

Table S24

female germline-list of genes from female germline cluster identified in hierarchical cluster (Fig. S7)

	+ Trl transcription_factor * DMGAGATRA_4 Trl * GAGA-581 Adf-2 isoform * 1e-05 contains similarity to the kelch/MIPP family * 6e-05 leukemia/lymphoma related factor LRF [BTB // zf-C2H2 // ZINC_FINGER_C2H2] CG9343 LD41963 70F4-70F4 dup:1/2 ID:101A10
CG9343	
	+ Ote motor_protein * 1e-174 OTE_DROME OTEFIN otefin - fruit fly (Drosophila melanogaster * 1e-176 DMOTEDA_2 Ote * * CG5581 LD41911 55C3-55C4 ID:101A4
CG5581	
	+ 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
CG6258	
	+ 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
CG2867	
	+ unknown * zinc finger protein(aa) * maf10(aa) * myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 6(aa) * ALL1 fu [PHD] CG1070 LD42009 84C1-84C3 dup:1/3 ID:101B2
CG1070	
	+ 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
CG1603	
	+ 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
CG3645	
	+ Gprk2 protein_kinase * 4e-45 protein kinase * GPRK2 * 1e-151 YQR1_CAEEL PROBABLE G PROTEIN-COUPLED RECEPTOR KINASE F19C6.1 * 1e-175 G protein-coupled receptor kinase 5; GR CG17998 LD42147 100C-100C dup:1/3 ID:101C4
CG17998	
CG12756	+ unknown * gene product(aa) * 8e-09 hypothetical protein * * CG12756 LD42148 64E3-64E3 ID:101C5
CG15634	+ unknown * CG15634 LD42284 25A4-25A4 ID:101D10
	+ 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
CG9834	
	+ EG:39E1.1 unknown * 5e-33 YNJ2_YEAST HYPOTHETICAL 45.5 KD PROTEIN IN YPT53-RHO2 INTERGENIC REGION * /match=(desc;; /ma * 6e-54 Similarity with yeast hypothetical prote [NLS_BP] CG11596 LD42227 2B17-2B17 dup:2/2 ID:101D3
CG11596	
	+ 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
CG12892	
CG17129	+ transcription_factor * [NLS_BP] CG17129 LD42420 61C9-61C9 dup:2/2 ID:101E10
	+ osa DNA_binding * eyelid(aa) * eld * 3e-05 YM42_YEAST HYPOTHETICAL 162.7 KD PROTEIN IN SIP18-SPT21 INTERGENIC REGION * 2e-37 coded for by C. elegans cDNA yk7c8.5; co [ARID // PRO_RICH // ANTIFREEZEI] CG7467 90C-90C dup:4/4 ID:101E12
CG7467	
CG5857	+ unknown * CG5857 LD42327 95C-95C dup:2/2 ID:101E3

+ Grip91 cytoskeletal_structural_protein * gamma-tubulin interacting protein(aa) * gamma-tubulin ring protein Dgrip91(aa) * 1e-123 spindle pole body protein spindle pole body protein spc98[DEHYDRATASE_SER_THR] CG10988 LD42379 12B7-12B7 dup:3/4 ID:101E5
 CG10988
 + 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
 CG2864
 + enzyme * 1e-89 predicted using Genefinder; Similarity to acid phosphatase * 1e-32 purple acid phosphatase like protein * Similarity to acid phosphatase * similar [PHOSPHO_ESTER] CG1637 LD42381 9F7-9F8 dup:2/2 ID:101E7
 CG1637
 + 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
 CG8378
 + Rep1 enzyme * Rep1 * 1e-121 DNA fragmentation factor DREP-1 * 1e-08 cell death activator CIDE-A * 4e-09 cell death-inducing DFFA-like effector a c CG8357 48E2-48E2 dup:3/3 ID:101E9
 CG8357
 + Pi3K21B signal_transduction * p60(aa) * DMPK57 Pi3K21B * p60 p * 2e-08 similar to vav proto-oncogene [PI3KINASEP85 // SH2DOMAIN // SH2] CG2699 LD42724 21B7-21B7 dup:2/2 ID:101F10
 CG2699
 + dock signal_transduction * dock * 6e-06 YG3D_YEAST HYPOTHETICAL 26.1 KD PROTEIN IN PAS5-CBF2 INTERGENIC REGION * 1e-157 SH2/SH3 adaptor protein * 4e-45 coded for by C. elegans[SH3DOMAIN // SH3 // NLS_BP // ATP_GTP_A] CG3727 LD42588 21D2-21D2 ID:101F2
 CG3727
 CG8121
 + unknown * CG8121 LD42595 85D9-85D9 ID:101F3
 + TH1 unknown * TH1(aa) * DMTH1X_3 TH1 * potential zinc-finger domains centered at aa and aa 364; kDa protein; putative(aa) * DMTH1X_3 TH1 CG9984 LD42626 14C4-14C4 ID:101F4
 CG9984
 + Pabp2 RNA_binding * HYPOTHETICAL 29.0 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION(aa) * DMROX2Y_3 Rox2 * RNA binding protein(aa) * 3e-39 Similarity to Bovine Poly-A bind [RNP_1 // RBD // rrm] CG2163 LD42638 44A7-44A8 ID:101F6
 CG2163
 + DNA_binding * X-linked nuclear protein(aa) * 8e-36 RA54_YEAST DNA REPAIR AND RECOMBINATION PROTEIN RAD54 RAD5 * 7e-41 RAD54 * 1e-145 strong similarity to the SNF2 [helicase_C // SNF2_N // NLS_BP] CG4548 LD42659 96E-96E2 dup:4/5 ID:101F7
 CG4548
 CG15312
 + transmembrane_receptor * [ig] CG15312 LD42756 9B1-9B1 ID:101G1
 + enzyme * No definition line found(aa) * predicted secreted protein(aa) * 3e-06 predicted secreted protein * [NLS_BP] CG1745 LD43003 10B15-10B15 dup:1/2 ID:101G12
 CG1745
 + 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
 CG9242
 + transcription_factor * zinc-finger-motif-protein * 1e-05 Bowel * 6e-05 predicted using Genefinder; similar to Zinc finger, C2H2 type (7 * 5e-14 zinc finger protein - mo[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG6791 87E1-87E1 dup:1/2 ID:101G3
 CG6791
 + Taf80 signal_transduction * 2e-17 TUP1_YEAST GLUCOSE REPRESSION REGULATORY PROTEIN TUP1 (FLOCCULATION SUPPRESSOR P * T2D4_DROME TRANSCRIPTION INITIATION FACTOR TFIIID KD SUBUN[GPROTEINBRPT // WD40_REGION // WD_REPEA] CG7704 LD42828 47C5-47C6 ID:101G5
 CG7704
 + grp protein_kinase * 5e-08 Ssp31 protein kinase * 2e-54 Ser/Thr kinase * 5e-13 serine/threonine kinase * 7e-27 Chk1; checkpoint kinase [PROTEIN_KINASE_DOM // pkinase] CG17161 LD42896 36A6-36A7 ID:101G7
 CG17161

CG5522 + GDP/GTP exchange factor for Ras GRF_CDC25, PH, PH_DOMAIN, RasGEF CG5522 dup:1/2 ID:101G8
+ BcDNA:GM10765 DNA_repair_protein * 5e-15 RA27_YEAST STRUCTURE SPECIFIC ENDONUCLEASE RAD27 hypothet * 2e-20 by match; 1-match_accession=SWISS-PROT:P397 * 5e-13 similar to the [53EXO_N_DOMAIN // 53EXO_I_DOMAIN // XPG]

CG10670 CG10670 LD43032 64C12-64C12 ID:101H3

CG6325 + unknown * [CYTOCHROME_C] CG6325 LD43055 86A5-86A6 ID:101H9
+ cell_cycle_regulator * pombe Cdc5-related protein(aa) * similar to MYB transforming protein; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA [MYB_1 // MYB_2 // myb_DNA-binding // MY] CG6905 LD43082 61C1-61C1 dup:2/2 ID:102A1

CG6905 dup:2/2 ID:102A1

CG5145 + unknown * CG5145 LD43096 77C2-77C2 ID:102A2
+ Chc transporter * DMCHC_2 Chc * CLH_YEAST CLATHRIN HEAVY CHAIN clathrin heavy chain - y * CLH_DROME CLATHRIN HEAVY CHAIN clathrin heavy chain - fr * CLH_CAEEL PRO[RCC1_2 // Clathrin_repeat // CLATHRIN_R] CG9012 LD43101 13F3-13F3 dup:1/3 ID:102A3

CG9012 LD43101 13F3-13F3 dup:1/3 ID:102A3

CG5787 + structural_protein * 7e-07 DR48_YEAST DDR48 STRESS PROTEIN (DNA DAMAGE-RESPONSIVE PROTEIN 48) (DDRP 48) (Y * 7e-07 M84D_DROME MALE SPECIFIC SPERM PROTEIN MST84DD testis- CG5787 LD43134 33F2-33F2 ID:102A8

CG5787 + unknown * ecdysone receptor isoform A - fruit fly (Drosophila melanogaster) (fragment)(aa) * EcR-A=ecdysone receptor isoform melanogaster, Peptide Partial, * CG8347 LD43136 42A9-42A9 ID:102A9

CG8347 + transcription_factor_binding * WD-repeat protein(aa) * 3e-05 YGA3_YEAST HYPOTHETICAL 62.8 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2 * 1e-07 Method: conceptual translation [WD40_REGION // WD40] CG11330 LD43270 26F5-26F6 ID:102B11

CG11330 + DNA_binding * TPR protein(aa) * 6e-74 PR06_YEAST PRE-MRNA SPLICING FACTOR PRP6 pre-mRNA splicing * 2e-12 62D9.a * 8e-08 contains similarity to multiple TPR domain [TPR_REGION // TPR_REPEAT // NLS_BP] CG6841 LD43276 75E2-75E3 ID:102B12

CG6841 + enzyme * 1e-98 PERO_DROME PEROXIDASE PRECURSOR myeloperoxidase (EC 1.11. * 6e-87 similar to eosinophil peroxidase and myelo-peroxydase * 2e-65 PERT_MOUSE THY [ANPEROXIDASE // PEROXIDASE_3] CG7660 LD43174 90C-90C ID:102B3

CG7660 + BcDNA:LD19168 transcription_factor_binding * endocrine regulator(aa) * BLASTX 6.3E-12 Rattus RNA helicase with domain mRNA, complete cds.(dna) * 9e-27 l(3)j1E6 l(3)j1E6 [ZINC_FINGER_C2H2 // PRO_RICH // NLS_BP] CG9776 LD43206 82A5-82A6 dup:2/2 ID:102B6

CG9776 + unknown * putative transposase(aa) * 3e-05 ORF1 * 2e-07 putative transposase * Hermes transposase [AMP_BINDING] CG11560 LD43225 68F3-68F3 ID:102B8

CG11560 + Orc4 DNA_replication_factor * 56-kDa subunit of recognition complex (ORC); Orc4p(aa) * recognition complex subunit 4-related protein Orp4p(aa) * recognition complex, subunit (yea [ATP_GTP_A2 // ATP_GTP_A] CG2917 LD43280 60D16-60D16 ID:102C1

CG2917 + unknown * 1e-21 BC10_HUMAN BLADDER CANCER KD PROTEIN 10kD protein * 1E-136* CG4867 LD43519 64E-64E ID:102D3

CG4867 + transcription_factor_binding * dMi-2 protein(aa) * D. melanogaster STS determined from European Mapping Project cosmid, sequence tagged site(dna) * 5e-06 YMW5_YEAST HYPOTH[BROMODOMAIN_2 // ZF_BBOX // PHD // PRO_] CG5206 LD43524

CG5206

92E-92E ID:102D5

CG1420 + unknown * Similarity to pre-mRNA splicing factor; cDNA EST comes from this gene; cDNA EST yk236g11.3 comes from this gene; cDNA EST yk274g3.3 comes from this [NLS_BP] CG1420 LD43674 98F7-98F8 dup:2/2 ID:102E11

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

CG2310 + unknown * 6e-08 No definition line found * 1e-13 signal peptidase:SUBUNIT=12kD * 3E-97* 1e-07 No definition line found [ATP_GTP_A] CG2310 LD43791 99B3-99B3 ID:102F8

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

CG1659 + unc-119 unknown * 1e-124 UNC-119 * 3e-59 U119_CAEEL UNC-119 PROTEIN unc-119 protein - Caenorhabd * 2e-65 UNC-119 * 2e-65 unc119 (C.elegans) homolog RETIN CG1659 LD43876 7A3-7A4 ID:102G3

CG2031 + unknown * nuclear matrix protein p84(aa) * 2e-07 T03G11.3 gene product * [HELIX_LOOP_HELIX // DEATH_DOMAIN] CG2031 LD43883 83C3-83C3 ID:102G4

CG5448 + syx1A transporter * DMSYX1A_4 syx1A * 4e-23 Sso2 protein * 1e-154 SYNA_DROME SYNTAXIN 1A syntaxin 1A melanogaster * 1e-103 syntaxin B (A [T_SNARE // Syntaxin // SYNTAXIN] CG5448 LD43943 95D9-95D9 dup:2/2 ID:102G6

CG1024 + CG1024 dup:1/3 ID:102G9

CG17184 + 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

CG7129 + 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

CG5553 + BcDNA:GM13640 enzyme * DNA primase, p58 subunit(aa) * putative dna primase large subunit(aa) * primase, polypeptide 2A (58kD)(aa) * PROBABLE DNA PRIMASE LARGE SUBUNIT(aa) CG5553 LD44074 77B4-77B4 ID:102H6

CG9874 + 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

CG8155 + 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

CG11248 + 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

CG11005 + enzyme * 3alpha-hydroxysteroid dehydrogenase (B-specific) (EC 1.1.1.50) - Pseudomonas sp. (strain * DMGLUTAC_9 Glt * DMADHA1_9 Adh * DMSCU scu [adh_short_C2 // GDHRDH // adh_short //] CG11005 LD44221 83B6-83B6 ID:103A10

CG3329 + Prosbeta2 endopeptidase * Pros bgr;2 * 3e-71 PRCF_YEAST PROTEASOME COMPONENT PUP1 PRECURSOR (MACROPAIN SUBUNIT PUP1) (PROTEIN * 1e-146 20S proteasome beta2 subunit * 4e-49 pr [PROTEASOME_B // PROTEASOME_PROTEASE //] CG3329 LD44234 71A3-71A3 ID:103A11

CG10107 + unknown * putative centromere protein(aa) * HYPOTHETICAL 75.7 KD PROTEIN T10F2.3 IN CHROMOSOME III(aa) * 6e-12 SMT4_YEAST SMT4 PROTEIN SMT4 protein - yeast (CG10107 LD44235 65C3-65C3 dup:1/2 ID:103A12

