

Table S2

genes with one expression peak

CG5581	+ Ote motor_protein * 1e-174 OTE_DROME OTEFIN otefin - fruit fly (Drosophila melanogas * 1e-176 DMOTEDA_2 Ote * * CG5581 LD41911 55C3-55C4 ID:101A4
CG6258	+ BcDNA:LD06837 DNA_replication_factor * Similarity to Human activator KD subunit (SW:AC13_HUMAN); cDNA EST CEESG65F comes from this gene; cDNA EST yk267e6.5 comes from this gene; cDNA EST [RFC] CG6258 LD41983 32D4-32D4 dup:2/2 ID:101B1
CG2867	+ Prat enzyme * AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPAT)(aa) * DMPRAT_2 Prat * 1e-55 PUR1_YE [Pribosyltran // PUR_PYR_PR_TRANSFER //] CG2867 LD42113 84E1-84E1 dup:1/3 ID:101B11
CG1603	+ transcription_factor * 5e-67 putative zinc finger protein * 6e-21 growth factor independence-1B * 4e-21 growth factor independent 1B (potential regulator of CDKN1A, tran * [zf-C2H2 // ZINC_FINGER_C2H2] CG1603 LD42046 43D3-43D3 ID:101B7
CG3645	+ unknown * similar to * conserved hypothetical protein, family(aa) * Yml080wp(aa) * hypothetical 35.8K protein (fis 5' - Escherichia coli(aa) [UPF0034 // FMN_ENZYMES] CG3645 LD42056 21B5-21B5 ID:101B8
CG15634	+ unknown * CG15634 LD42284 25A4-25A4 ID:101D10
CG9834	+ unknown * F35A5.8 gene product(aa) * CGI-61 protein(aa) * 2e-58 F35A5.8 gene product * 6e-06 antigen 6; AdamAS [NLS_BP] CG9834 LD42223 56C10-56C11 ID:101D2
CG11596	+ EG:39E1.1 unknown * 5e-33 YNJ2_YEAST HYPOTHETICAL 45.5 KD PROTEIN IN YPT53-RHO2 INTERGENIC REGION * /match=(desc;; /ma * 6e-54 Similairity with yeast hypothetical prote [NLS_BP] CG11596 LD42227 2B17-2B17 dup:2/2 ID:101D3
CG12892	+ DNA_binding * 3e-59 CAC2_YEAST CHROMATIN ASSEMBLY FACTOR P60 SUBUNIT (CAF-1 KD SUBUNIT) * 8e-33 HIRA * 4e-11 YZLL_CAEEL HYPOTHETICAL 43.1 KD TRP-ASP REPEATS CONTA [GPROTEINB // WD40_REGION // WD_REPEATS] CG12892 LD42270 47A9-47A9 ID:101D8
CG7467	+ osa DNA_binding * eyelid(aa) * eld * 3e-05 YM42_YEAST HYPOTHETICAL 162.7 KD PROTEIN IN SIP18-SPT21 INTERGENIC REGION * 2e-37 coded for by C. elegans cDNA yk7c8.5; co [ARID // PRO_RICH // ANTIFREEZEI] CG7467 90C-90C dup:4/4 ID:101E12
CG2864	+ Parg enzyme * poly(ADP-ribose) glycohydrolase * 6e-33 cDNA EST comes from this gene; cDNA EST co * 1e-100 poly(ADP-ribose) glycohydrolase * 1e-102 poly (ADP-ribos [NLS_BP // ATP_GTP_A] CG2864 LD42380 3F2-3F2 dup:5/5 ID:101E6
CG8378	+ BcDNA:LD29892 unknown * 4e-09 YKT7_CAEEL HYPOTHETICAL 53.2 KD PROTEIN C07A9.7 IN CHROMOSOME III * 1e-05 skm-BOP2 * 8e-52 inserted at base Both 5' and 3' ends of P element I [SET_DOMAIN] CG8378 48E10-48E10 dup:3/3 ID:101E8
CG8121	+ unknown * CG8121 LD42595 85D9-85D9 ID:101F3
CG9984	+ TH1 unknown * TH1(aa) * DMTH1X_3 TH1 * potential zinc-finger domains centered at aa and aa 364; kDa protein; putative(aa) * DMTH1X_3 TH1 CG9984 LD42626 14C4-14C4 ID:101F4
CG1745	+ enzyme * No definition line found(aa) * predicted secreted protein(aa) * 3e-06 predicted secreted protein * [NLS_BP] CG1745 LD43003 10B15-10B15 dup:1/2 ID:101G12
CG9242	+ enzyme * unknown(aa) * PROBABLE GMP SYNTHASE (GLUTAMINE-HYDROLYSING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)(aa) * guanine-monophosphate synthetase; GM [CPSGATASE // GMP_synt_C //

ANTSNTHASEII] CG9242 LD42771 39B4-39B4 dup:2/2 ID:101G2

+ Taf80 signal_transduction * 2e-17 TUP1_YEAST GLUCOSE REPRESSION REGULATORY PROTEIN TUP1 (FLOCCULATION SUPPRESSOR P * T2D4_DROME TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUN[GPROTEINBRPT // WD40_REGION // WD_REPEA] CG7704 LD42828 47C5-47C6 ID:101G5

CG7704 + transporter * similar to ABC transporters ; ABC transporter transmembrane * metal resistance protein, similar to multidrug resistance proteins and cystic fibrosi [ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG7806 LD42916 29A5-29A5 ID:101G9

CG7806 + 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 ID:102A1

CG6905 + storage_protein * s18 chorion protein(aa) * GCR protein - fruit fly (Drosophila melanogaster)(aa) * s19 chorion protein(aa)

CG5095 * ATP-DEPENDENT RNA HELICASE A (NUCLEAR CG5095 LD43171 15E5-15E5 ID:102B2

CG4497 + unknown * [GRAM_POS_ANCHORING] CG4497 LD43863 27E4-27E4 ID:102F12

CG5694 + unknown * CG5694 LD44026 31B4-31B4 dup:1/2 ID:102G12

+ motor_protein * ARFAPTIN 1(aa) * 3e-36 YL87_CAEEL HYPOTHETICAL 35.0 KD PROTEIN F54C8.7 IN CHROMOSOME III * 2e-82 por1 * AFP2_HUMAN ARFAPTIN (POR1 PROTEIN) arfaptin CG17184 LD44124 86D8-86D8 dup:2/2 ID:102H10

CG17184 + signal_transduction * 3e-07 hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae) (U1 * 3e-08 YKA7_CAEEL HYPOTHETICAL 39.7 KD PROTEIN IN CHROMOSOME III * 2e-1[P67PHOX // SH3DOMAIN // SH3 // PRO_RICH] CG7129 LD44138 90F7-90F7 ID:102H11

CG7129 + Tbp transcription_factor * Tbp * TRANSCRIPTION INITIATION FACTOR TFIID (TATA-BOX FACTOR) (TATA SEQUENCE-BINDING PROTEIN) (TBP) (TATA-BOX BINDING PROTEIN)(aa) * 4e-80 TF2D_YEAS [TFIID // TIFACTORIID // TBP] CG9874 LD44083 57F8-57F8 dup:1/2 ID:102H7

CG9874 + unknown * similar to Probable rabGAP domains; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST yk243e1.5 comes from this gene; cDNA EST [TBC // RAB_GAP] CG8155 LD44087 51F5-51F6 ID:102H8

CG8155 + motor_protein * ORF 73, contains large complex repeat CR sarcoma-associated * zip * 9e-17 transport protein USO1 - yeast (Saccharomyces cerevisiae) * 1e-17 nonmusc CG11248 LD44094 78F2-78F2 ID:102H9

CG11248 + unknown * CG4229 LD44179 77A1-77A1 ID:103A2

CG4229 + signal_transduction * Taf80 * katanin p80 subunit(aa) * 5e-07 YCW2_YEAST HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN CPR4-SSK2 * 4e-09 transcription ini[GPROTEINBRPT // GPROTEINB // WD40_REGIO] CG9910 LD44201 14B11-14B11 ID:103A6

CG9910 + signal_transduction * PACSIN(aa) * 3e-07 hypothetical protein YFR024c-a - yeast (Saccharomyces cerevisiae) * 7e-08 Cortactin * 1e-52 weakly similar to surface[FCH // CDC15_NT // P67PHOX // SH3DOMAIN] CG15694 LD44220 92F13-92F13 dup:2/2 ID:103A9

CG15694 + unknown * [NLS_BP] CG3995 89E12-89E12 dup:2/2 ID:103B9

CG3995 + 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 68D4-68D4 dup:2/2 ID:103C10

CG5940

+ pav motor_protein * 7e-35 YGW6_YEAST PUTATIVE KINESIN-LIKE PROTEIN YGL216W hypoth * PAV-KLP protein * 5e-91 Similar to kinesin-like protein; coded for by C. elegans cDN [kinesin // KINESIN_MOTOR_DOMAIN1 // KIN] CG1258 64B4-64B4 dup:1/2 ID:103C2

CG1258

CG9241 + function_unknown * Cdc23(aa) ** [NLS_BP] CG9241 LD44370 39B4-39B4 dup:1/2 ID:103C3

CG9018 + unknown * 1e-12 YKK4_CAEEL HYPOTHETICAL 30.2 KD PROTEIN C02F5.4 IN CHROMOSOME III ** [NLS_BP] CG9018 LD44521 62D3-62D3 dup:2/2 ID:103D5

CG8621 + motor_protein * CLIP-190 * 6e-05 microtubule binding protein D-CLIP-190 * 3e-05 myosin * 4e-06 ORF 73, contains large complex repeat CR sarcoma-associated herpesv CG8621 LD44526 65E6-65E6 dup:2/2 ID:103D6

CG4622 + unknown * F1N21.18(aa) * HYPOTHETICAL 51.8 KD PROTEIN ZK632.11 IN CHROMOSOME III(aa) * * [ZF_CCHC // PRO_RICH // zf-CCHC // NLS_B] CG4622 LD44757 60D5-60D5 dup:3/3 ID:103E12

CG5422 + RNA_binding CG5422 dup:2/2 ID:103E5

CG11104 + unknown * 7E-80* 4e-29 inserted at base Both 5' and 3' ends of P element Inverse PCR * [ATP_GTP_A] CG11104 LD44686 12B8-12B8 dup:2/2 ID:103E6

CG11980 + unknown * BLASTX 4.0E-27 YER156C|Protein of unknown function(dna) * HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION(aa) * 6e-60 similar to Yeast h CG11980 LD44814 85C3-85C3 dup:2/2 ID:103F9

CG5190 + unknown * F46F11.8 gene product(aa) * Yol093wp(aa) * unknown(aa) * 3e-13 hypothetical protein YOL093w - yeast (Saccharomyces cerevisiae) [NLS_BP] CG5190 LD44982 55C13-55D ID:103G10

CG8571 + smid endopeptidase * DMSMMIN_2 smallminded * smallminded(aa) * 3e-68 AFG2_YEAST AFG2 PROTEIN valosin-containing protein homolo * smallminded [ENDOLAPTASE // AAA // ATP_GTP_A] CG8571 65F5-65F6 dup:2/2 ID:103G2

CG10596 + Msr-110 unknown * Msr-110 * Msr-110=EN protein binding gene/engrailed nuclear homeoprotein-regula * * CG10596 LD44960 64E-64E dup:1/3 ID:103G6

CG10622 + enzyme * hypothetical protein(aa) * 3e-93 SUCB_YEAST PROBABLE SUCCINYL-COA LIGASE (GDP-FORMING), BETA-CHAIN PRECURSOR (SU * 1e-134 SCB2_CAEEL PROBABLE SUCCI [SUCCINYL_COA_LIG_3 // ligase-CoA] CG10622 LD44970 64E-64E ID:103G7

CG6422 + unknown * NY-REN-2 antigen(aa) * 1e-27 hypothetical protein YDR374c - yeast (Saccharomyces cerevisiae) (U * 9E-49* Similarity to A. thaliana gene product F21M [PRO_RICH] CG6422 LD44979 96B14-96B15 ID:103G8

CG17818 + rdgBbetatransporter * PHOSPHATIDYLINOSITOL TRANSFER PROTEIN BETA ISOFORM (PTDINS TRANSFER PROTEIN BETA) (PTDINSTP) (PI-TP-BETA)(aa) * BLASTX 3.1E-49 M.musculus mRNA for D [PITRANSFER] CG17818 LD44980 54E3-54E3 ID:103G9

CG1240 + unknown * 7e-07 hypothetical protein YOR295w - yeast (Saccharomyces cerevisiae) * 9e-09 weak similarity to D. melanogaster salivary gland-specific protein (PI [TUBULIN // NLS_BP] CG1240 LD45195 63A1-63A1 dup:2/2 ID:103H12

CG3605 + RNA_binding * spliceosome associated protein 145, SF3b subunit(aa) * spliceosome associated protein-like(aa) * BLASTX 7.8E-75 Human spliceosome associated protei [NLS_BP] CG3605 LD45152 23C4-23C4 ID:103H9

CG12225 + SPT6 structural_protein * 3e-79 SPT6_YEAST TRANSCRIPTION INITIATION PROTEIN SPT6 SPT6 pro * EMB5_CAEEL EMB-5 PROTEIN emb-5 protein - Caenorhabditis e * Supt6h * similar to e [S1] CG12225 LD45251 5E1-5E1 dup:3/5 ID:104A10

CG5739 + unknown * [NLS_BP] CG5739 LD45253 31B2-31B2 ID:104A11

CG5916 + unknown * short of similarity to human transforming protein (tre) * similar to human (TRE) transforming protein *

Ypl249cp(aa) * pollux(aa) [TBC // RAB_GAP] CG5916 LD45246 89B9-89B9 ID:104A9
+ snf RNA_binding * DMD25SNRN_2 snf * U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) (SEX DETERMINATION PROTEIN SNF)(aa) * 3e-05 YIS9_YEAST HYPOTHETICAL 12.8 [RNP_1 // RBD // rrm] CG4528 LD45302 4F1-4F2 dup:3/3 ID:104B7

CG4528

+ neur DNA_binding * finger protein neuralized - fruit fly (Drosophila melanogaster)(aa) * DMC3HC4ZF_2 neur * 3e-89 coded for by C. elegans cDNA yk27g3.5; coded for by C [zf-C3HC4 // ZF_RING] CG11988 LD45505 85C4-85C5 dup:1/2 ID:104C12

CG11988

+ bl RNA_binding * hnRNP-K protein(aa) * 1e-05 YB83_YEAST HYPOTHETICAL 45.8 KD PROTEIN IN PCS60-ABD1 INTERGENIC REGION * 4e-05 unknown * 9e-32 coded for by C. elegans CG13425 LD45549 57B1-57B1 dup:2/2 ID:104D5

CG13425

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

CG18426

CG11456

+ CG11456 dup:2/2 ID:104E6

+ motor_protein * symplekin(aa) * 6e-19 contains weak similarity to human microtubule-vesicle linker CL * symplekin * BLASTX 1.6E-16 Human symplekin mRNA, partial cds [NLS_BP] CG2097 LD45768 83C1-83C1 ID:104F6

CG2097

+ enzyme * 1e-07 BET4_YEAST TYPE II PROTEINS GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT (TYPE II PRO * 9e-11 similar to the protein prenyltransferase alpha subunit [PPTA] CG3073 LD45906 2F1-2F1 ID:104G2

CG3073

CG10916

+ unknown * CG10916 LD46221 55B9-55B9 dup:2/2 ID:105A10

+ BG:DS00004.12 unknown * hypothetical 23.1kd-like protein(aa) * 2e-17 YBF7_YEAST HYPOTHETICAL 23.1 KD PROTEIN IN SHP1-PTC3 INTERGENIC REGION * 9e-15 No definition line found CG1307 LD46144 84C4-84C4 ID:105A4

CG1307

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

CG17484

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

CG9556

CG4949

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

+ nucleic_acid_binding * 3e-05 YNN6_YEAST HYPOTHETICAL 49.4 KD PROTEIN IN NAM9-FPR1 INTERGENIC REGION * 2e-06 RU17_DROME U1 SMALL NUCLEAR RIBONUCLEOPROTEIN KD (U1 SNRNP KD) [PRO_RICH // NLS_BP] CG5146 LD46256 64E-64E ID:105B4

CG5146

CG4617

+ DNA_binding * hypothetical protein(aa) * 5e-16 HMGBCG protein * * [HMG] CG4617 LD46272 6F5-6F5 ID:105B7

CG4617

CG5726

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

CG5726

CG16753

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

+ Sry-delta transcription_factor * DMSRYG1_25 Sry- dgr; * serendipity beta protein(aa) * 2e-13 contains similarity to multiple C2H2-type zinc fingers (Pfam: zf-C2H2.hmm, sc * 2e-22 O [zf-C2H2 // ZINC_FINGER_C2H2_2] CG17958 LD46336 99D5-99D5 ID:105C3

CG17958

+ xl6 RNA_binding * similar to pre-mRNA splicing factor like protein; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA [RBD // ZF_CCHC // rrm // zf-CCHC // NLS] CG10203 LD46359 27C-27C ID:105C6

CG10203

CG10473

+ unknown * 4e-41 protein * 1e-09 putative protein * coded for by C. elegans cDNA yk93e11.5; coded for by C. elegans

cDNA yk103a11.5; * [NLS_BP] CG10473 LD46360 37B11-37B12 ID:105C7

+ transcription_factor * zinc finger homeodomain enhancer-binding protein-1(aa) * BLASTX 1.9E-18 H.sapiens OZF mRNA.(dna) * transcription factor RREB-1(aa) * similar to Z[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG3941 LD46363 59E3-59E3 ID:105C9

CG3941

CG18177 + unknown * CG18177 LD46538 67C-67C ID:105D12

CG8553 + SelD enzyme * SelD protein * 2e-93 similar to AIR synthase related proteins elegans * 1e-143 selenophosphate synthetase * 1e-159 SELD_HUMAN SELENIDE, WATER DIKINAS [AIRS] CG8553 LD46437 50F-50F dup:1/2 ID:105D2

CG9890 + unknown * 2e-42 similar to Zinc finger, C2H2 type; cDNA EST comes from * 5e-53 inserted at base 5' end of P element Inverse PCR * [zf-C2H2 // ZINC_FINGER_C2H2_2] CG9890 LD46465 59C3-59C3 ID:105D4

CG9418 + DNA_binding * Smarce1-related protein(aa) * 4e-05 ORF YBR089c-a * 0.00000000002 * 5e-09 ribosomal transcription factor UBF2 - Chinese hamster [HMG // HMG_box // PRO_RICH // NLS_BP] CG9418 LD46483 57C3-57C3 ID:105D6

+ transporter * nucleoporin Nup153 homolog(aa) * Ran/TC4-binding nucleopore protein(aa) * NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPOR [zf-RanBP // ZF_RANBP] CG4453 LD46585 14F2-14F2 dup:5/6 ID:105E3

CG4453

CG12135 + unknown * predicted using Genefinder; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this g CG12135 LD46621 8D10-8D10 dup:2/2 ID:105E7

CG11525 + * cyclin G1 - human (fragment)(aa) * cyclin G2(aa) * cyclin G - rat(aa) * cyclin G2(aa) CG11525 100D2-100D2 dup:3/3 ID:105F12

CG10385 + msl-1 transcription_factor * MALE-SPECIFIC LETHAL-1 PROTEIN(aa) * DMMSL1A_2 msl-1 * DMMSL1A_2 msl-1 * male-specific lethal-1 protein - fruit fly (Drosophila melanogaster) CG10385 LD46729 37A4-37A4 dup:4/4 ID:105F6

CG8253 + unknown * unknown protein(aa) * 2e-21 R06C7.6 * 1e-32 unknown protein * CG8253 LD46868 52D2-52D2 ID:105G11

CG7663 + structural_protein CUTICLE PROTEIN AMP1B CUTICLE, insect_cuticle CG7663 LD46979 ID:105H11

CG4813 + unknown * [ZF_RING] CG4813 LD46938 96F3-96F3 ID:105H5

CG2691 + unknown * protein(aa) * 3e-25 probable membrane protein YPL012w - yeast (Saccharomyces cerevisiae) * 7e-18 putative protein (fragment) * unknown [NLS_BP] CG2691 LD46946 12A5-12A6 dup:4/4 ID:105H6

CG2916 + 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 dup:1/2 ID:106A3

CG11678 + Actr13E cytoskeletal_structural_protein * DMARP_2 Actr13E * 2e-45 ACT_YEAST ACTIN actin - yeast (Saccharomyces cerevisiae) * ACTU_DROME ACTIN-LIKE PROTEIN 13E actin-related protein * 1e-70 [actin] CG11678 LD47054 13E15-13E16 ID:106A4

CG1381 + ribosomal_protein * ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG (L10E)(aa) * coded for by C. elegans cDNA CEESN26F; coded for by C. elegans cDNA CEESI89F; similar to 60S acidi [Ribosomal_L10] CG1381 LD47064 46E3-46E3 ID:106A5

CG11935 + unknown * CGI-67 protein(aa) * Similarity to S. Pombe BEM1/BUD5 suppressor; cDNA EST comes from this gene; cDNA EST yk482d4.3 comes from this gene; cDNA EST y [ESTERASE] CG11935 LD47093 96B19-96B19 ID:106A6

CG5519	+ Gbp signal_transduction * striatin, calmodulin-binding protein(aa) * WD-40-family-member * 3e-16 SFL2 gene product (AA 1-669) * 2e-19 transcription initiation factor IID-as[GPROTEINBRPT // WD40_REGION // WD_REPEA] CG5519 LD47390 55C13-55C13 ID:106C9
CG6157	+ dah unknown * dystrobrevin(aa) * similar to the kDA Torpedo acetylcholine receptor-associated protein; similar to rat apodystrophin-3, PIR Accession Number * dah [ZF_ZZ // ZZ] CG6157 LD47411 13C1-13C1 ID:106D2
CG6316	+ unknown * hypothetical protein(aa) * HSPC039 protein(aa) * 2e-11 LAS1_YEAST LAS1 PROTEIN LAS1 protein - yeast (Saccharomyc * CG6316 LD47413 70E1-70E1 ID:106D3
CG10754	+ RNA_binding * SP62_HUMAN; SAP 62; SF3A66(aa) * 1e-13 PR11_YEAST PRE-MRNA SPLICING FACTOR PRP11 PRP11 protein * 4e-94 Similarity to Human splicosome-associated pro [ZF_MATRIN // PRO_RICH] CG10754 LD47455 69E2-69E2 dup:2/2 ID:106D8
CG7845	+ transcription_factor * 8e-33 cDNA EST yk416a1.3 comes from this gene; cDNA EST yk466h2.3 comes * 1e-13 hypothetical protein * [NLS_BP // WD40] CG7845 LD47540 42A5-42A6 dup:2/2 ID:106E12
CG7269	+ RNA_binding CG7269 dup:2/2 ID:106E3
CG1671	+ signal_transduction * Ylr222cp(aa) * WD repeat protein(aa) * coatomer alpha subunit(aa) * BLASTX 2.6E-32 YLR222C Protein of unknown function, has beta-transducin (WD-[GPROTEINBRPT // WD40_REGION // WD_REPEA] CG1671 LD47550 46B13-46B14 ID:106F3
CG14965	+ motor_protein * CG14965 LD47616 63B13-63B13 ID:106G2
CG14954	+ unknown * CG14954 LD47625 63F4-63F4 ID:106G4
CG8399	+ unknown * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST yk226e12.3 com CG8399 LD47639 52E1-52E3 dup:2/2 ID:106G6
CG3281	+ transcription_factor * ovo * DMSPALTR_3 salr * 6e-29 GLAS_DROME GLASS PROTEIN finger protein glass - fruit fly [zf-C2H2 // ZINC_FINGER_C2H2 // HISTONE_] CG3281 LD47774 87A7-87A7 ID:106H11
CG8370	+ unknown * Similar to a C.elegans protein encoded in cosmid C27F2 * RW1 protein(aa) * 3e-57 coded for by C. elegans cDNA yk86c6.3; coded for by C. elegans cDNA [NLS_BP] CG8370 LD47858 52E1-52E1 dup:2/2 ID:107A9
CG5568	+ enzyme * 1e-19 FAT2_YEAST PEROXISOMAL-COENZYME A SYNTHETASE probable AMP * 3e-11 acetyl-CoA synthetase - fruit fly (Drosophila melanogaster) * 9e-40 similar [AMP-binding] CG5568 LD47944 64F3-64F3 ID:107B6
CG11990	+ unknown * 5e-17 probable membrane protein YLR418c - yeast (Saccharomyces cerevisiae) * 1e-10 unknown conserved hypothetical protein * [DLC_GAD_HDC_YDC] CG11990 LD47989 85C5-85C5 dup:3/3 ID:107B9
CG18140	+ Cht3 enzyme * chitinase(aa) * 2e-22 probable membrane protein YDR371w - yeast (Saccharomyces cerevisiae) * 2e-63 chitinase * 1e-44 CHIT_CAEEL PUTATIVE ENDOCHITIN CG18140 LP01426 40D5-40D5 dup:4/4 ID:107E10
CG10236	+ 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
CG6863	+ tok endopeptidase * tok * development protein tolkin - fruit fly (Drosophila melanogaster) * 1e-145 similar to developmentally important proteins like human BMP-1 [EGF // CUB // ASTACIN // Astacin // EGF] CG6863 LP01328 96A20-96A22 dup:3/3 ID:107E4
CG7252	+ 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 CG7252 LP01340 68E3-68E3 dup:2/2 ID:107E7

+ transcription_factor * DMRCPA_X kel * leucine-zipper-like transcriptional regulator, 1(aa) * 4e-12 YG52_YEAST HYPOTHETICAL 100.0 KD PROTEIN IN YHB1-PFK1 INTERGENIC REGION [BTB] CG3711 LP01394 1C5-1C5 dup:2/2 ID:107E9

CG3711

+ signal_transduction * similar to epidermal growth factor receptor kinase substrate; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST yk246h9.3 come [SH3 // PRO_RICH] CG8907 LP01469 92C1-92C1 ID:107F1

CG8907

+ 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 * steroid sulfotransferase 3(aa) * 7e-25 tyrosine-ester sulfotransferase * 2e-24 SUPM_HUMAN MONOAMINE-SULFATING PHENOL SULFOTRANSFERASE (SULFOTRANSFER [Sulfotransfer] CG5431 LP01553 59F4-59F4 ID:107F4

CG5431

+ cell_adhesion * DMSCA_3 sca * 4e-15 scabrous protein precursor - fruit fly (Drosophila melanogaster) * 2e-05 coded for by C. elegans cDNA yk9a2.5; coded for by C. e [fibrinogen_C] CG6788 LP01858 16E2-16E2 ID:107G11

CG6788

+ enzyme * STERYL-SULFATASE PRECURSOR (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC)(aa) * 5e-14 weakly similar to arylsulfatase B [Sulfatase // SULFATASE_2] CG5584 LP01735 75A2-75A2 ID:107G6

CG5584

CG16926

+ unknown * CG16926 LP01766 56D10-56D10 ID:107G8

+ Cdlc2 motor_protein * 8kd dynein light chain(aa) * Cdlc1 * dynein light chain 5(aa) * 1e-21 DYLL1_YEAST DYNEIN LIGHT CHAIN 1, CYTOPLASMIC dynein lig [Dynein_light // DYNEIN_LIGHT_1] CG5450 LP02196 22A-22A ID:108A1

CG5450

CG5468

+ unknown * CG5468 LP02501 97C1-97C1 ID:108A10

+ receptor * putative mitochondrial inner membrane protein import receptor(aa) * MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM44 PRECURSOR(aa) * P CG11779 91F4-91F4 dup:1/2 ID:108A11

CG11779

+ ligand_binding_or_carrier * 2e-08 galactose specific C-type lectin * 3e-10 lectin lambda * 7e-13 mannose receptor, C type MACROPH * 3e-08 C-type lectin-like protein [lectin_c // C_TYPE_LLECTIN_1 // C_TYPE_L] CG9134 LP02252 61F4-61F4 ID:108A3

CG9134

CG13627

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

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

CG5958

CG18596

+ unknown * CG18596 LP02352 96D4-96D4 ID:108A7

+ homology to bifunctional endo-1,4-beta-xylanase and RNA binding protein RGGm [Trypanosoma cruzi] GLUTELIN, PRO_RICH CG10953 LP02439 ID:108A8

CG10953

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

+ enzyme * 4e-06 cytochrome c oxidase subunit VIIa polypeptide (muscle) * 1e-05 COXK_BOVIN CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-HEART PRECURSOR (COX VIIA-M) (CG9603 LP02592 84F13-84F13 ID:108B5

CG9603

CG17754

+ actin_binding * kelch protein; ring canal component involved in cytoplasmic bridges; 77% Similarity to * 2e-93 kelch protein,

long form - fruit fly (*Drosophila mela* [BTB // Kelch] CG17754 LP02641 8D6-8D6 dup:2/2 ID:108B7

+ nucleic_acid_binding * 2e-06 Zinc finger-AT hook protein * 2e-13 protein * 5e-09 XFIN_XENLA XFIN PROTEIN Xfin protein (AA - * 2e-08 DMRNAD19A D19A [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG14438 LP02916 6C12-6C12 dup:2/3 ID:108C7

CG14438 + unknown * lbn * 1e-09 LBM_DROME LATE BLOOMER PROTEIN late bloomer me * 1e-11 lbn * [TM4_2] CG4471 LP02988 42E2-42E2 ID:108C9

CG4471 + unknown * putative DNA binding protein=son placenta, Peptide Partial, * * CG7924 LP03067 74E1-74E1 ID:108D3

CG7924 + unknown * CG7906 LP03104 74E1-74E1 ID:108D7

CG7906 + transporter * 4e-15 hypothetical protein YDR387c - yeast (*Saccharomyces cerevisiae*) (U * 2e-35 GTRL_DROME GLUCOSE TRANSPORTER-LIKE PROTEIN glucose transpo * 3e-[SUGRTRNSPORT // SUGAR_TRANSPORT_1 // SU] CG7801 LP03341 48B5-48B5 dup:2/2 ID:108E12

CG7801 + * CG11470 99B5-99B5 dup:4/4 ID:108E6

CG11470 + 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 + BcDNA:GH09358 unknown * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from thi CG2967 LP03505 9B6-9B7 dup:4/4 ID:108F7

CG2967 + unknown * CG1806 LP03706 11A3-11A3 ID:108G2

CG1806 + unknown * Ymr077cp(aa) * 2e-08 YMW7_YEAST HYPOTHETICAL 25.6 KD PROTEIN IN ABF2-CHL12 INTERGENIC REGION * 8e-05 No definition line found * 5e-59 l(2)rG270 l(2) CG4071 LP03791 58F1-58F1 ID:108G4

CG4071 + unknown * CG6981 LP03829 77A2-77A2 ID:108G7

CG6981 + enzyme Glycosyl transferasem, similar to N-acetylgalactosaminyltransferase GLYC_TRANS, Glycos_transf_2, RICIN_B_LEC] CG8182 LP03835 ID:108G9