CG9910 + 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
+ signal_transduction * PACSIN(aa) * 3e-07 hypothetical protein YFR024c-a - yeast (Saccharomyces cerevisiae) * 7e-08
Cortactin * 1e-52 weakly similar to surface[FCH // CDC15_NT // P67PHOX // SH3DOMAIN] CG15694 LD44220 92F13-92F13
CG15694 dup:2/2 ID:103A9
CG1503 + unknown * CG1503 LD44327 19E7-19E7 ID:103B10
+ unknown * 8e-74 GPI3_YEAST N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN
CG6401 (GLCN * 6e-92 similar to phosphatidylinositol biosynthetic protein; [Glycos_transf_1] CG6401 LD44262 54E7-54E7 ID:103B2
+ enzyme * isopeptidase T(aa) * 3e-68 UBPE_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (UBIQUITIN
THIOLESTERASE 14) * 1e-125 Similar to ubiquitin carboxyl-term [UBA // UCH_2_1 // UCH_2_2 // UCH_2_3 //] CG12082
CG12082 LD44295 63B10-63B11 ID:103B7
CG3995 + unknown * [NLS_BP] CG3995 89E12-89E12 dup:2/2 ID:103B9
+ CycA cell_cycle_regulator * cell cycle regulator cyclin) map_position:68E1-2 * DMCYCA_3 CycA * G2/MITOTIC-SPECIFIC
CYCLIN A(aa) * 2e-27 CG23_YEAST G2/MITOTIC-SPECIFIC[cyclin // HELIX_LOOP_HELIX // CYCLINS] CG5940 LD44443
CG5940 68D4-68D4 dup:2/2 ID:103C10
+ Cyp310a1cytochrome_P450 * cytochrome P450(aa) * DMLCPM Cyt-P450-rBF6-2 * 2e-29 cytochrome P450 monooxygenase *
CG10391 2e-17 similar to cytochrome P450 [EP450II // p450 // P450 // MITP450 // E] CG10391 LD44491 37A3-37A3 ID:103C12
+ pav motor_protein * 7e-35 YGW6_YEAST PUTATIVE KINESIN-LIKE PROTEIN YGL216W hypoth * PAV-KLP protein * 5e-91
Similar to kinesin-like protein; coded for by C. elegans cDN [kinesin // KINESIN_MOTOR_DOMAIN1 // KIN] CG1258 64B4-64B4
CG1258 dup:1/2 ID:103C2
CG9241 + function_unknown * Cdc23(aa) * * [NLS_BP] CG9241 LD44370 39B4-39B4 dup:1/2 ID:103C3
+ chaperone * 5e-33 Similarity to Xenopus P58 protein cDNA EST * 3e-78 GP36b glycoprotein * 3e-83 coded for by C.
CG5510 elegans cDNA yk74e11.5; coded for by C. elegans CG5510 95E3-95E3 dup:2/2 ID:103C4
+ hdc signal_transduction * cell cytoplasm) map_position:99F6-11 * 4e-98 hdc protein - fruit fly (Drosophila melanogaster) (Z *
CG15532 8e-11 similar to drosophila HCD protein * 1e-10 CG15532 LD44381 99F-99F3 dup:2/3 ID:103C5
CG6674 + tumor_suppressor * 2e-05 tumor suppressing STF cDNA * * CG6674 LD44422 67C5-67C5 ID:103C7
+ motor_protein * Nijmegen breakage syndrome (nibrin)(aa) * 2e-06 AMYH_YEAST GLUCOAMYLASE S1/S2 PRECURSOR
(GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPH * 1e-08 predicted u [FHA_DOMAIN // NLS_BP // FHA] CG6754 LD44438 67C-
CG6754 67C dup:1/2 ID:103C9
+ lswi DNA_binding * enzyme DNA dependent adenosinetriphosphatase) transcription factor binding transcription co-activator)
map_position:72A3 * enzyme DNA dependent ad [helicase_C // SNF2_N // NLS_BP // ATP_G] CG8625 LD44594 49B6-49B7
CG8625 ID:103D12
+ enzyme * DMANKY_5 Ank * calcium-independent phospholipase A2(aa) * Ca2+-independent phospholipase A2(aa) * 1e-
CG6718 08 ankyrin ankyrin m [ANK_REP // ank // ANK_REP_REGION] CG6718 LD44515 67C2-67C2 dup:2/2 ID:103D4
+ unknown * 1e-12 YKK4_CAEEL HYPOTHETICAL 30.2 KD PROTEIN C02F5.4 IN CHROMOSOME III * * [NLS_BP]
CG9018 CG9018 LD44521 62D3-62D3 dup:2/2 ID:103D5
+ motor_protein * CLIP-190 * 6e-05 microtubule binding protein D-CLIP-190 * 3e-05 myosin * 4e-06 ORF 73, contains large
CG8621 complex repeat CR sarcoma-associated herpesv CG8621 LD44526 65E6-65E6 dup:2/2 ID:103D6

CG5174 + unknown * 4e-14 YZG1_CAEEL HYPOTHETICAL 28.7 KD PROTEIN F13E6.1 IN CHROMOSOME X * 1e-13 D52 * 7e-20 tumor protein D52-like hD54+ins2 isoform * 3e-14 CSPP28 CG5174 LD44733 55C11-55C11 dup:3/3 ID:103E10

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

CG13605 + DNA_binding * 4e-06 probable finger protein YOL054w - yeast (Saccharomyces cerevisiae) * 5e-22 contains similarity to C3HC4-class zinc finger eleg * 1e-06 peroxis [zf-C3HC4] CG13605 LD44641 95D10-95D10 dup:2/2 ID:103E3

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

CG7832 + unknown * [NLS_BP // ANTIFREEZEI] CG7832 LD44696 88C10-88C10 dup:3/3 ID:103E7

CG11586 + unknown * 2e-37 YO14_CAEEL HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III * * [ZF_MATRIN // ZINC_FINGER_C2H2 // NLS_BP] CG11586 LD44732 64B5-64B5 dup:3/3 ID:103E9

CG8287 + Rab8 cell_cycle_regulator * Rab8 * rab8(aa) * rab1(aa) * 4e-55 SEC4_YEAST RAS-RELATED PROTEIN SEC4 GTP-binding protein SE [SIGMA54_INTERACT_1 // PRENYLATION // ra] CG8287 LD44762 76D5-76D5 ID:103F1

CG8390 + unknown * 5e-08 No definition line found * 5e-16 PSD-95/SAP90-associated protein-2 * 1e-16 PSD-95 binding protein * 1e-171 inserted at base Unknown 5' end of [NLS_BP] CG8390 LD44824 41E5-41E5 ID:103F11

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

CG7347 + motor_protein * 8e-05 myosin heavy chain * * [PRO_RICH] CG7347 LD44887 75B10-75B10 ID:103G1

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

CG3812 + enzyme * 3e-35 PLSC_YEAST PROBABLE 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (1-AGP ACYLTR * 2e-37 1-acylglycerol-3-phosphate O-acyltransferase melan * [GLYCEROL_ACYLTRANS] CG3812 LD44987 11B19-11B19 ID:103G11

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

CG8950 + transcription_factor * transcription factor IIIC102(aa) * putative transcription factor subunit, TPR domain s(aa) * Similarity with yeast transcription factor TAU 131KD s [TPR_REGION // TPR_REPEAT // TPR] CG8950 LD44919 53F5-53F5 ID:103G4

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

CG6912 + unknown * CG6912 LD45181 88E4-88E4 ID:103H11

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

CG7074 + chaperone * 3e-23 YBK4_YEAST HYPOTHETICAL 104.7 KD PROTEIN IN PKC1-RTG3 INTERGENIC REGION * 6e-07

CAF1_DROME CHROMATIN ASSEMBLY FACTOR P55 SUBUNIT (CAF-1 P55 SU CG7074 LD45056 23D1-23D1 ID:103H2
+ cell_cycle_regulator * hypothetical protein(aa) * 8e-23 hypothetical protein YLR127c - yeast (Saccharomyces cerevisiae) *
CG3060 3e-05 LI19_DROME LIN-19 HOMOLOG PROTEIN lin19 pro [CULLIN_2] CG3060 60A14-60A14 dup:2/3 ID:103H3
+ enzyme * protein(aa) * 3e-07 FMS1_YEAST FMS1 PROTEIN FMS1 protein - yeast (Saccharom * 6e-12 Cs protein
CG17149 [ADXRDTASE // NAD_BINDING] CG17149 LD45081 77A4-77A4 ID:103H4
+ RpL1 ribosomal_protein * DMRPL1R_2 RpL1 * 60S RIBOSOMAL PROTEIN L1 (L4)(aa) * PROBABLE 60S RIBOSOMAL
CG5502 PROTEIN L1(aa) * 1e-90 RL2A_YEAST 60S RIBOSOMAL PROTEIN L2A (RP2) riboso [RIBOSOMAL_L1E // NLS_BP //
Ribosomal_L4] CG5502 98B2-98B2 dup:2/3 ID:103H6
+ receptor * 1e-07 weak similarity with quinone oxidoreductase; cDNA EST * 2e-12 CGRP-receptor component protein;
CG4875 CGRP-RCP * 1e-13 CGRP-receptor component protei CG4875 LD45115 15B1-15B1 ID:103H8
+ RNA_binding * spliceosome associated protein 145, SF3b subunit(aa) * spliceosome associated protein-like(aa) * BLASTX
CG3605 7.8E-75 Human spliceosome associated protei [NLS_BP] CG3605 LD45152 23C4-23C4 ID:103H9
+ SPT6 structural_protein * 3e-79 SPT6_YEAST TRANSCRIPTION INITIATION PROTEIN SPT6 SPT6 pro * EMB5_CAEEL
CG12225 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
+ unknown * short of similarity to human transforming protein (tre) * similar to human (TRE) transforming protein *
CG5916 Ypl249cp(aa) * pollux(aa) [TBC // RAB_GAP] CG5916 LD45246 89B9-89B9 ID:104A9
+ * NY-REN-57 antigen(aa) * 4e-08 hypothetical protein YLR097c - yeast (Saccharomyces cerevisiae) (* 4e-53
CG5961 dJ341E18.2.1 (novel PUTATIVE protein) (isofo [TPR_REGION // FBOX_DOMAIN // TPR_REPEAT] CG5961 87C-87C dup:2/2
ID:104B12
+ snf RNA_binding * DMD25SNRN_2 snf * U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) (SEX
CG4528 DETERMINATION PROTEIN SNF)(aa) * 3e-05 YIS9_YEAST HYPOTHETICAL 12.8 [RNP_1 // RBD // rrm] CG4528 LD45302 4F1-
4F2 dup:3/3 ID:104B7
CG10825 + unknown * [NLS_BP] CG10825 LD45317 95F1-95F1 ID:104B8
+ neur DNA_binding * finger protein neuralized - fruit fly (Drosophila melanogaster)(aa) * DMC3HC4ZF_2 neur * 3e-89 coded for
CG11988 by C. elegans cDNA yk27g3.5; coded for by C [zf-C3HC4 // ZF_RING] CG11988 LD45505 85C4-85C5 dup:1/2 ID:104C12
+ unknown * R07E5.1 protein (clone R07E5) - Caenorhabditis elegans(aa) * 7e-49 inserted at base Both 5' and 3' ends of P
CG8833 element Inverse PCR * cDNA EST comes fr [PRO_RICH // D111_DOMAIN // NLS_BP] CG8833 LD45361 74B1-74B1 ID:104C2
+ signal_transduction * Plenty of SH3s; POSH(aa) * 5e-09 hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae)
CG4909 (U1 * 4e-05 DRK_DROME PROTEIN E(SEV)2B (SH2-SH3 A[zf-C3HC4 // ZINC_FINGER_C3HC4 // P67PHO] CG4909 LD45365
54D1-54D1 ID:104C3
+ unknown * BLASTX 6.9E-07 YJL064W|Protein of unknown function(dna) * BLASTX 8.2E-11 G.gallus PR264 mRNA.(dna) *
CG10084 2e-17 No definition line found * [ZF_CCCH // NLS_BP] CG10084 LD45403 37E5-37E5 dup:2/3 ID:104C7
+ DNA_binding * BLASTX 7.4E-06 Oryctolagus cuniculus preproacrosin mRNA, complete cds.(dna) * 5e-05 Y144_HUMAN
CG8715 HYPOTHETICAL PROTEIN The * CG8715 LD45430 44A3-44A4 dup:2/3 ID:104C8
+ transmembrane_receptor * HYPOTHETICAL PROTEIN * cysteine-rich protein (intestinal)(aa) * 4e-09 MLP2_DROME
CG4656 MUSCLE LIM PROTEIN MLP84B muscle L * 4e-18 gene product [LIM_DOMAIN_1 // LIM // LIM_DOMAIN_2 //] CG4656

LD45535 94E-94E dup:2/2 ID:104D3

CG13425 + 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

CG4878 + RNA_binding * 9e-87 IF3X_YEAST EUKARYOTIC TRANSLATION INITIATION FACTOR BETA SUBUNIT (EIF-3 BETA) * 3e-95 predicted using Genefinder; cDNA EST comes from this * [RBD // rrm // NLS_BP] CG4878 LD45560 54C11-54C11 dup:2/2 ID:104D8

CG18426 + 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

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

CG4925 + motor_protein * 9e-09 NUF1_YEAST NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110) * 6e-12 microtubule binding protein D-CLIP-190 * 2e-29 predicted using Genef CG4925 LD45682 72E5-72E5 dup:3/3 ID:104E9

CG1115 + unknown * [NLS_BP] CG1115 LD45836 82F10-82F11 dup:2/2 ID:104F10

CG1591 + endopeptidase * autoantigen(aa) * 1e-67 Ki antigen PA2 * 3e-65 Ki nuclear autoantigen - human Ki nuclear autoantigen * IGUP_HUMAN INTERFERON GAMMA UP-REGULATED PR CG1591 LD45860 11D10-11D10 dup:2/2 ID:104F11

CG2097 + 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

CG6192 + unknown * partner of Ral-binding protein 1(aa) * 3e-09 PAN1_YEAST PAN1 PROTEIN poly(A)-specific ribonuclease (EC * 6e-06 PAST-1 * 3e-05 contain EF-hand-like c [EPS // PRO_RICH // EF_HAND_2] CG6192 LD45769 32D3-32D4 ID:104F7

CG9126 + motor_protein * protein(aa) * stromal interaction molecule 1(aa) * 2e-53 cDNA EST comes from this gene; cDNA EST co * 1e-90 stromal cell protein [SAM_DOMAIN] CG9126 LD45776 13F14-13F14 ID:104F8

CG8067 + enzyme * 1e-45 ESTs and come from this gene. th * unknown * BIOC_SERMA BIOTIN SYNTHESIS PROTEIN BIOC the p * CG8067 LD45826 50C22-50C23 ID:104F9

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

CG2055 + * Protein kinase C-related kinase (PRKSD)(aa) * DMPKCR_2 Pkc53E * 2e-97 KPC1_YEAST PROTEIN KINASE C-LIKE (PKC 1) serine/threoni * 9e-57 p90 ribosomal [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG2055 45C-45C3 dup:2/3 ID:104G7

CG7108 + DNAPol-alpha50 DNA_replication_factor * DMDPRI_2 DNAPol- agr;50 * 8e-62 p48 DNA primase (AA 1-409) * PRI1_DROME DNA PRIMASE SMALL SUBUNIT (DNA PRIMASE KD SUBUNIT) (DNA POLYMERAS * 3e-64 N CG7108 LD46032 66C8-66C8 ID:104H2

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

CG6677 + ash2 transcription_factor * ash2 * trithorax protein ASH2 * 6e-83 Y17G7B.2a * 1e-134 similar to Drosophila ash2 [SPRY_DOMAIN // NLS_BP] CG6677 LD46053 96A17-96A17 ID:104H8

CG1307 + 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

CG17484 + 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

CG9556 + 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

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

CG4495 + transporter * atopy related autoantigen CALC(aa) * 4e-27 predicted using Genefinder; similar to EF hand (2 domains) * 2e-91 atopy related autoantigen CALC * 2e-40 [EF_HAND // efhand // EF_HAND_2] CG4495 LD46238 27E3-27E3 ID:105B3

CG5146 + 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

CG12942 + transcription_factor * 6e-14 YJF6_YEAST HYPOTHETICAL 98.9 KD ZINC FINGER PROTEIN IN BTN1-PEP8 INTERGENIC REG * 1e-18 SUHW_DROME SUPPRESSOR OF HAIRY WING PROTEIN Hw s * [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG12942 LD46263 47C6-47C6 ID:105B5

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

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

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

CG9293 + enzyme * similar to tumor suppressor p33ING1; similar to * Unknown protein(aa) * 5e-17 YNJ7_YEAST HYPOTHETICAL 37.0 KD PROTEIN IN RAS2-YPT53 INTERGENIC REGI [PHD // NLS_BP] CG9293 LD46333 34B6-34B6 ID:105C2

CG17958 + 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

CG10203 + 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

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

CG3941 + 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

CG4852 + enzyme * prenyl protein protease RCE1(aa) * 2e-17 RCE1_YEAST CAAX PRENYL PROTEASE (PRENYL PROTEIN-SPECIFIC ENDOPROTEASE 2) (PPS * 9e-22 caax prenyl protease CG4852 LD46418 64E-64E ID:105D1

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
CG17840	+ unknown * HYPOTHETICAL PROTEIN * 1e-117 YN65_YEAST HYPOTHETICAL 101.7 KD PROTEIN IN EGT2-KRE1 INTERGENIC REGION * 1e-118 Similarity to Yeast hypothetical 101. [SYJA_NTERM] CG17840 LD46494 24F6-24F6 dup:2/2 ID:105D7
CG4453	+ 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
CG12135	+ unknown * predicted using Genefinder; 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
CG4564	+ unknown * 1E-78* * CG4564 LD46629 6D4-6D6 dup:2/2 ID:105E8
CG5877	+ unknown * CG5877 13B9-13B9 ID:105F1
CG11525	+ * cyclin G1 - human (fragment)(aa) * cyclin G2(aa) * cyclin G - rat(aa) * cyclin G2(aa) CG11525 100D2-100D2 dup:3/3 ID:105F12
CG7081	+ chaperone * 2e-09 Similarity to Rat peroxisome assembly factor-1 (SW:PAF1_RAT) * 1e-33 peroxisome membrane protein PEX2 * 4e-32 peroxisomal membrane protein (35 [zf-C3HC4 // ZINC_FINGER_C3HC4 // ZF_RIN] CG7081 LD46714 66C8-66C8 dup:2/2 ID:105F3
CG14896	+ motor_protein * DMBNBR_2 bnb * mu2 * 1e-07 RRP1_DROME RECOMBINATION REPAIR PROTEIN (DNA-(APURINIC OR APYRIMIDINIC SITE) L * 2e-21 C. elegans UNC-89 CG14896 LD46725 89C4-89C4 dup:1/3 ID:105F5
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
CG4338	+ unknown * HYPOTHETICAL 32.6 KD PROTEIN C1F3.04C IN CHROMOSOME I(aa) * No definition line found(aa) * Yor006cp(aa) * 7e-49 YO06_YEAST HYPOTHETICAL 35.7 KD PROT CG4338 LD46811 88E9-88E9 ID:105G2
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
CG5954	+ l(3)mbt transcription_factor * tumor-suppressor(aa) * DMMBT163 l(3)mbt * tumor-suppressor * 2e-18 predicted using Genefinder; cDNA EST yk292d9.5 comes from this gen [NLS_BP] CG5954 LD46950 97F4-97F4 ID:105H7
CG5284	+ ion_channel * CHLORIDE CHANNEL PROTEIN (CLC-4)(aa) * chloride channel 4(aa) * Similarity to Rat chloride channel protein (PIR Acc. No. cDNA EST yk354e5.3 comes f [CLCHANNEL // CBS // SNF4_REP // voltage] CG5284 LD47154 72D5-72D5 ID:106A10
CG2264	+ * 4e-10 similar to thyroglobulin and EF hand domains elega * 8e-05 testican * 6e-09 testican-3 * 8e-05 EQST_ACTEQ EQUISTATIN [thyroglobulin_1 // THYROGLOBULIN_1 // k] CG2264 46D8-46D9 dup:2/2 ID:106A12
CG7983	+ signal_transduction * 5e-48 pdb 1GKY Guanylate Kinase (E.C.2.7.4.8) Complex With Guanosine Monophosphate * 2e-19 DLG1_DROME LETHAL(1)DISCS LARGE-1 TUMOR SUPPRESSOR PROTE [PRO_RICH] CG7983 LD47023 67E5-67E5

ID:106A2

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

CG11367 + unknown * clot.672(dna)* 7e-07 YEQ8_YEAST HYPOTHETICAL 58.0 KD PEPTIDASE IN PTP3-ILV1 INTERGENIC REGION * 5e-08 similar to the peptidase family M24B * 3e-12 CG11367 LD47277 79F2-79F2 dup:2/2 ID:106B10

CG8448 + chaperone * 2e-11 SCJ1_YEAST SCJ1 PROTEIN SCJ1 protein - yeast (Saccharomyce * 6e-11 Tid(56) protein - fruit fly (Drosophila melanogaster) * 2e-07 similar to DN [DNAJ_1 // DnaJ // DNAJ_2] CG8448 LD47190 52F8-52F9 dup:1/2 ID:106B3

CG10255 + cell_adhesion * 6e-23 adenylate cyclase * 2e-24 flightless-I unkn * 1e-40 Ras-binding protein SUR-8 leuc * 3e-44 Ras-binding protein SUR-8 [LRR // LEURICHRPT // PDZ // NLS_BP] CG10255 LD47229 51D6-51D6 dup:1/2 ID:106B6

CG9705 + unknown * calcium-regulated heat stable protein CRHSP-24(aa) * calcium-regulated heat stable protein CRHSP-24(aa) * RNA-binding protein PIPPIn - rat PIPPIn pr [CSD] CG9705 LD47312 73C-73C ID:106C2

CG4700 + Sema-2a unknown * semaphorin II precursor - fruit fly (Drosophila melanogaster)(aa) * semaphorin-like * semaphorin 2a precursor(aa) * DMDSEM_2 sema-I CG4700 LD47367 53C4-53C ID:106C6

CG3870 + ligand_binding_or_carrier * Rab2 * BACR37P7.a(aa) * 5e-33 YP51_YEAST GTP-BINDING PROTEIN YPT51/VPS21 GTP-binding pr * 7e-28 rab1 [ras // ATP_GTP_A // RASTRNSFRMNG] CG3870 LD47384 59E-59E ID:106C7

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

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

CG4643 + unknown * C26E6.5 gene product(aa) * 1e-36 C9 * 2e-38 C9 * [SPRY_DOMAIN // WD_REPEATS // GAMMA_CARB] CG4643 LD47425 49F13-49F13 ID:106D4

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

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 spliceosome-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

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

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

CG8600 + unknown * CG8600 LD47606 65F2-65F2 ID:106F12

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

CG13852 + unknown * CG13852 LD47553 96E1-96E1 ID:106F5

CG1453 + motor_protein * KINESIN CENTRAL MOTOR (XKCM1)(aa) * kinesin heavy chain member 2(aa) * kinesin-like (mitotic centromere-associated kinesin)(aa) * kinesin heavy c[kinesin // KINESIN_MOTOR_DOMAIN1 // KIN] CG1453 LD47558 10A6-10A8 dup:2/2 ID:106F6

CG5632 + transcription_factor_binding * hypothetical protein(aa) * 2e-05 serine-threonine kinase receptor-associated protein * 2e-05 WD-40 repeat protein * 3e-05 DMEST6P_15 Est-P [WD40_REGION // WD40] CG5632 LD47568 68F8-68F8 dup:1/2 ID:106F8

CG1395 + stg protein_tyrosine_phosphatase * DMCDC25_2 stg * 3e-21 MPIP_YEAST M-PHASE INDUCER PHOSPHATASE (MITOSIS INITIATION PROTEIN MIH1) (MITOT * cdc25 protein - fruit fly (D[Rhodanese // RHODANESE // MPIPHTASE] CG1395 LD47579 99A5-99A6 dup:3/3 ID:106F9

CG4920 + ea endopeptidase * DMEAST_4 ea * SERINE PROTEASE EASTER PRECURSOR(aa) * 5e-20 kallikrein * 8e-29 airway trypsin-like protease a [ANTENNAPEDIA // trypsin // CHYMOTRYPSIN] CG4920 LD47701 90E1-90E1 ID:106G12

CG14965 + motor_protein * CG14965 LD47616 63B13-63B13 ID:106G2

CG15737 + unknown * 5e-14 /match=(desc: * 6e-43 weak similarity to drosophila tyrosine kinase ele * 5e-23 The gene is expressed ubiquitously.; The protein * 1e-20 caffe [PAP_ASSOCIATED // PAP_CORE // PAP // PR] CG15737 LD47659 10F5-10F6 dup:1/2 ID:106G9

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

CG11484 + transcription_factor_binding * [UBA] CG11484 LD47780 102D1-102D3 ID:106H12

CG9523 + unknown * cDNA EST comes from this gene; cDNA EST comes from this gene(aa) * huntingtin interacting protein HYPE(aa) * 9e-84 cDNA EST comes from this gene; c [TPR_REGION // TPR_REPEAT] CG9523 LD47713 26D3-26D3 ID:106H2

CG2843 + unknown * 2e-09 YNY5_YEAST HYPOTHETICAL 20.4 KD PROTEIN IN RPA49-SUI1 INTERGENIC REGION * 2e-08 coded for by C. elegans cDNA yk127b8.5; coded for by C. elegans [NLS_BP] CG2843 LD47748 23A7-23A7 ID:106H9

CG2945 + cin unknown * BACR37P7.g(aa) * MOLYBDENUM COFACTOR SYNTHESIS PROTEIN CINNAMON(aa) * DMCOFACTO_2 cin * 3e-05 hypothetical protein YMR244c-a - yeast (Saccharomyces [MOCF_BIOSYNTHESIS_1 // MOCF_BIOSYNTHESI]

CG2945 LD47852 1A5-1A5 dup:1/3 ID:107A8

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

CG18543 + unknown * CG18543 LD47919 66C12-66C12 ID:107B1

+ enzyme * acid phosphatase (EC 3.1.3.2) Acph-1 precursor, lysosomal - fruit fly (Drosophila melanogaster)(aa) * 4e-56 PPAY_CAEEL PUTATIVE ACID PHOSPHATASE PRE [HIS_ACID_PHOSPHAT_1 // HIS_ACID_PHOSPHA] CG7899 LD47943 99D3-99D3 dup:2/2 ID:107B5

CG7899 + 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

CG5568 + unknown * No definition line found(aa) * protein(aa) * No definition line found * [NLS_BP] CG9646 LD47968 53F4-53F5 ID:107B7

CG9646 + unknown * Kelch-repeat protein, similar to Kel1 and Kel2; Kel3p(aa) * 2e-32 hypothetical protein YPL263c - yeast (Saccharomyces cerevisiae) * 9e-06 host cell [NLS_BP] CG4069 LD47970 69C4-69C4 ID:107B8

CG4069 + unknown * 5e-17 probable membrane protein YLR418c - yeast (Saccharomyces cerevisiae) * 1e-10 unknown conserved hypothetical protein * [DDC_GAD_HDC_YDC] CG11990 LD47989 85C5-85C5 dup:3/3 ID:107B9

CG11990 + unknown * 5e-20 YNZ5_YEAST HYPOTHETICAL 17.1 KD PROTEIN IN SIP3-MRPL30 INTERGENIC REGION * 3e-12 RNA helicase * 2e-25 cellular nucleic acid binding protein cl [ZF_CCHC // zf-CCHC] CG3800 LD48005 59B6-59B6 ID:107C1

CG3800 + transcription_factor * 4e-91 putative zinc finger protein * 8e-13 similar to Zinc finger, C2H2 type (4 domains); cDNA EST * 4e-27 MFG2_MOUSE ZINC FINGER PROTEIN MFG-2 z[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG1602 LD48073 43D3-43D3 ID:107C11

CG1602 + protein_phosphatase * myotubularin related protein 1(aa) * 3e-14 YJ80_YEAST HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-NNF1 INTERGENIC REGION * 2e-19 SET domain binding factor CG5026 LD48015 66E5-66E5 ID:107C5

CG5026 + shg cell_adhesion * DMDACHSOU_2 ds * EPITHELIAL-CADHERIN PRECURSOR (E-CADHERIN) (LIVER CELL ADHESION MOLECULE) (L-CAM)(aa) * DE-cadherin(aa) * DMDEC_1 shg [EGF_1 // EGF_2 // LAM_G_DOMAIN // Cadhe] CG3722 LP01248 57B19-57B20 ID:107D10

CG3722 + unknown * 8e-24 putative phosphatase ** CG12237 LP01149 18D10-18D10 ID:107D4

CG12237 + ribosomal_protein * MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3(aa) * 8e-35 RM09_YEAST MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L9 PRECURSOR (YML9) * 3e-40 RM03_CAEEL PUTATIVE MI [Ribosomal_L3] CG8288 LP01949 13E18-13E18 ID:107H3

CG8288 + unknown * queuine trna-ribosyltransferase(aa) * 7e-98 TGT_CAEEL PUTATIVE QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLA * TGT_BACSU QUEUINE TR CG4947 LP01967 21F1-21F1 ID:107H4

CG4947 + endopeptidase * SERINE PROTEINASE STUBBLE (STUBBLE-STUBBLOID PROTEIN)(aa) * 2e-22 similar to peptidase family S1 (trypsin family) * 7e-28 PLMN_MOUSE PLASMINOGEN PRE [trypsin // CHYMOTRYPSIN // TRYPSIN_HIS] CG7142 LP02004 90F6-90F6 ID:107H5

CG7142 + Akap200 signal_transduction * [PRO_RICH // NLS_BP] CG13388 29C1-29C3 dup:1/2 ID:108A9

CG13388 + CG1263 dup:2/2 ID:108B9

CG1263

CG13397 + enzyme * 1e-152 Naglu * 1e-153 N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB) * 1e-113 alpha-N-acetylglucosaminidase * alpha-N-acetylglucosaminida CG13397 LP03571 29C1-29C1 ID:108F10

CG10719 + brat transcription_factor * transcription factor(aa) * 1e-142 YOG2_CAEEL HYPOTHETICAL ZINC FINGER PROTEIN ZK112.2 IN CHROMOSOME III * 2e-38 protein * 9e-38 RING finger[ZF_BBOX // NHL // ZINC_FINGER_C2H2 // Z] CG10719 LP03649 37C4-37C dup:3/5 ID:108G1

CG4071 + 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

CG3628 + unknown * 1e-118 inserted at base Both 5' and 3' ends of P element Inverse PCR * 1e-118 inserted at base Both 5' and 3' ends of P element Inverse PCR * CG3628 67B4-67B4 dup:1/3 ID:109A10

CG9916 + 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

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

CG14214 + transporter * 2e-08 SSS1 protein - yeast (Saccharomyces cerevisiae) (X820 * 5e-24 S61G_CAEEL PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT S * 1e-26 S61G_CANFA PR [SecE // SECE_SEC61G] CG14214 LP05042 18D11-18D11 dup:1/2 ID:109C1

CG9699 + cytoskeletal_structural_protein * PEANUT PROTEIN(aa) * cell division control-related protein 2b(aa) * protein(aa) * BRAIN PROTEIN H5(aa) [ATP_GTP_A2 // GTP_CDC // PRO_RICH // AT] CG9699 LP06017 15A1-15A1 dup:1/2 ID:109F12

CG3127 + Pkg protein_kinase * 3-phosphoglycerate kinase; Pkg1p(aa) * DMPGKG_2 Pkg * PHOSPHOGLYCERATE KINASE(aa) * 1e-136 PGK_YEAST PHOSPHOGLYCERATE KINASE 3-phosphoglycerate kina [PGK // PGLYCERATE_KINASE // PHGLYCKINAS] CG3127 23A7-23A7 dup:2/3 ID:109G12

CG7702 + cell_adhesion * 1e-05 CCR4_YEAST GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL EFFECTOR (C * 4e-14 CHAO_DROME CHAOPTIN PRECURSOR (PHOTORECEPTOR CELL-SPE [LRR // LEURICHRPT // LRRCT] CG7702 LP06937 91B7-91B7 ID:109H12

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

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

CG4578 + CG4578 dup:2/2 ID:113D11

CG9437 + transcription_factor * DMADF1A_2 Adf1 * 6e-05 ADF1_DROME TRANSCRIPTION FACTOR ADF-1 (ADH DISTAL FACTOR 1) * 2e-67 inserted at base Both 5' and 3' ends of P element Inverse [NLS_BP] CG9437 SD02118 57C5-57C5 dup:2/2 ID:113E10

CG8465 + enzyme_inhibitor * protein(aa) * protein(aa) * protein(aa) * [ANK_REP // ank // ANK_REP_REGION] CG8465 SD02148 16B5-16B6 dup:2/4 ID:113F4

CG17938 + enzyme * similar to aspartyl-tRNA synthetase; cDNA EST yk250e3.3 comes from this gene(aa) * 2e-40 SYDM_YEAST ASPARTYL-TRNA SYNTHETASE, MITOCHONDRIAL (ASPARTA [tRNA-synt_2 // TRNASYNTHLYS // TRNASYNT] CG17938

SD02215 36A10-36A10 ID:113G1

CG8743 + unknown * [CHANNEL_PORE_CA_NA // CATION_CHANNEL_TR] CG8743 76C5-76C5 ID:113G11

+ nod motor_protein * DMKINLA_3 nod * KINESIN-LIKE PROTEIN NOD(aa) * 4e-19 Cin8p kinesin-related * 9e-46 similar to Kinesin motor domain; cDNA EST yk256h1.3 comes from t [kinesin // KINESIN_MOTOR_DOMAIN1 // KIN] CG1763 SD02282

CG1763 10C5-10C6 ID:113H6

+ signal_transduction * beta2-chimerin, cerebellar - human(aa) * beta2-chimerin, cerebellar - rat (fragment)(aa) * 2e-07 BEM2_YEAST GTPASE ACTIVATING PROTEIN BEM2/IP[RHO_GAP // RhoGAP // DAG_PE_BINDING_DOM] CG3208 SD02309

CG3208 5A8-5A8 dup:1/3 ID:113H7

+ * F22D3.3 gene product(aa) * 9e-05 YG24_YEAST HYPOTHETICAL 28.6 KD PROTEIN IN MUP1-SPR3 INTERGENIC REGION * [NLS_BP] CG8616 65E9-65E9 dup:2/2 ID:114B12