CG8182 + Cyp1 chaperone * DMCYP1_2 Cyp1 * 1e-63 CYPH_YEAST PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) * 2e-93 CYPH_DROME PEPTIDYL-PROLYL CIS-TRANS[pro_isomerase // CSA_PPIASE_1 // CSA_PP] CG9916 LP04479 14B15-14B15 dup:1/2 ID:109A7

CG9916 + unknown * CG18337 LP04503 47E1-47E1 ID:109A8

CG18337 + svr peptidase * carboxypeptidase precursor(aa) * svr * 1e-06 YHT2_YEAST HYPOTHETICAL 49.8 KD PROTEIN IN ACT3-YCK1 INTERGENIC REGION PRECURSOR * 2e-76 coded for by [CRBOXYPTASEA // NLS_BP // Zn_carbOpept] CG4122 LP04580 1B4-1B5 ID:109A9

CG4122 + DnaJ-60 chaperone * dnaJ-like protein(aa) * DMDNAJLP_2 DnaJ-60 * 3e-08 SCJ1_YEAST SCJ1 PROTEIN SCJ1 protein - yeast (*Saccharomyce* * 1e-114 dnaJ-like protein [DnaJ // DNAJ_2] CG12240 LP04971 60B9-60B9 dup:3/3 ID:109B12

CG12240 + CG12373 ID:109B8

CG12373 + 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 66B13-66B13 dup:1/2 ID:109C10

CG7387

CG9021 + unknown * Cr-Pil allergen(aa) * Cr-Pil * major allergen Per a * CG9021 LP05310 26A5-26A5 ID:109C12

CG8342 + m1 unknown * M1 protein(aa) * 4e-82 M1 protein * 3e-05 Similarity to Crayfish proteinase inhibitor cDNA ES * 5e-05 IOV7_CHICK OVOINHIBITOR PRECURSOR ovoinhibito CG8342 LP05127 96F10-96F10 ID:109C5

CG7438 + Myo31DF motor_protein * myosin-1A(aa) * didum * actin binding actin binding) map_position:31D-F * Myo31DF [myosin_head // IQ // MYOSINHEAVY // NLS] CG7438 LP05132 31E4-31E5 ID:109C6

CG11880 + unknown * NG22(aa) * 3e-97 coded for by C. elegans cDNA CEESB82F; coded for by C. elegans cDNA CEESB93F * 1e-79 NG22 * CG11880 LP05177 99A1-99A1 dup:1/4 ID:109C9

CG4839 + protein_kinase * 1e-57 KAPB_YEAST CAMP-DEPENDENT PROTEIN KINASE TYPE (PKA 2) * 1e-147 protein kinase (EC 2.7.1.37), cGMP-dependent - fruit fly (Drosophila melanog * [cNMP_binding // CNMP_BINDING_1 // CNMP_] CG4839 LP05330 31B-31B ID:109D1

CG10764 + endopeptidase * COAGULATION FACTOR X PRECURSOR (STUART FACTOR)(aa) * chymotrypsinogen B1(aa) * coagulation factor G beta chain precursor - horseshoe crab (Tachyleu [trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG10764 LP05421 54C3-54C3 ID:109D4

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

CG7758 + ppl enzyme * predicted using Genefinder(aa) * 5e-19 GCSH_YEAST GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR F * 3e-28 predicted using Genefinder * 7e-32 glycine c [LIPOYL] CG7758 LP05579 78C8-78C8 dup:2/2 ID:109E4

CG13263 + Cyt-c1 electron_transfer * CYTOCHROME C(aa) * 1e-32 pdb1YCC] Cytochrome C (Isozyme 1) (Reduced) Saccharomyces cerevisia * 2e-58 CYC1_DROME CYTOCHROME C-1 cytochrome c[CYTCHROMEIAB // cytochrome_c // CYTOCHR] CG13263 LP05614 36A7-36A7 dup:2/2 ID:109E5

CG6933 + structural_protein * peritrophin-48a precursor(aa) * peritrophin-44(aa) * SW-peritrophin-48 precursor(aa) * CG6933 LP05638 77A-77A dup:3/3 ID:109E6

CG11685 + actin_binding * 5e-06 alternatively spliced form * 9e-06 alpha-actinin * protein * 9e-06 alpha-actinin - rabbit (fragment) muscle alp [CH_DOMAIN] CG11685 LP05986 85F7-85F7 ID:109F10

CG9568 + unknown * CG9568 LP05845 29F8-29F8 ID:109F2

CG7576 + Rab3 signal_transduction * enzyme RHO small GTPase) map_position:47B * 2e-47 SEC4_YEAST RAS-RELATED PROTEIN SEC4 GTP-binding protein SE * 1e-127 RAB3_DROME RAS-RELATED PROTEI [ras // ATP_GTP_A // RASTRNSFRMNG] CG7576 LP05860 47B7-47B7 ID:109F3

CG10154 + structural_protein * peritrophin 1(aa) * 3e-08 Gasp precursor * 1e-07 R02F2.4 gene product * 2e-13 insect intestinal mucin IIM22 CG10154 LP06444 70A8-70A8 ID:109G11

CG3127 + Pgk protein_kinase * 3-phosphoglycerate kinase; Pgk1p(aa) * DMPGKG_2 Pgk * PHOSPHOGLYCERATE KINASE(aa) * 1e-136 PGK_YEAST PHOSPHOGLYCERATE KINASE 3-phosphoglycerate kina [PGK // PGLYCERATE_KINASE // PHGLYCKINAS] CG3127 23A7-23A7 dup:2/3 ID:109G12

CG12115 + unknown * [NLS_BP] CG12115 LP06283 8D2-8D2 ID:109G5

CG14455 + CG14455 LP06288 ID:109G6

CG2070 + enzyme * 8e-21 probable membrane protein YOR246c - yeast (*Saccharomyces cerevisiae*) * 1e-06 3-hydroxyacyl-CoA dehydrogenase type II * 1e-46 predicted using G [GDHRDH // adh_short] CG2070 LP06328 43E6-43E6 ID:109G7

CG7160 + 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

CG5084 + unknown * CG5084 LP06708 53E4-53E4 ID:109H7

CG3245 + PpN58A protein_phosphatase * serine-threonine protein phosphatase(aa) * PpN58A * 1e-108 PP12_YEAST SERINE/THREONINE PROTEIN PHOSPHATASE PP1-2 pho * 1e-174 serine-threonine prot[PHOSPHO_ESTER // STPHPHTASE // SER_THR_] CG3245 SD01703 58B1-58B1 ID:113A9

CG8114 + 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

CG9443 + 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

CG1676 + unknown * * 5e-87 lclprt_seq No definition line found * YB3C_SCHPO HYPOTHETICAL 60.9 KD PROTEIN C2F12.12C IN CHROMOSOME II * [NLS_BP] CG1676 SD01916 19D2-19D2 ID:113C9

CG9379 + actin_binding * TENSIN(aa) * 3e-63 coded for by *C. elegans* cDNA yk126c6.3; coded for by *C. elegans* cDNA yk125d8.5; * 2e-74 tensin - chicken tensin * coded for by *C. [SH2]* CG9379 SD01953 85D23-85D23 ID:113D1

CG17836 + unknown * [NLS_BP] CG17836 SD01985 91D4-91D4 dup:2/2 ID:113D3

none + none SD02145 ID:113F3

CG9042 + enzyme CG9042 ID:113F9

CG9177 + translation_factor * EUKARYOTIC TRANSLATION INITIATION FACTOR (EIF-5)(aa) * 2e-63 IF5_YEAST EUKARYOTIC TRANSLATION INITIATION FACTOR (EIF-5) * 2e-87 IF5_CAEEL EUKARYOTIC [EF_HAND] CG9177 SD02540 14A1-14A1 dup:2/3 ID:114C10

CG10355 + enzyme * sn-1,2-diacylglycerol cholinephosphotransferase(aa) * contains similarity to CDP-alcohol phosphotransferases(aa) * choline/ethanolaminephosphotrans [CDP_ALCOHOL_P_TRANSF // CDP_ALCOHOL_P_T] CG10355 SD02518 37F1-37F1 dup:3/5 ID:114C5

CG12109 + ligand_binding_or_carrier * chromatin assembly factor I (150 kDa)(aa) * chromatin assembly factor I p150 chain - human * [NLS_BP] CG12109 SD02526 7F4-7F5 dup:1/2 ID:114C7

CG12139 + receptor * dominant autoantigen gp - rat (fragment)(aa) * ST7 protein(aa) * 3e-12 NDL_DROME SERINE PROTEASE NUDEL PRECURSOR nudel protein * 1e-26 coded for by [LDLRA_2 // LDLRECEPTOR // ldl_recept_a] CG12139 SD02842 8D12-8E1 dup:2/2 ID:114G4

CG11130 + Rtc1 enzyme * RNA 3'-terminal phosphate cyclase(aa) * DMYP3G Rtc1 * PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE)(aa) * 4e-4 [RTC // RCT // NLS_BP] CG11130 SD02972 12B8-12B8 ID:114H11

CG7400 + transporter * fatty acid transport protein 4; FATP4(aa) * 1e-64 very long-chain fatty acyl-CoA synthetase * 1e-129 coded for by *C. elegans* cDNA yk83h3.3; coded f [AMP_BINDING // AMP-binding // NLS_BP] CG7400 SD02910 31E5-31E6 dup:4/4

ID:114H2

CG13097 + unknown * 8e-36 YJX2_YEAST HYPOTHETICAL 67.0 KD PROTEIN IN PRE3-SAG1 INTERGENIC REGION * 2e-38 cDNA EST yk337b8.5 comes from this gene; cDNA EST yk371b10.5 co [NLS_BP] CG13097 SD02943 29D1-29D1 ID:114H6

CG8485 + protein_kinase * 8e-50 SNF1_YEAST CARBON CATABOLITE DEREPRESSING PROTEIN KINASE p * 3e-30 p90 ribosomal S6 kinase * 1e-117 similar to serine/threonine kinase; cDNA E [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG8485 SD02969 50E8-50E8 ID:114H9

CG3864 + electron_transfer * thioredoxin(aa) * 8e-20 TRX1_YEAST THIOREDOXIN I (TR-I) thioredoxin I - yeast (Sacc * 1e-17 THIO_DROME THIOREDOXIN (DEADHEAD PROTEIN) thioredoxin-I [THIOREDOXIN // THIOREDOXIN_2 // thioered] CG3864 30C-30C2 ID:115A11

CG5919 + unknown * isopentenyl-diphosphate delta isomerase(aa) * 1e-44 IPPI_YEAST ISOPENTENYL-DIPHOSPHATE DELTA-ISOMERASE (IPP ISOMERASE) * 3e-33 YMX3_CAEEL HYPOTHETIC CG5919 SD03046 93D4-93D4 ID:115A12

CG15319 + CG15319 SD03263 ID:115D11

CG1074 + unknown * 3e-55 hypothetical protein YOL124c - yeast (Saccharomyces cerevisiae) (* 3e-51 hypothetical protein * Y724_METTH HYPOTHETICAL PROTEIN MTH724 methyl [N6_MTASE // N12N6MTFRASE] CG1074 SD03208 82C1-82C1 ID:115D7

CG6977 + cell_adhesion * DMDACHSOU_2 ds * contains similarity to multiple cadherin-type repeats(aa) * cadherin 18(aa) * DMDEC_1 shg [CADHERIN // cadherin] CG6977 SD03311 87A-87A dup:5/5 ID:115E6

CG14818 + EG:63B12.12 unknown * 9e-50 /match=(desc: * 7e-40 inserted at base Both 5' and 3' ends of P element Inverse PCR * CG14818 SD03316 2B14-2B14 dup:2/2 ID:115E7

CG6582 + Aac11 apoptosis_inhibitor * apoptosis inhibitor 5(aa) * Aac11(aa) * 1e-110 unknown * 1e-35 unknown protein CG6582 SD03364 36C3-36C3 ID:115F2

CG1474 + Es2 enzyme * HYPOTHETICAL 58.3 KD PROTEIN F42H10.7 IN CHROMOSOME III(aa) * ES2 protein(aa) * ES2 protein(aa) * Es2 CG1474 SD03464 7E7-7E7 ID:115G8

CG1528 + gammaCoptransporter * coat protein gamma-cop(aa) * COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)(aa) * 1e-123 COPG_YEAST COATOMER GAMMA SUBUNIT (GAMMA-COAT PROT CG1528 SD03531 100D-100D ID:115H4

CG13096 + unknown * PBK1 protein(aa) * 5e-11 predicted using Genefinder; Weak similarity to Mouse CSA-19 protei * 2e-16 PBK1 protein * 7e-08 hypothetical protein [NLS_BP] CG13096 SD03546 29D1-29D1 ID:115H5

CG14941 + esc transcription_factor * DMESCOMBS_4 esc * 3e-08 YCW2_YEAST HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN CPR4-SSK2 * extra sex combs protein - fruit fly (Dr[GPROTEINBRPT // RCC1_2 // WD40_REGION /] CG14941 SD03549 33B1-33B2 ID:115H6

CG6665 + unknown * HSPC012(aa) * * [NLS_BP] CG6665 SD03555 53E6-53E6 ID:115H7

CG8046 + transporter CG8046 SD03610 dup:1/2 ID:116A2

CG1973 + protein_kinase * unknown protein(aa) * 2e-22 hypothetical protein YOR112w - yeast (Saccharomyces cerevisiae) * 3e-06 CDK5_DROME CELL DIVISION PROTEIN KINASE HOMOLOG [PROTEIN_KINASE_DOM] CG1973 SD03656 99C2-99C2 ID:116A7

CG1803 + unknown CG1803 SD03837 dup:2/2 ID:116C2.2

CG4281 + EG:22E5.7 unknown * /match=(desc:(aa) * /match=(desc: * * CG4281 SD03946 2C5-2C6 dup:2/2 ID:116D9.2
+ 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
CG12706 + CG12706 SD04019 dup:2/4 ID:116E9.2
+ alpha-Adaptin transporter * highly similar to alpha-adaptin (rat and mouse)(aa) * DMALPADPT_2 agr;-Adaptin * adaptor-related
CG4260 protein complex AP-2, alpha subunit(aa) * ALPHA-AD CG4260 SD04083 21C2-21C2 dup:2/3 ID:116F9
CG9531 + CG9531 SD04586 dup:3/3 ID:117E5
+ cell_adhesion * robo * similar to IG (immunoglobulin) superfamily (17 domains), Low-density lipoprotein receptor domain
CG7981 class A (3 domains), Laminin EGF-like (Doma[LDLRA_2 // ig // RNP_1 // EGF_1 // EGF] CG7981 SD04592 3A2-3A3 dup:4/4
ID:117E7
CG17156 + transcription_factor CG17156 SD04616 dup:2/2 ID:117E9
+ protein_kinase * protein(aa) * cdc2-like protein kinase(aa) * 3e-65 CTK1_YEAST CTD KINASE ALPHA SUBUNIT (CTD
KINASE KD SUBUNIT) (CTDK-I ALPHA SUB * 6e-69 posi[PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG7597
CG7597 SD04681 78E1-78E1 dup:2/3 ID:117F7.2
+ unknown * 1e-28 weak similarity to chromosomal replicator initiator protein DNAA (* similar to a C.elegans protein
CG11943 encoded in cosmid * CG11943 SD04935 19A3-19A3 dup:3/7 ID:118A12
CG17436 + CG17436 ID:118A9
+ Mcm6 DNA_replication_factor Minichromosome maintenance 6, chromatin binding involved in pre-replicative complex
CG4039 formation MCM, MCM_1, MCM_2 CG4039 SD04977 dup:3/3 ID:118B11
CG1832 + transcription_factor CG1832 SD05094 dup:2/5 ID:118C8.2
CG9366 + enzyme CG9366 SD05212 ID:118D6
+ BcDNA:GH13356 enzyme beta galactosyltransferase MITOCH_CARRIER, XYLOSE_ISOMERASE_2 CG8536 SD05469
CG8536 dup:1/2 ID:118G11
CG7110 + unknown * [NLS_BP] CG7110 SD05480 34B7-34B7 dup:2/3 ID:118H1
CG8902 + CG8902 dup:2/4 ID:118H6
CG8159 + transcription_factor CG8159 SD05592 ID:119A8
CG9717 + transporter similar to sulfate transport protein, sulphate permease Sulfate_transp CG9717 SD05675 dup:1/2 ID:119C1
CG11168 + cytoskeletal_structural_protein CG11168 SD05685 ID:119C4
+ DNA_binding * selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and
CG7421 III(aa) * nucleolar phosphoprotein - African cla [NLS_BP // HISTONEH5] CG7421 SD05988 79A5-79A5 ID:119F11
CG5853 + transporter CG5853 SD06390 dup:2/3 ID:119G10.2
CG4427 + transcription_factor CG4427 SD06353 dup:2/2 ID:119G5.2
+ unknown * 3e-83 YOJ1_CAEEL HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN CHROMOSOME III * * CG14939
CG14939 33B1-33B1 dup:2/3 ID:119G8.2

CG11860 + BG:DS07851.11 unknown * CG11860 35C4-35C4 dup:2/2 ID:119H7

CG7090 + enzyme CG7090 SD06635 dup:1/2 ID:120A12.2

CG4510 + CG4510 SD09607 dup:1/2 ID:124A6.2

CG15613 + CG15613 SD09786 dup:1/2 ID:124C3.2

CG3616 + cytochrome_P450 CG3616 SD10018 dup:1/2 ID:124F2.2

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

+ structural_protein * unknown(aa) * Allele: hi4(aa) * gene is related to S.cerevisiae NIC96 gene.(aa) * 7e-24 NI96_YEAST

CG7262 KD NUCLEOPORIN-INTERACTING COMPONENT nucle CG7262 GH01087 88D8-88D8 ID:30A8

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

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

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

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

+ 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

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

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

+ motor_protein * protein(aa) * HYPOTHETICAL 123.7 KD PROTEIN C14C4.02 IN CHROMOSOME I(aa) * 2e-65

hypothetical protein YOL034w - yeast (Saccharomyces cerevisiae) * 3 [ATP_GTP_A2 // ATP_GTP_A] CG7783 GH01608 78E2-78E3 dup:2/2 ID:30E4

CG7783 + unknown * 8e-06 belong to the membrane protein group of Transmembrane Super * 8e-06 First identified non-mammalian

CG12143 member of the Transmembrane S * 9e-08 TM4SF CG12143 GH01773 42E-42E ID:30F9

+ enzyme * antennal-specific short-chain dehydrogenase/reductase(aa) * 4e-12 YM71_YEAST HYPOTHETICAL

OXIDOREDUCTASE IN MRPL44-MTF1 INTERGENIC REGION * 8e-08 Si [GDHRDH // adh_short] CG3301 GH01837 93D4-93D4 ID:30G3

CG3301 + receptor * 5e-14 cDNA EST comes from this gene; cDNA EST co * 3e-35 peripheral-type benzodiazepine receptor

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

CG12860 + unknown * [NLS_BP] CG12860 GH02210 51B11-51B11 ID:31A8

+ ion_channel * 2e-20 YMT1_YEAST HYPOTHETICAL 38.2 KD PROTEIN IN SUB1-ARGR1 INTERGENIC REGION * 8e-44

similar to phosphotransferase enzyme II and to members of the [ALDKETRDASE] CG3397 GH02366 87A8-87A8 dup:2/2

CG3397 ID:31B6

+ 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

CG5173 dup:1/3 ID:31C7

CG11201	+ enzyme * hypothetical protein(aa) * TUBULIN--TYROSINE LIGASE (TTL)(aa) * Ybr094wp(aa) * 2e-10 ORF2 [NLS_BP]
CG9759	CG11201 GH02545 27A1-27A1 ID:31C9
	+ unknown * CG9759 GH02603 87F-87F ID:31D2
CG5163	+ TflIA-S transcription_factor * 4e-16 TOA2_YEAST TRANSCRIPTION INITIATION FACTOR IIA SMALL CHAIN (TFIIA 13.5 KD SUBUNI * 5e-56 T2AG_DROME TRANSCRIPTION INITIATION FACTOR IIA GAMMA CG5163 GH03194 95C9-95C9 ID:31G12
	+ BcDNA:GH03108 chaperone * similar to DnaJ, prokaryotic heat shock protein, Zinc finger, C2H2 type; cDNA EST yk290e12.5 comes from this gene; cDNA EST yk290e12.3 comes from th [ZF_MATRIN // ZINC_FINGER_C2H2 // DNAJ_1] CG2790
CG2790	GH03108 60E5-60E5 ID:31G7
CG7974	+ contains similarity to hepatocellular carcinoma-associated antigen 59 NLS_BP CG7974 GH03217 ID:31H1
	+ enzyme * DMCSUC_5 Vha16 * VACUOLAR ATP SYNTHASE KD PROTEOLIPID SUBUNIT (DUCTIN)(aa) * ATP synthase subunit(aa) * proteolipid protein of the proton ATPase; P [VACATPASE // ATP-synt_C] CG7007 GH03514 90B1-90B1 ID:32A10
CG7007	
CG4784	+ structural_protein * 2e-05 DMEDG84A_3 Edg84A * * [CUTICLE // insect_cuticle] CG4784 GH03623 72F1-72F1 ID:32B4
	+ Vha26 enzyme * Vha26 * ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD(aa) * VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) (V-ATPASE KD SUBUN CG1088 GH03683 83B4-83B4 ID:32B5
CG1088	+ transcription_factor_binding * ankyrin-like with transmembrane domains 1(aa) * C. elegans ankyrin-related unc-44 * similar to ankyrin repeats; cDNA EST comes f[ANK_REP // ank // ANK_REP_REGION // CAT] CG10409 GH03924 84E1-84E1 dup:2/4 ID:32C10
CG10409	
	+ unknown * HYPOTHETICAL PROTEIN * 8e-06 development protein * HYPOTHETICAL PROTEIN * 8e-06 development protein CG1116 82F10-82F10 dup:1/4 ID:32C11
CG1116	
CG18178	+ unknown * CG18178 GH03795 67C-67C ID:32C3
	+ 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
CG12744	GH03826 46C1-46C1 dup:1/2 ID:32C5
CG4184	+ BcDNA:GH03922 unknown * CG4184 GH03922 21C3-21C dup:1/3 ID:32C9
	+ translation_factor * Eif4E * 1e-23 IF4E_YEAST EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CA * 2e-56 IF4E_DROME EUKARYOTIC TRANSLATION INITIATION [IF4E] CG8023 GH04024 66C-66C ID:32D6
CG8023	+ BcDNA:GH04245 motor_protein * contains TPR domain-like repeats(aa) * UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE KD SUBUNIT (O-GLCNAC TRANSFERASE [TPR_REGION // TPR_REPEAT // TPR // NLS_] CG10392 GH04245 41A1-41A2 dup:3/4 ID:32E11
CG10392	+ 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	
CG4468	+ unknown * CG4468 GH04205 92B9-92B9 dup:2/2 ID:32E8
	+ enzyme * alpha esterase(aa) * C. elegans esterase CM06B1 * similar to esterase(aa) * DMEST6P_15 Est-P [CYTOCHROME_B5 // ESTERASE // COesterase] CG5397 GH04232 21F2-21F2 dup:2/2 ID:32E9
CG5397	

+ apoptosis_inhibitor * 2e-81 SINA_DROME DEVELOPMENTAL PROTEIN SEVEN IN ABSENTIA devel * 8e-67 seven-in-absentia protein homologue-1 * 2e-73 siah-1A protein - mouse siah-1A [ZF_RING] CG13030 GH04279 73D1-73D1 ID:32F2
 CG13030
 + CG6186 dup:2/2 ID:32G1
 CG6186
 + unknown * CG6405 GH04442 33D5-33D5 ID:32G9
 CG6405
 + BcDNA:GH04753 enzyme * glutathione transferase (EC 2.5.1.18) D26 - fruit fly (Drosophila melanogaster)(aa) * glutathione transferase (EC 2.5.1.18) D21 - fruit fly (Drosoph [GST] CG16936 GH04753 60D14-60D14 dup:2/2 ID:33A11
 CG16936
 + unknown * HSPC015(aa) * 8e-45 hypothetical protein YOR173w - yeast (Saccharomyces cerevisiae) (* hypothetical protein YLR270w - yeast (Saccharomyces cerevisi CG2091 GH04919 83C-83C ID:33C2
 CG2091
 CG4250
 + unknown * [EGF_2] CG4250 GH05106 58F3-58F3 dup:2/2 ID:33D11
 + enzyme * HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN F01F1.6(aa) * antiquitin=26g turgor protein homolog {C-terminal} intestinal mucosa, Peptide Partial [aldehy // ALDEHYDE_DEHYDR_GLU] CG9629 GH05218 76A3-76A3 dup:2/2 ID:33E7
 CG9629
 CG3273
 + unknown * CG3273 GH05256 42B3-42B3 dup:2/2 ID:33E8
 + electron_transfer * 3e-17 cytochrome b5 * 1e-18 Similarity to Human cytochrome b5 (SW:CYB5_HUMAN); cDNA EST EMBL:D * 5e-18 CYB5_MOUSE CYTOCHROME B5 * 7e-22 cytochrome b [CYTOCHROME B5 // CYTOCHROME_B5_2 // NLS_] CG3566 GH05526 5E1-5E1 ID:33F10
 CG3566
 + 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
 + unknown * 1E-178* 1e-105 inserted at base Both 5' and 3' ends of P element Inverse PCR * CG6770 GH05738 33B12-33B12 ID:33H4
 CG6770
 CG10139
 + unknown * CG10139 GH05836 51B9-51B9 ID:34A1
 + unknown * 1e-21 BIM1_YEAST BIM1 PROTEIN hypothetical protein YER016w - y * 6E-40* 2e-74 coded for by C. elegans cDNA cm17d4; Similar to epoxide hydrolase. * 8 [EPOXYHYDROLASE // abhydrolase] CG15101 GH05945 55F4-55F4 dup:1/3 ID:34A12
 CG15101
 + acyl-CoA_dehydrogenase * fadE19(aa) * PROBABLE GLUTARYL-COA DEHYDROGENASE PRECURSOR (GCD)(aa) * acyl-Coenzyme A dehydrogenase, short/branched chain precursor(aa) * acyl-CoA [Acyl-CoA_dh] CG9547 GH06693 26D7-26D7 ID:34G1
 CG9547
 CG5538
 + unknown * [NLS_BP] CG5538 87C-87C dup:1/3 ID:34G11
 + enzyme * transcriptional adaptor (ADA2, yeast homolog)-3 like (PCAF histone acetylase complex)(aa) * 4e-32 ADA3-like protein * CG7098 16F7-16F7 dup:3/3 ID:34H7
 CG7098
 + 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
 CG10652
 + CG10652 ID:35A1
 + electron_transfer * 7e-19 C561_CAEEL PUTATIVE CYTOCHROME B561 (CYTOCHROME B-561) hy * 1e-20 cytochrome B561 * 2e-20 HCYTO B561 * 9e-24 cytochrome B561 CG8776 GH07176 49B8-49B8 dup:1/3 ID:35B5
 CG8776
 CG4152
 + 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 GH07290 35D6-35D6 ID:35C5

CG13480 + unknown * CG13480 GH07663 70E4-70E4 dup:2/2 ID:35E7
+ BG:DS00180.12 cell_adhesion * 7e-18 C901 protein * 2e-23 similar to EGF-like domain; cDNA EST yk299a12.3 comes from this * 7e-18 Ten-m2 * 1e-14 acetyl LDL receptor; SREC=scavenge [EGF_1 // EGF_2] CG8855 GH07762 34E1-34E1 ID:35F2

CG8855 + unknown * CG8701 GH07855 44B9-44B9 ID:35G4
CG8701 + transcription_factor * skeletal muscle LIM protein(aa) * DRAL gene product(aa) * skeletal muscle LIM-protein 1(aa) *
CG11916 testin(aa) [LIM] CG11916 GH07858 73D4-73D4 ID:35G5
+ motor_protein * very strong similarity to C. elegans myosin heavy chain B * 6e-09 MYS1_YEAST MYOSIN-1 ISOFORM
CG6059 (TYPE II MYOSIN) myosin heavy * 1e-12 nonmuscle myosin [PEROXIDASE_3] CG6059 GH07888 97E8-97E8 dup:1/2 ID:35G7
+ unknown * No definition line found(aa) * 8e-31 IPPI_YEAST ISOPENTENYL-DIPHOSPHATE DELTA-ISOMERASE (IPP
CG3308 ISOMERASE) * 4e-44 isopentenyl-diphosphate delta isome [UPF0006] CG3308 GH08045 93D4-93D4 ID:35H8
+ glycerol_kinase * 3e-59 GLPK_YEAST GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE)
(GLYCEROKINASE) (* 6e-86 similar to glycerol kinase * 1e-107 GLPK_MOUSE GLYCER [FGGY_KINASES_2 // FGGY]
CG8298 CG8298 GH09939 48D8-48D8 ID:37D12
+ cytoskeletal_structural_protein * 2e-21 contains similarity to leucine-rich repeats, strongest similarity is to rat leuc * 6e-37
CG5784 acidic nuclear phosphoprotein pp32 * 3e-37 PHA1_HUMAN [LRR] CG5784 GH10170 54F6-55A1 ID:37F6
+ BcDNA:GH10333 unknown * 2e-91 hypothetical protein * * [ALDOKETO_REDUCTASE_3] CG12152 GH10333 7B8-7B8
CG12152 ID:37G11
+ 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 //
CG11228 PROTEIN_KINASE_DOM // pkin] CG11228 GH10354 56D10-56D10 ID:37H3
+ Su(fu) unknown * DMSF_2 Su(fu) * Su(fu) protein(aa) * gene suppressor of fused protein - fruit fly (Drosophila melanogaster) *
CG6054 6e-80 Su(fu) protein CG6054 GH10488 87C8-87C8 ID:38A6
CG18284 + unknown * CG18284 GH10507 31F5-31F5 ID:38A9
+ BEAF-32 DNA_binding * boundary element-associated factor, 32k - fruit fly (Drosophila melanogaster)(aa) * 1e-146
CG10159 DMBEAF32A_2 BEAF-32 * boundary element associated factor [NLS_BP] CG10159 GH10592 51C3-51C3 ID:38B2
+ unknown * royal jelly protein RJP57-2 - honeybee(aa) * DMYELLOW_7 y * 9e-32 YELL_DROME YELLOW PROTEIN
CG9889 yellow protein - fruit fly (Dros * 2e-34 milk protein ma CG9889 GH10609 59D9-59D9 ID:38B4
CG3074 + endopeptidase similar to cysteine protease Peptidase_C1, THIOL_PROTEASE_HIS CG3074 GH10620 dup:1/3 ID:38B6
+ Cyp6a17 cytochrome_P450 * CYP6A2(aa) * 4e-43 YRV2_CAEEL PUTATIVE CYTOCHROME P450 T10B9.2 IN
CHROMOSOME II * 2e-68 cytochrome P450IIIA * 4e-67 cytochrome P450, subfamily IIIA [EP450II // p450 // P450 // MITP450 //
CG10241 C] CG10241 GH10635 51D2-51D2 ID:38B8
CG9133 + unknown * CG9133 GH10732 61F4-61F4 dup:1/3 ID:38C6
+ Su(H) DNA_binding * DMSUHA_2 Su(H) * RBJK_DROME J KAPPA-RECOMBINATION SIGNAL BINDING PROTEIN (RBP-J
CG3497 KAPPA) (SUPPRESSO * 1e-134 DNA-binding protein LAG-1 lag-1 ge * RB [LIPOCALIN] CG3497 GH10914 35C1-35C1 dup:2/2