CG8616 + transcription_factor * CCAAT-box-binding transcription factor(aa) * 6e-35 probable membrane protein YDR060w - yeast (Saccharomyces cerevisiae) * 1e-76 predicted using Gene [NLS_BP] CG7839 SD02424 70E1-68A3 ID:114B2

CG7839 + 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

CG9177 dup:2/3 ID:114C10

+ 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

CG10355 CG7434 + Rpl22 ribosomal_protein Ribosomal protein L22 60S subunit ANTIFREEZE1 CG7434 SD02522 ID:114C6

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

CG12109 + DNA_binding * 2e-33 inserted at base 5' end of P element Inverse PCR * * [MYB_1 // NLS_BP] CG15610 SD02691 53E-53E5 dup:2/2 ID:114E11

CG15610 + protein_kinase * nik-like; similar to * NCK interacting kinase(aa) * alternatively spliced serine/threonine protein kinase MIG-15(aa) * NIK [CNH // PROTEIN_KINASE_ST // TYRKINASE /] CG16973 62E8-62F1 dup:3/3 ID:114E8

CG16973 + 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

CG12139 8D12-8E1 dup:2/2 ID:114G4

+ 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

CG11130 + 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

CG13097 CG5444 + transcription_factor CG5444 dup:3/3 ID:115D3

+ 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

CG1074 ID:115D7

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

CG6285 + Eip74EF transcription_factor * DME74B_2 Eip74EF * ecdysone-induced protein E74B - fruit fly (Drosophila melanogaster)(aa) *
 5e-40 contains similarity to ETS domains * 3e-43 ELF[ETS_DOMAIN_1 // HSF_ETS // ETSDOMAIN //] CG6285 SD03570 74D3-
 74D4 ID:115H10

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

CG3743 + transcription_factor * metal-regulatory transcription factor 1(aa) * 1e-22 YJF6_YEAST HYPOTHETICAL 98.9 KD ZINC
 FINGER PROTEIN IN BTN1-PEP8 INTERGENIC REG * 1e-1[zf-C2H2 // ZINC_FINGER_C2H2_2 // NLS_BP] CG3743 SD03560
 67B3-67B3 dup:1/2 ID:115H9

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

CG5786 + ppan unknown * Peter Pan(aa) * 4e-35 SSF1_YEAST SSF1 PROTEIN SSF1 protein - yeast (Saccharomyc * 1e-53 contains
 similarity to human RNA-binding protein FUS/TLS * 1 [NLS_BP] CG5786 SD03871 95F1-95F1 dup:1/3 ID:116C10

CG10376 + protein_phosphatase CG10376 SD03870 dup:2/2 ID:116C9.2

CG4281 + EG:22E5.7 unknown * /match=(desc:(aa) * /match=(desc: * * CG4281 SD03946 2C5-2C6 dup:2/2 ID:116D9.2

CG9433 + Xpd DNA_repair_protein Xeroderma pigmentosum D nucleotide-excision repair DEAH_ATP_HELICASE, XRODRMPGMNTD
 CG9433 SD04012 dup:3/3 ID:116E7

CG10712 + translation_factor * 3e-06 Pdd1p Pdd1p thermoph * * [chromo // CHROMO_2] CG10712 79F5-79F5 dup:3/4 ID:116F1

CG4260 + alpha-Adaptin transporter * highly similar to alpha-adaptin (rat and mouse)(aa) * DMALPADPT_2 agr;-Adaptin * adaptor-related
 protein complex AP-2, alpha subunit(aa) * ALPHA-AD CG4260 SD04083 21C2-21C2 dup:2/3 ID:116F9

CG8409 + DNA_binding CG8409 dup:2/2 ID:116H11.2

CG11033 + DNA_binding * DNA (cytosine-5-)-methyltransferase 1(aa) * protein(aa) * HYPOTHETICAL 56.5 KD PROTEIN IN CAJ1-
 HOM3 INTERGENIC REGION(aa) * DNA (cytosine-5-)-methyl CG11033 SD04170 85C6-85C7 dup:1/5 ID:116H3

CG8948

CG8151 + CG8151 SD04652 ID:117F3

CG7623 + transporter CG7623 SD04658 dup:1/2 ID:117F5

CG7597 + protein_kinase * protein(aa) * cdc2-like protein kinase(aa) * 3e-65 CTK1_YEAST CTD KINASE ALPHA SUBUNIT (CTD

KINASE KD SUBUNIT) (CTDK-I ALPHA SUB * 6e-69 posi[PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG7597
 SD04681 78E1-78E1 dup:2/3 ID:117F7.2
 + dos signal_transduction * DMPHDOMPT_2 dos * Dos protein * 3e-20 Gab2 [PH // CYTOCHROME_C // PH_DOMAIN]
 CG1044 CG1044 SD04771 62F1-62F1 dup:2/7 ID:117G12
 CG3368 + RNP_1,UDP-glucose/GDP-mannose dehydrogen] CG3368 dup:3/5 ID:117H4
 + unknown * BLASTX 7.0E-38 YLR386W|Protein of unknown function(dna) * BLASTX 7.0E-38 YLR386W|Protein of unknown
 CG5608 function(dna) * BLASTX 7.0E-38 YLR386W|Protein o CG5608 SD04925 87C-87C dup:2/2 ID:118A11
 + unknown * 1e-28 weak similarity to chromosomal replicator initiator protein DNAA (* similar to a C.elegans protein encoded
 CG11943 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
 + lic protein_kinase (licorn) stress activated MAP kinase kinase 3 [Drosophila melanogaster] PROTEIN_KINASE_DOM,
 CG12244 PROTEIN_KINASE_ST, p] CG12244 SD04985 ID:118B12
 CG8013 + Su(z)12 a novel gene that affects zeste, Pc-G and PRE mediated silencing NLS_BP, PRO_RICH CG8013 SD04959 ID:118B5
 + unknown * 1e-149 inserted at base Both 5' and 3' ends of P element Inverse PCR * BLASTX 4.2E-08 Carrot gene for
 CG8929 extensin.(dna) * 2e-61 inserted at base Both 5 [PRO_RICH // NLS_BP] CG8929 SD04973 57A-57A dup:2/3 ID:118B9
 CG6556 + CG6556 SD05024 dup:1/8 ID:118C3
 CG1832 + transcription_factor CG1832 SD05094 dup:2/5 ID:118C8.2
 CG4141 + Pi3K92E enzyme 1-phosphatidylinositol 3-kinase PI3K-C2, PI3K-rbd, PI3Ka, PI3-PI4-kinase CG4141 SD05105 ID:118C9
 + dally cell_adhesion * dally * DALY_DROME DIVISION ABNORMALLY DELAYED PROTEIN PRECURSOR (DALLY PROTEIN)
 * 2e-10 similar to Glypican * 1e-24 GPCK_MOUSE K-GLYPICAN PRECURSO [Glypican] CG4974 SD05230 66E-66E3 dup:2/2
 CG4974 ID:118D10
 CG12210 + transporter CG12210 SD05285 dup:2/2 ID:118E11
 CG5119 + CG5119 dup:3/3 ID:118E4
 + S6klI protein_kinase ribosomal protein S6 kinase PROTEIN-KINASE-ATP, PROTEIN-KINASE-ST, T] CG17596 SD05277
 CG17596 dup:3/3 ID:118E6
 CG7143 + DNA_repair_protein CG7143 SD05329 dup:2/2 ID:118F3
 + AP-50 transporter clathrin adaptor protein AP50 Adap_comp_sub, CLATHRINADPT, CLAT_ADAPTO] CG7057 SD05403
 CG7057 ID:118G1
 + transporter * Ydr205wp(aa) * 5e-09 Zn/Cd resistance gene * 1e-06 cDNA EST yk447c2.5 comes from this gene; cDNA EST
 CG6672 co * 1e-06 zinc transporter ZnT-1 - mouse ZnT-1 [KININOGEN] CG6672 86D7-86D7 dup:1/2 ID:118G3
 + Rpn4 endopeptidase * proteasome (prosome, macropain) 26S subunit, non-ATPase, 13(aa) * 26S proteasome subunit
 CG10230 p40.5(aa) * 3e-43 hypothetical protein YDR427w - yeast (Sac [PCI_DOMAIN] CG10230 SD05423 95B5-95B5 dup:1/2 ID:118G4
 CG7110 + unknown * [NLS_BP] CG7110 SD05480 34B7-34B7 dup:2/3 ID:118H1
 CG9054 + Ddx1 RNA_binding Dead-box-1 Potential involvement of DDX1, a DEAD-box protein, in eye development ATP_GTP_A, DEAD,

HELICASE, SPRY, SPRY_DO] CG9054 SD05527 ID:118H11
 CG3086 + protein_kinase CG3086 dup:3/4 ID:118H2.2
 CG8902 + CG8902 dup:2/4 ID:118H6
 CG12238 + transcription_factor * requiem, apoptosis response zinc finger gene; neuroD4; ubi-d4(aa) * All-1 related protein(aa) *
 probable transcription factor requiem - mouse(aa) * [PHD] CG12238 SD05644 18D9-18D10 dup:2/3 ID:119B5
 + kis motor_protein * BLASTX 1.2E-06 Plasmodium falciparum GGM tandem repeat protein mRNA, partial cds.(dna) *
 kismet(aa) * 1e-07 contains similarity to chromo (chromatin [NLS_BP // ATP_GTP_A] CG3696 SD05649 21B4-21B4 dup:4/8
 CG3696 ID:119B7
 + RpS3A ribosomal_protein * DMRPS3A_2 RpS3A * ribosomal protein S3a(aa) * 3e-63 RS3A_YEAST 40S RIBOSOMAL
 PROTEIN RP10A ribosomal protein * 4e-78 RS3A_CAEEL PROBABLE 40S RIBOS[RIBOSOMAL_S3AE // Ribosomal_S3Ae //
 CG2168 NLS] CG2168 SD05650 101F1-101F1 ID:119B8
 CG8877 + CG8877 SD05715 dup:2/2 ID:119C11.2
 CG6406 + unknown * No definition line found(aa) * * CG6406 SD05904 54E7-54E7 dup:2/5 ID:119E11.2
 + 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
 + unknown * protein(aa) * 4e-83 cDNA EST comes from this gene; cDNA EST co * CG10080 SD05932 57F5-57F5 dup:2/3
 CG10080 ID:119F2
 + unknown * 3e-83 YOJ1_CAEEL HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN CHROMOSOME III * * CG14939 33B1-
 CG14939 33B1 dup:2/3 ID:119G8.2
 CG9799 + CG9799 SD06427 dup:3/3 ID:119H4.2
 CG4817 + DNA_binding CG4817 SD06504 dup:2/2 ID:119H6.2
 CG18273 + CG18273 SD06521 dup:2/2 ID:119H9.2
 CG12598 + unknown CG12598 SD06892 dup:1/2 ID:120D3.2
 + transcription_factor * GASTRULA ZINC FINGER PROTEIN XFG20-1 (XLCGF20.1)(aa) * ovo * ZINC FINGER PROTEIN
 CG10462 186(aa) * DMC115C2 [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG10462 SD07008 38A2-38A2 dup:1/3 ID:120E2.2
 CG10716 + translation_factor CG10716 SD07020 dup:1/2 ID:120E3.2
 CG1691 + RNA_binding CG1691 SD07045 dup:1/3 ID:120E7.2
 CG13185 + CG13185 SD07158 dup:1/3 ID:120G1.2
 CG5216
 CG4510 + CG4510 SD09607 dup:1/2 ID:124A6.2
 CG3140 + adenylate_kinase CG3140 SD09634 dup:1/2 ID:124A9.2
 CG12015 + enzyme CG12015 SD09929 dup:1/2 ID:124D10.2
 CG2952 + larval_serum_protein CG2952 SD09866 dup:1/2 ID:124D2.2
 CG11100 + CG11100 dup:1/4 ID:124D5.2
 CG3878 + signal_transduction * BLASTX 1.6E-48 Human mRNA for gene, partial cds.(dna) * 2e-13 weakly similar over a short to

metastasis-associated proteins mta-1 * 2e-10 n[ELM2 // myb_DNA-binding // ATP_GTP_A] CG3878 SD10063 18D3-18D3 dup:2/3 ID:124F11.2

CG15804 + motor_protein CG15804 SD10040 dup:1/2 ID:124F5.2

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

CG3458 + DNA_binding CG3458 SD10251 dup:1/2 ID:124H9.2

CG10293 + RNA_binding CG10293 SD10595 dup:1/2 ID:125D9.2

CG8944 + transcription_factor CG8944 SD10776 dup:1/2 ID:125F12.2

CG5013 + CG5013 SD10757 dup:1/2 ID:125F7.2

+ BcDNA:GH01073 RNA_binding * unknown(aa) * 7e-08 CYP6_YEAST PEPTIDYL-PROLYL CIS-TRANS ISOMERASE CYP6 (PPIASE) (ROTAMASE) * 7e-06 RNA-binding protein * 1e-103 Similarity to pepti [RBD // pro_isomerase // rrm // CSA_PPIA]

CG5808 CG5808 GH01073 96B1-96B1 ID:30A6

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

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

+ Traf2 signal_transduction * TNF-receptor-associated factor melanoga * 8e-06 YQ57_CAEEL HYPOTHETICAL 24.9 KD PROTEIN C16C10.7 IN CHROMOSOME III * 4e-38 TRAF6 * 1e-36 TNF recept[RNP_1 // zf-C3HC4 // ZINC_FINGER_C3HC4]

CG10961 CG10961 GH01161 7D14-7D14 ID:30B3

+ unknown * Ykr081cp(aa) * 5e-49 YK61_YEAST HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC

CG7993 REGION * ORF YKR401 * CG7993 GH01229 90F1-90F1 ID:30B8

+ transcription_factor * crol * 1e-32 CROL ALPHA * 1e-17 final three exons similar to C2H2-type zinc finger * 1e-31 kruppel-

CG12397 type zinc finger protein [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG12397 GH01265 42B3-42B3 ID:30B9

+ DNA_binding * ISWI PROTEIN (IMITATION SWI PROTEIN) (NUCLEOSOME REMODELING FACTOR KD SUBUNIT) (NURF-140) (CHRAK KD SUBUNIT)(aa) * DMISWI_6 lswi * 8e-94 YAB9_YEAST [helicase_C // SNF2_N] CG5899 GH01406

CG5899 33A1-33A1 ID:30C10

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

CG14228 18E1-18E1 ID:30C2

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

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

+ dim-7 unknown * RanBP7(aa) * 1e-73 NMD5_YEAST NONSENSE-MEDIATED MRNA DECAY PROTEIN NMD5 * 8E-26*

CG7935 RanBP7/importin [IBN_NT] CG7935 GH01576 66B9-67E3 dup:3/3 ID:30E1

+ Rab2 enzyme * Ypt31p(aa) * Rab2 * RAB2, member RAS oncogene family(aa) * rab14(aa) [SIGMA54_INTERACT_1 // ras // ATP_GTP_A] CG3269 GH01619 42C6-42C6 dup:2/2 ID:30E6

CG3269

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

+ lwr enzyme * 4e-50 UBC9_YEAST UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN LIGASE) (UB * 1e-92 ubiquitin-conjugating enzyme * 3e-73 similar to ubiqui [UBIQUITIN_CONJUGAT // UQ_con // UBIQUIT] CG3018 GH02236

CG3018 21C5-21C5 ID:31A12

CG8611 + BcDNA:GH02833 RNA_binding * DMDBP45A_18 Dbp45A * pit * 3e-64 DBP7_YEAST ATP-DEPENDENT RNA HELICASE DBP7 probable purin * 1e-58 helicase pitchoun [helicase_C // HELICASE // DEAD // NLS_B] CG8611 GH02833 16A1-16A2 dup:3/3 ID:31E5

CG6758 + unknown * actin-fragmin kinase(aa) * putative protein kinase(aa) * HYPOTHETICAL 143.1 KD PROTEIN F33C8.1 IN CHROMOSOME X PRECURSOR(aa) * 4e-10 YG52_YEAST HYP [FBOX_DOMAIN] CG6758 GH02866 58C5-58C5 dup:2/2 ID:31E7

CG2790 + BcDNA:GH03108 chaperone * similar to DnaJ, prokaryotic heat shock protein, Zinc finger, C2H2 type; cDNA EST yk290e12.5 comes from this gene; cDNA EST yk290e12.3 comes from th [ZF_MATRIN // ZINC_FINGER_C2H2 // DNAJ_1] CG2790 GH03108 60E5-60E5 ID:31G7

CG12127 + BcDNA:GH02974 unknown * 2e-35 YJ05_CAEEL HYPOTHETICAL 85.1 KD NUCLEASE C41D11.5 simila * YKK3_CAEEL HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III >g * CG12127 8D6-8D6 dup:1/2 ID:31G9

CG7974 + contains similarity to hepatocellular carcinoma-associated antigen 59 NLS_BP CG7974 GH03217 ID:31H1
+ 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 + unknown * CG18178 GH03795 67C-67C ID:32C3

CG18178 + transcription_factor * pleiomorphic adenoma gene-like 2; PLAG-like 2(aa) * DMZFH1_2 zfh1 * 1e-06 ZFH1_DROME ZINC-FINGER PROTEIN (ZINC-FINGER HOMEODOMAIN PROTEIN [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG12744 GH03826 46C1-46C1 dup:1/2 ID:32C5

CG12744 + BcDNA:GH03922 unknown * CG4184 GH03922 21C3-21C dup:1/3 ID:32C9

CG4184 + unknown * 1e-05 house-keeping protein - mouse house-keeping protein m * * CG3910 GH04071 85F8-85F8 ID:32D11

CG3910 + G_protein_linked_receptor * transcription factor (binds GC-rich sequences)(aa) * Similarity to Human GC-rich DNA-binding factor (GCF) cDNA EST yk238e11.3 comes from this gene; [NLS_BP] CG1965 GH04034 84C1-84C1 dup:2/2 ID:32D9

CG1965 + 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 + Trip1 translation_factor * 3e-80 IF34_YEAST EUKARYOTIC TRANSLATION INITIATION FACTOR DELTA SUBUNIT (EIF-3 DELTA * IF34_DROME EUKARYOTIC TRANSLATION INITIATION FACTOR DEL[GPROTEINBRPT // WD40_REGION // WD_REPEA] CG8882 GH04085 25B-25B dup:2/2 ID:32E2

CG8882 + * Ribosomal protein S7A (rp30); Rps7ap(aa) * 40S RIBOSOMAL PROTEIN S7(aa) * 9e-44 RP30_YEAST 40S RIBOSOMAL PROTEIN RP30 ribosomal protein * 1e-59 simi [Ribosomal_S7e] CG1883 99E3-99E4 dup:2/2 ID:32F11

CG1883 + unknown * HSPC015(aa) * 8e-45 hypothetical protein YOR173w - yeast (Saccharomyces cerevisiae) (* hypothetical protein YLR270w - yeast (Saccharomyces cerevisi CG2091 GH04919 83C-83C ID:33C2

CG2091 + unknown * CG3273 GH05256 42B3-42B3 dup:2/2 ID:33E8

CG3273

CG5649 + kin17 DNA_binding * kin17 * KIN17 protein - mouse(aa) * 9e-25 RTS2_YEAST ZINC FINGER PROTEIN RTS2 RTS2 protein - yeast * 1e-127 KIN17 protein [ZINC_FINGER_C2H2 // NLS_BP] CG5649 GH05550 77B4-77B4 ID:33F12

CG9356 + unknown * R12B2.2 gene product(aa) * basic-leucine zipper nuclear factor(aa) * basic-leucine zipper nuclear factor * CG9356 GH05665 85D15-85D15 ID:33G8

CG3613 + 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

CG10139 + unknown * CG10139 GH05836 51B9-51B9 ID:34A1

CG9769 + translation_factor * 2e-16 hypothetical protein YOR261c - yeast (Saccharomyces cerevisiae) * 1e-17 PRSC_DROME 26S PROTEASOME REGULATORY SUBUNIT S12 (PROTEASOME SUBUNIT P [Mov34 // MPN_DOMAIN] CG9769 GH05855 82D6-82D6 ID:34A2

CG7098 + 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

CG10652 + CG10652 ID:35A1

CG8233 + unknown * 1e-16 coded for by C. elegans cDNA yk86d12.3; coded for by C. elegans cDNA yk86d12.5 * * CG8233 GH07168 50E1-50E1 dup:4/5 ID:35B3

CG8495 + ribosomal_protein * Similar to 40S ribosomal protein S29; coded for by C. elegans cDNA cm10c2; coded for by C. elegans cDNA yk61d8.5; coded for by C. elegans cDNA yk10 [RIBOSOMAL_S14 // Ribosomal_S14] CG8495 GH07263 86D1-86D1 dup:1/2 ID:35C1

CG4152 + I(2)35DfRNA_binding * MTR4_YEAST ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4) * YH27_CAEEL PUTATIVE HELICASE W08D2.7 IN CHROMOSOME IV * 1e-153 hypoth [HELICASE // DEAD // ATP_GTP_A] CG4152 GH07290 35D6-35D6 ID:35C5

CG8108 + BcDNA:GH07921 RNA_binding * homeobox-containing protein Wariar(aa) * 3e-05 PEP_DROME ZINC FINGER PROTEIN ON ECDYSONE PUFFS PEP prote * 3e-05 Pep protein - fruit fly (Dr[ZINC_FINGER_C2H2 // NLS_BP // CYTOCHROM] CG8108 GH07921 67C3-67C3 dup:1/4 ID:35G10

CG3922 + RpS17 ribosomal_protein * DMRPS17_9 RpS17 * 6e-26 R17B_YEAST 40S RIBOSOMAL PROTEIN S17B (51B) ribosomal prot * 6e-61 RS17_DROME 40S RIBOSOMAL PROTEIN S17 ribosomal protein S1 [RIBOSOMAL_S17E // Ribosomal_S17e] CG3922 GH07989 67B3-67B3 ID:35H4

CG3223 + unknown * [UBA // PHOSPHOPANTETHEINE] CG3223 GH08043 84E6-84E6 dup:1/2 ID:35H7

CG3570 + unknown * 9e-30 inserted at base Both 5' and 3' ends of P element Inverse PCR * * CG3570 GH09390 60D8-60D8 dup:1/3 ID:37A3

CG5784 + cytoskeletal_structural_protein * 2e-21 contains similarity to leucine-rich repeats, strongest similarity is to rat leuc * 6e-37 acidic nuclear phosphoprotein pp32 * 3e-37 PHA1_HUMAN [LRR] CG5784 GH10170 54F6-55A1 ID:37F6

CG12152 + BcDNA:GH10333 unknown * 2e-91 hypothetical protein * * [ALDOKETO_REDUCTASE_3] CG12152 GH10333 7B8-7B8 ID:37G11

CG11228 + protein_kinase * Pak * DMAURG_2 aur * MST1(aa) * SERINE/THREONINE-PROTEIN KINASE PLO1(aa) [TYRKINASE // PROTEIN_KINASE_DOM // pkin] CG11228 GH10354 56D10-56D10 ID:37H3

CG6054 + Su(fu) unknown * DMSF_2 Su(fu) * Su(fu) protein(aa) * gene suppressor of fused protein - fruit fly (Drosophila melanogaster) *

6e-80 Su(fu) protein CG6054 GH10488 87C8-87C8 ID:38A6

CG14683 + unknown * 1e-45 YABC_ECOLI HYPOTHETICAL 34.9 KD PROTEIN IN FRUR-FTSL INTERGENIC REGION (ORFB) >g * 1E-170* hypothetical protein * hypothetical protein CG14683 GH10770 86C2-86C2 ID:38C10

CG7146 + unknown * protein(aa) * cDNA EST yk269g12.5 comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene CG7146 GH10703 90F6-90F6 ID:38C3

CG3497 + Su(H) DNA_binding * DMSUHA_2 Su(H) * RBJK_DROME J KAPPA-RECOMBINATION SIGNAL BINDING PROTEIN (RBP-J KAPPA) (SUPPRESSO * 1e-134 DNA-binding protein LAG-1 lag-1 ge * RB [LIPOCALIN] CG3497 GH10914 35C1-35C1 dup:2/2 ID:38D10

CG2910 + BcDNA:GH11110 RNA_binding * 6e-06 heterogeneous nuclear RNP protein clone pHRP40.2 - fruit fly (Drosophila melan * 2e-25 contains similarity to RNA recognition motifs (Pfam; rr [RBD // rrm] CG2910 GH11110 43F7-43F8 dup:1/3 ID:38F3

CG10415 + TflIEalpha transcription_factor * 6e-23 T2EA_YEAST TRANSCRIPTION INITIATION FACTOR IIE, ALPHA SUBUNIT (TFIIE-ALPHA) (TRA * TFIIE large subunit * 7e-35 cDNA EST yk210d12.5 comes from CG10415 GH11150 68C13-68C13 ID:38F9

CG18174 + Rpn11 endopeptidase * BLASTX 2.4E-33 MPR1|Protein with similarity to S. pombe PAD1 gene product(dna) * PAD1 PROTEIN(aa) * 1e-110 MPR1_YEAST MPR1 PROTEIN MPR1 protein - ye [Mov34 // MPN_DOMAIN] CG18174 GH11304 25C3-25C3 ID:38G10

CG3460 + Nmd3 unknown * 1e-115 NMD3_YEAST NONSENSE-MEDIATED MRNA DECAY PROTEIN Nmd3p * 1e-125 Similarity to Yeast nonsense-mediated mRNA decay protein (SW:NMD3_Y * 1e-143 CG [CYTOCHROME_C] CG3460 GH11261 2E1-2E1 ID:38G5

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

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

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

CG12795 + unknown * 2e-40 predicted using Genefinder * 4e-18 putative zinc finger protein * [PRENYLATION // zf-AN1 // NLS_BP] CG12795 GH11689 25A3-25A3 ID:39B10

CG7238 + BcDNA:GH11690 unknown * 2e-08 hypothetical protein YLR424w - yeast (Saccharomyces cerevisiae) (U * 1e-102 weak similarity with viral DNA polymerase (Swiss Prot accession nu [PRO_RICH // D111_DOMAIN // NLS_BP // AT] CG7238 GH11690 27E1-27E1 ID:39B11

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

CG8615 + ribosomal_protein * ribosomal protein L18(aa) * 1e-52 RL18_YEAST 60S RIBOSOMAL PROTEIN L18 (RP28) ribosomal prot * 1e-67 similar to Eukaryotic ribosomal protein L18; c [RIBOSOMAL_L18E // Ribosomal_L18e] CG8615 GH11604 65E9-65E9 dup:3/3 ID:39B4

CG15010 + signal_transduction * 3e-48 cdc4, incomplete, len: 579, CAI, 0.15, CC4_YEAST CELL DIVISI * 2e-61 Slimb * 5e-32

YKY4_CAEEL HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CO[GPROTEINBRPT // F-box // WD_REPEATS //] CG15010
GH11648 64B4-64B4 dup:2/3 ID:39B6
+ BcDNA:GH12174 DNA_binding * 1e-05 eyelid * 6e-45 YP83_CAEEL HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN
CHROMOSOME II * 5e-06 FMO5_MOUSE DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FO [ARID] CG3274 GH12174
CG3274 42B2-42B3 dup:4/4 ID:39E10
+ unknown * 2e-10 YEA3_YEAST HYPOTHETICAL 14.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION * 7e-28
CG6302 prefoldin subunit * 2e-68 I(3)j9B4 I(3)j9B4 inserted at base Bo CG6302 GH12095 70E1-70E1 dup:2/2 ID:39E2
+ EG:115C2.11 unknown * 2e-37 hypothetical protein YOL133w - yeast (Saccharomyces cerevisiae) * 9e-60 /match=(desc: * 8e-
CG16982 50 Similarity to yeast hypothetical protein PIR acc [ZF_RING] CG16982 GH12110 1B10-1B10 dup:2/2 ID:39E4
CG9119 + unknown * 2e-25 No definition line found ** CG9119 61F3-61F3 dup:5/5 ID:39E5
CG17420 + CG17420 dup:2/2 ID:39E6
+ CBP calcium_binding * CBP * sarcoplasmic calcium-binding protein(aa) * 1e-161 sarcoplasmic calcium-binding protein * 4e-23
SCP_PERVT SARCOPLASMIC CALCIUM-BINDING PROTEIN [EF_HAND // NLS_BP // efhand // EF_HAND_] CG1435
CG1435 GH12350 7A4-7A4 ID:39F9
+ protein_phosphatase * Hop * DMPPY_2 PpY-55A * serine/threonine protein phosphatase PPT1(aa) * 7e-88 PPT1_YEAST
SERINE/THREONINE PROTEIN PHOSPHATASE T (PPT) [TPR_REGION // PHOSPHO_ESTER // STPHPTA] CG8402
CG8402 GH12714 85E6-85E6 ID:40B1
+ TppII peptidase * tripeptidyl peptidase II; dTPP II; subtilisin-like serine protease * 1e-135 YQS6_CAEEL HYPOTHETICAL
SUBTILASE-TYPE PROTEINASE F21H12.6 IN CHROMOSOME [Peptidase_S8 // SUBTILASE_SER // SUBTIL] CG3991
CG3991 GH12811 49F7-49F7 ID:40B7
+ structural_protein * nuclear pore protein; Nsp1p(aa) * nucleoporin p62(aa) * similar to nucleoporins(aa) * NUCLEAR PORE
CG6251 GLYCOPROTEIN P62 (NUCLEOPORIN P62)(aa) CG6251 GH12838 53B1-53B1 ID:40B9
+ signal_transduction * centaurin beta 1A(aa) * BLASTX 1.6E-48 Human mRNA for gene, partial cds.(dna) * HYPOTHETICAL
CG6742 PROTEIN * centaurin beta2(aa) [ANK_REP // ArfGap // GLYCOSYL_HYDROL_F5] CG6742 GH12888 94E-94E dup:1/2 ID:40C1
+ unknown * Similar to Plasmodium falciparum glutamic acid-rich protein precursor * cDNA EST comes from this gene; cDNA
CG10955 EST comes from this gene; cDNA EST come [PRO_RICH] CG10955 GH12904 58D6-58D6 dup:1/3 ID:40C2
+ E2f2 transcription_factor * E2f2 * 1e-174 E2F-like transcription factor (E2F2) * 7e-14 predicted using Genefinder; cDNA EST
CG1071 comes from this * 3e-18 E2F5_MOUSE TRANSCRIPTION FAC CG1071 GH13089 39B3-39B3 ID:40D1
+ unknown * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST yk410c1.3 comes from this
CG12113 gene; cDNA EST yk410c1.5 comes from this gene; cDNA [ATP_GTP_A] CG12113 GH13214 7F1-7F3 ID:40D10
+ translation_factor * BLASTX 4.7E-83 Human translation initiation factor eIF3 p66 subunit mRNA, complete cds.(dna) *
CG10161 HYPOTHETICAL 64.2 KD PROTEIN R08D7.3 IN CHROMOSOME II CG10161 GH13209 97D8-97D8 dup:3/4 ID:40D9
+ transcription_factor * HYPOTHETICAL 43.4 KD PROTEIN C6F12.11C IN CHROMOSOME I(aa) * transcription factor
CG10563 IIC63(aa) * 1e-05 TFC1_YEAST TRANSCRIPTION FACTOR TAU KD SUBUNIT CG10563 GH13253 37C1-37C1 dup:2/2
ID:40E1
+ transcription_factor * zf30C * DMSPALTR_3 salr * 5e-05 YEW0_YEAST PUTATIVE 50.3 KD ZINC FINGER PROTEIN IN
CG2199 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

CG9238 + protein_phosphatase * smooth muscle protein phosphatase type 1-binding subunit(aa) * 4e-11 GIP2_YEAST GLC7-INTERACTING PROTEIN hypothetical prote * 8e-19 similar to glyc CG9238 GH13364 70E-70E dup:2/2 ID:40F1

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

CG12389 + Fpps enzyme * 8e-80 FPPS_YEAST FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DI * farnesyl pyrophosphate synthase melanogas * 2e-37 predicted [polyprenyl_synt // POLYPRENYL_SYNTHET_1] CG12389 GH13450 47E5-47E6 dup:2/2 ID:40F5

CG8314 + transcription_factor * DNZDHHC/NEW1 zinc finger protein 11(aa) * 3e-15 probable membrane protein YLR246w - yeast (Saccharomyces cerevisiae) * 1e-67 No definition line foun [ZF_DHHC] CG8314 GH13672 52E1-52E1 dup:1/2 ID:40G10

CG3041 + Orc2 DNA_replication_factor * recognition complex, subunit (yeast homolog)-like(aa) * ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT (XORC2)(aa) * Orc2 * ORIGIN RECOGNITION COMPLE[ALDOKETO_REDUCTASE_3 // SUBTILASE_ASP] CG3041 GH13824 88A4-88A4 ID:40H11