ID:38D10

CG7624 + signal_transduction * glucosyltransferase; Die2p(aa) * 1e-16 DIE2_YEAST DIE2 PROTEIN DIE2 protein - yeast (Saccharom * 6e-23 Similarity to Yeast DIE2 protein elega * 4e-4 [SH3] CG7624 GH10931 68A6-68A7 ID:38D12

CG6567 + enzyme * 2e-12 probable membrane protein YLR118c - yeast (Saccharomyces cerevisiae) * 2e-21 Similarity to some prokaryotic esterases; cDNA EST com * 3e-26 ly [ESTERASE] CG6567 GH11067 86C7-86C7 dup:2/2 ID:38E12

CG7486 + Dredd endopeptidase * DREDD isoform delta * 2e-16 interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans * 1e-18 caspase-8 caspase-8 * 5e-18 caspas[CASPASE_P10 // ICE_p10 // CASPASE_P20 /] CG7486 GH10971 1B10-1B10 dup:2/2 ID:38E5

CG6456 + unknown * 9e-07 prepro-APGWamide * APGWamide * [NLS_BP] CG6456 GH11008 74B-74B dup:2/2 ID:38E7

CG3573 + EG:86E4.5 * dJ454M7.1.2 (Lowe Oculocerebrorenal Syndrome protein OCRL-1) (isoform 2)(aa) * /match=(desc;; /match=(desc;; /motif=(desc;; EST /matc [IPPC] CG3573 2B16-2B17 dup:2/2 ID:38E8

CG2950 + RNA_binding * 3e-18 predicted using Genefinder; similar to KH domain family of RNA b * 3e-12 predicted using Genefinder; similar to KH domain family of RNA b * [KH-domain // KH_DOMAIN] CG2950 GH11071 25B3-25B3 dup:1/2 ID:38F1

CG3129 + Rab-RP4 enzyme * Rab4 * rab-related protein 4(aa) * 2e-29 SEC4_YEAST RAS-RELATED PROTEIN SEC4 GTP-binding protein SE * 1e-32 strong similarity to the YPT1 sub-family [SIGMA54_INTERACT_1 // SAR1GTPBP // ras] CG3129 GH11193 5A12-5A12 ID:38G1

CG16857 + BcDNA:GH11322 cell_adhesion * Pxn * 6e-20 roundabout * 2e-15 hemicentin precursor * 1e-10 rig-1 protein [ig // fn3] CG16857 GH11322 24E4-24E4 dup:2/5 ID:38G12

CG10599 + unknown * [NLS_BP] CG10599 GH11223 37B3-37B3 ID:38G3

CG11089 + unknown * 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase(aa) * 5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) trans [ATP_GTP_A] CG11089 GH11240 96B4-96B5 ID:38G4

CG5686 + flp signal_transduction * 2e-35 IRS1_MOUSE INSULIN RECEPTOR SUBSTRATE-1 insulin receptor sub * 9e-35 IRS1_HUMAN INSULIN RECEPTOR SUBSTRATE-1 (IRS-1) insulin * 2e-35 IRS1_RAT [INSULINRSI // PH_DOMAIN] CG5686 GH11263 31C1-31C3 ID:38G6

CG7157 + Acp36DE signal_transduction * 36DE accessory gland protein(aa) * 1e-156 accessory gland protein Acp36DE * 1e-124 Acp36DE * CG7157 GH11288 36F6-36F6 ID:38G8

CG4766 + BcDNA:GH11415 unknown * 1e-104 mab-21 * 1e-139 CAGR1 cell fate specificati * 1e-140 XMAB21 * cDNA EST yk376f11.5 comes from this gene; cDNA EST yk282h5.5 comes CG4766 GH11415 5D1-5D1 ID:38H10

CG3624 + cell_adhesion * [ig] CG3624 GH11432 58D7-58D7 dup:2/2 ID:38H12

CG8913 + enzyme * peroxinectin - signal crayfish(aa) * ovoperoxidase(aa) * peroxidase(aa) * coded for by C. elegans cDNA yk30f1.3; coded for by C. elegans cDNA yk40 [ANPEROXIDASE // PEROXIDASE_3] CG8913 GH11385 92C1-92C1 ID:38H5

CG6015 + 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 GH11406 94A1-94A1 ID:38H8

CG17567 + unknown * 1E-78* * CG17567 GH11551 37C-37C ID:39A10

CG9373 + RNA_binding * polyadenylate binding protein II - human(aa) * myelin gene expression factor 2(aa) * DMB52_2 B52 * Gbp1p protein - Chlamydomonas reinhardtii(aa) [RBD // rrm] CG9373 GH11495 86C1-86C1 dup:1/2 ID:39A4

CG4107 + Pcaf enzyme * Pcaf SPTR(aa) * BLASTX 2.0E-35 GCN5[Component of the nucleosomal histone acetyltransferase (Spt-Ada-Gcn5-Acetyltransferase or SAGA) complex(dna) * B [NLS_BP] CG4107 GH11602 69C3-69C3 dup:2/2 ID:39B3

CG17027 + unknown * MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE (IMP 2) (INOSITOL MONOPHOSPHATASE 2)(aa) * MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE (IMP) (INOSITOL MONOPHOSPHATASE [inositol_P // INFBPHTASE // INOSHPHT] CG17027 GH11740 72C1-72C1 ID:39C2

CG13928 + unknown * inserted at base Both 5' and 3' ends of P element Inverse PCR * * CG13928 GH11843 62A-62A ID:39C8

CG15095 + 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

CG9284 + unknown * CG9284 GH11908 58A2-58A2 ID:39D1

CG11045 + transporter * Contains similarity to equilibrative nucleoside transporter from Homo sapiens. ESTs and come from this gene.(aa) * NBMPR-insensitive nucleoside tr [DERENTRNSPT] CG11045 GH12067 26E2-26E2 ID:39D11

CG6014 + BcDNA:GH11973 unknown * 2e-05 CD94 C-type lectin receptor muscucu * 4e-05 regenerating islet-derived alpha (pancreatic stone protein, pancreatic thread protein) * 7e-05 PA2 [lectin_c // C_TYPE_LLECTIN_2 // NLS_BP] CG6014 GH11973 78D4-78D4 dup:3/3 ID:39D7

CG3274 + BcDNA:GH12174 DNA_binding * 1e-05 eyelid * 6e-45 YP83_CAEEL HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II * 5e-06 FMO5_MOUSE DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FO [ARID] CG3274 GH12174 42B2-42B3 dup:4/4 ID:39E10

CG6302 + unknown * 2e-10 YEA3_YEAST HYPOTHETICAL 14.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION * 7e-28 prefoldin subunit * 2e-68 l(3)j9B4 l(3)j9B4 inserted at base Bo CG6302 GH12095 70E1-70E1 dup:2/2 ID:39E2

CG9119 + unknown * 2e-25 No definition line found * * CG9119 61F3-61F3 dup:5/5 ID:39E5

CG17420 + CG17420 dup:2/2 ID:39E6

CG4929 + CG4929 dup:2/2 ID:39E8

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

CG5973 + 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 GH12376 27F7-28A1 ID:39F12

CG3832 + Phm enzyme * Phm * 4e-65 peptidylglycine alpha-hydroxylating monooxygenase * 8e-05 similar to peptidyl-glycine alpha-amidating monooxygenases elega * 5e-09 AMD_M [PAMONOXGNASE // Cu2_monooxygen // CU2_M] CG3832 GH12243 60A14-60A14 ID:39F4

CG4750 + peptidase * PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III(aa) * Chain A, Bovine Lens Leucine Aminopeptidase Complexed With L-Leucine Phosphonic Acid(aa) * [Peptidase_M17] CG4750 GH12543 53C-53C ID:39G10

CG3318 + Dat ligand_binding_or_carrier * DMNAT1_2 Aanat1 * N-acetyltransferase(aa) * aralkylamine N-acetyltransferase (EC 2.3.1.87) - fruit fly (Drosophila melano * CG3318 GH12636 60B9-60B9 ID:39H12

CG9668 + 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

CG6251 + structural_protein * nuclear pore protein; Nsp1p(aa) * nucleoporin p62(aa) * similar to nucleoporins(aa) * NUCLEAR PORE GLYCOPROTEIN P62 (NUCLEOPORIN P62)(aa) CG6251 GH12838 53B1-53B1 ID:40B9

CG4995 + transporter * similar to ADP/ATP translocase(aa) * 2e-17 probable membrane protein YPL134c - yeast (*Saccharomyces cerevisiae*) * 1e-32 colt * 1e-58 similar to mito [mito_carr // MITOCARRIER // MITOCH_CARR] CG4995 GH13054 31D8-31D8 ID:40C11

CG7470 + metabolism * DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMA [GLU5KINASE // PROA // aldedh // GLUTAMA] CG7470 GH12945 79B3-79B3 dup:1/5 ID:40C6

CG6372 + peptidase * Chain A, Bovine Lens Leucine Aminopeptidase Complexed With L-Leucine Phosphonic Acid(aa) * 6e-20 YOJ6_CAEEL PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROM [LAMNOPPTDASE // Peptidase_M17] CG6372 GH13022 68C1-68C1 dup:2/2 ID:40C9

CG1071 + E2f2 transcription_factor * E2f2 * 1e-174 E2F-like transcription factor (E2F2) * 7e-14 predicted using Genefinder; cDNA EST comes from this * 3e-18 E2F5_MOUSE TRANSCRIPTION FAC CG1071 GH13089 39B3-39B3 ID:40D1

CG12113 + unknown * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST yk410c1.3 comes from this gene; cDNA EST yk410c1.5 comes from this gene; cDNA [ATP_GTP_A] CG12113 GH13214 7F1-7F3 ID:40D10

CG8343 + ligand_binding_or_carrier * mannose receptor, C type 1(aa) * 1e-05 similar to Lectin C-type domain short and long forms (2 domains) * 9e-06 lectin lambda * 6e-0[lectin_c // C_TYPE_LECTIN_1 // C_TYPE_L] CG8343 GH13116 42A10-42A10 dup:2/2 ID:40D2

CG10563 + transcription_factor * HYPOTHETICAL 43.4 KD PROTEIN C6F12.11C IN CHROMOSOME I(aa) * transcription factor IIC63(aa) * 1e-05 TFC1_YEAST TRANSCRIPTION FACTOR TAU KD SUBUNIT CG10563 GH13253 37C1-37C1 dup:2/2 ID:40E1

CG2199 + transcription_factor * zf30C * DMSPALTR_3 salr * 5e-05 YEW0_YEAST PUTATIVE 50.3 KD ZINC FINGER PROTEIN IN PAK1-RPS26B INTERGENIC REGIO * 9e-06 spalt-related [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG2199 GH13336 61F7-61F7 dup:2/2 ID:40E10

CG7283 + ribosomal_protein * ribosomal protein L10a(aa) * 60S RIBOSOMAL PROTEIN L10A (CSA-19)(aa) * 60S RIBOSOMAL PROTEIN L10A(aa) * 2e-06 predicted using Genefinder; Weak simil [Ribosomal_L1] CG7283 GH13356 68D3-68D3 dup:3/3 ID:40E11

CG9489 + actin_binding * 2e-12 putative actin-binding protein UNC-115 * 2e-11 protein * 2e-05 talin homologue * 5e-05 qua CG9489 GH13330 85E5-85E5 dup:3/3 ID:40E9

CG12750 + RNA_binding * LET 858(aa) * conserved hypothetical protein(aa) * BLASTX 7.4E-44 *Caenorhabditis elegans* Nucampholin (let-858) mRNA, complete cds.(dna) * BLASTX 3 [NLS_BP] CG12750 GH13383 36F7-36F7 dup:3/3 ID:40F2

CG14718 + RNA_binding * 3e-16 RNA-binding protein cabeza - fruit fly (*Drosophila melanogaster*) (* 4e-14 EWS_MOUSE RNA-BINDING PROTEIN EWS RNA-binding protein E * 2e-15 TLS [RBD // zf-RanBP // rrm // ZF_RANBP] CG14718 GH13594 86F1-86F1 ID:40G5

CG5790 + protein_kinase * serine/threonine protein kinase; Cdc7p(aa) * protein kinase Cdc7(aa) * DMSTPK Pk61C * HsCdc7(aa) [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG5790 GH13884 36F-36F ID:41A7

CG9010 + enzyme * *C. elegans* glyceraldehyde 3-phosphate dehydrogenase * GLYCERALDEHYDE 3-PHOSPHATE

DEHYDROGENASE II (GAPDH II)(aa) * GLYCERALDEHYDE 3-PHOSPHATE DEHYDR [G3PDHDRGNASE // gpdh // GAPDH]
 CG9010 GH13901 53E6-53E6 ID:41A8
 CG7251 + unknown * [NLS_BP] CG7251 GH13914 27D1-27D1 ID:41A9
 CG1112 + alpha-Est7 enzyme * alpha esterase(aa) * alpha esterase(aa) * alpha esterase(aa) * alpha esterase(aa)
 [CARBOXYLESTERASE_B_1 // ESTERASE // COe] CG1112 GH13950 84D5-84D5 dup:3/3 ID:41B1
 CG7131 + unknown * CG7131 GH14048 90F7-90F7 ID:41B9
 CG9775 + unknown * [NLS_BP] CG9775 GH14260 82D2-82D2 dup:1/2 ID:41C10
 + 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
 CG7567 + unknown * CG7567 GH14364 99B5-99B5 ID:41D8
 + signal_transduction * 2e-17 activin beta precursor * 3e-14 CET-1 * 2e-22 IHBA_MOUSE INHIBIN BETA A CHAIN
 PRECURSOR (ACTIVIN BETA-A CHAIN) * 5e-23 inhibin, beta A[TGF-beta // TGF_BETA // TGF_BETA_2 // Z] CG16987
 CG16987 GH14433 23B2-23B2 dup:2/2 ID:41E2
 + electron_transfer * 9e-06 PDI_YEAST PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) / DOLICHYL-
 DIPHOSPHOOLIGOS * 2e-08 PDI_DROME PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) [THIOREDOXIN // THIOREDOXIN_2 // thiored]
 CG3315 CG3315 GH14562 4F2-4F2 ID:41F1
 + structural_protein * 3e-05 MAGE tumor antigen D1 * 5e-13 FMRA_ANTEL ANTHO-RFAMIDE NEUROPEPTIDE
 PRECURSOR Antho-RFa * LWamide neuropeptide precursor protein * 33K hydroxy CG11395 GH14572 54A2-54A2 dup:2/2
 CG11395 ID:41F2
 + eff enzyme * DMUBCD1_2 eff * Ubiquitin conjugating enzyme(aa) * similar to ubiquitin conjugating enzymes(aa) * ubiquitin
 CG7425 conjugating enzyme(aa) [UBIQUITIN_CONJUGAT // UQ_con // UBIQUIT] CG7425 GH14739 88D2-88D2 ID:41G8
 + HmgZ DNA_binding * 2e-07 cerevisiae mitochondrial protein gene, complete gene produc * 5e-42 HMGZ_DROME HIGH
 CG17921 MOBILITY GROUP PROTEIN Z (HMG-Z) high mob * 2e-11 SSRP_CAE [HMG // HMG_box // NLS_BP] CG17921 GH14749
 57F8-57F9 ID:41G9
 + * ribosomal protein L24(aa) * Ribosomal protein L24B (rp29) (YL21) (L30B); Rpl24bp(aa) * 60S RIBOSOMAL PROTEIN
 CG9282 L24 (L30)(aa) * Similar to 60S ribosoma [Ribosomal_L24e // NLS_BP] CG9282 34B6-34B6 dup:1/5 ID:42A12
 CG8136 + unknown * CG8136 GH14973 85B2-85B2 dup:1/2 ID:42A2
 CG2149 + unknown * [NLS_BP] CG2149 GH15120 44B9-44B9 dup:1/2 ID:42B2
 + unknown * 2e-81 YN28_YEAST HYPOTHETICAL 41.2 KD PROTEIN IN PLC1-SEC21 INTERGENIC REGION * 4e-94
 CG14213 C26E6.3 gene product * 1e-124 protein involved in sexual devel CG14213 GH15157 18D10-18D10 ID:42B4
 + 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
 CG2127 + unknown * [EF_HAND // NLS_BP] CG2127 GH15271 44B9-44B9 ID:42C3
 CG11993 + Mst85C unknown * CG11993 LD21554 85C6-85C6 ID:43A6

CG14722	+ 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 86F6-86F6 ID:43A8
CG4747	+ motor_protein * 1e-34 3-hydroxyisobutyrate dehydrogenase * 1e-10 inserted at base Both 5' and 3' ends of P element Inverse PCR * YKWC_BACSU HYPOTHETICAL 30.7 KD PR CG4747 LD22344 30F5-30F5 ID:43B10
CG7055	+ DNA_binding * SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1(aa) * BAF57(aa) * 1e-08 HMG1-related DNA-binding [HMG // HMG_box // PRO_RICH] CG7055 LD22182 8C17-8D1 ID:43B5
CG17252	+ BCL7-like CG17252 LD22180 dup:2/2 ID:43B6
CG7139	+ BcDNA:LD21293 enzyme * unknown(aa) * 1e-27 unknown * [ATP_GTP_A2 // ATP_GTP_A] CG7139 LD22250 79C2-79C3 ID:43B9
CG2925	+ noi RNA_binding * noi * noisette(aa) * 1e-30 PR09_YEAST PRE-MRNA SPLICING FACTOR PRP9 PRP9 protein - ye * noisette [ZF_MATRIN] CG2925 LD22754 83B4-83B4 ID:43C11
CG7538	+ Mcm2 DNA_replication_factor * BLASTX 4.1E-84 Homo sapiens mRNA for DNA replication licensing factor (huMCM2), complete cds.(dna) * BLASTX 4.1E-84 Homo sapiens mRNA for DNA replic [MCM // MCM_1 // MCM_2] CG7538 LD22409 84F-84F dup:1/2 ID:43C3
CG7752	+ transcription_factor CG7752 ID:43C7
CG8295	+ unknown * myelodysplasia/myeloid leukemia factor 1(aa) * Y17G7B.17(aa) * 6e-27 myeloid leukemia factor myelodysplasia/myel * t(3;5)(q25.1;p34) fusion gene CG8295 LD22883 52D11-52D11 dup:2/2 ID:43D3
CG8569	+ transcription_factor * 6e-09 predicted using Genefinder; cDNA EST comes from this g * 4e-05 hepatoma-derived growth factor * 2e-20 BS69 protein - human binds directly to a [PWWP // NLS_BP] CG8569 LD22977 49A10-49A10 dup:2/2 ID:43D7
CG3004	+ signal_transduction G-protein beta-subunit 6 GPROTEINBRPT, RCC1_2, WD40, WD40_REGION,] CG3004 LD23129 dup:3/3 ID:43E6
CG6538	+ TflIFbeta transcription_factor * TflIF bgr; * TRANSCRIPTION INITIATION FACTOR IIF, BETA SUBUNIT (TFIIF-BETA)(aa) * 6e-05 T2FB_YEAST TRANSCRIPTION INITIATION FACTOR IIF, BETA SUBUNIT CG6538 LD23340 86C4-86C4 dup:1/2 ID:43F2
CG6254	+ transcription_factor * zinc-finger protein - African clawed frog(aa) * 1e-15 YJF6_YEAST HYPOTHETICAL 98.9 KD ZINC FINGER PROTEIN IN BTN1-PEP8 INTERGENIC REG * 6[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG6254 LD23879 85F13-85F13 dup:1/2 ID:43F9
CG8153	+ 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 // NLS_BP] CG8153 51F4-51F5 dup:1/3 ID:43G11
CG7600	+ NLS_BP, PLANT_GLOBIN CG7600 LD25031 dup:1/2 ID:43H1
CG1906	+ protein_phosphatase * DPP2C1(aa) * protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform(aa) * 3e-44 P2C2_YEAST PROTEIN PHOSPHATASE 2C HOMOLOG (PP2C-2) [PP2C_1 // PP2C // PP2C_2] CG1906 LD25115 99B6-99B6 ID:43H5
CG11154	+ ATPsyn-beta * DMATPSYNB ATPsyn- bgr; * 1e-173 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor - yeast (Sacch * ATPB_DROME ATP SYNTHASE BETA CHAIN [ATP-synt_ab // ATP-synt_ab_C // ATPASE_] CG11154 102F6-102F6 dup:3/4 ID:43H8

CG14641 + * ORF; Method: conceptual translation supplied by author.(aa) * similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST comes from [rrm] CG14641 82A-82A dup:2/4 ID:44A11

CG8301 + transcription_factor homology to uncharacterized human zinc finger proteins ZINC_FINGER_C2H2, ZINC_FINGER_C2H2_2, zf] CG8301 LD25464 dup:1/4 ID:44A2

CG3183 + motor_protein * 1e-155 inserted at base 5' end of P element Inverse PCR * * [bZIP] CG3183 LD25484 42B3-42B3 dup:1/2 ID:44A3

CG9768 + huckebein transcription_factor specific RNA polymerase II transcription factor ZINC_FINGER_C2H2, ZINC_FINGER_C2H2_2, zf] CG9768 LD25709 dup:2/3 ID:44B3

CG5383 + Similar sequences have been identified in Caenorhabditis elegans , Homo sapiens and Schizosaccharomyces pombe CG5383 LD25827 dup:2/2 ID:44B7

CG16788 + RNA_binding * son3 protein - human (fragment)(aa) * SON DNA binding protein(aa) * Pad-1(aa) * similar to RNA binding proteins(aa) [RBD // rrm // NLS_BP] CG16788 LD26185 85D25-85D25 ID:44C10

CG11329 + unknown * 1e-16 inserted at base 5' end of P element Inverse PCR * * CG11329 LD26217 26F6-26F6 ID:44C11

CG2087 + PEK protein_kinase * 8e-30 protein kinase GCN2 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) * 2e-24 eIF-2alpha kinase * 2e-55 similar to serine/threonine kinase (2 do [Bacterial_PQQ // PROTEIN_KINASE_ST // P] CG2087 LD25978 83A8-83A8 ID:44C5

CG12340 + BcDNA:LD26050 motor_protein * 1e-05 strong similarity to the SNF2/RAD54 family of helicases; partial CDS * 1e-104 inserted at base Both 5' and 3' ends of P element Inverse PCR * [fn3] CG12340 LD26128 47C-47C dup:2/4 ID:44C9

CG5363 + cdc2 protein_kinase * CDK5 kinase(aa) * DMCD2_2 cdc2 * 1e-101 CC28_YEAST CELL DIVISION CONTROL PROTEIN protein kinase * 1e-174 CC2_DROME CELL DIVISION CONTROL PROT[PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG5363 LD26702 31D11-31D11 dup:3/3 ID:44E11

CG4785 + CG4785 LD26982 dup:2/2 ID:44F11

CG16892 + ligand_binding_or_carrier * 4e-05 fizzy-related protein * 1e-05 transducin (beta)-like transducin (beta) like pr * 1e-05 hypothetical protein * 5e-07 DMRNAFRP fzf CG16892 LD26813 8D7-8D8 dup:2/2 ID:44F4

CG5222 + unknown unknown protein CIT987SK_2A8_1 [Homo sapiens] CG5222 LD26912 dup:1/2 ID:44F9

CG4303 + Bap60 Brahma associated protein 60kD NLS_BP, PRO_RICH CG4303 LD27052 dup:1/2 ID:44G4

CG11906 + 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 LD27134 56C7-56C8 ID:44G9

CG3847 + transcription_factor * 2e-10 CROL GAMMA * 5e-16 predicted using Genefinder; similar to Zinc finger, C2H2 type (5 d * 1e-11 zinc finger protein - mouse zinc finger protein [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG3847 LD27244 5E5-5E5 ID:44H4

CG3511 + chaperone * DMNINAA_7 ninaA * DMCYP1_2 Cyp1 * 5e-23 CYPC_YEAST PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C PRECURSOR (PPIASE) (ROTAMASE) (* 1e-20 CYPH_DROME PEPTIDYL [pro_isomerase // CSA_PPIASE_2 // WD40_R] CG3511 LD27277 60D5-60D5 dup:1/2 ID:44H8

CG15112 + 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 ID:45A1
 + transcription_factor similar to crol protein ZINC_FINGER_C2H2, ZINC_FINGER_C2H2_2, z] CG2678 LD27553 dup:1/2 ID:45A10
 CG2678
 CG18608 + unknown * CG18608 LD27570 56A-56A dup:1/2 ID:45A11
 + BcDNA:LD22910 endopeptidase * reserved(aa) * 1e-12 UBP9_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (UBIQUITIN THIOLESTERASE 9) (* 1e-08 UBPX_CAEEL PROBABLE UBIQUITIN CARBOXYL[UCH_2_2 // UCH_2_3 // PRO_RICH // UCH-2] CG15817 99A5-99A5 dup:2/2 ID:45A6
 CG15817
 CG8632 + embryonic lung protein [Homo sapiens] CG8632 LD27783 dup:1/2 ID:45B7
 CG11970 + BcDNA:LD23876 similar to nuclear factor related to kappa B binding protein CG11970 LD28082 dup:2/4 ID:45C12
 + RNA_binding * similar to RNA recognition motif. (aka RRM, RBD, or RNP domain) (2 domains); cDNA EST yk211a9.5 comes from this gene; cDNA EST yk266e11.5 comes from [RNP_1 // RBD // rrm // NLS_BP] CG4806 LD27920 60D10-60D10 ID:45C2
 CG4806
 CG9506 + protein_phosphatase * CG9506 LD27991 28D1-28D1 dup:1/2 ID:45C6
 CG7825 + Rad17 DNA_repair_protein DNA repair protein ATP_GTP_A, ATP_GTP_A2, RFC CG7825 LD27993 ID:45C7
 CG10018 + DNA_repair_protein homology to mouse and human SNM1 protein NLS_BP CG10018 LD28027 dup:1/2 ID:45C8
 + unknown * 1e-106 probable membrane protein YPL217c - yeast (Saccharomyces cerevisiae) * 2e-11 No definition line found * 1E-152* 1e-100 conserved hypothetical [NLS_BP // ATP_GTP_A] CG7728 LD28182 73E3-73E4 dup:3/3 ID:45D11
 CG7728
 CG5003 + unknown * [FBOX_DOMAIN] CG5003 LD28210 98B2-98B2 ID:45D12
 CG6994 + cytoskeletal_structural_protein CG6994 LD28101 dup:2/2 ID:45D5
 CG9213 + enzyme CG9213 LD28117 dup:2/2 ID:45D7
 + unknown * 5e-24 hypothetical protein YDL087c - yeast (Saccharomyces cerevisiae) * 4e-34 YP68_CAEEL HYPOTHETICAL 37.0 KD PROTEIN IN CHROMOSOME II (U2 * 2e-23 p [NLS_BP] CG7564 LD28402 74D1-74D1 dup:4/4 ID:45E12
 CG7564
 CG6391 + enzyme * nudix (nucleoside diphosphate linked moiety X)-type motif 3(aa) * 7e-40 diphosphoinositol polyphosphate phosphohydrolase (A * [MUTT // mutT] CG6391 LD28241 67F4-67F4 dup:3/4 ID:45E3
 CG14749 + CG14749 dup:3/3 ID:45F10
 CG8783 + unknown Conserved gene telomeric to alpha globin cluster [Homo sapiens] CG8783 LD28428 dup:2/3 ID:45F2
 CG14657 + unknown CG14657 LD28447 ID:45F4
 + ribosomal_protein * 1e-48 RL7A_YEAST 60S RIBOSOMAL PROTEIN YL17-A ribosomal protein * 4e-66 ribosomal protein L17 60S RIBOSOM * 1e-65 RL17_RAT 60S RIBOSOMAL PROTEIN L17 [Ribosomal_L22 // RIBOSOMAL_L22] CG3203 6C10-6C10 dup:1/5 ID:45G12
 CG3203
 CG5965 + unknown * Cys-rich protein(aa) * FIM protein(aa) * zinc finger protein 261(aa) * BLASTX 3.6E-13 Dictyostelium discoideum sp96 gene for spore coat protein SP9 CG5965 97F4-97F4 dup:2/3 ID:45G2
 + unknown * phosphatidylinositol glycan, class B(aa) * 2e-29 YGO2_YEAST HYPOTHETICAL 72.6 KD PROTEIN IN MRF1-SEC27 INTERGENIC REGION * 5e-08 coded for by C. ele CG12006 64C4-64C4 dup:2/2 ID:45H10
 CG12006
 CG10640 + CG10640 dup:4/4 ID:45H8

CG5263	+ smg * cloned by ability to arrest the cell cycle when expressed in the fission yeast Schizosaccharomyces pombe(aa) * 1e-124 cloned by ability to arrest th
CG6605	+ motor_protein CG6605 ID:46B12
CG9805	+ translation_factor eukaryotic translation initiation factor 3 subunit NLS_BP, PCI_DOMAIN CG9805 ID:46B4
CG4916	+ RNA_binding CG4916 dup:2/2 ID:46C4
CG7563	+ calpain CG7563 dup:1/4 ID:46C8
CG1101	+ CG1101 dup:4/5 ID:46D7
CG8730	+ drosha RNA binding ribonuclease III DSRBD, PRO_RICH, RIBONUCLEASE_III, RNASE] CG8730 LD29995 dup:2/3 ID:46F12
CG10082	+ unknown * PiUS(aa) * 6e-18 KCS1 protein - yeast (Saccharomyces cerevisiae) (Z49 * 7e-27 cDNA EST comes from this gene * 2e-43 Similar to S.cerevisiae protein CG10082 LD29913 57F6-57F6 dup:2/2 ID:46F6
CG3021	+ CG3021 LD29918 dup:1/2 ID:46F9
CG7288	+ endopeptidase * hypothetical protein unip - 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
CG17681	+ unknown * CG17681 LD30009 36E-36E ID:46G4
CG6819	+ transmembrane_receptor * nucleoporin Nup84(aa) * 6e-46 nucleoporin 88kD 88kDa nuclear * 3e-47 nucleoporin Nup84 * CG6819 LD30108 87C7-87C7 ID:46G7
CG2260	+ transcription_factor_binding * 4e-71 YER2_YEAST HYPOTHETICAL 62.3 KD PROTEIN IN PTP3-ILV1 INTERGENIC REGION * 9e-94 Similarity to Yeast hypothetical protein YER2 (SW:YER2_YEAS[WD40_REGION // WD_REPEATS // WD40] CG2260 LD30339 7D11-7D11 ID:46H10
CG5930	+ Transcription factor IIA L transcription_factor general RNA polymerase II transcription factor, PHOSPHOPANTETHEINE CG5930 LD30231 dup:2/2 ID:46H2
CG1647	+ glass transcription_factor photoreceptor determination ZINC_FINGER_C2H2 CG1647 LD30287 dup:2/2 ID:46H5
CG14005	+ unknown * CG14005 LD30293 26A2-26A2 dup:2/3 ID:46H6
CG12298	+ 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 ID:46H7
CG1677	+ CG1677 LD30482 ID:47A10
CG2682	+ transcription_factor CG2682 ID:47A11
CG8617	+ CG8617 LD30408 dup:1/2 ID:47A4
CG8749	+ snRNP70KRNA_binding * U1 SMALL NUCLEAR RIBONUCLEOPROTEIN KD (U1 SNRNP KD) (SNRNP70)(aa) * DMRNP70K_6 snRNP27D * ribonucleoprotein antigen(aa) * small nuclear ribonucleopr [RNP_1 // RBD // rrm // NLS_BP] CG8749 LD30455 27C7-27C7 dup:1/2 ID:47A8
CG9797	+ transcription_factor * b34I8.1 (Kruppel related Zinc Finger protein 184)(aa) * 2e-15 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * 8e-24 SUHW_DROME SUPPRESSO[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG9797 LD30467 85B2-85B2 ID:47A9
CG6502	+ E(z) transcription_factor * enhancer of zeste (Drosophila) homolog 2(aa) * enhancer of zeste homolog (Drosophila)(aa) *