CG8684 + enzyme * METHIONYL-TRNA SYNTHETASE (METHIONINE--TRNA LIGASE) (METRS)(aa) * 2e-67 SYMM_YEAST METHIONYL-TRNA SYNTHETASE, MITOCHONDRIAL (METHIONINE--TRNA LIGASE [tRNA-synt_1 // TRNASYNTHMET] CG8684 GH13807 88B5-88B5 ID:40H7

CG10590 + unknown * 3e-66 EMP70 protein precursor - yeast (Saccharomyces cerevisiae) * 2e-88 Similarity to Yeast endosomal P24A protein (SW:EM70_YEAST); cDNA E * 4e-93 [CRYSTALLIN_BETAGAMMA] CG10590 GH13842 64E3-64E3 ID:41A2

CG5355 + endopeptidase * PROTEASE II (OLIGOPEPTIDASE B)(aa) * 6e-06 contains similarity to prolyl oligopeptidase family (Pfam: Prolyl_oligopep.hmm * prolyl endopeptidase PRO [PROLIGOPTASE // Peptidase_S9 // ESTERAS] CG5355 GH13952 31E1-31E1 ID:41B2

CG10800 + Rca1 unknown * Rca1 * Rca1 * Rca1 * 6e-25 inserted at base 5' end of P element Inverse PCR [NLS_BP] CG10800 GH14043 27C-27C ID:41B8

CG5701 + RhoBTB ligand_binding_or_carrier * protein(aa) * protein(aa) * 6e-24 RHO1_YEAST RHO1 PROTEIN transforming protein RHO1 - yeast * 9e-27 RHO1_DROME RAS-LIKE GTP-BINDING PR[BTB // PRO_RICH // ras // ATP_GTP_A //] CG5701 GH14096 77B6-77B6 dup:1/2 ID:41C1

CG2493 + peptidase * similar to lysosomal carboxypeptidase; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes f [ESTERASE // abhydrolase] CG2493 GH14278 38D1-38D1 ID:41D1

CG5827 + ribosomal_protein * 60S RIBOSOMAL PROTEIN YL35 (L37A)(aa) * 60S RIBOSOMAL PROTEIN L37A(aa) * 3e-31 ribosomal protein L37a 60S RIBOS * 1e-33 60S ribosomal protein L37A CG5827 GH14367 25C4-25C4 ID:41D9

CG5258 + ribosomal_protein * similar to Ribosomal protein L7Ae; cDNA EST comes from this gene(aa) * 2e-18 NHP2_YEAST HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN hi * 2e-27 similar [Ribosomal_L7Ae // L7ARS6FAMILY // NUCLE] CG5258 GH14757 70F6-70F6 ID:41G10

CG7425 + eff enzyme * DMUBCD1_2 eff * Ubiquitin conjugating enzyme(aa) * similar to ubiquitin conjugating enzymes(aa) * ubiquitin

conjugating enzyme(aa) [UBIQUITIN_CONJUGAT // UQ_con // UBIQUIT] CG7425 GH14739 88D2-88D2 ID:41G8
 + * 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
 + EG:63B12.8 unknown * 1e-50 PEP8_YEAST VACUOLAR PROTEIN SORTING/TARGETING PROTEIN PEP8 * /match=(desc;;
 /ma * 1e-111 YLNO_CAEEL HYPOTHETICAL 37.4 KD PROTEIN T20D3.7 IN CH [NLS_BP] CG14804 GH15034 2B13-2B13
 CG14804 ID:42A6
 + unknown * 2e-81 YN28_YEAST HYPOTHETICAL 41.2 KD PROTEIN IN PLC1-SEC21 INTERGENIC REGION * 4e-94
 CG14213 C26E6.3 gene product * 1e-124 protein involved in sexual devel CG14213 GH15157 18D10-18D10 ID:42B4
 CG10539 + protein_kinase CG10539 GH15161 ID:42B6
 + signal_transduction * serine/threonine kinase with Dbl- and pleckstrin homology domains(aa) * actin-filament binding
 protein Frabin(aa) * 5e-12 ROM1_YEAST RHO1 GDP-GTP E [GRF_DBL // RhoGEF // PRO_RICH // NLS_BP] CG8606 LD21492
 CG8606 65F2-65F2 ID:43A5
 CG11993 + Mst85C unknown * CG11993 LD21554 85C6-85C6 ID:43A6
 + transcription_factor_binding * 6e-06 DIP2_YEAST DOM34 INTERACTING PROTEIN DIP2 protein - y * 2e-06 similar to beta
 transducin proteins containing TRP-ASP domains el * 6e-11 ap[WD40_REGION // WD_REPEATS // WD40] CG14722 LD21659
 CG14722 86F6-86F6 ID:43A8
 + RNA_binding * RNA helicase isolog(aa) * RNA helicase HEL117 - rat(aa) * protein(aa) * putative ATP-dependent RNA
 CG6227 helicase(aa) [helicase_C // ANTIFREEZE1 // AA_TRANSFE] CG6227 LD21880 13C1-13C1 dup:1/4 ID:43A9
 + motor_protein * 1e-34 3-hydroxyisobutyrate dehydrogenase * 1e-10 inserted at base Both 5' and 3' ends of P element
 CG4747 Inverse PCR * YKWC_BACSU HYPOTHETICAL 30.7 KD PR CG4747 LD22344 30F5-30F5 ID:43B10
 CG3510 + CycB cell_cycle_regulator G2/MITOTIC-SPECIFIC CYCLIN B CYCLINS, cyclin CG3510 dup:2/4 ID:43B3
 + DNA_binding * SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1(aa) *
 CG7055 BAF57(aa) * 1e-08 HMG1-related DNA-binding [HMG // HMG_box // PRO_RICH] CG7055 LD22182 8C17-8D1 ID:43B5
 CG17252 + BCL7-like CG17252 LD22180 dup:2/2 ID:43B6
 + BcDNA:LD21293 enzyme * unknown(aa) * 1e-27 unknown * [ATP_GTP_A2 // ATP_GTP_A] CG7139 LD22250 79C2-79C3
 CG7139 ID:43B9
 + not endopeptidase * PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C (UBIQUITIN
 THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN[UCH_2_1 // UCH_2_3 // UCH-
 CG4166 1 // NLS_BP /] CG4166 LD22730 75D1-75D1 dup:1/2 ID:43C10
 + noi RNA_binding * noi * noisette(aa) * 1e-30 PR09_YEAST PRE-MRNA SPLICING FACTOR PRP9 PRP9 protein - ye *
 CG2925 noisette [ZF_MATRIN] CG2925 LD22754 83B4-83B4 ID:43C11
 + Mcm2 DNA_replication_factor * BLASTX 4.1E-84 Homo sapiens mRNA for DNA replication licensing factor (huMCM2),
 complete cds.(dna) * BLASTX 4.1E-84 Homo sapiens mRNA for DNA replic [MCM // MCM_1 // MCM_2] CG7538 LD22409 84F-
 CG7538 84F dup:1/2 ID:43C3
 + enzyme * 1e-34 GLO2_YEAST HYDROXYACYLGLUTATHIONE HYDROLASE ISOZYME (GLYOXALASE II) (GLX II) * 8e-
 CG4365 60 similar to Metallo-beta-lactamase superfamily el * 3e-85 [lactamase_B] CG4365 77E-77E dup:1/3 ID:43C6

CG7752 + transcription_factor CG7752 ID:43C7
+ signal_transduction * DM60AP * 1e-11 60A_DROME 60A PROTEIN PRECURSOR TGF-beta-related protein * 2e-09
protein homolog * 1e-14 BMP2_MOUSE BONE MORPHOGENETIC PROTEIN PRECUR [TGF-beta // TGF_BETA //

CG1901 TGF_BETA_2] CG1901 102D1-102D1 dup:2/2 ID:43C8
+ Arf51F ligand_binding_or_carrier * ADP-RIBOSYLATION FACTOR 3(aa) * DMARF3A_3 Arf51F * 1e-65 ARF2_YEAST ADP-
RIBOSYLATION FACTOR ADP-ribosylation fac * 3e-67 ARF1_CAEEL PUTATIVE A[ARF // arf // SAR1GTPBP // ATP_GTP_A //]

CG8156 CG8156 LD22876 51F6-51F6 ID:43D4
+ 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

CG8569 + bves CG1754 LD22978 dup:2/2 ID:43D8
CG1754 + enzyme * [NLS_BP] CG12124 LD23314 8D5-8D5 dup:4/4 ID:43E11
CG12124 + car transporter * 9e-22 SLP1 protein homolog - Caenorhabditis elegans SLP-1 protei * 1e-116 vacuolar protein sorting
homolog r-vps33a * SLP1_CAEEL SLP-1 PROTEIN * C5 [Sec1 // CYTOCHROME_C] CG12230 LD23088 18D5-18D5 dup:3/3
ID:43E5

CG12230 + signal_transduction G-protein beta-subunit 6 GPROTEINBRPT, RCC1_2, WD40, WD40_REGION,] CG3004 LD23129
CG3004 dup:3/3 ID:43E6
+ signal_transduction * putative WD-repeat protein(aa) * katanin (80 kDa)(aa) * 4e-12 hypothetical protein YCL039w - yeast
(Saccharomyces cerevisiae) * 1e-09 L2DT_D[GPROTEINBRPT // WD40_REGION // WD_REPEA] CG7611 LD23260 78E1-78E1
dup:5/5 ID:43E8

CG7611 + CG5926 dup:2/2 ID:43E9
CG5926 + 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

CG6538 + Mat1 transcription_factor CDK7/cyclin H assembly factor NLS_BP, ZF_RING, ZINC_FINGER_C3HC4, zf-C] CG7614 LD23429
CG7614 ID:43F4
+ Bub3 signal_transduction * WD-40 repeat protein(aa) * 7e-49 YET7_YEAST HYPOTHETICAL 40.5 KD TRP-ASP REPEATS
CONTAINING PROTEIN IN NUP157-PDH * 7e-72 predicted using Genefinder [GPROTEINBRPT // WD40_REGION //

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

CG6254 85F13-85F13 dup:1/2 ID:43F9
+ mus210 DNA_repair_protein * DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS HOMOLOG (XERODERMA
PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN HOMOLOG) (XPCDM)(aa) * DMXPCCF_2 Xpcc * 4e- [MYB_1 //

CG8153 NLS_BP] CG8153 51F4-51F5 dup:1/3 ID:43G11
+ cytoskeletal_structural_protein * actin-related protein; Arp8p(aa) * 1e-26 ARP8_YEAST ACTIN-LIKE PROTEIN ARP8
probable membrane pr * 9e-05 actin isolog * 4e-05 DNARP87C_2 Arp87C [ATPASE_ALPHA_BETA] CG7846 LD24980 16D7-
16D7 ID:43G12

CG7846 + dbbe unknown * DMDRIBBLE dbbe * dribble(aa) * 9e-98 YCF9_YEAST HYPOTHETICAL 37.2 KD PROTEIN IN CHA1-PRD1
CG4258

INTERGENIC REGION * 5e-88 similar to human REV interacting CG4258 LD24634 21E3-21E3 ID:43G5

CG4735 + chaperone * FK506-binding protein 6(aa) * FK506-binding protein - Arabidopsis thaliana(aa) * FKBP (FK506 binding protein) 13; peptidylprolyl cis-trans isomerase [FKBP // FKBP_PPIASE_3 // TPR_REPEAT] CG4735 LD24746 60A4-60A4 ID:43G6

+ Dom transcription_factor * DOMINA protein (WHN-homologue)(aa) * 1e-12 FKH2_YEAST FORK HEAD PROTEIN HOMOLOG FKH2 protein - y * 4e-16 SLP1_DROME FORK HEAD DOMAIN TRANSCRIPTION F [Fork_head // FORKHEAD] CG4029 LD24749 86A2-86A3 ID:43G7

CG4029 LD24749 86A2-86A3 ID:43G7

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

CG7600 + NLS_BP, PLANT_GLOBIN CG7600 LD25031 dup:1/2 ID:43H1

CG17322 + enzyme UDP-glycosyltransferase UDPGT CG17322 LD25345 dup:1/2 ID:43H10

+ Srp54k ligand_binding_or_carrier * 1e-119 SR54_YEAST SIGNAL RECOGNITION PARTICLE KD PROTEIN HOMOLOG (SRP54) * similar to signal recognition particle protein (SRP54); cDNA EST E * SR5 [SRP54 // ATP_GTP_A] CG4659 LD25385 64C12-64C12 dup:1/3 ID:43H11

CG4659 64C12-64C12 dup:1/3 ID:43H11

+ enzyme possible protein methyltransferase N12N6MTFRASE, N6_MTASE, SAM_BIND CG9666 LD25448 dup:1/3 ID:43H12

CG9666 ID:43H12

+ DNA_binding * protein(aa) * 6e-24 hypothetical protein YPR031w - yeast (Saccharomyces cerevisiae) * 2e-25 zinc finger protein CEZF gene * 1e-31 maf10 [PHD] CG15439 LD25123 24F4-24F4 dup:2/2 ID:43H4

CG15439 + 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

CG1906 99B6 ID:43H5

CG9967 + CG9967 LD25280 dup:1/2 ID:43H7

CG9967 + 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

CG11154 dup:3/4 ID:43H8

+ * 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

CG14641 + transcription_factor homology to uncharacterized human zinc finger proteins ZINC_FINGER_C2H2, ZINC_FINGER_C2H2_2, zf] CG8301 LD25464 dup:1/4 ID:44A2

CG8301 + motor_protein * 1e-155 inserted at base 5' end of P element Inverse PCR * * [bZIP] CG3183 LD25484 42B3-42B3 dup:1/2 ID:44A3

CG3183 ID:44A3

+ unknown * 4e-21 YS48_CAEEL HYPOTHETICAL 66.5 KD PROTEIN ZK177.8 IN CHROMOSOME II (U * 2e-20 MG11_MOUSE INTERFERON-GAMMA INDUCIBLE PROTEIN MG11 unkn * 4e-20 hy CG9670 LD25913 76A5-76A6 dup:3/3 ID:44B11

CG9670 ID:44B11

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

CG7531 + huckebein transcription_factor specific RNA polymerase II transcription factor ZINC_FINGER_C2H2, ZINC_FINGER_C2H2_2, zf] CG9768 LD25709 dup:2/3 ID:44B3

CG9768 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

+ 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

CG2087 + 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

CG12340 + unknown CG13322 LD26432 dup:2/3 ID:44D11

CG13322 + aret RNA_binding * aret * 8e-06 polyadenylate-binding protein * 1e-148 testis-specific RNP-type RNA binding protein * 2e-29 elav-type ribonucleoprotein coded [RBD // HUDSXL RNA // rrm] CG6319 33D-33D4 dup:3/3 ID:44D5

CG6319 + signal_transduction * Polyadenylation Factor I subunit; Pfs2p(aa) * 3e-17 alpha-COP (Z466 * 3e-18 lissencephaly-1 * 3e-15 SEL-10 [GPROTEINBRPT // WD40_REGION // WD40] CG1109 LD26389 83B7-83B7 dup:2/3 ID:44D6

CG1109 + CHROMO_2, chromo CG18622 LD26416 dup:2/3 ID:44D9

CG18622 + Sr-CII cell_adhesion Scavenger receptor class C, type II MAM, MAM_2, SOMATOMEDIN_B, Somatomedin_B] CG8856 LD26673 dup:3/3 ID:44E10

CG8856 + 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

CG5363 + CG11504 LD26477 dup:3/3 ID:44E2

CG11504 + endopeptidase * Saccharolysin (oligopeptidase yscD); Prd1p(aa) * NEUROLYSIN PRECURSOR (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOP [Peptidase_M3] CG11771 LD26931 98F1-98F1 dup:4/5 ID:44F10

CG11771 + CG4785 LD26982 dup:2/2 ID:44F11

CG4785 + protein_phosphatase * 4e-56 P2C2_YEAST PROTEIN PHOSPHATASE 2C HOMOLOG (PP2C-2) hyp * 9e-20 unknown * 1e-108 P2C2_CAEEL PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (PP2C) * 4 [PP2C // PP2C_1 // PP2C_2] CG17746 64A3-64A3 dup:4/4 ID:44F12

CG17746 + 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 fzr CG16892 LD26813 8D7-8D8 dup:2/2 ID:44F4

CG16892 + unknown CG7725 LD26833 dup:2/2 ID:44F6

CG7725 + unknown unknown protein CIT987SK_2A8_1 [Homo sapiens] CG5222 LD26912 dup:1/2 ID:44F9

CG5222 + Bap60 Brahma associated protein 60kD NLS_BP, PRO_RICH CG4303 LD27052 dup:1/2 ID:44G4

CG4303 + transporter * multiple drug resistance protein 1(aa) * 1e-180 cadmium resistance protein YCF1 - yeast (Saccharomyces cerevisiae) * 3e-34 MDR4_DROME MULTIDRUG RES[ATP_GTP_A2 // ABC_TRANSPORTER // TUBULI] CG11897 LD27104 99A2-99A3 dup:1/2 ID:44G6

CG11897

CG10372 + Faf unknown * Fly Fas-associated factor (FFAF)(aa) * Faf * 1e-12 probable membrane protein YDL091c - yeast (Saccharomyces cerevisiae) * 7e-10 similar to mouse FAF [UX_DOMAIN] CG10372 LD27106 37A4-37A4 dup:1/2 ID:44G7

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

CG10923 + Klp67A motor_protein kinesin family protein 3B ATP_GTP_A, KINESINHEAVY, KINESIN_MOTOR_D] CG10923 LD27326 dup:2/2 ID:44H12

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

CG2678 + transcription_factor similar to crol protein ZINC_FINGER_C2H2, ZINC_FINGER_C2H2_2, z] CG2678 LD27553 dup:1/2 ID:45A10

CG18608 + unknown * CG18608 LD27570 56A-56A dup:1/2 ID:45A11

CG15817 + 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

CG12785 + unknown * Ygr090wp(aa) * hypothetical protein(aa) * 4e-17 YG2L_YEAST HYPOTHETICAL 140.5 KD PROTEIN IN CTT1-PRP31 INTERGENIC REGION CG12785 LD27528 89B17-89B17 dup:2/2 ID:45A9

CG1506 + Ac3 enzyme adenylyl cyclase isoform DAC3 [Drosophila melanogaster] GUANYLATE_CYCLASES, GUANYLATE_CYCLASES_] CG1506 LD27878 dup:2/2 ID:45B12

CG9446 + actin_binding * has homology to the Dictyostelium and human actin-binding protein coronin; Crn1p(aa) * coronin-1(aa) * 3e-76 CORO_YEAST CORONIN-LIKE PROTEIN hypothe [WD40_REGION // ARGINASE_2 // WD_REPEATS] CG9446 42C8-42C8 dup:3/3 ID:45B2

CG8632 + embryonic lung protein [Homo sapiens] CG8632 LD27783 dup:1/2 ID:45B7

CG11274 + unknown * Ser/Arg-related nuclear matrix protein (plenty of prolines 101-like)(aa) * 7e-33 cDNA EST comes from this gene; cDNA EST co * 2e-43 plenty-of-prolin [RIBOSOMAL_S12 // NLS_BP] CG11274 LD28048 69F2-69F2 dup:1/2 ID:45C10

CG11970 + BcDNA:LD23876 similar to nuclear factor related to kappa B binding protein CG11970 LD28082 dup:2/4 ID:45C12

CG4806 + 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

CG5126 + unknown * CG5126 LD27921 21F1-21F1 dup:1/2 ID:45C3

CG10739	+ lio protein_kinase * LIO_DROME LINOTTE PROTEIN linotte protein mela * lio * * [NLS_BP] CG10739 LD27947 37C-37C dup:2/2 ID:45C4
CG9506	+ protein_phosphatase * CG9506 LD27991 28D1-28D1 dup:1/2 ID:45C6
CG7825	+ Rad17 DNA_repair_protein DNA repair protein ATP_GTP_A, ATP_GTP_A2, RFC CG7825 LD27993 ID:45C7
CG10018	+ DNA_repair_protein homology to mouse and human SNM1 protein NLS_BP CG10018 LD28027 dup:1/2 ID:45C8
CG4609	+ fax failed axon connections protein CG4609 LD28084 dup:2/2 ID:45D1
CG7728	+ 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
CG5003	+ unknown * [FBOX_DOMAIN] CG5003 LD28210 98B2-98B2 ID:45D12
CG6994	+ cytoskeletal_structural_protein CG6994 LD28101 dup:2/2 ID:45D5
CG14650	+ chaperone * 2e-09 HLJ1_YEAST HLJ1 PROTEIN HLJ1 protein - yeast (Saccharom * 2e-09 DNJ1_DROME DNAJ PROTEIN HOMOLOG (DROJ1) droj1 * 1e-26 YQ07_CAEEL HYPOTHETICAL [GRAM_POS_ANCHORING // DnaJ // DNAJPROTE] CG14650 LD28109 82C1-82C1 dup:3/3 ID:45D6
CG9213	+ enzyme CG9213 LD28117 dup:2/2 ID:45D7
CG7564	+ 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
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
CG9933	+ Weak homology to SNF2 family (CHD1 subfamily) chromodomain protein [Arabidopsis thaliana] CHROMO_2 CG9933 LD28372 dup:5/5 ID:45E9
CG14749	+ CG14749 dup:3/3 ID:45F10
CG1658	+ Doa protein_kinase * PROTEIN KINASE DOA (PROTEIN DARKENER OF APRICOT)(aa) * DMDOA_2 Doa * 2e-60 ORF YLL019c * 1e-127 Similarity to Drosophila Doa kinase (PIR Acc. No. cD [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG1658 98F-98F2 dup:3/3 ID:45F12
CG8783	+ unknown Conserved gene telomeric to alpha globin cluster [Homo sapiens] CG8783 LD28428 dup:2/3 ID:45F2
CG12179	+ EG:66A1.2 transcription_factor_binding * map_position:4C6 * map_position:4C6 * map_position:4C6 * by match; 1-mat CG12179 LD28429 4C6-4C7 ID:45F3
CG14657	+ unknown CG14657 LD28447 ID:45F4
CG4300	+ unknown spermine synthase SAM_BIND CG4300 LD28457 ID:45F5
CG1091	+ unknown * 7e-10 /match=(desc: * 9e-10 K10D2.3 gene product * 1e-10 The gene is expressed ubiquitously.; The protein * 1e-09 caffeine-induced death protein >g [PAP_ASSOCIATED // PAP_CORE // PAP // AA] CG1091 84C1-84C1 dup:3/3 ID:45F7
CG2947	+ chaperone * 1e-07 STI1_YEAST HEAT SHOCK PROTEIN STI1 stress-induced protein * 1e-08 Hsp70/Hsp90 organizing protein homolog * 1e-54 similar to TPR Domain (2 doma [RNP_1 // TPR_REGION // TPR_REPEAT // TP] CG2947 3F6-3F6 dup:3/4 ID:45F9
CG12000	+ CG12000 ID:45G11

+ ribosomal_protein * 1e-48 RL7A_YEAST 60S RIBOSOMAL PROTEIN YL17-A ribosomal protein * 4e-66 ribosomal protein
 L17 60S RIBOSOM * 1e-65 RL17_RAT 60S RIBOSOMAL PROTEIN L17 [Ribosomal_L22 // RIBOSOMAL_L22] CG3203 6C10-
 CG3203 6C10 dup:1/5 ID:45G12
 + unknown * Cys-rich protein(aa) * FIM protein(aa) * zinc finger protein 261(aa) * BLASTX 3.6E-13 Dictyostelium discoideum
 CG5965 sp96 gene for spore coat protein SP9 CG5965 97F4-97F4 dup:2/3 ID:45G2
 + sgg protein_kinase * DMSGG46_2 sgg * 5e-98 MDS1_YEAST SERINE/THREONINE-PROTEIN KINASE MDS1/RIM11 pr *
 CG2621 zeste-white 3-A - fruit fly (Drosophila melanogaster) * 1e-141 pred [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG2621
 3B2-3B3 dup:1/2 ID:45G9
 + unknown * phosphatidylinositol glycan, class B(aa) * 2e-29 YGO2_YEAST HYPOTHETICAL 72.6 KD PROTEIN IN MRF1-
 CG12006 SEC27 INTERGENIC REGION * 5e-08 coded for by C. ele CG12006 64C4-64C4 dup:2/2 ID:45H10
 CG11207 + unknown CG11207 dup:2/2 ID:45H2
 CG2890 + CG2890 dup:2/3 ID:45H3
 CG10640 + CG10640 dup:4/4 ID:45H8
 + smg * cloned by ability to arrest the cell cycle when expressed in the fission yeast Schizosaccharomyces pombe(aa) * 1e-124
 CG5263 cloned by ability to arrest th CG5263 66F1-66F1 dup:1/5 ID:46A10
 CG8309 + CG8309 dup:2/3 ID:46A12
 CG8379 + * CG8379 85B4-85B4 dup:1/3 ID:46A2
 + ncd motor_protein * DMCLARET_4 ncd * 3e-75 KAR3_YEAST KINESIN-LIKE PROTEIN KAR3 (NUCLEAR FUSION
 CG7831 PROTEIN) * NCD_DROME CLARET SEGREGATIONAL PROTEIN * 4e-61 YNZ2_CAEEL PU [kinesin //
 KINESIN_MOTOR_DOMAIN1 // KIN] CG7831 99C5-99C5 ID:46A9
 + protein_kinase * DMTKABL3_2 Abl * TAK1 (TGF-beta-activated kinase)(aa) * TGF-beta activated kinase 1b(aa) * TGF-beta
 CG1388 activated kinase 1c(aa) [PROTEIN_KINASE_ST // EGF_1 // TYRKINASE] CG1388 19E1-19E1 dup:1/4 ID:46B1
 CG6605 + motor_protein CG6605 ID:46B12
 CG9805 + translation_factor eukaryotic translation initiation factor 3 subunit NLS_BP, PCI_DOMAIN CG9805 ID:46B4
 + unknown * MA3(aa) * 3e-70 apoptosis protein MA-3 - mouse apoptosis-i * 1e-69 nuclear protein H731 - human nuclear
 CG10990 antigen H731 * nuclear antigen H731-like pr [RCC1_2 // NLS_BP] CG10990 12B8-12B8 ID:46B7
 CG4916 + RNA_binding CG4916 dup:2/2 ID:46C4
 CG7563 + calpain CG7563 dup:1/4 ID:46C8
 CG2028 + protein_kinase CG2028 ID:46D10
 CG5991 + enzyme PHOSPHATIDYLSERINE DECARBOXYLASE PROENZYME CG5991 ID:46D2
 CG2034 + CG2034 ID:46D4
 CG1101 + CG1101 dup:4/5 ID:46D7
 + transcription_factor * host cell factor C1 (VP16-accessory protein)(aa) * HOST CELL FACTOR C1 (HCF) (VP16
 CG1710 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF)(aa) * host cell factor 2(a CG1710 LD29768 102B3-102B3 dup:3/3 ID:46E3
 + shn transcription_factor * 5e-05 pdb|2ADR| Adr1 Dna-Binding Domain From Saccharomyces Cerevisiae, Nmr, Structures *
 CG7734 transcription factor * 2e-28 similar to 11-S plant[PTS_HPR_SER // zf-C2H2 // ZINC_FINGER_C] CG7734 LD29807 47D5-47D6

dup:4/4 ID:46E6

CG3820 + transporter * ATP-DEPENDENT RNA HELICASE GLH-1(aa) * 1e-08 EAST_DROME SERINE PROTEASE EASTER
 PRECURSOR serine protein * 6e-22 similar to nucleoporin; cDNA EST com CG3820 LD29808 59B4-59B4 dup:3/4 ID:46E7

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

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

CG8730 + drosha RNA binding ribonuclease III DSRBD, PRO_RICH, RIBONUCLEASE_III, RNASE] CG8730 LD29995 dup:2/3 ID:46F12

CG5742 + transcription factor binding involved in cytoskeleton organization and biogenesis which is a component of the plasma
 membrane ANK_REP, ANK_REP_REGION, NLS_BP, ank CG5742 LD29875 ID:46F2

CG7913 + protein_phosphatase regulatory subunit B' of serine-threonine protein phosphatase 2A ANTIFREEZEI, B56 CG7913
 LD29902 dup:1/3 ID:46F5

CG10647 + some homology to T-box transcription factor tbx2, procollagen, type VIII, alpha 1 and putative protein kinase CG10647
 LD29922 dup:1/2 ID:46F7

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

CG3021 + CG3021 LD29918 dup:1/2 ID:46F9

CG7288 + endopeptidase * hypothetical protein unsp - 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

CG3309 + unknown * 3e-62 No definition line found * No definition line found * CG3309 LD30005 4F2-4F2 dup:1/2 ID:46G3

CG17681 + unknown * CG17681 LD30009 36E-36E ID:46G4

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

CG9949 + SEVEN IN ABSENTIA DNA binding ubiquitin-dependent protein degradation ZF_RING CG9949 LD30265 ID:46H3

CG1647 + glass transcription_factor photoreceptor determination ZINC_FINGER_C2H2 CG1647 LD30287 dup:2/2 ID:46H5

CG14005 + unknown * CG14005 LD30293 26A2-26A2 dup:2/3 ID:46H6

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

CG4164 + chaperone It encodes a chaperone involved in proteolysis and peptidolysis which is a component of the mitochondrion
 DNAJPROTEIN, DNAJ_1, DNAJ_2, DnaJ CG4164 LD30318 ID:46H8

CG1677 + CG1677 LD30482 ID:47A10

CG2682 + transcription_factor CG2682 ID:47A11

CG12306 + protein_kinase CG12306 ID:47A2

CG8617 + CG8617 LD30408 dup:1/2 ID:47A4

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

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

CG12202 + translation_factor * 1e-85 NAT1_YEAST N-TERMINAL ACETYLTRANSFERASE (AMINO-TERMINAL, ALPHA-AMINO, ACETYLTR * 1e-123 N-terminal acetyltransferase * O-linked GlcNAc tran[TPR_REGION // TPR_REPEAT // NLS_BP] CG12202 LD30511 18C8-18D1 dup:3/6 ID:47B1

CG7764 + transcription_factor * general transcription factor IIH, polypeptide (52kD subunit)(aa) * TFIIH subunit Tfb2; has homology to CAK and human IIH subunits; Tfb2p(aa) * 9e-71 CG7764 LD30622 71D3-71D4 ID:47B11

CG9231 + * 2e-14 pIL2 hypothetical protein - rat (fragment) growth and trans ** CG9231 76B9-76B9 dup:2/2 ID:47B12

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

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

CG7133 + 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

CG4274 + 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

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

CG17299 + SNF4Agamma protein_kinase * SNF4A ggr; * protein kinase protein serine/threonine kinase) map_position:93C * 8e-29 SNF4_YEAST NUCLEAR PROTEIN SNF4 (REGULATORY PROTEIN CAT3) * 1 [CBS // SNF4_REP // NLS_BP] CG17299 LD30628 93C4-95F5 dup:1/11 ID:47C1

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

CG6226 + 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

CG6962 + CG6962 ID:47C2

CG8631 + 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

CG14222 + unknown * 2e-34 hypothetical protein YPR131c - yeast (*Saccharomyces cerevisiae*) (* 8e-20 contains similarity to N-terminal acetyltransferase complex subunit [Acetyltransf] CG14222 LD30731 18D9-18D9 dup:1/2 ID:47C6

CG11490 + unknown CG11490 dup:1/3 ID:47C9

CG7536 + unknown * xenotropic and polytropic murine leukemia virus receptor X3(aa) * polytropic murine leukemia virus receptor SYG1(aa) * predicted using Genefinder; CG7536 LD30826 16F7-16F7 ID:47D1

CG2670 + 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

CG11982 + transcription_factor * putative ring zinc finger protein NY-REN-43 antigen(aa) * putative protein(aa) * hypothetical protein, similar to PRAJA1 * DMGOLTHA_3 gol [zf-C3HC4 // ZF_RING] CG11982 LD30985 85C4-85C4 dup:3/3 ID:47D12

CG15104 + unknown * 3e-05 No definition line found * 1e-32 topoisomerase I-binding RS protein * 8e-11 ring finger protein * tumor protein p53-binding protein p53 bindin [zf-C3HC4 // ZINC_FINGER_C3HC4 // NLS_BP] CG15104 56A-56A dup:3/3 ID:47D3

CG7940 + cytoskeletal_structural_protein * actin-like protein; (2 actin domains)(aa) * 2e-71 ARP5_YEAST ACTIN-LIKE PROTEIN ARP5 probable nuclear pro * 3e-18 ACTU_DROME ACTIN-LIKE PROTEIN 13E [NLS_BP // actin] CG7940 90E5-90E6 dup:1/2 ID:47D6