DM180_2 E(z) * ENHANCER OF ZESTE PROTEIN(aa) [SET_DOMAIN // SET // NLS_BP] CG6502 LD30505 67E4-67E4 ID:47B2

+ transcription_factor * similar to PHD-finger. (2 domains), SET domain; cDNA EST yk453a7.5 comes from this gene; cDNA EST yk453a7.3 comes from this gene; cDNA EST yk273c7.3 [PHD] CG5591 LD30514 60A9-60A9 dup:2/2 ID:47B3

CG5591

CG3508 + unknown * HMBA-inducible(aa) * 3e-11 HIS1 protein * [NLS_BP] CG3508 LD30520 88C11-88C11 ID:47B4

+ chaperone * 1e-09 SCJ1_YEAST SCJ1 PROTEIN SCJ1 protein - yeast (Saccharomyce * 4e-11 csp29 cysteine string protein * 6e-12 similar to DnaJ, prokaryotic heat sho [DnaJ // DNAJPROTEIN // DNAJ_2] CG7133 LD30543 79C3-79C3 ID:47B6

CG7133 + fzy cell_cycle_regulator * fzy * 2e-76 YGA3_YEAST HYPOTHETICAL 62.8 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2 * Method: conceptual translation supplied by au[WD40_REGION // FIZZY_DOMAIN // WD_REPEA] CG4274 LD30572 35F8-35F8 dup:1/2 ID:47B7

CG4274

CG18683 + unknown * CG18683 LD30576 99C6-99C6 ID:47B8

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

CG6549 + FK506-bp1 ligand_binding_or_carrier * DMFKBP39_2 FK506-bp1 * KD FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE)(aa) * 7e-24 hypothetical protein YLR4[FKBP // FKBP_PPIASE_2 // FKBP_PPIASE_3] CG6226 LD30817 90E1-90E1 ID:47C12

CG6226

CG6962 + CG6962 ID:47C2

+ msl-3 tumor_suppressor * MALE-SPECIFIC LETHAL-3 PROTEIN(aa) * DMMSL3_2 msl-3 * 7e-08 hypothetical protein * DMMSL3_2 msl-3 CG8631 LD30726 65E5-65E5 dup:1/2 ID:47C5

CG8631 + transcription_factor * with similarity to Homo sapiens TAFII55 encoded by Genbank Accession Number and C. elegans unknown protein encoded by Genbank Accession Number * an CG2670 LD30980 84E1-84E1 ID:47D11

CG2670 + Mcm3 DNA_replication_factor * Mcm3 * DNA replication factor MCM3(aa) * 1e-168 MCM3_YEAST MINICHROMOSOME MAINTENANCE PROTEIN minichrom * MCM3 [MCM // MCM_1 // MCM_2] CG4206 LD30950 4F2-4F2 ID:47D8

CG4206 + protein_phosphatase * 4e-25 PVH1_YEAST PROTEIN-TYROSINE PHOSPHATASE YVH1 (PTPASE YVH1) * 8e-13 puckered protein * 1e-14 predicted using Genefinder; similar to D[PTS_HPR_SER // DSPc // TYR_PHOSPHATASE_] CG14211 LD31102 18D9-18D9 dup:2/2 ID:47E10

CG14211

CG6506 + unknown * CG6506 LD31003 16D6-16D6 dup:3/3 ID:47E2

+ cell_adhesion THYROGLOBULIN PRECURSOR 4_DISULFIDE_CORE, ATP_GTP_A, EGF_1, THYR] CG5639 LD31017 dup:2/2 ID:47E4

CG5639 + tos DNA_repair_protein * DMTOSCAP1_2 tos * Tosca(aa) * 7e-47 EXO1_YEAST EXONUCLEASE I (EXO I) (DHS1 PROTEIN) DHS1 pr * Tosca [53EXO_N_DOMAIN // 53EXO_I_DOMAIN // XPG] CG10387 LD31018 37A4-37A4 dup:2/2 ID:47E5

CG10387 + chaperone * 1e-10 XDJ1 protein - yeast (Saccharomyces cerevisiae) Xdj1p: H * 2e-08 DNJ1_DROME DNAJ PROTEIN HOMOLOG (DROJ1) droj1 * 6e-56 predicted using Genefin [DNAJ_1 // DnaJ // DNAJ_2 // NLS_BP] CG7872 LD31069 13E3-13E3 dup:2/2 ID:47E9

CG7872 + unknown * 7e-05 YHOB_DROME TRANSPOSABLE ELEMENT HOBO KD HYPOTHETICAL PROTEIN * 9e-05 transposase * 7e-05 ORF1 * Hermes transposase CG17153 LD31163 68F3-68F3 ID:47F2

CG17153

CG7197 + ligand_binding_or_carrier * 3e-51 ARF1_YEAST ADP-RIBOSYLATION FACTOR ADP-ribosylation fac * 3e-49

ARF1_DROME ADP-RIBOSYLATION FACTOR ADP-ribosylation fac * 1e-52 ARFL_CA[arf // SAR1GTPBP // RASTRNSFRMNG]
 CG7197 LD31204 66C5-66C5 dup:2/5 ID:47F5
 + RNA_binding * 13878, ribosomal protein S14 (not transcribed)(aa) * 9e-84 PR43_YEAST PRE-MRNA SPLICING FACTOR
 RNA HELICASE PRP43 (HELICASE JA1) * 8E-32* 5e-90 YQZN [HELICASE // NLS_BP // Ribosomal_S14 //] CG12211 LD31543
 18C8-18C8 ID:47G11
 CG12211 + motor_protein * coded for by C. elegans cDNA yk38d7.3; coded for by C. elegans cDNA cm06h5; coded for by C. elegans
 cDNA yk38d7.5(aa) * Yml093wp(aa) * 5e-33 YMJ3_Y [NLS_BP] CG12301 LD31322 71D4-71D4 dup:1/2 ID:47G3
 CG12301 + motor_protein * CG8149 LD31448 86C1-86C1 ID:47G6
 CG8149 + cell_adhesion * tip associating protein(aa) * tip associating protein(aa) * tip associating protein(aa) CG4118 LD31449
 CG4118 77A1-73A7 dup:1/2 ID:47G7
 CG18592 + * CG18592 25C3-25C3 dup:1/2 ID:47H11
 CG7494 + * contains weak similarity to HIV P17 matrix protein * 7e-13 RL1_SERMA 50S RIBOSOMAL PROTEIN L1 ribosomal
 protein L1 - S * RL1_HAEDU 50S RIBOSOMAL P [Ribosomal_L1] CG7494 84F9-84F9 dup:2/2 ID:47H12
 CG11063 + transcription_factor * DMMLP84B_2 Mlp84B * ajuba; jub(aa) * BLASTX 7.1E-07 Human LIM protein (LPP) mRNA, partial
 cds.(dna) * 8e-06 LRG1 [LIM_DOMAIN_1 // LIM // LIM_DOMAIN_2 //] CG11063 LD31670 12B9-12B9 ID:47H4
 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
 CG1657 + unknown * hypothetical protein(aa) * 4e-06 VPS9_YEAST VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN
 VPS9 * 3e-31 C05D9.6 gene product * 1e-14 Rab5 GDP/GTP exch [RAS_GTPASE_ACTIV_2 // PTS_HPR_HIS // NL] CG1657
 LD31729 10B8-10B8 dup:2/2 ID:47H8
 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
 CG10364 + msb1l unknown * CG10364 LD32040 37F2-37F2 ID:48A8
 CG8961 + transcription_factor * 5e-87 inserted at base 5' end of P element Inverse PCR ** [zf-C2H2 // ZINC_FINGER_C2H2 //
 ZINC_FIN] CG8961 LD32631 53F5-53F5 ID:48D3
 CG6509 + signal_transduction * protein(aa) * BLASTX 4.9E-08 Mus musculus TDAG51 (TDAG51) mRNA, complete cds.(dna) *
 BLASTX 7.3E-13 Rattus PSD-95/SAP90-related gene (chapsyn isoform) [GUANYLATE_KINASE_2 // PDZ // NLS_BP] CG6509
 LD32687 33A2-33A2 ID:48D7
 CG6418 + RNA_binding * 4e-80 DBP2_YEAST P68-LIKE PROTEIN RNA helicase DBP2 - yeast (Sac * 1e-68 RM62_DROME
 PUTATIVE ATP-DEPENDENT RNA HELICASE P62 RNA he * 1e-154 similar [helicase_C // HELICASE // DEAD // DEAD_] CG6418 LD32732 67F4-67F4 dup:2/2 ID:48D8
 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
 CG10043 + rtGEF signal_transduction * 5e-60 rho type GEF * 6e-62 rtGEF * rtGEF * rho type GEF(aa) [GRF_DBL // RhoGEF //
 SH3DOMAIN // SH3 /] CG10043 LD33092 38C7-38C8 dup:2/2 ID:48F9
 CG3704 + unknown * Yjr072cp(aa) * ATP(GTP)-binding protein(aa) * HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN
 CHROMOSOME III(aa) * putative protein(aa) [ATP_GTP_A] CG3704 LD33276 1D1-1D1 ID:48G10

+ unknown * protein(aa) * 3e-09 PC11_YEAST PCF11 PROTEIN hypothetical protein YDR228c - * 3e-21 YRR2_CAEEL
 CG10228 HYPOTHETICAL 91.1 KD PROTEIN R144.2 IN CHROMOSOME III [PRENYLATION // PRO_RICH // NLS_BP // CY] CG10228
 LD33132 51D2-51D2 ID:48G2
 + motor_protein * kda paraneoplastic cerebellar degeneration-associated antigen Peptide, * MYOSIN HEAVY CHAIN D
 CG1962 (MHC D)(aa) * CLIP-190 * 7e-05 microtubule binding pro [NLS_BP] CG1962 38E-38E dup:3/5 ID:48G3
 + DNA_binding * protein(aa) * 3e-65 YEZ9_YEAST PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2
 CG15835 INTERGENIC REGION > * 2e-26 Similarity to Human XE169 protein (SW:X CG15835 LD33386 43F5-43F5 ID:48H3
 + chromatin_binding * pheromone response pathway suppressor; Srm1p(aa) * similar to RCC1 proteins(aa) * regulator of
 CG9135 chromosome condensation(aa) * retinitis pigmentosa [RCC1 // RCC1_2 // RCCNDNSATION] CG9135 LD33431 26B3-26B3
 dup:1/2 ID:48H4
 CG18124 + BG:DS01068.4 unknown * 1e-05 mtDBP protein * AAs * * CG18124 LD33443 35A1-35A1 ID:48H5
 + enzyme * 1e-10 FMS1_YEAST FMS1 PROTEIN FMS1 protein - yeast (Saccharom * 6e-11 Cs protein * 8e-33 No definition
 CG7737 line found * 2e-13 protein [ADXRDTASE // AMINEOXDASEF // NAD_BINDIN] CG7737 LD33764 47D6-47D7 dup:1/2 ID:49A10
 + transcription_factor * transcription factor 17(aa) * zinc finger protein(aa) * RENAL TRANSCRIPTION FACTOR KID-1
 CG7357 (TRANSCRIPTION FACTOR 17)(aa) * crol [zf-C2H2 // ZINC_FINGER_C2H2_2] CG7357 LD33778 93B1-93B1 ID:49A11
 CG15736 + transcription_factor * CG15736 LD33780 11A4-11A4 ID:49A12
 + unknown * similar to the postsynaptic membrane 43K protein from Xenopus * LGN protein(aa) * 4e-13 C10A gene
 CG5692 product * 2e-29 hypothetical protein [TPR_REGION // TPR_REPEAT // NLS_BP] CG5692 LD33695 98A3-98A3 ID:49A6
 + Caf1 signal_transduction * Caf1 * Rack1 * CHROMATIN ASSEMBLY FACTOR P55 SUBUNIT (CAF-1 P55 SUBUNIT)
 CG4236 (DCAF-1)(aa) * 2e-73 HAT2_YEAST HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT hy [GPROTEINBRPT //
 WD40_REGION // WD_REPEA] CG4236 LD33761 88E8-88E8 ID:49A9
 + unknown * 1e-27 cDNA EST yk476a1.5 comes from this gene * 4e-28 Unknown * cDNA EST comes from this gene; cDNA
 CG3887 EST yk256g7.5 come * F28H7.4 CG3887 LD33828 25C1-25C1 ID:49B2
 + RNA_binding * 3e-05 NSR1_YEAST NUCLEAR LOCALIZATION SEQUENCE BINDING PROTEIN (P67) * 7e-06 protease
 CG10837 * 3e-05 Similarity to Bovine Poly-A binding protein II cDNA * [RNP_1 // RBD // rm] CG10837 LD33831 cyto_unknown ID:49B3
 + unknown * 6e-97 N2,N2-dimethylguanosine tRNA methyltransferase c * 1e-105 similar to N2,N2-dimethylguanosine tRNA
 CG6388 methyltransferase; cDNA ES * 1E-125* 1e-111 [SAM_BIND] CG6388 LD33880 33D5-33E ID:49B7
 + unknown * 3e-47 YKT6_YEAST HYPOTHETICAL 22.7 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION * 7e-53
 CG1515 YMP8_CAEEL HYPOTHETICAL 82.6 KD PROTEIN IN CHROMOSOME III * 1e- [SYNAPTOBREVN // synaptobrevin] CG1515
 LD34211 7C8-7C8 ID:49C12
 + unknown * Ydl060wp(aa) * No definition line found(aa) * 8e-91 hypothetical protein YDL060w - yeast (Saccharomyces
 CG7338 cerevisiae) * 0.00000000006 [NLS_BP] CG7338 LD34093 78D-78D dup:2/4 ID:49C5
 + unknown * RRM3/PIF1 helicase homolog(aa) * PIF1(aa) * putative helicase(aa) * DNA helicase homolog(aa) [NLS_BP //
 CG3238 ATP_GTP_A] CG3238 LD34105 25A3-25A3 ID:49C6
 CG7869 + motor_protein * [SNF2_N // NLS_BP] CG7869 LD34474 70E1-70E1 ID:49D11
 + CH1-2 endopeptidase * COP9 complex homolog subunit 1-2 DCH1-2(aa) * 3e-14 YE28_CAEEL HYPOTHETICAL 47.6 KD
 CG3889 PROTEIN F49C12.8 IN CHROMOSOME IV * 1e-157 GPS1_HUMAN G PROTEIN [PCI_DOMAIN // PCI] CG3889 LD34304

75E2-75E2 dup:1/2 ID:49D6

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

+ TFIIS transcription_factor * 2e-20 DST1 DNA strand transferase alpha * 1e-124 TFS2_DROME TRANSCRIPTION ELONGATION FACTOR S-II (RNA POLYMERASE II ELONGATION FA * 3e-42 TFS2_CAEEL [TFIIS] CG3710 LD34766 35C1-35C1 ID:49F1

CG3710 + DNA_binding * zinc finger protein (RING finger, C3HC4 type)(aa) * 4e-34 YL23_YEAST HYPOTHETICAL 29.7 KD PROTEIN IN REC102-SFH1 INTERGENIC REGION * 5e-65 similar t [ZF_CCCH // zf-C3HC4 // ZINC_FINGER_C3HC] CG4973 LD35003 92C4-92C4 ID:49F12

CG4973 + unknown * [NLS_BP] CG9754 LD34845 57D4-57D4 ID:49F8

CG9754 + Dox-A2 endopeptidase * component of the regulatory module of the 26S proteasome, homologous to human p58 subunit; Rpn3p(aa) * proteasome (prosome, macropain) 26S subunit, [PCI_DOMAIN // PCI // TPR_REPEAT] CG10484 LD34970 37B12-37B12 dup:3/3 ID:49F9

CG10484 + DNA_binding * 1e-125 hypothetical protein YDR334w - yeast (Saccharomyces cerevisiae) (* 1e-67 iswi protein - fruit fly (Drosophila melanogaster) ISWI p * 2e-67 p [helicase_C // DNA_LIGASE_A1 // MYB_3 //] CG9696 LD35056 57D5-57D8 dup:3/4 ID:49G4

CG9696 + 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 + 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 + unknown * CG5107 GH01257 99B4-99B4 ID:54C4

CG5107 + 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 + 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 GH01326 28C2-28C2 dup:1/3 ID:54C9

CG13796 + 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 + unknown * CG7058 GH01369 17E1-17E1 ID:54D2

CG7058 + 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

CG6959 + defense/immunity_protein * cuticular molt protein precursor(aa) * 2e-29 peptidoglycan recognition protein precursor * 2e-31 TNF superfamily, member (LTB)-like (peptidoglycan r CG8995 GH01554 13F1-13F1 dup:2/2 ID:54E9

CG8995 + * CG10680 38B1-38B1 dup:2/3 ID:54F11

CG10680

CG14942 + enzyme * 2e-07 CN1C_RAT CALCIUM/CALMODULIN-DEPENDENT 3',5'-CYCLIC NUCLEOTIDE PHOSPHODIESTERASE ** [kazal // KAZAL] CG14942 GH01602 33B2-33B2 dup:2/2 ID:54F6

+ unknown * PROTEIN 22A3(aa) * 8e-46 YL22_YEAST HYPOTHETICAL 28.3 KD PROTEIN IN PPR1-SNF7 INTERGENIC REGION * 4e-56 YOM4_CAEEL HYPOTHETICAL 29.1 KD PROTEIN W06E [UPF0023] CG8549 GH01786 66D10-66D10 ID:54G12

CG8549

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

CG5778 + CG5778 GH02030 ID:55A10

CG5588 + Mtl enzyme CG5588 GH01976 ID:55A4

CG18214 + unknown * guanine nucleotide exchange factor UNC-73A(aa) * * CG18214 GH01987 61E2-61E2 dup:1/2 ID:55A5

CG11317 + transcription_factor * [ZINC_FINGER_C2H2 // ZINC_FINGER_C2H2_2] CG11317 GH02265 100B5-100B5 ID:55B5

+ 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

CG3413

+ unknown * 2e-22 YKQ5_YEAST HYPOTHETICAL 105.7 KD PROTEIN IN TPK3-PIR1 INTERGENIC REGION * 6e-36 Mcd4p homolog * 1e-18 hypothetical protein * unknown protein CG6790 GH02677 86E15-86E15 ID:55D6

CG6790

+ Dgp-1 translation_factor * 1e-07 EF1A_YEAST ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) translat * 8e-05 EF11_DROME ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (50 KD FEMALE-SPECIFIC PR [NLS_BP // GTP_EFTU // ATP_GTP_A] CG5729 GH02692 55B9-55B9 dup:2/4 ID:55D7

CG5729

+ Chi DNA_binding * neural src interacting protein, long form; NSIP long form(aa) * Nuclear LIM interactor(aa) * short form of CHIP(aa) * CHIP(aa) [NLS_BP] CG3924 GH02919 60B1-60B1 dup:3/4 ID:55E11

CG3924

+ unknown * molybdenum cofactor biosynthesis protein E isolog(aa) * molybdenum cofactor synthesis 2(aa) * 8e-28 similar to molybdenum cofactor biosynthesis pro CG10238 GH02855 96B20-96B20 dup:2/2 ID:55E4

CG10238

+ unknown * 6e-05 centromere protein E CENTROMERIC * 6e-05 CENP-E protein * CG4714 GH03085 50A1-50A1 ID:55F11

CG4714

+ serpin * THYROXINE-BINDING GLOBULIN PRECURSOR (T4-BINDING GLOBULIN)(aa) * alpha-1-antichymotrypsin precursor(aa) * 8e-42 Similar to serine protease inhibito [serpin] CG9334 GH03095 38E9-38E9 ID:55G1

CG9334

+ tim transcription_factor * TIM_DROME TIMELESS PROTEIN TIM * 3e-16 timeless * 3e-16 UNKNOWN timeless homolog * TIM CG3234 GH03106 23F3-23F5 ID:55G2

CG3234

+ transcription_factor * LTG19 - human(aa) * BLASTX 1.2E-10 Caenorhabditis elegans cosmid ZK354.(dna) * 1e-11 YNK7_YEAST HYPOTHETICAL 26.0 KD PROTEIN IN CYB5-LEU4 INTERGENIC [NLS_BP] CG4913 GH03493 90E1-90E1 dup:1/2 ID:55H10

CG4913

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

CG12106 + unknown * 1e-05 bup=5'of bmi-1 proviral insertion locus Peptide, s * * CG12106 GH03263 8D2-8D2 ID:55H2

CG1844 + unknown * 1E-172 * * CG1844 GH03581 10F4-10F4 ID:56A8

CG9803 + unknown * [PRO_RICH] CG9803 GH03629 59D6-59D6 ID:56B1

CG10706 + ion_channel * calcium-activated potassium channel rSK3(aa) * 2e-52 Weak similarity to potassium channel proteins; cDNA

EST * 3e-41 intermediate conductance potass [CHANNEL_PORE_K] CG10706 GH03729 4F5-4F7 ID:56B10

CG3124 + unknown * CG3124 GH03736 59D4-59D4 ID:56B12

CG9861 + DNA_binding * [NLS_BP] CG9861 GH03827 59D6-59D6 ID:56C11

CG1220 + Kaz1 enzyme_inhibitor * 3e-67 KAZ1-type serine protease inhibitor-like protein type gamma * KAZ1-type serine protease inhibitor-like protein type epsilon * KAZ1-type serine [kazal] CG1220 GH03839 61A6-61A6 dup:2/3 ID:56D1

CG7041 + chromatin_binding HUMAN HETEROCHROMATIN PROTEIN 1 HOMOLOG GAMMA (HP1 BETA) CHROMODOMAIN, CHROMO_1, CHROMO_2, Chromo] CG7041 GH03916 ID:56D7

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

CG3652 + structural_protein * Similarity to Yeast YIP1 protein cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from t CG3652 GH04132 24F1-24F1 dup:2/3 ID:56F4

+ transcription_factor * 7e-10 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * 2e-37 transcription factor YY1 homolog * 1e-14 contains similarity to C2H2-type z[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG3445 67B4-67B4 dup:3/4 ID:56G10

CG3445

CG6541 + Mst33A unknown * [NLS_BP] CG6541 GH04277 33A3-33A3 ID:56G4

CG7896 + cell_adhesion * protein(aa) * DMCONNECTN_1 Con * 4e-18 adenylate cyclase * 1e-25 CAPRICIOUS [LRR // LEURICHRPT // LRRCT] CG7896 GH04292 99D3-99D3 dup:1/2 ID:56G8

CG3918 + NLS_BP, ZF_CCHC CG3918 ID:56H5

CG2017 + unknown * 1e-102 predicted using Genefinder; Weak similarity to elongation factors; * 1e-90 putative G-protein * 3e-90 GTP binding protein putative G-protein [GTP_EFTU // ATP_GTP_A] CG2017 GH04432 83C4-83C4 dup:3/3 ID:56H9

CG5931 + RNA_binding * Putative RNA helicase(aa) * BRR2_YEAST PRE-MRNA SPLICING HELICASE BRR2 hypothetical * 1e-23 mus308 * similar to Helicases conserved C-terminal doma [EF_HAND // HELICASE // DEAD // ATP_GTP_] CG5931 GH04577 72C1-72C1 dup:1/2 ID:57B1

CG4963 + transporter * similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST comes from this gene(aa) * 6e-50 MRS3_YEAST MITOCHONDRIAL RNA SPLICING PROTEIN MRS [mito_carr // MITOCARRIER // MITOCH_CARR] CG4963 GH04641 98B2-98B2 dup:2/2 ID:57B5

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

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

CG18004 + unknown * CG18004 GH04870 47C6-47C6 dup:2/2 ID:57D2

+ 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

CG6069

+ unknown * hypothetical protein - Chinese hamster (fragment)(aa) * DHFR-coamplified protein * hypothetical protein - Chinese hamster (fragment)(aa) * 4e-44 ins [ACTININ_1] CG7231 GH04938 30C1-30C1 dup:2/3 ID:57D8
 CG7231
 CG9686 + unknown * CG9686 GH05060 9A2-9A2 dup:2/2 ID:57E11
 + CaMKI protein_kinase * CaMKI * calcium/calmodulin dependent protein kinase I(aa) * 1e-28 KCC1_YEAST
 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE I * 5e-17 Contains si[PROTEIN_KINASE_ST // TYRKINASE // PROTE] CG1495 GH04968 102B7-102B7 dup:7/7 ID:57E2
 CG1495 + chaperone * DMCYP1_2 Cyp1 * 1e-10 CYPH_YEAST PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) * 1e-14 CYPH_DROME PEPTIDYL-PROLYL CIS-TRANS [pro_isomerase // CSA_PPIASE_2 // ZF_BBO] CG5071 GH04969 96E6-96E6 dup:2/2 ID:57E3
 CG5071 + transporter * WHITE PROTEIN HOMOLOG(aa) * 4e-43 ORF YOL075c * 7e-39 SCRT_DROME SCARLET PROTEIN scarlet protein mel * 4e-37 Similarity to Drosophila white protein[ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG17646 GH05015 22F3-22F3 dup:3/3 ID:57E6
 CG17646
 CG15867 + unknown CG15867 GH05072 ID:57F2
 CG13607 + unknown * CG13607 GH05104 95D10-95D10 ID:57F5
 none + none GH05253 ID:57G7
 + transcription_factor_binding * oxidoreductase(aa) * 3e-20 YULF_BACSU HYPOTHETICAL 36.5 KD PROTEIN IN GBSA-TLPB INTERGENIC REGION * YMO1_RHIME HYPOTHETICAL 36.4 KD PROTEIN IN MOC [GFO_IDH_MocA] CG13280 GH05468 36A9-36A10 dup:2/2 ID:57H11
 CG13280 + Dhc64C motor_protein * DMCYTHA_2 Dhc64C * DYHC_YEAST DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) dynein he * DYHC_DROME DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) dynein h * DYHC_CA [CRYSTALLIN_BETAGAMMA // THIOL_PROTEASE_] CG7507 64C-64C dup:2/3 ID:58B4
 CG7507
 CG9689 + unknown * CG9689 GH05731 9A2-9A2 ID:58B9
 + chaperone * DMHSP60_2 Hsp60 * CHAPERONIN HOMOLOG HSP60 PRECURSOR (HEAT SHOCK PROTEIN 60) (HSP-60)(aa) * MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYT [CHAPERONINS_CPN60 // TCOMPLEXTCP1 // CH] CG2830 GH05807 21D1-21D1 ID:58C8
 CG2830 + 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
 CG2077 + enzyme * 659aa long hypothetical 3-hydroxybutyryl-CoA dehydratase(aa) * PhaB(aa) * 9e-10 YDAK_YEAST HYPOTHETICAL 56.3 KD PROTEIN IN ARO3-KRS1 INTERGENIC REGI [ECH] CG9577 GH06131 19C1-19C1 dup:2/2 ID:58E12
 CG9577 + 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 + cell_adhesion * sdk * DMNRGAA_3 Nrg * fra * 8e-23 LAR_DROME PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (PROTEIN-TYROSINE-PHOSPHAT [ig // FNTYPEIII // fn3] CG8619 GH06134 65E7-65E7 dup:2/2 ID:58F1
 CG8619 + transcription_factor * 6e-06 TF3A_YEAST TRANSCRIPTION FACTOR IIIA (TFIIIA) transcriptio * 2e-11 zinc finger motif protein * 5e-09 similar to Zinc finger, C2H2 typ[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG10631 GH06278 38A2-38A dup:1/3 ID:58G1
 CG10631

CG3380	+ transporter * organic anion transporter-K2(aa) * solute carrier family (prostaglandin transporter), member 2(aa) * SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (O
CG3748	+ unknown * CG3748 GH06504 30B-30B ID:58H11
CG5089	+ unknown * [NLS_BP] CG5089 GH06435 53C8-53C9 dup:2/2 ID:58H4
CG3950	+ DNA_binding * Ser/Arg-related nuclear matrix protein (plenty of prolines 101-like)(aa) * elastic titin(aa) * 1e-11 C. elegans
CG10204	UNC-89 * 8e-07 MAPB_MOUSE MICROTUBU [NLS_BP] CG3950 GH06555 6B1-6B3 ID:59A3
	+ CG10204 102B4-102B5 ID:59A6
CG2727	+ 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
CG7557	+ unknown * [ATP_GTP_A] CG7557 GH07076 68C3-68C3 ID:59C11
CG5467	+ unknown * CG5467 GH07007 97B9-97B9 ID:59C8
CG6761	+ unknown * CG6761 GH07092 67B12-67B12 ID:59D1
	+ transporter * 9e-43 hypothetical protein YLR348c - yeast (Saccharomyces cerevisiae) (U * 1e-74 Oxoglutarate/malate carrier protein - Caenorhabditis elegans * 8e-2 [mito_carr // MITOCARRIER // MITOCH_CARR] CG4323 GH07093 92E7-92E7 ID:59D2
CG4323	
	+ * TRIACYLGLYCEROL LIPASE (LIPASE, PANCREATIC)(aa) * 2e-16 VIT1_DROME VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1) vitell * 2e-19 LIPL_MOUSE LIPOPROTEIN L [lipase] CG10116 73D5-73D5 dup:2/2 ID:59D6
CG10116	
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	
	+ peptidase * alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)(aa) * 8e-98 AAP1_YEAST ALANINE/ARGININE [ALADIPTASE // Peptidase_M1 // HEMOPEXIN] CG11955 GH07390 99A5-99A5 dup:2/3 ID:59F7
CG11955	
none	+ none GH07529 ID:59G6
	+ enzyme * DMADHA1_9 Adh * DMSCU scu * 7e-17 SP19_YEAST SPORULATION PROTEIN SPS19 (SPORULATION-SPECIFIC PROTEIN SPX19) * 4e-05 3-hydroxyacyl-CoA dehydrogenase [CPSASE_2 // adh_short_C2 // GDHRDH // a] CG2907 GH07691 83B6-83B6 ID:59H8
CG2907	
	+ endopeptidase * kuz * a disintegrin and metalloprotease domain (ADAM) 10(aa) * 1e-109 kuzbanian * 1e-102 ADAM similar to [DISINTEGRINS_2 // ADAM_MEPRO // ZINC_PR] CG1964 GH07695 99C1-99C1 ID:59H9
CG1964	
CG8678	+ CG8678 dup:1/2 ID:60A10
CG3092	+ unknown * CG3092 GH07743 59D-59D dup:1/2 ID:60A5
	+ unknown * cDNA EST yk429e10.5 comes from this gene; cDNA EST yk431d3.5 comes * gene e1 protein - mouse * is a human counterpart of mouse e1 gene. * 7e-20 hypo CG14967 GH07785 63C1-64A3 dup:1/3 ID:60A7
CG14967	
CG6332	+ unknown * [NLS_BP] CG6332 GH07879 93F14-93F14 dup:1/2 ID:60B8
CG3151	+ 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
 GH07919 23C1-23C2 dup:1/2 ID:60C1
 + endopeptidase * coded for by C. elegans cDNA CEESC71F; similar to the S25B family of peptidases(aa) *
 PROTEASOME COMPONENT C7-I (MACROPAIN SUBUNIT C7-I) (MULTI[PROTEASOME_B // PROTEASOME_PROTEASE //
] CG17302 GH07971 23A3-23A3 dup:1/3 ID:60C10
 CG17302 + unknown * [DNA_LIGASE_A1] CG11018 GH07940 56E2-56E2 dup:1/2 ID:60C2
 CG11018 + Rpl7 ribosomal_protein RL7_DROME 60S RIBOSOMAL PROTEIN L7 CG4897 Ribosomal_L30, THIOL_PROTEASE_HIS
 CG4897 ID:60C3
 CG9338 + unknown * CG9338 GH07967 38F1-38F1 dup:1/2 ID:60C9
 + Cpn ligand_binding_or_carrier * 1e-128 CPN_DROME CALPHOTIN calcium-binding protein calphotin - f * 1e-129 calphotin -
 CG4795 Drosophila calphotin * 1e-131 binding or carrier, G * DMCLPTN_6 CG4795 GH08002 87B4-87B4 dup:1/2 ID:60D1
 + unknown * 7e-30 weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase * 1e-58 CGI-16 protein * 6e-27
 CG1774 hypothetical protein * contains weak simil CG1774 GH08048 100D2-100D2 dup:2/3 ID:60D2
 + cell_adhesion * DMLACH_2 Lac * 1e-09 LACH_DROME LACHESIN PRECURSOR lachesin melanoga * 5e-06 hemicentin
 CG5308 precursor * 4e-05 elastic titin [ig] CG5308 GH08163 86E9-86E10 dup:2/3 ID:60D7
 + endopeptidase * 3e-11 TBP6_YEAST PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG 6) * 3e-
 08 MEI1_CAEEL MEIOTIC SPINDLE FORMATION PROTEIN MEI-1 mei-1 * 0.000 CG14183 GH08353 76E3-76E4 dup:3/3
 CG14183 ID:60E12
 CG18380 + unknown * CG18380 GH08307 47A-47A dup:2/2 ID:60E5
 + enzyme * SUCCINYL-COA SYNTHETASE ALPHA CHAIN (SCS-ALPHA)(aa) * DMSUCCOAA Scs agr; * 9e-77
 SUCA_YEAST PROBABLE SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN [SUCCINYL_COA_LIG_2 // ligase-CoA
 CG6255 // SUC] CG6255 GH08383 92A6-92A6 dup:2/4 ID:60F3
 CG7669 + unknown * [NLS_BP] CG7669 GH08407 91A-91A dup:1/2 ID:60F7
 CG11656 + unknown * CG11656 GH08448 87D9-87D9 dup:1/2 ID:60F9
 + cytoskeletal_structural_protein * Similarity to some phosphatases and kinases; cDNA EST comes from this gene(aa) * 2e-
 87 Similarity to some phosphatases and kinases; cDNA ES[PX // RA_DOMAIN // BEM_DOMAIN] CG3138 GH08671 5B2-5B2
 CG3138 dup:1/2 ID:60G12
 CG14830 + * 1E-102* * CG14830 65E10-65E10 dup:2/3 ID:60H4
 CG9445 + unknown * CG9445 42C7-42C7 dup:3/3 ID:61B11
 CG13432 + unknown CG13432 GH08941 dup:1/2 ID:61B12
 + sif signal_transduction (still life) Guanine-nucleotide dissociation stimulators CDC24 family signatur GRF_DBL, NLS_BP,
 CG5406 PDZ, PH_DOMAIN, PRO_RIC] CG5406 GH08923 dup:1/2 ID:61B8
 CG18404 + unknown * CG18404 GH09039 99E5-99E5 dup:1/2 ID:61C7
 CG6304 + unknown * [NLS_BP] CG6304 GH09088 36A14-36A14 dup:2/3 ID:61D2
 CG8508 + unknown * CG8508 GH09161 87E2-87E2 dup:1/2 ID:61D9
 CG4653 + endopeptidase * TRYPSIN DELTA PRECURSOR(aa) * Ser12 * Ser6 * Dvtry-1 trypsin precursor(aa) [trypsin //

CHYMOTRYPSIN // TRYPSIN_HIS] CG4653 GH09333 15A1-15A1 ID:61F1

CG8919 + unknown * coded for by C. elegans cDNA cm16h1; coded for by C. elegans cDNA yk13a7.5; coded for by C. elegans cDNA yk13a7.3; similar to S. cerevisiae SAC3 pro [RBD] CG8919 GH09410 15E1-15E1 dup:2/3 ID:61F10

+ enzyme * DMCATHPO_2 Cat * CATALASE(aa) * 1e-110 CATA_YEAST CATALASE A catalase (EC 1.11.1.6), peroxisomal - * 1e-158 catalase (EC 1.11.1.6) - Caenorhabditis [CATALASE // catalase // CATALASE_1] CG9314 GH09387 29E4-29E4 dup:1/2 ID:61F8

CG9314 + BG:DS04095.1 unknown * CG4891 GH09478 35F1-35F1 dup:1/2 ID:61G1

CG4891 + nAcRalpha-96Ab ion_channel * DMARD1_2 nAcR bgr;-64B * DMNARAS nAcR bgr;-96A * DMDA2_2 nAcR agr;-96Ab * ACH2_DROME ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-LIKE CHAIN PRECU[NICOTINICR // neur_chan // NEUROTR_ION_] CG6844 GH09582 96A2-96A2 dup:1/3 ID:61G11

CG6844 + SP2353 cell_adhesion agrin-like ATP_GTP_A, EGF, EGF_1, EGF_2, LAM_G_DOMA] CG8403 GH09608 dup:1/3 ID:61G12

CG8403 + enzyme * 7e-62 SYWM_YEAST TRYPTOPHANYL-TRNA SYNTHETASE, MITOCHONDRIAL (TRYPTOPHAN--TRNA LIGASE) * 1e-60 SYWM_CAEEL PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE, MIT [TRNASYNTHTRP // tRNA-synt_1b // AA_TRNA] CG7441 GH09538 75A4-75A4 dup:1/3 ID:61G8

CG7441 + unknown * [NLS_BP] CG9312 GH09754 87F13-87F13 dup:1/2 ID:61H8

CG9312 + 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 ID:62A7

CG10327 + unknown * [NLS_BP] CG11074 GH09884 42F2-42F2 ID:62A8

CG11074 + unknown * [PRO_RICH // NLS_BP] CG2467 GH09980 10F7-10F8 dup:2/2 ID:62B5

CG2467 + unknown * similar to human 5'-nucleotidase * cytosolic IMP-GMP specific 5'-nucleotidase(aa) * CYTOSOLIC PURINE 5'-NUCLEOTIDASE(aa) * 1e-145 similar to human 5 [NLS_BP] CG6247 GH10029 17A11-17A11 ID:62B8

CG6247 + unknown * similar to several putative T1/ST2receptor binding protein precursors(aa) * 3e-14 EM24_YEAST ENDOSOMAL P24B PROTEIN PRECURSOR (24 KD ENDOMEMBRANE P [EMP24_GP25L] CG9308 GH10235 58B9-58B9 ID:62C9

CG9308 + chaperone * 5e-06 YB05_YEAST HYPOTHETICAL 44.1 KD PROTEIN IN RPB5-CDC28 INTERGENIC REGION * 1e-10 Hsp70/Hsp90 organizing protein homolog * 1e-08 coded for by C. [TPR_REGION] CG6980 GH10293 98E1-98E1 ID:62D2

CG6980 + unknown * CG6130 GH10346 90E4-90E4 ID:62D6

CG6130 + motor_protein * 2e-05 cellular myosin heavy chain * 8e-07 myosin heavy chain, neuronal - rat * 1e-05 Klp68D * myosin heavy chain IIb CG4681 GH10544 60D6-60D6 dup:2/2 ID:62E11

CG4681 + ligand_binding_or_carrier * 1e-22 YBE9_YEAST HYPOTHETICAL 16.1 KD PROTEIN IN SEC17-QCR1 INTERGENIC REGION * 8e-21 putative zinc-binding protein melanogaste * 1e-18 No definitio CG15309 GH10478 9B6-9B6 dup:2/2 ID:62E4

CG15309 + unknown * CG11191 GH10486 43F9-43F9 dup:2/2 ID:62E6

CG11191 + tafazzin unknown * 2e-17 hypothetical protein YPR140w - yeast (Saccharomyces cerevisiae) (* 4e-39 ZK809.2 * 1e-59 tafazzin TAFAZZIN * 2e-40 Similar to tafazzins prote [GLYCEROL_ACYLTRANS // TAFAZZIN] CG8766 GH10529 49C1-49C1 dup:2/2 ID:62E9

CG8766 + enzyme * DMHISSEAC_3 Rpd3 * histone deacetylase mHDA1(aa) * histone deacetylase HDA2(aa) * histone deacetylase,

CG1770

shares sequence similarity with Rpd3p, Hos1p [LECTIN_LEGUME_BETA // Hist_deacetyl] CG1770 GH10588 11E1-11E3 dup:1/3 ID:62F3

CG10577 + signal_transduction * protein(aa) * 1e-31 Sec7p * 2e-76 similar to S. cerevisiae protein transport protein SEC7 * 1e-38 cytohesin [SEC7 // Sec7 // NLS_BP] CG10577 GH10594 78B1-78B1 dup:1/2 ID:62F7

CG10742 + unknown * 1e-36 predicted using Genefinder; Similarity to Human leukocyte surface * 7e-22 CD63_MOUSE CD63 ANTIGEN CD63/ME491 antigen homolog - mou * 3e-44 tet [transmembrane4 // TMFOUR // TM4_2] CG10742 GH10778 3A9-3A9 dup:1/2 ID:62G10

CG3544 + metabolism * xylulokinase (H. influenzae) homolog(aa) * xylulose kinase(aa) * xylulokinase(aa) * HYPOTHETICAL 60.3 KD PROTEIN R08D7.7 IN CHROMOSOME III(aa) [FGGY] CG3544 GH10780 21E1-21E1 ID:62G11

CG2666 + enzyme * similar to chitin synthases(aa) * 9e-13 CHS3_YEAST CHITIN SYNTHASE (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 3) * 8e-06 hyaluronan synthase * 8e- CG2666 GH10726 83A5-83A5 ID:62G3

CG4462 + transporter * 1e-21 putative organic cation transporter * 1e-08 similar to C. elegans protein and to rat synaptic vesicle protein (PIR:S3 * 3e-14 organic cation t CG4462 GH10729 92B9-92B10 ID:62G4

CG10374 + chaperone * 6e-06 cargo selection protein TIP47 * placental protein 17b1; PP17b1 * adipose differentiation-related protein * 2e-06 cargo selection protein TIP47 [NLS_BP] CG10374 GH10767 95B8-95B9 ID:62G9

CG17564 + unknown * 7E-86* * CG17564 GH10882 37D3-37D3 ID:62H12

CG5125 + ninaC motor_protein * DMNINAC_2 ninaC * ligand binding or carrier calmodulin binding) protein kinase protein serine/threonine kinase) cell non-muscle myosin) map_posit [myosin_head // PROTEIN_KINASE_TYR // IQ] CG5125 GH10824 27F5-27F6 ID:62H5

CG16868 + unknown * 6e-05 transducer * 6e-05 chemotactic transducer * [VWA_DOMAIN] CG16868 GH11109 56F16-56F16 dup:1/2 ID:63B9

CG14630 + unknown * 2e-15 YHC1_YEAST HYPOTHETICAL 53.1 KD PROTEIN IN SPO11-OPI1 INTERGENIC REGION * 1e-44 similar to gamma-butyrobetaine,2-oxoglutarate dioxygenase; cDN CG14630 GH11273 1E1-1E1 ID:63C11

CG11390 + PebIII ligand_binding_or_carrier * PebIII * 2e-48 ejaculatory bulb specific protein III * 2e-31 chemosensory protein CSP-sg1 * olfactory protein CG11390 GH11257 60B1-60B1 ID:63C9

CG17119 + unknown * 1e-16 ERS1_YEAST TRANSMEMBRANE PROTEIN ERS1 (ERD SUPPRESSOR) ER * 6e-39 similarity to the transmembranous domains of yeast ERS1 protein; c * 5e-76 c [TONB_DEPENDENT_REC_1] CG17119 GH11342 94D12-94D12 ID:63D3

CG18418 + unknown * CG18418 GH11346 65A10-65A10 ID:63D4

CG11352 + jim transcription_factor * stripe a/b protein - fruit fly (Drosophila melanogaster)(aa) * zinc finger protein/embryonic muscle development-related transcriptional re[ZINC_FINGER_C2H2 // zf-C2H2 // ZINC_FIN] CG11352 GH11419 79F3-79F3 dup:3/3 ID:63D8

CG6441 + unknown * CG6441 GH11511 28A1-28A1 dup:2/2 ID:63E3

CG12638 + CG12638 GH11525 dup:2/2 ID:63E7

CG7794 + cytoskeletal_structural_protein * DMTUBA1_2 agr;Tub84B * 1e-117 TBA1_YEAST TUBULIN ALPHA-1 CHAIN tubulin alpha-1 chain * 1e-132 TBA1_DROME TUBULIN ALPHA-1 CHAIN tubulin alpha-1 chain [tubulin] CG7794 GH11574 90D2-90D2 ID:63F2

CG3306 + unknown * CG3306 GH11578 67B9-67B9 ID:63F3

CG1324 + unknown * [ATP_GTP_A] CG1324 GH11587 19E3-19E3 ID:63F6

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

+ RNA_binding * putative RNA-binding protein(aa) * Wbscr1(aa) * 7e-05 NSR1_YEAST NUCLEAR LOCALIZATION
SEQUENCE BINDING PROTEIN (P67) * 2e-13 RNA recognition motif-t [RNP_1 // RBD // rrm // NLS_BP] CG1340 GH11731

CG1340 100A-100A dup:2/2 ID:63G10

+ motor_protein * 3e-08 hook1 protein * p230 peripheral membrane pr * autoantigen, subfamily a, > * CG14039 GH11749

CG14039 25C3-25C3 dup:1/4 ID:63G11

+ Sin3A transcription_factor * 3e-58 SIN3_YEAST PAIRED AMPHIPATHIC HELIX PROTEIN regulatory * transcription factor *
2e-31 cDNA EST comes from this gene; cDNA EST co * 1e-135 co-r [ATPASE_ALPHA_BETA // NLS_BP] CG8815 GH11769

CG8815 49B2-49B3 dup:1/2 ID:63G12

CG14355 + unknown * CG14355 GH11706 88A12-88B1 ID:63G5

CG11404 + unknown * CG11404 GH11730 79E-79E ID:63G9

CG10286 + unknown * CG10286 GH12023 83E6-83E6 dup:1/2 ID:64A12

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

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

CG3541 DMDUSKY_1 dy * similar to cuticlin CG3541 GH12163 60D7-60D8 dup:1/2 ID:64C4

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

CG15560 tectorin * 2e-16 tectorin alpha alpha-tectorin * 1e-15 alpha CG15560 GH12365 100B8-100B8 ID:64D8

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

+ 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 GH12627 79F3-79F3 ID:64F10

CG11146 + signal_transduction Shb=Src homology 2 protein ANTIFREEZE1, SH2 CG11146 ID:64F5

+ 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

CG3982 + unknown * CG3982 GH12755 67B3-67B3 dup:2/2 ID:64G10

+ 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 + endopeptidase * DMEAST_4 ea * serine proteinase(aa) * 1e-09 easter * 5e-07 anticoagulant protein C [trypsin //
TRYPSIN_CATAL] CG17837 GH12831 92F5-92F5 dup:2/2 ID:64H6

CG17837 + protein_phosphatase * DMPP1A1_2 Pp1 agr;-96A * serine-threonine protein phosphatase(aa) * type 1-related protein
phosphatase(aa) * 1e-110 PP12_YEAST SERINE/THREONINE PR[PHOSPHO_ESTER // STPHPTASE // SER_THR_] CG10138

CG10138 phosphatase(aa) * 1e-110 PP12_YEAST SERINE/THREONINE PR[PHOSPHO_ESTER // STPHPTASE // SER_THR_] CG10138

CG10138 GH12873 58B9-58B9 ID:65A1

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

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

+ protein_kinase * 5e-06 DRK_DROME PROTEIN E(SEV)2B (SH2-SH3 ADAPTOR PROTEIN DRK) * 1e-05 SEM5_CAEEL
SEX MUSCLE ABNORMAL PROTEIN sem-5 protein - * 9e-12 stac * 6e-13 s [SH3] CG8179 GH12942 52A2-52A4 dup:1/2
ID:65A6

CG8179

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

+ DNA_binding * putative chromatin structure regulator(aa) * HYPOTHETICAL PROTEIN IN REGION E(aa) * TEX
CG5253 PROTEIN(aa) * similar to hypothetical proteins(aa) [NLS_BP] CG5253 GH13080 94B10-94B11 ID:65B8

+ transcription_factor * Pcaf SPTR(aa) * CREB-BINDING PROTEIN(aa) * HAT A1(aa) * 5.9 kb fsh membrane protein(aa)
CG7229 [BROMODOMAIN_2 // BROMODOMAIN_1 // bromo] CG7229 GH13144 56C-56C ID:65C2

+ unknown * FLAGELLAR RADIAL SPOKE PROTEIN 4(aa) * radial spokehead(aa) * 9e-13 predicted using Genefinder;
CG3121 similar to Sugar transporter; cDNA EST * 5e-55 radia [ER_TARGET] CG3121 GH13165 60A16-60A16 dup:1/2 ID:65C3

CG2209 + unknown * CG2209 GH13175 11D3-11D3 ID:65C5

+ 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

CG3483

+ enzyme * 2e-20 alpha-alpha-trehalase * 1e-102 similar to family glycosyl hydrolases; most similar to trehalase * 1e-124
TREHA_HUMAN TREHALASE PRECURSOR (ALPHA [Trehalase // TREHALASE_1 // GLHYDRLASE3] CG9364 GH13461
57B20-57C dup:4/4 ID:65D10

CG9364

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

CG6903 + unknown * CG6903 GH13389 4D1-4D1 ID:65D4

+ unknown * conserved protein(aa) * 1e-133 YP65_CAEEL HYPOTHETICAL 81.5 KD PROTEIN IN CHROMOSOME II (U2
* 1e-125 YYAL_BACSU HYPOTHETICAL 78.8 KD PROTEIN IN TET [CARBOXYPEPT_ZN_2] CG8613 GH13403 50F6-50F6
ID:65D5

CG8613

+ RpP2 ribosomal_protein * DMRP21C_2 RpP2 * 60S ACIDIC RIBOSOMAL PROTEIN P1 (RP21C) (ACIDIC RIBOSOMAL
PROTEIN RPA2)(aa) * 5e-14 acidic ribosomal protein P1.e.A, cytosolic - ye [60s_ribosomal // RIBOSOMALP2] CG4087 GH13422
21C2-21C2 dup:3/3 ID:65D7

CG4087

+ enzyme * 1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (P5C DEHYDROGENASE)(aa) * UNKNOWN(aa) *
Similar to aldehyde dehydrogenase; coded for by C. elegans cDNA cm1 [aldehy // NLS_BP] CG6670 GH13449 93F-93F10
dup:2/2 ID:65D9

CG6670

+ enzyme * peritrophin-95 precursor(aa) * 4e-29 triacylglycerol lipase (EC 3.1.1.3) precursor, pancreatic - mouse * 2e-29
lipase * 7e-31 pdb[1BU8] Rat Pancrea [DOLALLERGEN // TAGLIPASE // ESTERASE //] CG6296 100D1-100D1 dup:2/2 ID:65E4

CG6296

CG18227 + CG18227 dup:2/2 ID:65E6

CG1314 + unknown * CG1314 GH13802 19E4-19E4 ID:65F10

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
CG5198	+ unknown * SMC2orf(aa) * CD2 antigen (cytoplasmic tail)-binding protein 2(aa) * 1e-08 YHV6_YEAST HYPOTHETICAL 40.4 KD PROTEIN IN SPO16-REC104 INTERGENIC REGIO CG5198 GH13760 33D1-33D1 ID:65F7
CG6676	+ cell_adhesion * coded for by C. elegans cDNA yk9a2.5; coded for by C. elegans cDNA yk9a2.3; similar to fibrinogen-like protein A precursor(aa) * 3(aa) * FIBRINOGEN [FIBRIN_AG_C_DOMAIN // fibrinogen_C] CG6676 GH13859 58C2-58C2 ID:65G3
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
CG3372	+ unknown * CG3372 GH14065 60C1-60C1 ID:65H8
CG3184	+ chaperone * hypothetical protein(aa) * 3e-22 YB96_YEAST HYPOTHETICAL 43.3 KD PROTEIN IN ALG7-ENP1 INTERGENIC REGION * WD-40 repeat protein * [WD40_REGION // WD40] CG3184 GH14157 6C7-6C7 ID:66A12
CG8043	+ DNA_binding * component of CCR4 transcriptional complex; Caf17p(aa) * putative protein(aa) * Similarity to S.pombe hypothetical protein C21E11.07 (SW:YAL7_SCHPO CG8043 GH14121 85B-85B ID:66A7
CG4416	+ transcription_factor ZINC_FINGER_C2H2, ZINC_FINGER_C2H2_2, zf] CG4416 GH14307 dup:2/3 ID:66B10
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
none - noe gene	+ noe none - noe gene GH14418 ID:66C11
CG3090	+ Sox14 DNA_binding * DMDSOX14 Sox14 * putative(aa) * POP-1 PROTEIN(aa) * SOX-2(aa) [HMG // HMG_box // NLS_BP] CG3090 GH14320 60A14-60A14 dup:1/3 ID:66C2
CG10097	+ Brassica napus 'male sterility protein 2' EMBL:X99922 CG10097 ID:66C5
CG11871	+ unknown * CG11871 GH14385 86A1-86A1 ID:66C8
CG17919	+ ligand_binding_or_carrier * 5e-13 DKA1_YEAST DKA1 PROTEIN (NSP1 PROTEIN) (TFS1 PROTEIN) DKA * 3e-44 OBA5_DROME PUTATIVE ODORANT-BINDING PROTEIN A5 PRECURSOR (ANTENNAL PROTEIN 5 [PBP] CG17919 GH14494 83E-83E ID:66D10
CG8909	+ receptor * LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (LDL RECEPTOR 1)(aa) * low density lipoprotein receptor-related protein 7(aa) * LDL receptor member LR3(a [LDLRA_2 // LDLRECEPTOR // EGF // EGF_2] CG8909 GH14506 13F10-13F12 ID:66D12
none	+ none GH14469 ID:66D6
CG4810	+ translation_factor * HYPOTHETICAL 64.2 KD PROTEIN R08D7.3 IN CHROMOSOME III(aa) * UNKNOWN(aa) * eIF3 p66(aa) * 9e-98 putative elongation initiation factor subunit CG4810 GH14470 87B5-87B5 ID:66D7
CG3565	+ enzyme_activator * 2e-40 inserted at base Both 5' and 3' ends of P element Inverse PCR * * [EF_HAND_2] CG3565 GH14476 60D8-60D8 ID:66D8
CG8332	+ CG8332 dup:3/5 ID:66D9
CG16791	+ unknown * 2e-24 cDNA EST CEMSE83F comes from this gene; cDNA EST comes * * CG16791 GH14545 93D6-93D6

dup:3/3 ID:66E5

CG6265 + endopeptidase * phosphate regulator(aa) * endothelin converting enzyme, ECE=putative zinc-binding metalloprotease aortic endothelial cells, Peptide, * Similarity t CG6265 GH14576 97E2-97E3 dup:2/2 ID:66E8

+ endopeptidase * similar to the M13 or zinc metalloprotease family of peptidases(aa) * endothelin converting enzyme 1(aa) * endothelin converting enzyme-2 - bovine [CNMP_BINDING_2 // NEPRILYSIN // PRENYLA] CG9507 GH14621 28D1-28D1 ID:66F3

CG9507

CG1394 + unknown * CG1394 GH14622 10A11-10A11 ID:66F4

+ cell_adhesion * 4e-06 UNC-89 * 6e-05 VGR2_MOUSE VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR PRECURSOR (VEGFR-2) (PR * 1e-05 protein tyrosine phosphatase, receptor t [ig] CG7607 GH14648 68A8-68A8 ID:66F6

CG7607 + 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

CG3427

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

+ enzyme * 2e-15 FOX2_YEAST PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL * 4e-14 3-hydroxyacyl-CoA dehydrogenase type II * 3e-42 strong [GDHRDH // adh_short] CG3603 GH14791 3C5-3C5 ID:66G11

CG3603 + enzyme * Ac76E * type VIII adenylyl cyclase - human(aa) * Ac35C * ADENYLATE CYCLASE, TYPE VIII (ATP PYROPHOSPHATE-LYASE) (CA(2+)/CALMODULIN ACTIVATED ADENYLY [guanylate_cyc // GUANYLATE_CYCLASES_2] CG5983 GH14744 36A2-36A2 ID:66G6

CG5983

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

+ transcription_factor * ZINC-FINGER PROTEIN (ZINC-FINGER HOMEODOMAIN PROTEIN 1)(aa) * DMDROSOPH_4 wdn * transcriptional repressor(aa) * DMBTDGN_2 btd [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG8591 GH14774 65F4-65F4 ID:66G9

CG8591

CG9137 + unknown * CG9137 GH14903 61F4-61F4 ID:66H10

CG9137

CG18314 + unknown * CG18314 GH14918 64B9-64B9 dup:1/3 ID:66H11

CG18314

CG18369 + unknown * CG18369 GH15231 50B9-50B9 ID:67C11

+ endopeptidase * cathepsin L-like protease precursor(aa) * cysteine proteinase 1(aa) * cathepsin H(aa) * Cp1 [PAPAIN // Peptidase_C1 // THIOL_PROTEAS] CG11459 GH15170 83E1-83E1 ID:67C4

CG11459

CG4232 + CG4232 58F2-58F2 dup:1/2 ID:67D1

+ 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

CG7626 + And ligand_binding_or_carrier * similar to calmodulin-like protein.(aa) * Homo sapiens(aa) * CALMODULIN(aa) * Eip63F-1 [efhand // EF_HAND_2] CG17769 GH15245 99D1-99D1 ID:67D2

CG17769

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

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

CG15848

CG18437 + unknown * CG18437 GH15426 98A6-98A6 dup:2/2 ID:67E2
+ enzyme * 1e-12 FOX2_YEAST PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE)
(MULTIFUNCTIONAL * 0.000000000000002* 2e-26 predicted using Genefinder; Similar [GDHRDH // adh_short // ADH_SHORT]

CG17121 CG17121 GH15451 94D12-94D12 dup:2/2 ID:67E8
+ transcription_factor * ash1 * polybromo protein - chicken(aa) * DMFSA_2 fs(1)h * similar to HMG (high mobility group)
box, Bromodomain (5 domains), Zinc finger, C2H2 [BROMODOMAIN_2 // BAH // HMG // HMG_box] CG11375 98E1-98E1
dup:1/2 ID:67G4

CG11375 + motor_protein * 6e-31 tektin * 3e-54 testicular tektin B1-like protein * 4e-52 tektin B1 * tektin A1 - sea urchin
(Strongylocentrotus purpuratus) [TEKTIN] CG3085 GH15825 59C3-59C3 dup:2/4 ID:68A12

CG3085 + ligand_binding_or_carrier * antennal binding protein X(aa) * Pbprp1 * 3e-06 PBP1_DROME PHEROMONE-BINDING
CG8462 PROTEIN-RELATED PROTEIN PRECURSOR (PBPRP-1) * 4e-08 Pbprp1 [PBP_GOBP] CG8462 GH15777 56E5-56E5 ID:68A5
+ 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-
CG5443 97B2 ID:68B3

CG14891 + unknown * CG14891 GH16156 92A1-92A1 ID:68C12
+ 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 CG4550 92B8-92B9 dup:1/5 ID:68C2

CG14477 + unknown * CG14477 54B16-54B17 ID:68C6
+ transporter * K05B2.5 gene product(aa) * 1e-13 YKW1_YEAST HYPOTHETICAL 52.3 KD PROTEIN IN FRE2 5'REGION *
CG8468 2e-82 /match=(desc; /ma * 1e-40 predicted using Genefin CG8468 GH16148 50E-50E7 dup:2/5 ID:68C9

CG17349 + unknown * E04F6.2 gene product(aa) * 1E-130* CG17349 GH16267 37D6-37D7 ID:68D11
+ Ace enzyme * DMACHE_5 Ace * cell growth and maintenance acetylcholine catabolism) cell growth and maintenance
carbamate resistance) cell growth and maintenance [CHOLNESTRASE // ESTERASE // COesterase] CG17907 GH16177 87E3-
CG17907 87E3 dup:2/2 ID:68D2
+ protein_kinase * protein kinase C, mu(aa) * DMPKC98F_2 Pkc98E * protein kinase C, mu(aa) * 6e-42 DUN1_YEAST DNA
DAMAGE RESPONSE PROTEIN KINASE DUN1 protei [DAG_PE_BINDING_DOMAIN // PROTEIN_KINASE] CG7125 GH16373
CG7125 90F8-90F9 dup:3/3 ID:68E7
+ * 3e-30 No definition line found * 5e-48 SCF complex protein Skp2 * 1e-42 S-phase kinase-associated protein (p45) cyclin
CG9772 A/CDK2-associate * YKK7_CAEE FBOX_DOMAIN CG9772 ID:68F1

CG12191 + cell_adhesion * 8e-05 adhesion molecule L1.1 * [ig] CG12191 GH16485 61D4-61D4 ID:68F12
+ BG:DS02252.2 cytoskeletal_structural_protein * 2e-48 tektin * 2e-34 testicular tektin B1-like protein * 3e-59 tektin A1 - sea
CG4767 urchin (Strongylocentrotus purpuratus) * tektin C1 [TEKTIN] CG4767 GH16413 35E-35E ID:68F2
+ signal_transduction * (putative) small GTPase, similar to Gtr1; Gtr2p(aa) * yeast gtr2 homolog, novel small GTPase
subfamily protein(aa) * homologous to the yeast YGR163 [CRYSTALLIN_BETAGAMMA // ATP_GTP_A] CG8707 GH16429 44B-
CG8707 44B ID:68F3

CG4759	+ * ribosomal protein L27 homolog(aa) * 7e-26 RL27_YEAST PROBABLE 60S RIBOSOMAL PROTEIN L27 ribosomal p * 5e-27 RL27_CAEEL 60S RIBOSOMAL PROTEIN L27 rib [RIBOSOMAL_L27E // NLS_BP] CG4759 96E10-96E10 dup:2/2 ID:68F8
CG2088	+ BcDNA:GH02712 motor_protein * BLASTX 8.9E-08 YOL155C Protein with similarity to S. cerevisiae glucan 1,4-alpha-glucosidase(dna) * BLASTX 2.5E-06 P.falciparum interspersed repeat [PRO_RICH] CG2088 GH16490 43E5-43E6 dup:1/3 ID:68G1
CG4067	+ 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 GH16587 86C2-86C2 dup:2/2 ID:68G5
none	+ none GH16763 ID:68H11
CG10426	+ enzyme * pharbin(aa) * 7e-35 YNK6_YEAST HYPOTHETICAL 133.3 KD PROTEIN IN CYB5-LEU4 INTERGENIC REGION * 2e-31 /match=(desc;; /ma * 4e-17 similar to Inositol p [IPPC // PRENYLATION] CG10426 GH16681 69A3-69A3 ID:68H4
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
CG8278	+ enzyme * 1e-05 cyclophilin Dicyp-2 * * [PRENYLATION] CG8278 GH17930 44F2-44F2 ID:70A2
CG4983	+ DNA_repair_protein * CG4983 GH17939 33A5-33A5 ID:70A4
CG9363	+ enzyme * MALEYLACETOACETATE ISOMERASE (MAAI)(aa) * glutathione transferase zeta 1(aa) * 6e-50 similar to glutathione S-transferase * 3e-05 GTC_MOUSE GLUTATHI [GST] CG9363 GH17960 85D18-85D18 ID:70A5
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
CG3492	+ chaperone * [CSA_PPIASE_2 // PRENYLATION] CG3492 GH18016 60D2-60D2 ID:70B2
CG18403	+ very low density lipoprotein receptor - mouse CG18403 ID:70B7
CG6614	+ unknown * [TPR_REGION // NLS_BP // ATP_GTP_A] CG6614 GH18077 33A5-33A5 ID:70C2
CG18033	+ msta unknown * /match=(desc:(aa) * map_position:2E3 * 7e-06 t-BOP * 5e-13 putative Bop-like zinc finger protein CG18033 GH18166 2E2-2E2 dup:2/2 ID:70D4
CG15097	+ actin_binding * protein(aa) * Similarity to Drosophila ring canal protein cDNA EST comes from this gene; cDNA EST comes from this gene(aa) * 1e-116 kelch protein, I [BTB // KELCHREPEAT // Kelch] CG15097 GH18278 55F2-55F3 dup:2/2 ID:70E1
CG4384	+ defense/immunity_protein * 3e-13 peptidoglycan recognition protein precursor * 4e-17 TNF superfamily, member (LTB)-like (peptidoglycan recognition * 8e-17 cuticular molt prote CG4384 67A8-67A8 dup:3/3 ID:70E2
CG18568	+ unknown * CG18568 GH18325 50C21-50C21 dup:2/2 ID:70E3
CG5835	+ unknown * CG5835 GH18370 91F4-91F4 dup:2/2 ID:70E9
CG6882	+ unknown * CG6882 GH18452 65A3-65A3 ID:70F7
CG8838	+ unknown * [NLS_BP // ATP_GTP_A] CG8838 GH18521 25A1-25A1 ID:70G2
CG10143	+ enzyme * secretory component(aa) * mollusk-derived growth factor; MDGF * AGSA_APLCA ATRIAL GLAND-SPECIFIC

ANTIGEN PRECURSOR (AGSA) * [NLS_BP // A_deaminase] CG10143 GH18530 51B10-51B10 ID:70G4

CG12022 + unknown * CG12022 GH18574 62E1-62E1 ID:70G8

CG3342 + unknown * 1e-05 protein ** CG3342 GH18625 6A4-6A4 ID:70H2

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

+ unknown * T03G11.3 gene product(aa) * CGI-62 protein(aa) * 1e-16 T03G11.3 gene product * CG10999 GH18838 83C3-83C3 dup:1/2 ID:71A3

CG10999

CG16783 + signal_transduction fizzy-related protein FIZZY_DOMAIN, WD40 CG16783 ID:71B5

+ 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 31D5-31D6 dup:2/2 ID:71B8

CG5390

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

+ unknown * 5e-05 unknown * 6e-16 unknown protein * YDOC_SCHPO HYPOTHETICAL 13.4 KD PROTEIN C15A10.12C

CG9067 IN CHROMOSOME I * CG9067 GH19135 47E3-47E3 ID:71C7

+ cell_adhesion * 7e-06 NTRI_RAT NEUOTRIMIN PRECURSOR (GP65) neurotrimin - rat * * [ig] CG10946 GH19181

CG10946 7C8-7C8 ID:71D1

+ transporter * mitochondrial carrier protein-like; similar to * 4e-13 probable membrane protein YPR011c - yeast

CG2616 (Saccharomyces cerevisiae) * 6e-11 colt * 3e-61 YQ [mito_carr // MITOCH_CARRIER] CG2616 GH19222 84D10-84D10 ID:71D5

+ 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

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

+ peptidase * 1e-34 YHT2_YEAST HYPOTHETICAL 49.8 KD PROTEIN IN ACT3-YCK1 INTERGENIC REGION

PRECURSOR * 3e-44 similar to zinc carboxypeptidases (Pfam: Zn_carbOpept [CARBOXYPEPT_ZN_1 // CRBOXYPTASEA //

Zn_] CG12374 GH19395 49C2-49C2 dup:2/2 ID:71E6

CG12374

+ protein_phosphatase * enolase-phosphatase E-1(aa) * Similarity to klebsiella oxytoca E-1 enzyme (TREMBL ID * 1e-24

UTR4_YEAST UTR4 PROTEIN (UNKNOWN TRANSCRIPT PROTEIN) U [Hydrolase // HADHALOGNASE] CG12173 GH19505

CG12173 83A1-83A1 ID:71F4

+ 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

CG2854 + unknown * CG2854 GH19593 2F4-2F4 ID:71G3

+ 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

CG1744

+ unknown * 1e-24 YLS5_CAEEL HYPOTHETICAL 55.1 KD PROTEIN F09G8.5 IN CHROMOSOME III * 2e-25 c21ORF-

CG15208 HumF09G8.5 * 5e-08 outer arm dynein light chain reinhar * 2e- CG15208 GH19655 9F12-9F12 ID:71G8

CG14408 + unknown * 2e-22 similarity to C. elegans protein C01C10.4 * 1e-36 SH3-domain binding protein * 1e-36 SH3 binding

protein SH3 binding protein sapien * YKL4_CA CG14408 GH19670 12F7-13A1 ID:71G9
 + enzyme * citrate synthase(aa) * CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR(aa) * PROBABLE CITRATE
 SYNTHASE, MITOCHONDRIAL PRECURSOR(aa) * citrate synthase. Nu [citrate_synt // CITRATE_SYNTHASE // CIT] CG14740
 CG14740 GH19789 87B1-87B1 ID:71H12
 CG2998 + ribosomal_protein Ribosomal protein S28B Ribosomal_S28e CG2998 ID:72A2
 CG3195 + CG3195 ID:72B11
 CG18396 + Mst98Cb unknown * CG18396 GH20038 98C2-98C2 ID:72C1
 + unknown * predicted using hexExon; MAL3P6.28 Hypothetical protein, len: aa; Similarity to model organism hypothetical
 CG18042 proteins (C.elegans, D.melanogaster, S. CG18042 GH20177 31B1-31B1 ID:72D3
 CG9483 + unknown * CG9483 GH20208 29F3-29F3 ID:72D7
 + unknown * weak similarity with B1-hordein (Swiss Prot accession number cDNA EST comes from this gene; cDNA EST
 comes from this gene; cDNA EST comes from this [SAM_DOMAIN // SAM // PRO_RICH] CG7915 GH20255 66B7-66B7 dup:4/4
 CG7915 ID:72E4
 + Cyp12c1 cytochrome_P450 * CYTOCHROME P450 CYP12A2(aa) * 1e-08 ERG5_YEAST CYTOCHROME P450 (C-22
 STEROL DESATURASE) * 2e-24 cytochrome P450 cytochrome P4 * 5e-21 YRV8_CAEEL[EP450II // p450 // P450 // MITP450 //
 CG4120 C] CG4120 GH20281 75D2-75D2 dup:2/2 ID:72E6
 + enzyme * similar to aspartate aminotransferase(aa) * 1e-99 aspartate aminotransferase cerevisiae, Peptide Partial, * 1e-
 157 similar to aspartate aminotransfe [aminotran_1 // AA_TRANSFER_CLASS_1 // T] CG4233 GH20337 22B8-22B8 dup:2/2
 CG4233 ID:72F2
 + Taf30alpha transcription_factor * 9e-08 hypothetical protein YDR145w - yeast (Saccharomyces cerevisiae) * 2e-59
 T2DA_DROME TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUNIT ALPHA/22 K [HIST_TAF] CG17358 GH20363
 CG17358 86F1-86F1 dup:1/3 ID:72F4
 + enzyme * Yjr105wp(aa) * 9e-49 ADK_YEAST PUTATIVE ADENOSINE KINASE ribokinase homolog * 2e-78 Similarity to
 Human adenosine kinase cDNA EST EMBL:Z1 * 2e-50 AD [ADENOKINASE // MITOCH_CARRIER // HELIX_] CG3809 GH20396
 CG3809 87B5-87B5 ID:72F8
 CG3557 + unknown * CG3557 GH20409 23E4-23E4 ID:72F9
 + chaperone * KD CHAPERONIN, CHLOROPLAST PRECURSOR (PROTEIN CPN10) (PROTEIN GROES)(aa) *
 chaperonin 10(aa) * 6e-17 CH10_YEAST KD HEAT SHOCK PROTEIN, MITOCHONDRIA [CHAPERONIN10 // cpn10] CG9920
 CG9920 GH20473 88A10-88A10 ID:72G3
 + transporter * 3e-19 nervous system antigen nerv * 5e-06 Similarity to Shrimp sodium/potassium-transporting ATPase beta
 CG11703 cha * 7e-10 ATNB_MOUSE SODIUM/POTASSIUM-TRA CG11703 GH20514 91F10-91F10 ID:72G7
 CG14021 + unknown * CG14021 GH20612 25D5-25D6 dup:2/2 ID:72H2
 + unknown * /match=(desc;; /match=(desc:(aa) * 1e-77 /match=(desc;; /ma * 1e-05 E02C12.6 gene product * 1E-151
 CG9497 CG9497 GH20717 26C4-26C4 ID:73A1
 CG1521 + transporter homology to uncharacterized human and C.elegans proteins MgtE CG1521 GH20809 ID:73A10
 CG1648 + unknown * 2e-12 inserted at base 5' end of P element Inverse PCR * * CG1648 GH20817 46B10-46B10 dup:2/3

ID:73A11
+ transcription_factor * BLASTX 1.3E-19 Human super cysteine rich protein mRNA, partial cds.(dna) * GAGA factor class A-isoform(aa) * 8e-32 alternatively spliced form * 8e- [BTB // zf-C2H2 // ZINC_FINGER_C2H2] CG12236 GH20830 5C6-5C6 ID:73B1
CG12236
- Ket cytoskeletal_structural_protein * BM KETTIN(aa) * titin(aa) * titin(aa) * Titin [ig // AA_TRNA_LIGASE_II_1 // SH3 // NLS]
CG1915
CG1915 GH20861 62C2-62C3 dup:2/2 ID:73B8
+ CtBP enzyme * CtBP * C-terminal binding protein CtBP2(aa) * C-terminal binding protein(aa) * similar to the D-isomer specific 2-hydroxyacid dehydrogenases family [2-Hacid_DH] CG7583 GH20987 87D9-87D11 dup:1/2 ID:73C12
CG7583
+ enzyme * UNKNOWN(aa) * 7e-63 PUT2_YEAST DELTA-1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE PRECURSOR (P5C DEHYDROG * 8e-11 alternatively spliced form; /prediction [aldedh] CG6661 GH20963 70C11-70C11 ID:73C5
CG6661
CG2750
+ enzyme * No definition line found(aa) * * [ATP_GTP_A] CG2750 GH20980 11A7-11A7 ID:73C8
+ 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
CG14704
CG10752
+ unknown * CG10752 GH21086 69E8-69E8 ID:73D8
+ Hr46 steroid_hormone_receptor * DMDHR3A_2 Hr46 * HR3_DROME PROBABLE NUCLEAR HORMONE RECEPTOR HR3 (DHR3) st * 4e-67 CHR3 gene product * 2e-71 ROR1_MOUSE NUCLEAR RECEPTOR ROR-A[STROIDFINGER // hormone_rec // THYROIDH] CG11823 GH21112 46F4-46F ID:73D9
CG11823
CG6740
+ unknown * CG6740 GH21172 67C-67C dup:2/2 ID:73E7
+ 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
CG8918
+ 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
CG8086
+ 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
CG12449
+ 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
CG5411
+ 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
CG7045
+ 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
CG11961
+ unknown * 2e-06 hypothetical protein * hypothetical protein * UVS2_NEUCR UVS-2 PROTEIN uvs2 protein - Neurospora crassa * [GLYCOSYL_HYDROL_F5 // zf-C3HC4 // ZINC_] CG7388 GH21463 66A12-66A12 dup:1/3 ID:73G4
CG7388

+ transporter * 2e-64 coded for by C. elegans cDNA yk54h9.5; coded for by C. elegans cDNA yk54h9.3; si * 4e-70
 CG7571 PGT_HUMAN PROSTAGLANDIN TRANSPORTER (PGT) prostaglandin CG7571 GH21536 74D1-74D1 dup:2/2 ID:73H1
 + motor_protein * 3e-05 F35D11.11 gene product * 2e-06 hyaluronan receptor - human * 3e-06 tetravalent M protein=hybrid
 CG10193 molecule containing amino-terminal subunit * Si [PRO_RICH] CG10193 GH21577 95C3-95C3 dup:2/2 ID:73H4
 CG6652 + motor_protein * 6e-13 unknown * * [NLS_BP] CG6652 GH21622 73E4-73E4 dup:2/2 ID:73H9
 + Orct transporter * DMORCT2_2 Orct * 3e-10 YGK4_YEAST PROBABLE METABOLITE TRANSPORT PROTEIN YGL104C *
 CG6331 putative organic cation transporter [sugar_tr] CG6331 GH21655 95F2-95F2 ID:74A1
 + EG:4F1.1cell_adhesion * /match=(desc:; /match=(desc:(aa) * sarcoglycan, delta (35kD dystrophin-associated glycoprotein)(aa)
 CG14808 * 4e-06 delta sarcoglycan * 9e-05 delta-sarcogl CG14808 GH21860 2B8-2B9 ID:74B10
 + unknown * 1e-23 hypothetical protein YDL219w - yeast (Saccharomyces cerevisiae) * 3e-32 predicted using Genefinder *
 CG5270 5e-27 SPAC8C9.05, len:149aa; similarity: [FYVE_DOMAIN // FYVE] CG5270 GH21817 86E5-86E5 ID:74B5
 + BcDNA:GH04802 ion_channel * 5e-05 TOK1_YEAST OUTWARD-RECTIFIER POTASSIUM CHANNEL TOK1 (TWO-DOMAIN
 OUTWARD RECTIFIER * 1e-18 C24H11.8 * 8e-06 TWIK-related acid-sensitive K+ channel [CHANNEL_PORE_K] CG1688 46B4-
 CG1688 46B5 dup:2/2 ID:74B7
 + weak homology to leucine carboxyl methyltransferase [Homo sapiens] and receptor protein kinase-like protein
 CG14768 [Arabidopsis thaliana] CG14768 GH21888 ID:74C2
 CG2457 + inaF ion_channel * INAF protein(aa) * 1e-115 INAF protein * * CG2457 GH21930 10D5-10D6 dup:1/2 ID:74C7
 CG3246 + unknown * CG3246 25A3-25A3 dup:2/2 ID:74E11
 CG6684 + CG6684 dup:2/2 ID:74E3
 + protein_kinase * coded for by C. elegans cDNA CEESC01F; coded for by C. elegans cDNA cm11b7; coded for by C.
 elegans cDNA cm11b8; Similar to protein kinase.(aa) * 1e [DAG_PE_BINDING_DOMAIN // DAG_PE-bind //] CG10737 56B6-
 CG10737 56C ID:74F1
 + 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
 + Cyp28d1 cytochrome_P450 * cytochrome P450 monooxygenase CYP28A2(aa) * 8e-48 CYP6A2 * 2e-32 YRVA_CAEEL
 PUTATIVE CYTOCHROME P450 T10B9.10 IN CHROMOSOME II * 3e-49 cytochrome P4 [EP450II // p450 // P450 // MITP450 //
 CG10833 C] CG10833 GH22460 25C9-25C9 ID:74H2
 CG9336 + unknown * CG9336 GH22472 38F1-38F1 ID:74H4
 + Abdominal B transcription_factor HOMEODOMAIN, HOMEODOMAIN_1, HOMEODOMAIN_2, HTHREP] CG10291 GH22693 dup:4/5
 CG10291 ID:75B6
 CG8960 + unknown * CG8960 GH22765 62D2-62D2 ID:75C5
 CG10311 + unknown * CG10311 GH22794 89B22-89B22 ID:75C7
 + enzyme * 1e-151 GLS1_CAEEL PUTATIVE GLUTAMINASE DH11.1 (GLS) (L-GLUTAMINE AMIDOHYDROLASE) * 1e-
 170 protein * 1e-171 GLSK_RAT GLUTAMINASE, KIDNEY ISOFORM PREC [ANK_REP // ank // ANK_REP_REGION] CG8772
 CG8772 GH22838 49B8-49B8 dup:2/2 ID:75D1
 CG2081 + unknown * CG2081 GH22911 10A3-10A3 dup:2/2 ID:75E4

CG7905 + unknown * CG7905 GH22919 66B6-66B7 dup:2/2 ID:75E5
+ enzyme * PHOSPHOMANNOMUTASE (PMM)(aa) * 2e-91 YM8L_YEAST HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION * 1e-114 similar to Phosphoglucomutase a [PGM_PMM // PGMPMM] CG10202 GH22984 51C5-51C5 ID:75F1

CG10202 + transmembrane_receptor * 3e-78 D-CD36 protein - fruit fly (*Drosophila melanogaster*) * 5e-35 predicted using Genefinder; similar to CD36 family; cDNA EST yk265 * 4e-53 scaven [CD36] CG12789 GH23019 28A1-28A1 ID:75F12

CG12789 + 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 // efhand // EF_HAND_2] CG10126 GH22994 87D3-87D3 ID:75F5

CG10126 + Klp68D motor_protein * Klp68D * KINESIN-LIKE PROTEIN KLP68D(aa) * 1e-38 Cin8p kinesin-related * 1e-115 Similarity to urchin kinensin-2 (PIR Acc. No. cDNA EST EM [kinesin // KINESINHEAVY] CG7293 GH23075 68D2-68D2 ID:75G8

CG7293 + unknown * 2e-22 YNQ8_YEAST HYPOTHETICAL 28.8 KD PROTEIN IN PSD1-SKO1 INTERGENIC REGION * 2e-27 YO23_CAEEL HYPOTHETICAL 23.3 KD PROTEIN ZK688.3 IN CHROMOSOME I [ATP_GTP_A] CG6028 GH23390 93F14-93F14 ID:76B10

CG6028 + alpha-Est8 enzyme * agr;-Est8 * alpha esterase(aa) * agr;-Est3 * alpha esterase [CARBOXYLESTERASE_B_1 // CARBOXYLESTERAS] CG1121 GH23353 85A1-84D5 ID:76B3

CG1121 + 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

CG10341 + protein_kinase * bt * hep * 8e-21 SPK1_YEAST PROTEIN KINASE SPK1 (SERINE-PROTEIN KINASE 1) * 2e-20 p90 ribosomal S6 kinase [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG1760 GH23573 10C3-10C3 ID:76D10

CG1760 + enzyme * 4e-10 match to * 3e-06 hypothetical protein * [NLS_BP] CG13773 GH23590 27C3-27C3 ID:76D12

CG13773 + ion_channel * 1e-15 chloride channel protein CLC-1 - yeast (*Saccharomyces cerevisiae*) * 1e-108 similar to *T. marmorata* chloride channel protein (SP:CLCH_TORMA, * [CLCHANNEL // CBS // voltage_CLC] CG6942 GH23529 86F9-86F9 ID:76D5

CG6942 + 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 + enzyme * fructose-1,6-bisphosphatase; Fbp1p(aa) * fructose-bisphosphatase 1(aa) * fructose-1,6-bisphosphatase precursor(aa) * fructose-1,6-bisphosphatase ho [FBPASE // FBPase // INFBPHPTASE // FBP] CG10611 38A-38A dup:3/3 ID:76F10

CG10611 + 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 + 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 GH23741 66D-66D dup:4/5 ID:76G2

CG5962 + rha motor_protein * RADHA protein(aa) * 1e-10 similar to *C. elegans* UNC-89 and titins * 3e-07 ORF 73, contains large complex repeat CR sarcoma-associated herpesv * YL CG11908 GH23783 96D-96D ID:76G7

CG11908 CG7655 + transmembrane_receptor * CG7655 GH23865 90C-90C ID:76H10

CG3192 + CG3192 ID:76H8

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

+ 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

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

+ unknown * UBIQUINONE BIOSYNTHESIS PROTEIN COQ4 HOMOLOG(aa) * CGI-92 protein(aa) * 4e-38 COQ4_YEAST

CG3877 UBIQUINONE BIOSYNTHESIS PROTEIN COQ4 Coq4p * 3e-48 putative CG3877 GH24045 78A1-78A1 dup:1/2 ID:77B7

+ enzyme * cDNA EST yk478b4.5 comes from this gene; cDNA EST comes from this gene; cDNA EST yk456b12.5 comes from this gene; cDNA EST comes from this gene(aa) [PHD] CG17446 GH24056 8D7-8D7 ID:77B9

CG17446 + 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 CG7529 GH24077 78D7-78D7 ID:77C1

+ unknown * R01H10.7(aa) * inositol polyphosphate 4-phosphatase, type II(aa) * inositol polyphosphate 4-phosphatase type II-alpha(aa) * 4e-58 inositol polypho [PH_DOMAIN] CG1846 GH24251 12E1-12E1 dup:2/2 ID:77D3

CG1846 + enzyme * flavin containing monooxygenase 3(aa) * T3P18.10(aa) * similar to Flavin-binding monooxygenase-like(aa) * similar to flavin-containing monooxygenase [ADXRTASE // FADPNR // FMO-like // PNDR] CG3006 GH24271 60A13-60A13

CG3006 ID:77D7

+ transcription_factor * ORFveg132; similar to Caenorhabditis elegans ORF F59B10.1 encoded by EMBL Accession Number

CG3328 * protein(aa) * 2e-70 similarity to a transmembranous of [CASPASE_HIS] CG3328 GH24458 60B9-60B10 dup:3/3 ID:77E12

+ phyl signal_transduction * phyl * 1e-175 phyllopod * phyllopod - fruit fly (Drosophila melanogaster) ORF * phyllopod [NLS_BP]

CG10108 CG10108 GH24326 51A-51A2 dup:2/2 ID:77E4

+ enzyme * CYSTEINYL-TRNA SYNTHETASE (CYSTEINE--TRNA LIGASE) (CYSRS)(aa) * 5e-52 YNY7_YEAST

CG8257 PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (CYSTEINE--TRNA LIGASE [TRNASYNTHCYS // tRNA-synt_1e]

CG8257 CG8257 GH24360 50E2-50E2 dup:3/3 ID:77E7

CG11440 + wunen * similarity to phosphatidic acid phosphatase PA_PHOSPHATASE CG11440 ID:77F12

+ transmembrane_receptor * DMLRR47_3 Lrr47 * 8e-06 LRR47 protein - fruit fly (Drosophila melanogaster) (* 6e-06 Ras-binding protein SUR-8 leuc * 6e-06 Ras-binding protein SUR [LRR // LEURICHRPT] CG2143 GH24470 9C2-9C2 ID:77F3

CG2143 + unknown * glycine-, glutamate-, thienylcyclohexylpiperidine-binding protein(aa) * 1e-59 protein * 1E-170* CG10137

CG10137 37F1-37F1 ID:77F4

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

+ Cyp6d4 cytochrome_P450 * THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)(aa) * Similar to cytochrome P450(aa) * cytochrome P450(aa) * CYTOCHROME P450 4A11 PRECURSOR (CYP1A11) [EP450II // p450 // P450 // MITP450 // B]

CG12800 CG12800 GH24669 94C4-94C4 ID:77G11

+ endopeptidase * 2e-11 similar to Zinc-binding metalloprotease; cDNA EST come * 3e-14 NEP_MOUSE NEPRILYSIN (NEUTRAL ENDOPEPTIDASE) (NEP) (ENKEPHALINASE) (CD10) * 2e[NEPRILYSIN // PRENYLATION // ZINC_PROTE]

CG3239 CG3239 GH24674 5A1-5A1 dup:1/3 ID:77G12

CG7178 + CG7178 dup:2/2 ID:77H12

CG7106 + ligand_binding_or_carrier * Acp29AB * mannan-binding lectin; collectin(aa) * 2e-16 accessory gland protein Acp29AB * 4e-08 FCE2_MOUSE LOW AFFINITY IMMUNOGLOBULIN EPSILON FC [lectin_c // C_TYPE_LLECTIN_2] CG7106 GH24720 28D3-28D3 dup:1/2 ID:77H5

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

CG12120 + unknown * CG12120 GH24835 8D4-8D4 ID:78A1

CG5453

CG16719 + unknown * hypothetical protein(aa) * 3e-10 hypothetical protein * CG16719 GH24859 67B11-67B11 ID:78A4

CG10750 + unknown * CG10750 GH24871 37D3-37D3 dup:1/3 ID:78A7

CG17617 + EG:23E12.5 unknown * /match=(desc;; /match=(desc:(aa) * /match=(desc;; /ma * * CG17617 GH24929 cyto_unknown ID:78B1

CG10553 + unknown CG10553 ID:78B2

CG10347 + unknown * 8e-10 partial CDS * * CG10347 10F2-10F2 dup:3/3 ID:78B3

CG3795 + EG:9D2.4endopeptidase * DMC9D2 * /motif=(desc;; /motif=(desc;; /motif=(desc;; /match=(desc;; /m * 2e-20 kallikrein * 1e-28 mesotrypsinogen mesotrypsino [trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG3795 GH24985 2B8-2B8 ID:78B4

CG14935 + * 2e-67 MAZS_YEAST PROBABLE ALPHA-GLUCOSIDASE FSP2 (MALTASE) (FLOCCULENT SPECIFIC PROTE * 1e-154 MAL2_DROME POSSIBLE MALTASE PRECURSOR (LARVAL VISCERA [ALPHAAMYLASE // PRENYLATION // alpha-am] CG14935 33B2-33B2 dup:1/2 ID:78C1

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

CG4059 + ftz-f1 steroid hormone receptor steroid receptor beta FTZ-F1 [Drosophila melanogaster] NUCLEAR_RECEPTOR, STRDHORMONER, STROIDFI] CG4059 GH25189 dup:3/3 ID:78D6

CG3751 + CG3751 dup:1/2 ID:78D9

CG7443 + unknown * CG7443 GH25351 84F11-84F11 dup:2/2 ID:78E10

CG6730 + Cyp4d21 cytochrome_P450 * DMC152A3 * Cyp4e2 * DMCYP4D2_12 Cyp4d2 * 1e-112 cytochrome P450 cytochrome P4 CG6730 GH25251 28A6-28B1 dup:2/2 ID:78E3

CG6470 + transcription_factor * [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG6470 GH25257 17B5-17B5 dup:2/2 ID:78E4

CG17210 + unknown * 6e-32 antigen 5-related * 1e-19 antigen 5-related protein * 6e-34 Ag5r2 * VA3_SOLIN VENOM ALLERGEN III (ALLERGEN SOL I 3) (SOL I III) CG17210 GH25284 86D8-86D8 dup:2/2 ID:78E5

CG1274 + enzyme * thioredoxin peroxidase (antioxidant enzyme)(aa) * 2e-58 TSA1_YEAST THIOL-SPECIFIC ANTIOXIDANT PROTEIN (PRP) thiol * 3e-72 similar to M. musculus MER [AhpC-TSA] CG1274 GH25379 63B5-63B5 ID:78F1

CG7724 + enzyme * 8e-11 YGA1_YEAST PUTATIVE BETA-HYDROXYSTEROID DEHYDROGENASE/DELTA 5-->4-ISOMERASE (* 2e-12 weakly similar to dihydrokaempferol 4-reductase * 2e-21 [3Beta_HSD] CG7724 GH25466 73E5-73E5 dup:2/2 ID:78F12

CG1615 + Ork1 ion_channel * potassium channel, subfamily K, member (TASK-2); TASK-2(aa) * two P domain potassium channel

ORK1(aa) * Ork1 * BLASTX 8.1E-08 Mus musculus TREK-1 K [CHANNEL_PORE_K] CG1615 GH25390 9F8-9F10 ID:78F2
 + transporter * sodium-dicarboxylate cotransporter SDCT1(aa) * 8e-08 YJT8_YEAST HYPOTHETICAL 97.7 KD
 MEMBRANE PROTEIN IN PRP21-UBP12 INTERGENIC REGIO * 4e-29 YKG6_C CG4961 GH25396 92C4-92C4 dup:2/2
 ID:78F3
 CG4961
 CG1835 + unknown * [NLS_BP] CG1835 GH25431 19E2-19E2 ID:78F5
 none + none GH25455 ID:78F8
 CG17975 + sut2 transporter * GLUCOSE TRANSPORTER TYPE 7, HEPATIC MICROSOMAL(aa) * Contains similarity to Pfam domain:
 (sugar_tr), Score=356.0, E-value=1.3e-103, N=1(aa) * solute CG17975 GH25507 44A4-44A4 dup:2/2 ID:78G4
 CG1540 + cell_adhesion * similar to the BPTI/Kunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor
 (TFPI)(aa) * similar to Kunitz/Bovine [ig // EGF_1 // BPTI_KUNITZ // Kunitz_BP] CG1540 GH25513 98D2-98D2 dup:1/3 ID:78G5
 CG5641 + transcription_factor * interleukin enhancer binding factor 2, 45kD(aa) * 2e-37 predicted using Genefinder; Similarity to
 Human NF45 protein (TR:Q * 5e-19 zinc finger RNA b [25A_SYNTH_2] CG5641 GH25564 87B15-87B15 ID:78H1
 + BcDNA:GH06348 enzyme * predicted using Genefinder; Similarity to Human pyruvate carboxylase cDNA EST comes from this
 gene; cDNA EST comes from this gene; cDNA EST comes f [CPSase_L_chain] CG1516 GH25836 46B14-46C1 dup:5/8
 CG1516 ID:79B10
 + * Chain B, * 305aa long hypothetical * lysosomal * PUTATIVE N4-(BETA-N-ACETYLGLUCOSAMINYL)-L-
 ASPARAGINASE PRECURSOR (GLYCOSYLASPARAGINASE) (ASPARTYLG [Asparaginase_2] CG1827 45F4-45F4 dup:2/2
 CG1827 ID:79B3
 + ligand_binding_or_carrier * GTP binding protein, almost identical to Gsp1p; Gsp2p(aa) * 3e-70 GSP2_YEAST GTP-
 BINDING NUCLEAR PROTEIN GSP2/CNR2 GTP-bind * 3e-23 rab11 * 6e[ras // GTPRANTC4 // ATP_GTP_A // RASTRN]
 CG7815 CG7815 GH25818 75F9-75F9 ID:79B9
 CG11473 + unknown * No definition line found(aa) * 6e-23 No definition line found * No definition line found * No definition line found
 CG11473 5A9-5A9 ID:79C12
 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
 CG13515 + unknown * CG13515 GH25860 58F4-58F4 ID:79C4
 CG17470 + unknown * CG17470 GH26094 38E-38E dup:2/2 ID:79E10
 CG8509 + enzyme_activator * HYPOTHETICAL 45.1 KD PROTEIN IN IMP2-DNA43 INTERGENIC REGION(aa) * phosphotyrosyl
 phosphatase activator(aa) * similar to hosphotyrosyl phosphatase CG8509 GH26069 13F1-13F1 dup:2/2 ID:79E2
 CG11475 + unknown * hypothetical protein(aa) * Hrt2p(aa) * F31D4.2(aa) * hypothetical protein(aa) [NLS_BP] CG11475 GH26080
 58C1-58C1 dup:2/2 ID:79E5
 CG10446 + transcription_factor * segmentation protein hairy - fruit fly (Drosophila melanogaster)(aa) * DMHAIRG_5 h * 3e-07 lin-22 *
 2e-18 HES1_MOUSE TRANSCRIPTION FACTOR HES-1 (HAI [HLH // HELIX_LOOP_HELIX_2] CG10446 37B10-37B10
 dup:2/2 ID:79F1
 CG5398 + transporter * aquaporin 2(aa) * 1e-07 YFF4_YEAST HYPOTHETICAL 70.5 KD PROTEIN IN AGP3-DAK3 INTERGENIC
 REGION * 8e-05 BIB_DROME NEUROGENIC PROTEIN BIG BRAIN bib pr [MINTRINICP // MIP] CG5398 GH26134 59F1-59F1
 ID:79F5

CG4715 + unknown * CG4715 GH26159 21E-21E ID:79F9

CG12136 + unknown * [AA_TRNA_LIGASE_I // NLS_BP] CG12136 GH26280 8D10-8D10 ID:79G11

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

CG10365 + unknown * contains similarity to E. coli cation transport protein * 6e-16 YEZ3_YEAST HYPOTHETICAL 26.3 KD PROTEIN IN RAD4-CHD1 INTERGENIC REGION * 3e-22 cont CG10365 GH26317 95B5-95B5 ID:79H4

CG4108 + unknown * contains similarity to BC-2 protein * 1e-45 developmental protein * hypothetical protein * [NLS_BP] CG4108 GH26351 75D2-75D2 ID:79H7

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

+ da transcription_factor * TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-[HLH // HELIX_LOOP_HELIX // PEROXIDASE_1] CG5102 da 31E1-31E1 dup:3/3 ID:8-31 cntrlBA11

CG5102

CG13201 + ix CG13201 ix dup:2/2 ID:8-31 cntrlBA6

+ 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

CG3772

CG1378 + tll steroid_hormone_receptor CG1378 tll dup:2/2 ID:8-31 cntrlBC1

+ ttk transcription_factor * DNA-binding protein ttk - fruit fly (Drosophila melanogaster)(aa) * DMDNABPMR_2 ttk * DNA binding protein * 3e-06 contains sim[BTB // zf-C2H2 // ZINC_FINGER_C2H2 // Z] CG1856 HK or ttK 100E1-100E1 dup:5/7 ID:8-31 cntrlBC2

CG1856

CG1374 + tsh transcription_factor CG1374 tsh dup:3/3 ID:8-31 cntrlBD3

+ pros transcription_factor * DMPROS_3 pros * PRO_DROME PROTEIN PROSPERO homeotic protein prospero - f * 4e-58 HM26_CAEEL HOMEOBOX 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

CG17228

+ 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 HOMEOBOX PROT CG1028 ANTP 84B-84D11 dup:3/3 ID:8-31 cntrlBE12

CG1028

CG2956 + twist transcription_factor CG2956 twist dup:3/5 ID:8-31 cntrlBG3

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

+ motor_protein * BACR37P7.j(aa) * MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND * * CG9392 GH26462 76C1-76C1 ID:80B3

CG9392

+ actin_binding * 4e-21 alternatively spliced form * 2e-31 similar to actin binding domain of alpha-actinin and spectra beta chain * 6e-30 mouse smoothelin, large iso [CH_DOMAIN // CH] CG3960 GH26714 6B3-6C1 dup:3/3 ID:80D12

CG3960

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

CG4669 + unknown * [PRO_RICH] CG4669 GH26702 64D1-64D1 ID:80D8

CG5758 + unknown * CG5758 GH26746 36E-36E dup:2/2 ID:80E5

CG7977 + RpL23a ribosomal_protein * ribosomal protein L23a(aa) * 5e-38 RL25_YEAST 60S RIBOSOMAL PROTEIN L25 (YL25) (RP61L) rib * 5e-38 RL2C_CAEEL PROBABLE 60S RIBOSOMAL PROTEIN L23A ([Ribosomal_L23 // RIBOSOMAL_L23 // NLS_B] CG7977 62A11-62A11 dup:3/3 ID:80E8

CG7445 + fln cytoskeletal_structural_protein * DMFLIGHT_2 fln * FLIGHTIN (MUSCLE PROTEIN 27)(aa) * 2e-19 CMP-N-acetylneuraminic acid synthetase * myofibrillar protein flightin - fruit fly (Drosop CG7445 GH26786 76E2-76E2 dup:3/3 ID:80E9

CG17137 + ion_channel * Vdac * DMMITPORN_2 porin * 1e-09 POR2_YEAST OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION * 3e-66 voltage dependent anion-sele [Euk_porin // EUKARYTPORIN] CG17137 GH26967 32B3-32B3 ID:80G10

CG15084 + unknown * 3e-12 YKJ5_YEAST 32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION * 1e-64 YS19_CAEEL HYPOTHETICAL 42.1 KD PROTEIN IN CHROMOSOME III * 1e-17 unknown * CG15084 GH26994 55F4-55F4 ID:80H2

CG7920 + enzyme * 2e-08 ACH1_YEAST ACETYL-COA HYDROLASE (ACETYL-COA DEACYLASE) (ACETYL-COA ACYLASE) * 1e-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

CG1607 + transporter * amino acid transporter chain (AmAt-L-Ic) ASUR4(aa) * Similarity to Human membrane protein E16 (SW:E16_HUMAN); cDNA EST comes from this gene; cDNA ES [AROMATIC_AA_PERMEASE_2 // aa_permeases] CG1607 GH27380 100C-100C ID:81C11

CG2968 + CG2968 ID:81C7

CG7077 + enzyme * antennal-specific short-chain dehydrogenase/reductase(aa) * BLASTX 3.5E-15 YMR226C|Protein with similarity to insect-type alcohol dehydrogenase, rib [adh_short] CG7077 GH27329 94A14-94A14 dup:2/2 ID:81C8

CG8279 + enzyme * phosphodiesterase 6B, cGMP-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant); PDEB(aa) * 7e-45 YBZJ_CAEEL PROBABLE 3 [PDEase // PDIESTERASE1 // PDEASE_I // P] CG8279 GH27433 89E3-88C6 dup:2/2 ID:81D9

CG1227 + protein_kinase * similar to serine/threonine kinase(aa) * 3e-37 hypothetical protein YPL236c - yeast (Saccharomyces cerevisiae) * 2e-17 SNF1A/AMP-activated protein k [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG1227 84C7-84C7 dup:3/3 ID:81E11

CG17323 + * UDP-GLUCURONOSYLTRANSFERASE 2B13 PRECURSOR, MICROSOMAL (UDPGT)(aa) * UDP-GLUCURONOSYLTRANSFERASE 2B20 PRECURSOR, MICROSOMAL (UDPGT)(aa) * similar t [UDPGT] CG17323 37B3-37B3 dup:1/2 ID:81G12

CG14735 + unknown * CG14735 GH27720 87A10-87A10 ID:81G2

CG8813 + transcription_factor * CG8813 GH27752 23B5-23B5 dup:1/2 ID:81G5

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

CG4948 + structural_protein * Gasp precursor(aa) * 1e-09 Gasp precursor * 3e-07 R02F2.4 gene product * 9e-13 insect intestinal mucin IIM22 CG4948 GH28017 66F4-66F4 dup:3/3 ID:82B4

CG5735 + RNA_binding * protein(aa) * 2e-49 ovarian protein - fruit fly (Drosophila melanogaster) s * 8e-75 YLF1_CAEEL HYPOTHETICAL 42.4 KD PROTEIN C40H1.1 IN CHROMOSOME II [RNP_1 // RBD // PFKB_KINASES_1 // rrm] CG5735 GH28038 66E4-66E4 dup:2/3 ID:82B7

CG4405 + nucleic_acid_binding * unknown(aa) * weak similarity with BRKA gene from Bordetella Pertussis; cDNA EST comes from this gene; cDNA EST comes from this gene(aa) * 2e-52 (P CG4405 GH28348 30B11-30B12 dup:2/3 ID:82C11

CG17838 + RNA_binding * hypothetical protein(aa) * heterogeneous nuclear ribonucleoprotein R(aa) * 1e-08 RN15_YEAST MRNA 3'-END PROCESSING PROTEIN RNA15 RNA15 pro * 6e-16 p [RBD // rrm // NLS_BP] CG17838 GH28335 92F10-92F10 dup:2/5 ID:82C6

CG9676 + endopeptidase * Ser12 * DMEAST_4 ea * Ser6 * DMSTUBBLE_1 Sb [trypsin // CHYMOTRYPSIN // TRYPSIN_HIS] CG9676 15A1-15A1 dup:1/3 ID:82C8

CG7206 + unknown * CG7206 GH28353 16F7-16F7 dup:2/2 ID:82D1

CG8854 + unknown * CG8854 GH28507 48F3-48F3 ID:82D12

CG17645 + enzyme * phosphoglyceromutase - fruit fly (Drosophila melanogaster)(aa) * DMPGLY_4 Pglym78 * 3e-72 PMG1_YEAST PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE 1 [PGAM // PG_MUTASE] CG17645 GH28416 87B7-87B7 ID:82D6

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

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

CG8588 + unknown * clot.599(dna)* 1e-104 l(3)j1D5 l(3)j1D5 inserted at base Both 5' and 3' ends of P element Inverse PCR * CG8588 GH28656 65F4-65F4 dup:3/4 ID:82F1

CG17397 + transcription_factor * 8e-09 C24H11.6 * 1e-31 SRB7 SRB protein * SRB7 (suppressor of RNA polymerase B, yeast) homolog RNA polymerase * CG17397 GH28678 cyto_unknown ID:82F4

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

CG8006 + unknown * CG8006 GH28769 67E7-67E7 ID:82G2

CG5413 + CREG unknown * CREG * 1e-112 cellular repressor of E1A-stimulated genes CREG * 8e-25 cellular repressor of E1A-stimulated genes CREG * 2e-22 UNKNOWN cellular repre CG5413 GH28782 90A6-90A6 ID:82G3

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

CG8857 + ribosomal_protein * 5e-46 RS41_YEAST 40S RIBOSOMAL PROTEIN RP41 (YS12) (S18A / S18B) * 4e-56 Similarity to Human 40S ribosomal protein S11 (SW:RS11_HUMAN); cDN * [RIBOSOMAL_S17 // Ribosomal_S17 // RIBOS] CG8857 GH28880 48F1-48F1 dup:2/2 ID:82H8

CG14226 + protein_phosphatase * 3e-10 PTP9_DROME PROTEIN-TYROSINE PHOSPHATASE 99A PRECURSOR (RECEPTOR-LINKED PROTEIN-T * 1e-10 myotactin form A * 1e-08 protein tyrosine phosphatase [fn3] CG14226 GM13503 18D13-18D13 ID:83A10

+ ribosomal_protein * 2e-08 predicted using Genefinder; Similarity to Human 60S ribosomal prot * 1e-22 RL28_MOUSE 60S
 CG12740 RIBOSOMAL PROTEIN L28 ribosomal protein L * 1e-22 ri CG12740 GM13756 64A3-64A3 ID:83B2
 CG14303 + unknown * 7E-86 * CG14303 GM13930 91B6-91B6 ID:83B9
 + ribosomal_protein * 60S RIBOSOMAL PROTEIN L21(aa) * 7e-46 R21A_YEAST 60S RIBOSOMAL PROTEIN L21E A
 ribosomal protein * 5e-50 RL21_CAEEL PROBABLE 60S RIBOSOMAL PROTEIN L2 [RIBOSOMAL_L21E // Ribosomal_L21e]
 CG12775 CG12775 GM14242 40D2-40D2 ID:83C2
 CG8501 + unknown * CG8501 HL07915 48C5-48C5 ID:83C9
 CG6219 + unknown * anon-fe1G5 * anon1G5 * 1e-124 anon1G5 [NLS_BP] CG6219 LD21372 95E7-95E7 ID:83D11
 + 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
 CG9300 + unknown * [SUGAR_TRANSPORT_2] CG9300 76B8-76B8 dup:2/2 ID:83E12
 + Bsg25D motor_protein * BSG2_DROME BLASTODERM SPECIFIC PROTEIN 25D bsg25D protein * 1e-05 contains similarity
 CG14025 to kinesin (PFam: kinesin.hmm, score: 10.52 and 16.62) * 6e-1 CG14025 LD21844 25D2-25D2 dup:2/2 ID:83E8
 + protein_kinase mitotic checkpoint control protein kinase B-like PROTEIN_KINASE_ATP CG14030 LD22858 dup:1/2
 CG14030 ID:83H1
 + MRG15 DNA_binding * MRG15(aa) * MORF-related gene 15(aa) * 4e-19 hypothetical protein YPR023c - yeast
 CG6363 (Saccharomyces cerevisiae) * 4e-10 predicted using Genefinder; cDN [NLS_BP] CG6363 LD22902 88E9-88E10 dup:2/2 ID:83H4
 CG7946 + unknown CG7946 ID:84A8
 + Rpl27A ribosomal_protein * ribosomal protein L27a.e - yeast (Saccharomyces cerevisiae)(aa) * Rpl27Ab * 2e-71
 RL2B_DROME 60S RIBOSOMAL PROTEIN L27A Rpl27a * 2e-44 RL2A_MOUSE 60 [L15] CG15442 24F5-24F5 dup:6/6
 CG15442 ID:84B6
 + metastasis-associated-1-like-protein unknown * metastasis associated gene 1-like 1(aa) * 3e-74 similar to metastasis-
 associated protein mta-1 (GB:U0 * 1e-128 metastasis associat[ELM2 // myb_DNA-binding // zf-C2H2 // Z] CG2244 LD24461
 CG2244 83B6-83B6 ID:84C10
 + TfiIB transcription_factor * TfiIB * 3e-43 TF2B_YEAST TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) (TRANSCRIPTION
 FACTOR E) * 1e-174 TF2B_DROME TRANSCRIPTION INITIATION FACTOR I[TIFACTORIIB // transcript_fac2 // TFIIB] CG5193
 CG5193 LD24035 33D1-33D1 ID:84C6
 + DNA_replication_factor * replication control protein 1(aa) * CDC6 protein(aa) * 7e-31 CC6_YEAST CELL DIVISION
 CG5971 CONTROL PROTEIN cell division * 3e-30 recognition complex subu [AAA // ATP_GTP_A] CG5971 LD25083 66D-66D ID:84D11
 + unknown * 1e-133 inserted at base Both 5' and 3' ends of P element Inverse PCR * 1e-133 inserted at base Both 5' and 3'
 CG2446 ends of P element Inverse PCR * CG2446 LD24866 10D4-10D5 dup:2/2 ID:84D4
 CG10267 + transcription_factor CG10267 dup:2/2 ID:84E4
 CG11866 + unknown * 5e-37 protein * [FBOX_DOMAIN] CG11866 46E4-46E4 dup:2/2 ID:84H7
 + glu DNA_binding * 1e-123 hypothetical protein YLR086w - yeast (Saccharomyces cerevisiae) (* 2e-34 Cap * 1e-100
 Similarity with the yeast chromosome segregation prot[ATP_GTP_A2 // DA_BOX // NLS_BP // ATP_G] CG11397 LD25919 36A7-
 CG11397 36A7 dup:3/3 ID:85B2

+ unknown * unknown(aa) * 5e-26 hypothetical protein YDR214w - yeast (*Saccharomyces cerevisiae*) * 9e-55 cDNA EST
 CG1416 CEMSC45R comes from this gene; cDNA EST yk436a5 CG1416 LD25951 39F1-39F1 dup:2/2 ID:85B7
 CG14233 + meso18E unknown * meso18E* CG14233 LD26007 18E2-18E3 ID:85C1
 CG2190 + unknown * [PRENYLATION] CG2190 LD26151 11D5-11D5 ID:85C10
 CG10281 + TflIFalpha transcription_factor * DMTFAC5_2 TflIF agr; * coded for by C. elegans cDNA yk79f12.5; coded for by C. elegans
 cDNA cm17c10; coded for by C. elegans cDNA yk98e4.5; coded fo [NLS_BP] CG10281 LD26157 84A4-84A4 ID:85C11
 + G-salpa60A signal_transduction * DMGNB_2 G-o agr;47A * 2e-39 GBA1_YEAST GUANINE NUCLEOTIDE-BINDING
 CG2835 PROTEIN ALPHA-1 SUBUNIT (GP1-ALPHA) * GBS1_DROME GUANINE NUCLEOTIDE-BINDIN[GPROTEINA // G-alpha //
 GPROTEINAQ // G] CG2835 LD26182 60A12-60A12 ID:85C12
 CG18145 + unknown * mitochondrial and cytoplasmic fumarase (fumarate hydratase); Fum1p * FUMARATE HYDRATASE,
 MITOCHONDRIAL PRECURSOR (FUMARASE) * Contains similarity to CG18145 31B-31B dup:2/2 ID:85C2
 CG7109 + mts protein_phosphatase microtubule star Ser/Thr protein phosphatase CG7109 LD26077 dup:2/2 ID:85C5
 CG17255 + unknown * 2e-05 BAT2 * 2e-05 BAT2 * CG17255 LD26094 9C2-9C2 dup:2/4 ID:85C6
 CG10591 + unknown * [COLLAGEN_REP // PRO_RICH] CG10591 LD26105 64E-64E3 ID:85C7
 CG16989 + EG:34F3.4 unknown * /match=(desc;; /ma * * CG16989 LD26306 1C2-1C2 ID:85D12
 + EG:30B8.3 ligand_binding_or_carrier * /match=(desc;; /match=(desc:(aa) * 1e-171 62D9.a * 1e-11 cellular retinaldehyde-
 CG3191 binding protein; CRALBP * 1e-11 retinaldehyde-binding protein C [CRETINALDHBP // CRAL_TRIO] CG3191 LD26231 2F1-2F1
 dup:2/2 ID:85D2
 + signal_transduction * 3e-07 secreted polypeptide spatzie precursor - fruit fly (*Drosophila melanogaster*) * 3e-07
 CG9972 SPZ_DROME SPAETZLE PROTEIN PRECURSOR * 4e-09 spz * CG9972 LD26258 63A-63E4 ID:85D5
 CG1646 + DNA_binding similarity to pre-mRNA processing protein NLS CG1646 LD26426 dup:3/3 ID:85E11
 CG8290 + motor_protein * 7e-07 No definition line found * 1e-15 ATRX protein * 2e-15 X-linked nuclear protein * 6e-06 putative
 protein [NLS_BP // CYTOCHROME_C] CG8290 48D7-48D8 dup:3/3 ID:85E2
 CG3726 + transcription_factor * pipsqueak(aa) * 8e-29 BTB domain * 2e-07 contains similarity to the kelch/MIPP family * 7e-07 BAZF
 [BTB] CG3726 LD26392 5C8-5C8 dup:2/2 ID:85E5
 CG8352 + unknown * 2e-40 No definition line found * 2e-09 hypothetical protein * 1E-180* Hypothetical protein [NLS_BP] CG8352
 LD26402 65B4-65B5 dup:4/4 ID:85E6
 CG2158 + structural_protein * 7e-06 bK217C2.1 (Rat RTP60 (nuclear pore complex protein Npap60) isolog) * 4e-11 RTP60 *
 [Ran_BP1 // RAN_BP1 // RANBP1_WASP] CG2158 LD26583 44A7-44A7 dup:3/3 ID:85F12
 CG6474 + e(y)1 transcription_factor * TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUNIT (TAFII-42) (TAFII40) (P42)
 (ENHANCER OF YELLOW PROTEIN)(aa) * e(y)1 * 2e-12 YM75_YEAST HYPOTHETICAL [HIST_TAF] CG6474 LD26511 16D4-
 CG12234 16D5 ID:85F5
 CG7824 + unknown exportin CG12234 LD26789 dup:1/2 ID:85G12
 CG10274 + unknown * unknown(aa) * 2e-14 unknown * * [PPASE // NLS_BP] CG7824 LD26655 99C6-99C7 ID:85G3
 + transcription_factor * 2e-11 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * Zinc finger-AT hook
 protein * 3e-15 contains multiple of strong similarity to C2H2[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG10274 LD26701

65A6-65A6 ID:85G6

CG9351 + unknown * 1e-35 YNU1_YEAST HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION * 1e-118
No definition line found * 3e-51 hypothetical protein * 5e-50 [RANBP1_WASP] CG9351 LD26904 87F8-87F9 dup:3/4 ID:85H10
+ EcR steroid_hormone_receptor * ECDYSONE RECEPTOR (ECDYSTEROID RECEPTOR) (20-HYDROXY-ECDYSONE
RECEPTOR) (20E RECEPTOR)(aa) * DMECR_4 EcR * 8e-14 ecdysteroid receptor * 6e-51 [STROIDFINGER // hormone_rec //
zf-C4 //] CG1765 LD26915 42A7-42A8 ID:85H12

CG1765

CG10016 + transcription_factor ZINC_FINGER_C2H2, ZINC_FINGER_C2H2_2, zf] CG10016 LD26791 dup:2/2 ID:85H2
+ * 1e-155 inserted at base Both 5' and 3' ends of P element Inverse PCR * * [NLS_BP] CG8580 65F4-65F5 dup:2/2
ID:85H4

CG8580

CG14100 + unknown * 6e-11 hypothetical protein * hypothetical protein * YG73_SYNY3 HYPOTHETICAL TRNA/RRNA
METHYLTRANSFERASE * [SpoU_methylase] CG14100 LD26903 76B9-76B9 dup:1/2 ID:85H9
+ function_unknown * coded for by C. elegans cDNA yk36f5.3; coded for by C. elegans cDNA yk36f5.5; similar to glucose
repression mediator protein (SP:CYC8_YEAST, * ubiqu [TPR_REGION // TPR_REPEAT // TPR] CG5640 LD27005 31C7-31D1
dup:2/2 ID:86A10

CG5640

CG17540 + RNA_binding * 2e-14 predicted using Genefinder; Similarity to Arabidopsis DNA-damage-r * 8e-43 splicing factor (45kD);
SPF 45kDa splicing factor; SPF * 2e-17 D111 [D111_DOMAIN] CG17540 LD27025 cyto_unknown ID:86A12
+ bcd transcription_factor * DNA-binding-protein,transcription-factor(aa) * DMBCDG_3 bcd * 1e-125 bcd protein * 8e-52
homeotic protein bicoid - fruit fly (Drosophila ps[RNP_1 // HOMEBOX_1 // homeobox // HOME] CG1034 LD27003 84D1-84D1
dup:1/2 ID:86A8

CG1034

CG5452 + dnk enzyme * 1e-145 deoxynucleoside kinase * 2e-31 DCK_MOUSE DEOXYCYTIDINE KINASE (DCK) deoxycytidine kina *
1e-49 thymidine kinase * 2e-30 DCK_RAT DEOXYCYTIDINE [ATP_GTP_A] CG5452 94A3-94A3 dup:2/2 ID:86C1

CG5452

CG6005 + NLS_BP CG6005 LD27322 dup:2/2 ID:86D10
+ RNA_binding * 6e-05 NOP3_YEAST NUCLEOLAR PROTEIN (MITOCHONDRIAL TARGETING SUPPRESSOR PROTEIN)
* 1e-32 contains similarity to RNA recognition motifs (RNP) * 2e-50 C [RNP_1 // RBD // rrm] CG13298 LD27466 65A6-65A6
dup:2/2 ID:86E10

CG13298

CG12085 + poly-U-binding-splicing-factor RNA_binding * sia binding protein 1(aa) * 4e-13 PABP_YEAST POLYADENYLATE-BINDING
PROTEIN, CYTOPLASMIC AND NUCLEAR (PABP) (ARS CO * 3e-14 polyadenylate-bind[RNP_1 // RBD // rrm] CG12085
LD27486 62A4-62A4 dup:2/2 ID:86E12

CG12085

CG3338 + Similar to a hydrophilic protein that is peripherally associated with the late Golgi in yeast. Homology to uncharacterized
proteins in Arabidopsis, h CG3338 LD27356 dup:3/3 ID:86E2

CG3338

CG6066 + unknown * O1(aa) * 2e-31 predicted protein of unknown function thal * * [NLS_BP] CG6066 LD27582 97E8-97E8
ID:86F10

CG6066

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

CG10417

CG17912 + transcription_factor * CROL ALPHA(aa) * zinc finger protein 207(aa) * predicted using Genefinder; similar to Zinc finger,
C2H2 type; cDNA EST comes from this gene; cDNA E CG17912 LD27810 36A7-36A8 dup:3/3 ID:86H6

CG17912

+ protein_phosphatase * 7e-33 protein-tyrosine phosphatase; PTPase; MPTP-MEG2 * 1e-32 protein tyrosine phosphatase, non-receptor type * 7e-40 protein-tyrosine-phosphatase ([G_PROTEIN_RECEPTOR // CRAL_TRIO] CG3102 LD27988 8F2-8F2 ID:87A10
 CG3102
 + Rad23 DNA_repair_protein * DHR23(aa) * 2e-30 UV excision repair protein UV exci * 9e-05 ubiquitin / ribosomal protein S27a - fruit fly (Drosophila melanogaster) * 4e-38 Simila [UBA // ubiquitin // UBIQUITIN_2] CG1836 102A8-102A8 dup:1/3 ID:87A11
 CG1836
 + ion_channel * similar to S. cerevisiae HAP4 transcriptional activator (SP:HAP4_YEAST, similar to regulatory domain of PI3-kinase P85-alpha subunit (phosphatidylin [PDZ] CG1976 LD28013 100F1-100F2 ID:87A12
 CG1976
 + sl enzyme * 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) gamma-D - fruit fly (Drosophila melanogaster)(aa) * DMCS_2 sl * phospholipa [PHPLIPASEC // SH2DOMAIN // C2 // PIPLC] CG4200 LD27939 14B18-14C1 ID:87A7
 CG4200
 + receptor * 4e-16 VT11_YEAST VESICLE TRANSPORT V-SNARE PROTEIN VT11 proba * 3e-27 cDNA EST yk433f11.3 comes from this gene; cDNA EST yk433f11.5 come * 3e-32 put CG3279 LD27967 61C9-61C9 dup:1/3 ID:87A9
 CG3279
 + enzyme_activator * 1e-29 YQK1_CAEEL HYPOTHETICAL 55.9 KD PROTEIN C56G2.1 IN CHROMOSOME III (U * 6e-32 AKAP121 * 9e-33 A kinase anchor protein, 149kD * 9e-35 A-kinase a [TUDOR] CG3249 LD28079 4F8-4F9 dup:2/3 ID:87B11
 CG3249
 + lola transcription_factor * DMPIPSQ1_3 psq * BtbV * lola * 1e-171 LOLS_DROME LOLA PROTEIN, SHORT ISOFORM (LONGITUDINALS LACKING PROTEIN) [BTB] CG12052 LD28033 47A-47A ID:87B3
 CG12052
 + transmembrane_receptor * InR * INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)(aa) * 2e-52 INSR_DROME INSULIN-LIKE RECEPTOR PRECURSOR insulin recep[Recep_L_domain // Furin-like] CG10702 LD28036 37B13-37B13 dup:2/3 ID:87B4
 CG10702
 + unknown * splicing factor 30, survival of motor neuron-related; SPF 30(aa) * SMN gene * CG17454 LD28068
 CG17454
 cyto_unknown ID:87B8
 + protein_kinase * CASEIN KINASE I, GAMMA ISOFORM (CKI-GAMMA 1)(aa) * CASEIN KINASE I, ALPHA ISOFORM (CKI-ALPHA)(aa) * 1e-89 CK12_YEAST CASEIN KINASE I HOMOLOG casein [pkinase] CG6963 LD28216 89B17-89B19 ID:87C12
 CG6963
 + Mcm5 DNA_replication_factor * Mcm5 * 1e-176 MCM5_YEAST MINICHROMOSOME MAINTENANCE PROTEIN (CELL DIVISION CONTROL PROTEIN * MCM5 homolog * MCM5_CAEEL DNA REPLICATION LICENSIN[MCM // MCM_1 // MCM_2 // NLS_BP] CG4082 LD28351 86C5-86C5 dup:3/5 ID:87D11
 CG4082
 + unknown * * 1e-05 HR12_MOUSE HEAT-RESPONSIVE PROTEIN heat-responsive prot * 7e-05 UK14_HUMAN 14.5 KD TRANSLATIONAL INHIBITOR PROTEIN (P14.5) (UK114 ANTIGEN H [UPF0076 // PROTEIN_KINASE_ATP] CG1578 LD28359 10E3-10E4 dup:4/5 ID:87D12
 CG1578
 CG2061
 + BcDNA:LD28247 G protein-coupled receptor 69A CRYSTALLIN_BETAGAMMA CG2061 LD28247 dup:2/3 ID:87D2
 + RNA_binding * dJ222E13.3.2 (PUTATIVE partial isoform 2)(aa) * DMBNBR_2 bnb * CG6961 LD28479 17D5-17D5 dup:3/4 ID:87F6
 CG6961
 + protein_kinase * 5e-49 PAN3_YEAST PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN3 (PAB1P-DEPEN * 2e-92 YOT7_CAEEL HYPOTHETICAL 76.2 KD PROTEIN ZK632.7 IN CH [AA_TRNA_LIGASE_II_2 // ANTIFREEZE] CG11486 63F4-63F4 dup:1/6 ID:87G3
 CG11486
 CG17521
 + Qm ribosomal_protein 60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) RIBOSOMAL_L10E, Ribosomal_L10e

CG17521 ID:87H3

CG17033 + CG17033 ID:87H8

CG1218 + CG1218 ID:87H9

CG5821 + RNA_binding CG5821 ID:88A7

+ sop ribosomal_protein * Ribosomal protein S2 (S4) (rp12) (YS5); Rps2p(aa) * sop * 2e-73 RS4_YEAST 40S RIBOSOMAL PROTEIN S4 (OMNIPOTENT SUPPRESSOR PROTEIN SUP44) (RP12) (* 1 [Ribosomal_S5 // RIBOSOMAL_S5] CG5920 33A1-33A1 dup:1/2 ID:88A8

CG5920

CG18041 + CG18041 ID:88B6

CG11177 + CG11177 ID:88C8

CG8116 + unknown * 1e-108 inserted at base 3' end of P element Inverse PCR * * CG8116 85B2-85B2 dup:1/2 ID:88D7

+ unknown * histone acetyltransferase 1(aa) * histone acetyltransferase; Hat1p(aa) * weak similarity with SINR protein (Swiss Prot accession number cDNA EST co [NLS_BP] CG2051 83C-83C dup:2/3 ID:88F12

CG2051

CG16901 + CG16901 ID:88G12

CG1596|unknown|CT3517 + CG1596|unknown|CT3517 ID:88G5

CG7471 + enzyme CG7471 ID:88H1

+ RNA_binding * pre-mRNA cleavage factor Im (68kD)(aa) * 2e-16 Similarity to Brassica glycine-rich RNA-binding protein (SW:GR10_B * 2e-29 HPBR11-7 protein - human H [RBD // rrm // PRO_RICH // NLS_BP] CG7185 66C6-66C7 dup:3/5 ID:88H10

CG7185

+ EG:EG0007.12 unknown * by content; by motif; 2-match_description=ATP/GTP-binding site motif A (P-I...(aa) * by content; 1-meth * by content; 1-meth * CG4857 4B1-4B2 dup:3/3 ID:88H5

CG4857

CG11723 + transcription_factor * [AA_TRNA_LIGASE_II_1] CG11723 22C3-22C3 dup:2/2 ID:88H7

CG5094 + chaperone CG5094 dup:2/2 ID:88H9

+ * 6e-24 predicted using Genefinder; similar to zinc-finger protein; cDNA E * 8e-05 DNA-binding protein BZP - golden hamster DNA-binding prot * 2e-06 z [zf-C2H2 // ZINC_FINGER_C2H2 // PRO_RICH] CG1244 62F2-62F2 dup:2/5 ID:89A1

CG1244

CG9277 + betaTub56D cytoskeletal_structural_protein beta-1 tubulin TUBULIN, TUBULIN_B_AUTOREG, tubulin CG9277 ID:89A3

+ unknown * predicted using Genefinder(aa) * 3e-12 predicted using Genefinder * * [SAM_DOMAIN] CG16812 34A10-34A10 dup:1/4 ID:89A4

CG16812

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

+ * C15H9.5 gene product(aa) * 5e-05 by content; 1-meth * 5e-70 C15H9.5 gene product * 1e-05 NEUM_MOUSE NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (P CG12121 8D4-8D5 dup:2/3 ID:89B4

CG12121

CG12269

+ RpS3 * Ribosomal protein S3 (rp13) (YS3); Rps3p(aa) * 40S RIBOSOMAL PROTEIN S3(aa) * DMRPS3_2 RpS3 * 8e-82 RS3_YEAST 40S RIBOSOMAL PROTEIN S3 (YS3) (RP13) [KH-domain // RIBOSOMAL_S3 // Ribosomal_] CG6779 94F1-94F1 dup:2/2 ID:89B9

CG6779

CG2186 + homolog of a human hypothetical protein DKFZp434D1319.1 NLS_BP CG2186 LD29862 dup:1/2 ID:89C10

CG10954 + P34-ARC actin_binding PROBABLE ARP (actin related protein) 2/3 COMPLEX 34 KDA SUBUNIT CG10954 LD29815 dup:2/3

ID:89C2

CG8924 + transcription_factor * 4e-30 alternatively spliced form * 4e-07 BAC1_MOUSE TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) * 2e-07 actin binding protein MAYV [BTB] CG8924 LD29820 13F14-13F14 ID:89C4

CG5014 + * VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPOBREVIN BINDING PROTEIN (VAP-33)(aa) * 2e-09 SCS2_YEAST SCS2 PROTEIN SCS2 protein - yeast (Saccharomy * 6e [MSP_domain // MSP_DOMAIN] CG5014 4A2-4A2 dup:2/3 ID:89D12

CG3333 + Nop60B enzyme * CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5)(aa) * major low affinity kDa Centromere/microtubu CG3333 LD30073 60B10-60B10 dup:4/4 ID:89E9

CG7490 + RpP0 * DMAP3A_2 RpP0 * ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG (L10E) (RIBOSOMAL PROTEIN L10)(aa) * 60S ACIDIC RIBOSOMAL PROTEIN P0 (DEOXYRIBONUCLEASE (APURINI [60s_ribosomal // Ribosomal_L10] CG7490 79C3-79C3 dup:3/3 ID:89F5

CG4985 + transcription_factor neural zinc finger factor 3; NZF-3 [Rattus norvegicus] ATPASE_ALPHA_BETA, zf-C2HC CG4985 LD30401 dup:2/2 ID:89H10

CG12050 + unknown unknown protein [Arabidopsis thaliana] NLS_BP, WD40_REGION CG12050 LD30416 dup:2/2 ID:89H12

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

CG6241 + unknown * 8e-07 TAFI68 * 7e-06 transcription factor SL1 * [NLS_BP] CG6241 LD35363 85F13-85F13 ID:95A2

CG5108 + ribosomal_protein * cDNA EST yk433f11.3 comes from this gene; cDNA EST yk433f11.5 comes from this gene(aa) * 9e-05 YJ83_YEAST PUTATIVE 40S RIBOSOMAL PROTEIN YJR113C pro [Ribosomal_S7] CG5108 LD35371 31D11-31D11 ID:95A3

CG11266 + RNA_binding * splicing factor (CC1.3)(aa) * 5e-12 polyadenylated RNA-binding protein PUB1 - yeast (Saccharomyces cerevisiae) >g * 7e-11 RNA-binding protein * 1e-1 [RNP_1 // RBD // rrm // NLS_BP] CG11266 LD35730 27D-27D3 dup:1/2 ID:95C11

CG6376 + E2f transcription_factor * E2f * E2F * 1e-19 predicted using Genefinder; cDNA EST comes from this * 5e-35 E2F3_MOUSE TRANSCRIPTION FACTOR E2F3 (E2F-3) transcripti [NLS_BP] CG6376 LD35741 93F1-93F1 dup:2/3 ID:95C12

CG4621 + unknown * BLASTX 1.2E-22 Human YL-1 mRNA for YL-1 protein (nuclear protein with DNA-binding ability), complete cds.(dna) * transcription factor-like 1(aa) * t [NLS_BP] CG4621 LD35676 34A3-34A3 ID:95C3

CG7705 + unknown * CG7705 LD35690 91B7-91B8 ID:95C5

CG7281 + CycC cell_cycle_regulator * DMCYCLCG_2 CycC * cyclin C(aa) * cyclin C protein(aa) * cyclin C(aa) CG7281 LD35705 88D8-88D8 dup:3/3 ID:95C8

CG7558 + 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 LD35711 66B8-66B8 ID:95C9

CG3735 + unknown * 8e-73 YIJ1_YEAST HYPOTHETICAL 84.0 KD PROTEIN IN SGA1-KTR7 INTERGENIC REGION * 1e-119 dJ434O14.5 (novel PUTATIVE protein similar to YIL091C yeast hy CG3735 LD35854 60A11-60A11 ID:95D10

CG9425	+ RNA_binding * HYPOTHETICAL PROTEIN * 3e-23 YKB7_YEAST HYPOTHETICAL 78.3 KD PROTEIN IN RAM2-ATP7 INTERGENIC REGION * 9e-11 cDNA EST yk384f3.5 comes from this gene; [zf-CCCH] CG9425 LD35863 70F6-70F6 dup:3/3 ID:95D12
CG7948	+ Rad51 DNA_repair_protein * DMDMRBA_1 Rad51 * 2e-97 RA51_YEAST DNA REPAIR PROTEIN RAD51 RAD51 protein - yeast * 1e-176 RA51_DROME DNA REPAIR PROTEIN RAD51 HOMOLOG (RECA PROTEIN [HHH // RECA_1 // RECA_2 // ATP_GTP_A] CG7948 LD35801 99D5-99D6 ID:95D3
CG7838	+ 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 42A1-42A1 ID:95D5
CG3287	+ motor_protein * 1e-34 cDNA EST comes from this gene; cDNA EST co * 3e-61 protein * 4e-19 SAD1_SCHPO SPINDLE POLE BODY ASSOCIATED PROTEIN SAD1 sp * 4e-29 inserted at CG3287 LD35815 42D1-42D1 dup:2/2 ID:95D6
CG1708	+ cos motor_protein * cos * 3e-20 YGW6_YEAST PUTATIVE KINESIN-LIKE PROTEIN YGL216W hypoth * kinesin-related protein; KRP; Costal2 * 1e-21 Similarity to Mouse kinensin-lik [kinesin // KINESIN_MOTOR_DOMAIN2 // KIN] CG1708 LD35834 43B2-43B2 ID:95D7
CG3594	+ RNA_binding * 8e-06 hypothetical protein YPR112c - yeast (Saccharomyces cerevisiae) (U * 1e-05 similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); c [RBD // rrm // NLS_BP] CG3594 LD36016 60D15-60D15 dup:2/2 ID:95E12
CG9062	+ signal_transduction * 5e-11 CC4_YEAST CELL DIVISION CONTROL PROTEIN cell division * 8e-25 Lis1 homolog * 1e-127 YPR4_CAEEL HYPOTHETICAL 77.0 KD TRP-ASP REPEATS CO[GPROTEINBRPT // WD40_REGION // WD_REPEA] CG9062 LD35961 47E3-47E3 dup:4/4 ID:95E7
CG17081	+ motor_protein * 6e-08 F35D11.11 gene product * YL17_CAEEL HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME X (* [NLS_BP] CG17081 LD35990 71B2-71B2 dup:3/3 ID:95E9
CG7892	+ nmo protein_kinase * nmo * 2e-58 HOG1_YEAST MITOGEN-ACTIVATED PROTEIN KINASE HOG1 (MAP KINASE HOG1) (OSMOSENSING * nemo, form I - fruit fly (Drosophila melanogaster) [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG7892 LD36031 67D9-66B4 dup:2/2 ID:95F4
CG1943	+ unknown * CG1943 LD36048 84C1-84C1 ID:95F5
CG2102	+ nucleic_acid_binding * castor protein - fruit fly (Drosophila sp.)(aa) * neuroblast cell lineage zinc finger protein ming - fruit fly (Drosophila melan * l(3)j1C2 l(3)j1C[CRYSTALLIN_BETAGAMMA // ZINC_FINGER_C2H] CG2102 LD36057 83C1-83C1 ID:95F7
CG7546	+ ubiquitin * BAT3(aa) * 2e-05 ubiquitin-like protein DSK2 - yeast (Saccharomyces cerevisiae) * 3e-14 BAT3 * 2e-15 Scythe [UBIQUITIN_1 // ubiquitin // UBIQUITIN_2] CG7546 LD36241 67B10-67B10 dup:1/2 ID:95G12
CG4454	+ unknown * CG4454 LD36125 32A1-32A1 dup:2/3 ID:95G2
CG8326	+ motor_protein * CG8326 LD36157 16B10-16B10 ID:95G4
CG5175	+ CG5175 ID:95H10
CG12363	+ Dlc90F motor_protein * Tctex protein(aa) * DMTCTEXPR_2 Tctex * 1e-61 Tctex protein * 7e-14 predicted using Genefinder; cDNA EST yk460f12.5 comes from this ge CG12363 LD36705 90F7-90F7 ID:96B11
CG1341	+ Rpt1 endopeptidase * 1e-166 PRS7_YEAST 26S PROTEASE REGULATORY SUBUNIT HOMOLOG (CIM5 PROTEIN) (TAT-

BINDING * 4e-48 transitional endoplasmic reticulum ATPase TER94 * PRS [AAA // ATP_GTP_A] CG1341 LD36653 43E6-43E6
dup:1/3 ID:96B9

+ Csp chaperone * cysteine string protein 1(aa) * 2e-16 MAS5_YEAST MITOCHONDRIAL PROTEIN IMPORT PROTEIN
MAS5 (PROTEIN YDJ1) * 4e-19 similar to the DNA-J domain foun [4FE4S_FERREDOXIN // DNAJ_1 // DnaJ // D] CG6395
LD36856 79E1-79E2 dup:1/4 ID:96C8

CG6395 + thr unknown * three rows protein * thr * THR_DROME THREE ROWS PROTEIN chromosome disjunction prot [NLS_BP]
CG5785 LD37031 54F5-54F6 dup:2/2 ID:96D10

CG4877 + unknown * [NLS_BP] CG4877 LD36996 72F1-72F1 dup:2/2 ID:96D5

CG13626 + unknown * 1e-05 No definition line found * [T_SNARE] CG13626 LD37002 96A14-96A14 ID:96D6

+ Noa36 nucleic_acid_binding * nucleolar protein, putative(aa) * 1e-111 cysteine-rich protein * 1e-110 Zn finger factor *
[NLS_BP] CG10009 LD37139 98D3-98D3 dup:2/2 ID:96E5

CG10009 + transporter * 4e-09 maltose permease - Bacillus stearothermophilus maltose pe * transcription factor IIE - African clawed
frog * TflIE&agr; CG7334 LD37218 68C13-68C13 ID:96F3

CG7334 + fs(1)K10DNA_binding * regulatory protein K10, oocyte-specific - fruit fly (Drosophila melanogaster)(aa) * DMK10G_4 fs(1)K10 *
CG3218 4e-58 K10_DROME DNA-BINDING PROTEIN K10 * 62 [PRO_RICH] CG3218 LD37240 2F1-2F1 ID:96F7

CG3218 + unknown * 8e-08 predicted using Genefinder; similar to WW domain * 1e-07 inserted at base Both 5' and 3' ends of P
element Inverse PCR * [WW_rsp5_WWP // WW_DOMAIN_1 // NLS_BP //] CG8949 15D1-15D1 ID:96G10

CG8949 + function_unknown * 2e-05 hypothetical protein YDL115c - yeast (Saccharomyces cerevisiae) * 5e-09 hypothetical protein *
CG10528 2e-43 inserted at base 5' end of P element Inve CG10528 LD37329 38A-38A4 dup:1/3 ID:96G3

CG10528 + EG:EG0007.10 unknown * by content; * 1e-92 by content; 1-meth * 1E-94* CG4865 LD37360 4B1-4B1 ID:96G8

CG4865 + B52 RNA_binding * transcription, DNA-dependent mRNA splicing) RNA binding RNA binding) nucleic acid binding pre-
mRNA splicing factor) * DMB52_2 B52 * 52K active ch [RBD // rrm // NLS_BP] CG10851 LD37428 87F7-87F7 ID:96H1

CG10851 + unknown * CG6311 LD37618 74D2-74D2 dup:1/2 ID:96H12

CG6311 + RNA_binding * * 3e-33 cDNA EST yk500a3.3 comes from this gene; cDNA EST yk500a3.5 comes * 2e-64 inserted at
base Unknown 5' end of P element Plasmid rescue * CG2503 LD37523 82E1-82E1 ID:96H6

CG2503 + * 2e-14 cDNA EST yk448c11.3 comes from this gene; cDNA EST com * * CG10978 83C-83C dup:2/4 ID:97A5

CG10978 + unknown * [KININOGEN] CG2961 LD38046 9B7-9B7 ID:97C11

CG2961 + transcription_factor * Cys2/His2 zinc finger protein(aa) * ovo * fruit fly STS clone SP6(dna) * zinc finger protein NY-REN-
CG4639 21 antigen(aa) [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG4639 LD38072 94E-94E ID:97D4

CG4639 + unknown * CG8928 LD38104 13F14-13F14 ID:97D7

CG8928 + EG:8D8.4unknown * /match=(desc:(aa) * 5e-48 hypothetical protein YDR365c - yeast (Saccharomyces cerevisiae) (U * 6e-34
CG11417 cDNA EST comes from this gene * 4e-60 hypothet [NLS_BP] CG11417 LD38432 2A2-2A2 dup:2/2 ID:97F9

CG11417 + unknown * 5e-10 FIP1_YEAST FIP1 PROTEIN FIP1 protein - yeast (Saccharom * 3e-16 contains similarity to S. cerevisiae
CG1078 FIP1 * 2e-13 YAAA_SCHPO HYPOTHETICAL 37.3 [PRO_RICH // NLS_BP] CG1078 LD38592 82C2-82C2 dup:1/3 ID:97G11

CG1078 + unknown * weak similarity to ATP/GTP-binding site motif A * 2e-40 weak similarity to ATP/GTP-binding site motif A elega *
CG5924 1e-63 POM1 chabaudi * [ATP_GTP_A] CG5924 LD38710 33A1-33A1 dup:1/2 ID:97H9

+ BcDNA:GH07910 protein_kinase * 7e-22 CC5_YEAST CELL CYCLE PROTEIN KINASE CDC5/MSD2 protein ki * 3e-12 p90
 ribosomal S6 kinase * 1e-121 YKT3_CAEEL PUTATIVE SERINE/THREONINE-[PFKB_KINASES_1 // PROTEIN_KINASE_ST //]
 CG2829 LD38852 3F4-3F6 dup:5/6 ID:98B2
 + unknown * 4e-14 YPT2_CAEEL HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III * 5e-05 unknown
 CG8441 protein * * [NLS_BP] CG8441 LD38910 52F7-52F7 dup:2/2 ID:98B9
 + unknown * 1e-75 hypothetical protein * repressor of the gab DTP gene cluster * Y039_MYCPN HYPOTHETICAL
 CG10639 PROTEIN MG039 HOMOLOG glycerol- * CG10639 LD39082 37B8-37B8 ID:98C7
 + transcription_factor * 0.00000000006* 9e-25 YMB4_CAEEL HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN
 CG1624 CHROMOSOME III * 4e-13 TIF1 protein - mouse TIF1 isoform Pepti * 8e-24 brai [NHL] CG1624 LD39167 43C5-43C7 ID:98D2
 CG14764 + unknown * CG14764 LD39211 43F6-43F6 ID:98D5
 + unknown * CGI-25 protein(aa) * Unknown protein(aa) * 5e-61 R05G6.4 gene product * [NLS_BP] CG6179 LD39230
 CG6179 17A10-17A10 ID:98D7
 + sta ribosomal_protein * 6e-69 NABA_YEAST 40S RIBOSOMAL PROTEIN SA HOMOLOG A (NUCLEIC ACID-BINDING
 CG14792 PROTEIN NAB1 * 1e-143 RSP4_DROME 40S RIBOSOMAL PROTEIN SA (P40) (STUBARIST RIBOSOMALS2,
 RIBOSOMAL_S2_1 CG14792 ID:98D8
 CG6425 + unknown * CG6425 LD39291 97C3-97C3 dup:2/2 ID:98E3
 + asf1 cell_cycle_regulator * involved in silencing; Asf1p(aa) * Similarity with yeast anti-silencing protein I (Swiss Prot accession
 CG9383 number cDNA EST comes from this gene; cDNA CG9383 LD39377 76C1-76C1 dup:2/2 ID:98E8
 + DNA_binding * 2e-15 YJ89_YEAST HYPOTHETICAL 85.0 KD PROTEIN IN STE24-ATP2 INTERGENIC REGION * 8e-26
 Similarity to Human XE169 protein (SW:XE169_HUMAN); cDNA EST E [ARID // PRO_RICH // NLS_BP] CG3654 LD39559 67B5-
 CG3654 67B5 dup:3/3 ID:98F11
 CG1896 + unknown * [NLS_BP] CG1896 LD39576 100E2-100E2 dup:2/2 ID:98F12
 CG6141 + RpL9 ribosomal_protein 60S RIBOSOMAL PROTEIN L9 RIBOSOMAL_L6_2, Ribosomal_L6 CG6141 ID:98F7
 + mod DNA_binding * DNA-BINDING PROTEIN MODULO(aa) * DMLA9_4 mod * 3e-05 Similarity to Human spliceosome-
 associated protein SAP62 (PIR Acc. * 5e-05 NUCL_MOUSE NUCLEOLIN [RBD // rrm // NLS_BP // ATP_GTP_A] CG2050
 CG2050 100F5-100F5 dup:3/3 ID:98F9
 + BcDNA:LD27873 actin_binding * 1e-06 RNA-binding protein * 1e-06 NAB2_YEAST NUCLEAR POLYADENYLATED RNA-
 BINDING PROTEIN NAB2 * 3e-88 inserted at base Both 5' and 3' ends of P eleme [NLS_BP] CG5720 95F-98B1 dup:5/8
 CG5720 ID:98G12
 + EG:95B7.7 transcription_factor * /motif=(desc;; /motif=(desc;; /motif=(desc;; /match=(desc:(aa) * /motif=(desc;; /motif=(desc;;
 /motif=(de * 3e-29 similar to Zinc finger, C2H2 type[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG2712 LD39664 3B6-3B6
 CG2712 ID:98G8
 CG10944 + RpS6 ribosomal_protein 40S RIBOSOMAL PROTEIN S6 NLS_BP, RIBOSOMAL_S6E CG10944 ID:98H3
 + Dp transcription_factor * DMDPRTF_2 Dp * transcription factor * 6e-59 similar to transcription factor DP-1; cDNA EST comes
 CG4654 f * 5e-72 TDP1_MOUSE TRANSCRIPTION FACTOR DP-1 (E2F CG4654 LD39905 49F13-49F13 dup:2/2 ID:99A2
 + BcDNA:LD23181 protein_phosphatase * 1e-41 inserted at base Both 5' and 3' ends of P element Inverse PCR * *
 CG6542 [TYR_PHOSPHATASE_1] CG6542 LD39930 54C1-54C3 ID:99A6

+ chaperone * M-phase phosphoprotein 11(aa) * zuotin related factor 2(aa) * strong similarity to mouse DNAJ-like protein MTJ1 * 6e-41 ZUO1_YEAST ZUOTIN zuotin - [MYB_3 // DnaJ // DNAJ_2 // NLS_BP] CG10565 LD40027 78C1-78C1 dup:2/2 ID:99B6
 CG10565
 + transcription_factor * 3e-09 TF3A_YEAST TRANSCRIPTION FACTOR IIIA (TFIIIA) transcriptio * 3e-15 CROL ALPHA * 2e-06 similar to Zinc finger, C2H2 type (3 domains)[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG12941 LD40262 47C6-47C6 dup:1/2 ID:99C12
 CG12941
 + gammaTub23C cytoskeletal_structural_protein * similar to Tubulin (2 domains); cDNA EST CEMSG51F comes from this gene(aa) * gamma-tubulin 3(aa) * TUBULIN ALPHA-4 CHAIN(aa) * DMTUBA4_2 agr;Tub67C [TUBULIN // tubulin] CG3157 LD40196 23C2-23C2 ID:99C6
 CG3157
 CG8374 + dmt unknown * [NLS_BP] CG8374 LD40216 85E5-85E5 ID:99C7
 + electron_transfer * Protein with glutaredoxin activity; Grx3p(aa) * predicted using Genefinder; cDNA EST CEMSA40F comes from this gene; cDNA EST CEMSA40R comes from [AA_TRNA_LIGASE_II_2 // THIOREDOXIN_2] CG6523 LD40224 34B6-34B6 dup:1/2 ID:99C9
 CG6523
 + receptor * 7e-05 CRM1_YEAST CHROMOSOME REGION MAINTENANCE PROTEIN CRM1 * 1e-120 protein * 6e-28 inserted at base Both 5' and 3' ends of P element Inverse PCR * [IBN_NT] CG7212 LD40304 90E-90E5 dup:2/3 ID:99D6
 CG7212
 + unknown * Loc7p(aa) * 13S condensin XCAP-D2 subunit(aa) * gene product is related to yeast protein * 8e-38 hypothetical protein YLR272c - yeast (Saccharomyce [NLS_BP] CG1911 LD40412 99B-99B dup:2/2 ID:99E3
 CG1911
 + RNA_binding * DMB52_2 B52 * ASF/SF2 homolog(aa) * nuclear phosphoprotein SRp55 - fruit fly (Drosophila melanogaster)(aa) * dJ862K6.2.1 (splicing factor, (SRP55-1) [RBD // rrm] CG6987 LD40489 89B21-89B21 dup:2/3 ID:99F1
 CG6987
 + ligand_binding_or_carrier * fast-twitch myosin light chain 1(aa) * DMTNC41C_2 TpnC41C * 1e-35 CC31_YEAST CELL DIVISION CONTROL PROTEIN cell division * 5e-32 CALM_DROME CALMO[EF_HAND // efhand // EF_HAND_2] CG17493 LD40645 cyto_unknown ID:99F11
 CG17493
 + DNA_binding * 9e-09 ssrp2 * 4e-09 contains similiarity to HMG boxes * 3e-19 mitochondrial transcription factor A * 6e-27 transcription factor 6-like (mitochondria [HMG // HMG_box // NLS_BP] CG4217 LD40493 92E11-92E11 ID:99F2
 CG4217
 + unknown * No definition line found(aa) * 4e-13 No definition line found * [WW_rsp5_WWP // NLS_BP // WW_DOMAIN_2] CG11820 LD40504 98F6-98F6 dup:1/2 ID:99F5
 CG11820
 + RNA_binding * 2e-16 SME1_YEAST SMALL NUCLEAR RIBONUCLEOPROTEIN E HOMOLOG SME1 * 1e-27 predicted using Genefinder * 1e-30 small nuclear ribonucleoprotein E * 8e-33 [BTB // Sm] CG7102 LD40565 28D5-28D5 ID:99F7
 CG7102
 CG9839 + unknown * [CYTOCHROME_C] CG9839 LD40589 85E9-85E9 ID:99F8
 + signal_transduction * Caf1 * Nle * Taf80 * 5e-13 T2D4_YEAST TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUNIT (TAFII-90) [GPROTEINBRPT // WD40_REGION // WD_REPEA] CG6724 LD40657 32A5-32A5 ID:99G1
 CG6724
 + RNA_binding * Bub3 * WD-40 repeat protein(aa) * HYPOTHETICAL 41.4 KD TRP-ASP REPEATS CONTAINING PROTEIN F10G8.3 IN CHROMOSOME I(aa) * HYPOTHETICAL RAE1-LIKE PROTE [GPROTEINBRPT // WD40_REGION // WD_REPEA] CG9862 LD40776 57F6-57F6 ID:99G12
 CG9862
 + unknown * HYPOTHETICAL 96.2 KD PROTEIN C08B11.4 IN CHROMOSOME II(aa) * predicted using Genefinder(aa) * 3e-05 /match=(desc: * 7e-38 cDNA EST comes from this CG8185 LD40680 52A9-52A10 dup:1/2 ID:99G3
 CG8185
 CG5589 + RNA_binding * 1e-89 ROK1_YEAST ATP-DEPENDENT RNA HELICASE ROK1 ATP-dependen * 1e-41 VASA_DROME

VASA PROTEIN vasa mel * 1e-81 similar to ATP dependent RNA helicase [helicase_C // HELICASE // DEAD // NLS_B] CG5589
 LD40692 75A2-75A2 dup:1/3 ID:99G4
 + transporter * CGI-19 protein(aa) * 5e-07 probable membrane protein YPL244c - yeast (Saccharomyces cerevisiae) * 7e-83
 CG7853 No definition line found * 2e-40 putative pr CG7853 LD40702 73E4-73E4 ID:99G5
 + enzyme * Yjr084wp(aa) * acyl-protein thioesterase(aa) * 1e-22 probable membrane protein YLR118c - yeast
 CG7351 (Saccharomyces cerevisiae) * 3e-67 YPI7_CAEEL HYPOTH [TNF_1] CG7351 LD40777 68C10-68C10 dup:2/3 ID:99H1
 + unknown * 7e-41 SS72_YEAST SSU72 PROTEIN hypothetical protein YNL222w - * 7e-57 coded for by C. elegans cDNA
 CG14216 yk10c10.3; coded for by C. elegans cDNA yk37e8.3; CG14216 LD40846 18D12-18D12 ID:99H10
 + * BLASTX 2.3E-13 TRA1|Homolog of human TR-AP which associates with a domain of c-Myc essential for cellular
 CG2905 transformation(dna) * predicted using Gen [PI3_4_KINASE_3] CG2905 41A1-41A1 ID:99H3
 + DNA_repair_protein * DMDNAPOLD_2 DNAPol- dgr; * DNA polymerase zeta subunit; Rev3p(aa) * 1e-152 DPOZ_YEAST
 CG1925 DNA POLYMERASE ZETA CATALYTIC SUBUNIT DNA-dire * 2e-69 DPOD_D[DNAPOLB // DNA_POLYMERASE_B //
 CG1404 DNA_pol_] CG1925 LD40801 43E16-43E17 ID:99H4
 + enzyme CG1404 ID:99H5
 + motor_protein * * similar to S. pombe phosphoprotein * BLASTX 2.1E-09 P.falciparum merozoite surface antigen (MSA-2)
 CG8176 gene, complete cds.(dna) * BLASTX 5.7E-22 Homo [ZINC_PROTEASE] CG8176 LD40806 86C1-85D23 dup:3/3 ID:99H6
 + sec23 unknown * COPII protein, homolog of s. cerevisiae SEC23p(aa) * SC23_YEAST PROTEIN TRANSPORT PROTEIN
 CG1250 SEC23 protein transpo * S23A_MOUSE PROTEIN TRANSPORT PRO CG1250 LD40826 83B6-83B6 dup:3/4 ID:99H8
 CG12758 + unknown * [NLS_BP] CG12758 trimmed 55F8-55F13 dup:2/3 ID:Farhad's BA1
 CG6044 + unknown * CG6044 Igg2(4036) 58D7-58D7 dup:1/2 ID:Farhad's BA10
 CG10934 + CG10934 GH26058 dup:2/3 ID:Farhad's BA12
 + BcDNA:LD24639 enzyme * F17F8.28(aa) * sperm associated antigen 2(aa) * UDP-N-acetylglucosamine pyrophosphorylase;
 CG9535 Qri1p(aa) * 3e-88 QRI1_YEAST HYPOTHETICAL 53.5 KD PROTEIN [ATP_GTP_A] CG9535 LD24639 26D5-26D5 dup:2/3
 ID:Farhad's BB11
 + BcDNA:GH02976 structural_protein * 5e-28 Gasp precursor * 9e-11 cDNA EST comes from this gene; cDNA EST yk369a9.5
 CG4778 come * 4e-08 peritrophin * 6e-30 Gasp CG4778 ck00178 30F6-30F6 dup:3/3 ID:Farhad's BD2
 CG1124 + unknown CG1124 ck00336 dup:2/2 ID:Farhad's BD9
 CG5848 + cytoskeletal_structural_protein CG5848 cactus dup:3/4 ID:Path + Ctrl1 + kras198
 + protein_kinase * DMFGFR1_2 htl * connectin/titin(aa) * fll-1(aa) * FTL4(aa) [ig // PROTEIN_KINASE_TYR //
 CG8222 PROTEIN_KIN] CG8222 VEGFR 78F1 28F4-28F5 dup:9/12 ID:Path + Ctrl1 + kras305