CG4206 + 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

CG14211 + 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

CG7730 + unknown * CG7730 LD31138 73E4-73E4 dup:2/2 ID:47E12

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

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

CG10387 + 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

CG6719 + chaperone * 7e-25 PA10_YEAST PAC10 PROTEIN PAC10 protein - yeast (*Sacchar* * 7e-27 YFM9_CAEEL HYPOTHETICAL 20.9 KD PROTEIN T06G6.9 IN CHROMOSOME I * 2e-43 VBP1_H CG6719 LD31046 86E4-86E4 dup:4/4 ID:47E7

CG7872 + 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

CG4943 + enzyme * 1e-109 RSP5_YEAST UBIQUITIN--PROTEIN LIGASE RSP5 hypothetical pr * 2e-48 similar to hypothetical proteins from yeast (YKL162) and rat (PIR: * 3e-90 [HECT_DOMAIN // HECT // WW_rsp5_WWP // C] CG4943 LD31242 54D3-54D3 dup:2/3 ID:47F12

CG17153 + 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

CG7035 + Cbp80 RNA_binding * cap-binding protein - human(aa) * nuclear cap binding protein, 80kD(aa) * 4e-17 GCR3_YEAST GCR3 PROTEIN (STO1 PROTEIN) (SUT1 PROTEIN) * by match; 1- [NLS_BP] CG7035 LD31211 4C7-4C7 ID:47F4

+ ligand_binding_or_carrier * 3e-51 ARF1_YEAST ADP-RIBOSYLATION FACTOR ADP-ribosylation fac * 3e-49 ARF1_DROME ADP-RIBOSYLATION FACTOR ADP-ribosylation fac * 1e-52 ARFL_CA[arf // SAR1GTPBP // RASTRNSFRMNG] CG7197 LD31204 66C5-66C5 dup:2/5 ID:47F5

CG8440 + signal_transduction CG8440 ID:47F8

CG5100 + unknown * [PRO_RICH // NLS_BP] CG5100 LD31243 77C4-77C4 dup:1/4 ID:47G1

+ RNA_binding * putative protein(aa) * homologous to mouse gene PC326:GenBank Accession Number * putative protein(aa) * 5e-08 Cdc40p [WD40_REGION // WD40] CG8001 LD31538 62B1-62B2 dup:1/2 ID:47G10

CG8001 + 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 77A1-73A7 dup:1/2 ID:47G7

CG4118 + * CG18592 25C3-25C3 dup:1/2 ID:47H11

CG18592 + * 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

CG7494 + unknown CG1530 ID:47H2

CG1530 + msi RNA_binding * DMMUSASH_3 msi * 9e-41 NAB4_YEAST NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4 * musashi * 2e-31 heterogeneous ribonuclear particel protein homol [RNP_1 // RBD // rrm // ANTIFREEZEI] CG5099 LD31631 96E5-99B9 ID:47H3

CG5099 + 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

CG10997 + enzyme * PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR (LYSYL HYDROXYLASE) (LH)(aa) * PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR ([GLYC_TRANS // HTH_LYSR_FAMILY] CG6199 LD31687 68A8-68A8 dup:3/4 ID:47H7

CG6199 + 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

CG1657 + transcription_factor * 1e-11 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * 4e-20 CROL BETA * 2e-08 similar to Zinc finger, C2H2 type (4 domains); cDNA EST *[ZF_MATRIN // zf-C2H2 // ZINC_FINGER_C2H] CG17806 LD32088 93B1-93B1 ID:48A11

CG17806 + unknown * CG5676 LD31953 31C4-31C4 dup:1/2 ID:48A3

CG5676

CG10364 + msb1l unknown * CG10364 LD32040 37F2-37F2 ID:48A8

CG1753 + enzyme * cystathionine beta-synthetase; CBS(aa) * BLASTX 8.7E-06 CYS4[Cystathionine beta-synthase (beta-CTSase), converts serine and homocysteine to cystathi [CBS // SNF4_REP // S_T_dehydratase // C] CG1753 LD32051 19E6-19E6 ID:48A9

+ ligand_binding_or_carrier * RasGAP-associated protein p56dok-2(aa) * docking protein 1(aa) * 1e-13 FAT2_YEAST PEROXISOMAL-COENZYME A SYNTHETASE probable AMP * 5e-14 Contains si [AMP-binding // PH_DOMAIN] CG2079 LD32155 7A4-7A4 dup:3/3 ID:48B2

CG2079 + unknown * DMPPP_2 Arr2 * 1e-41 ARRB_DROME PHOSRESTIN I (ARRESTIN B) (ARRESTIN 2) (49 KD ARRESTIN-LIKE PROTEIN) * 1e-45 ARRB_CAEEL PROBABLE BETA-ARRESTIN coded [ARRESTIN // arrestin // ARRESTINS // AT] CG1487 LD32202 100F5-100F5 ID:48B3

CG1487 + unknown * 1e-141 YQT5_CAEEL HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III (U * 1e-132 putative protein * similar to hypothetical proteins * YLEA_HAE [UPF0004] CG6345 LD32258 86A6-86A6 ID:48B4

CG6345 + weak homology to extensin-like protein [Lycopersicon esculentum], proline-rich protein PRP2 precursor [Lupinus luteus] CG15486 LD32537 ID:48C11

CG15486 + unknown * clot.500(dna)* * CG3883 LD32410 21D2-21D2 ID:48C2

CG3883 + unknown * 3e-26 YKJ5_YEAST 32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION * 3e-47 similar to S. cerevisiae YJU2 protein * 5e-67 unknown * 1e-35 hypothetical p CG8435 LD32459 52F5-52F5 ID:48C4

CG8435 + RnrS enzyme * 1e-113 RIR2_YEAST RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE R * 1e-107 RIR2_DROME PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTA [RIBORED_SMALL] CG8975 LD32770 48D8-48D8 ID:48D10

CG8975 + 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

CG8961 + 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

CG6509 + 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

CG6418 + motor_protein * ARX(aa) * 1e-58 UBA2_YEAST UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN * 2e-28 ubiquitin activating enzyme * 1e-67 simila[UBA_NAD // ThiF_family // NAD_BINDING /] CG7528 LD33023 67E3-67E3 dup:5/5 ID:48E10

CG7528 + unknown * 1e-142 inserted at base Both 5' and 3' ends of P element Inverse PCR * * CG15893 LD32923 5E4-5E4 dup:2/2 ID:48E5

CG15893 + 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

CG10206 + Mat89Bb unknown * Mat89Ba * contains similarity to drosophila ovary2 * ovary2 * ovary2 CG6814 LD33046 89B17-89B17 dup:2/3 ID:48F1

CG6814 + BG:DS09218.3 chaperone * 8e-19 ERP5_CAEEL PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR * 4e-21 CG4455

protein disulfide isomerase-related protein * 9e-21 ERP5_RAT PROBABLE PRO CG4455 LD33101 35F10-35F10 dup:2/3 ID:48F10

CG18551 + unknown * CG18551 LD33058 88E1-88E1 ID:48F3

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

CG10228 + unknown * protein(aa) * 3e-09 PC11_YEAST PCF11 PROTEIN hypothetical protein YDR228c - * 3e-21 YRR2_CAEEL HYPOTHETICAL 91.1 KD PROTEIN R144.2 IN CHROMOSOME III [PRENYLATION // PRO_RICH // NLS_BP // CY] CG10228 LD33132 51D2-51D2 ID:48G2

CG1962 + motor_protein * kda paraneoplastic cerebellar degeneration-associated antigen Peptide, * MYOSIN HEAVY CHAIN D (MHC D)(aa) * CLIP-190 * 7e-05 microtubule binding pro [NLS_BP] CG1962 38E-38E dup:3/5 ID:48G3

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

CG8000 + unknown * hypothetical protein(aa) * 4e-25 YMO9_YEAST HYPOTHETICAL 20.9 KD PROTEIN IN PLB1-HXT2 INTERGENIC REGION * 9e-21 Closely related to Arabidopsis thal [NLS_BP] CG8000 LD33361 67E4-67E4 ID:48H2

CG15835 + DNA_binding * protein(aa) * 3e-65 YEZ9_YEAST PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION > * 2e-26 Similarity to Human XE169 protein (SW:X CG15835 LD33386 43F5-43F5 ID:48H3

CG9135 + chromatin_binding * pheromone response pathway suppressor; Srm1p(aa) * similar to RCC1 proteins(aa) * regulator of chromosome condensation(aa) * retinitis pigmentosa [RCC1 // RCC1_2 // RCCNDNSATION] CG9135 LD33431 26B3-26B3 dup:1/2 ID:48H4

CG18124 + BG:DS01068.4 unknown * 1e-05 mtDBP protein * AAs * * CG18124 LD33443 35A1-35A1 ID:48H5

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

CG1454 + wdn transcription_factor * DMDROSOPH_4 wdn * 3e-18 YJF6_YEAST HYPOTHETICAL 98.9 KD ZINC FINGER PROTEIN IN BTN1-PEP8 INTERGENIC REG * SRYC_DROME SERENDIPITY LOCUS PRO[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG1454 LD33455 98E4-98E4 dup:2/3 ID:48H7

CG6543 + enzyme * ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (SHORT CHAIN ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATASE 1)(aa) * 1e-17 YDAK_YEAST HYPOTHETICAL 56 [ECH // ENOYL_COA_HYDRATASE] CG6543 LD33482 50C14-50C14 ID:48H8

CG7737 + enzyme * 1e-10 FMS1_YEAST FMS1 PROTEIN FMS1 protein - yeast (Saccharom * 6e-11 Cs protein * 8e-33 No definition line found * 2e-13 protein [ADXRDTASE // AMINEOXDASEF // NAD_BINDIN] CG7737 LD33764 47D6-47D7 dup:1/2 ID:49A10

CG7357 + transcription_factor * transcription factor 17(aa) * zinc finger protein(aa) * RENAL TRANSCRIPTION FACTOR KID-1 (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

CG12276 + enzyme * SUMO-1 activating enzyme subunit 1(aa) * Similar to ubiquitin activating proteins; Aos1p(aa) * 6e-30

RH31_YEAST DNA DAMAGE TOLERANCE PROTEIN RHC31 ([UBA_NAD // ThiF_family] CG12276 LD33652 87B15-87B15 ID:49A3

CG5692 + unknown * similar to the postsynaptic membrane 43K protein from Xenopus * LGN protein(aa) * 4e-13 C10A gene product * 2e-29 hypothetical protein [TPR_REGION // TPR_REPEAT // NLS_BP] CG5692 LD33695 98A3-98A3 ID:49A6

CG7878 + RNA_binding * DMRM62RH_2 Rm62 * RNA helicase(aa) * mitochondrial DEAD box protein(aa) * VASA PROTEIN(aa) [helicase_C // KH-domain // KH_DOMAIN //] CG7878 LD33749 84F1-84F1 ID:49A7

CG12235 + motor_protein * 5e-05 ARPX_YEAST ACTIN-LIKE PROTEIN ARP10 hypothetical protei * 3e-16 ACT3_DROME ACTIN 57B actin * 1e-20 Similar to actin-like protein. * 9e-19 acti [actin] CG12235 LD33759 18D11-18D11 ID:49A8

CG4236 + Caf1 signal_transduction * Caf1 * Rack1 * CHROMATIN ASSEMBLY FACTOR P55 SUBUNIT (CAF-1 P55 SUBUNIT) (DCAF-1)(aa) * 2e-73 HAT2_YEAST HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT hy [GPROTEINBRPT // WD40_REGION // WD_REPEA] CG4236 LD33761 88E8-88E8 ID:49A9

CG3887 + unknown * 1e-27 cDNA EST yk476a1.5 comes from this gene * 4e-28 Unknown * cDNA EST comes from this gene; cDNA EST yk256g7.5 come * F28H7.4 CG3887 LD33828 25C1-25C1 ID:49B2

CG10837 + RNA_binding * 3e-05 NSR1_YEAST NUCLEAR LOCALIZATION SEQUENCE BINDING PROTEIN (P67) * 7e-06 protease * 3e-05 Similarity to Bovine Poly-A binding protein II cDNA * [RNP_1 // RBD // rrm] CG10837 LD33831 cyto_unknown ID:49B3

CG1913 + CG1913 dup:6/7 ID:49B9

CG2984 + Pp2C1 protein_phosphatase * DPP2C1(aa) * 5e-10 P2C3_YEAST PROTEIN PHOSPHATASE 2C HOMOLOG (PP2C-3) prob * DPP2C1 * 6e-16 P2C2_CAEEL PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (PP2 [PP2C_1 // PP2C // PP2C_2 // FRD_SDH_FAD] CG2984 LD34192 4C8-4C8 ID:49C11

CG1515 + unknown * 3e-47 YKT6_YEAST HYPOTHETICAL 22.7 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION * 7e-53 YMP8_CAEEL HYPOTHETICAL 82.6 KD PROTEIN IN CHROMOSOME III * 1e- [SYNAPTOBREVN // synaptobrevin] CG1515 LD34211 7C8-7C8 ID:49C12

CG7338 + unknown * Ydl060wp(aa) * No definition line found(aa) * 8e-91 hypothetical protein YDL060w - yeast (Saccharomyces cerevisiae) * 0.00000000006 [NLS_BP] CG7338 LD34093 78D-78D dup:2/4 ID:49C5

CG3238 + unknown * RRM3/PIF1 helicase homolog(aa) * PIF1(aa) * putative helicase(aa) * DNA helicase homolog(aa) [NLS_BP // ATP_GTP_A] CG3238 LD34105 25A3-25A3 ID:49C6

CG3024 + EG:84H4.1 chaperone * by content; by match; 2-match_description=TORSINA.; 2-match_species=HOMO SAP...(aa) * 7e-55 similarity to 35.1KD hypothetical yeast protein (Swiss [CLPPROTEASEA] CG3024 LD34179 4C7-4C7 ID:49C9

CG7654 + transporter * MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM20 HOMOLOG (MITOCHONDRIAL KD OUTER MEMBRANE PROTEIN) (OUTER MITOCHONDRIAL MEMBRANE RECEPTOR TOM20)(aa) * 2e [NLS_BP] CG7654 LD34461 76E2-76E2 ID:49D10

CG7869 + motor_protein * [SNF2_N // NLS_BP] CG7869 LD34474 70E1-70E1 ID:49D11

CG3959 + pelo unknown * pelo * 9e-61 DOM34 protein - yeast (Saccharomyces cerevisiae) (X77 * PELO_DROME PELOTA PROTEIN pelota * 1e-120 YNU6_CAEEL HYPOTHETICAL 42.9 KD PROT CG3959 LD34262 30C6-30C7 ID:49D2

CG8988 + peptidase * 1e-62 S2P * 2e-62 S2P * SP2 metalloprotease * S2P metalloprotease [ZINC_PROTEASE // SREBPS2PTASE] CG8988 LD34294 48C-48C ID:49D4

CG4050 + cell_cycle_regulator * DMUNKNOWN anon-DM192 * unknown product(aa) * 4e-05 CC27_YEAST CELL DIVISION

CONTROL PROTEIN cell division * 1e-139 unknown product [TPR_REGION // TPR_REPEAT // TPR] CG4050 57C2-57C2
dup:3/4 ID:49D5

+ CH1-2 endopeptidase * COP9 complex homolog subunit 1-2 DCH1-2(aa) * 3e-14 YE28_CAEEL HYPOTHETICAL 47.6 KD
PROTEIN F49C12.8 IN CHROMOSOME IV * 1e-157 GPS1_HUMAN G PROTEIN [PCI_DOMAIN // PCI] CG3889 LD34304 75E2-
75E2 dup:1/2 ID:49D6

+ Keren signal_transduction * DMSH2P_2 spi * 6e-39 SPIT_DROME PROTEIN SPITZ PRECURSOR probable EGF-like gro *
8e-07 heregulin precursor, splice form alpha - human * 5e-08 neu d[EGF_1 // EGF // EGF_2 // PRO_RICH] CG8056 LD34429
74E3-74E4 dup:2/3 ID:49D9

+ enzyme * peptidylglycine alpha-amidating monooxygenase(aa) * 9e-38 strong similarity to the carboxyl-half of peptidyl-
glycine alpha-amidating monoo * 7e-65 A [PAMONOXGNASE // NHL // NLS_BP] CG12130 LD34757 46C10-46C10 dup:2/2
ID:49E12

+ enzyme * nuclear protein methyltransferase (mono- and asymmetrically dimethylating enzyme); Hmt1p(aa) * protein N-
methyltransferase 3(aa) * protein N-methy [SAM_BIND] CG6563 LD34544 88E8-88E8 dup:2/2 ID:49E3

+ unknown * 2e-41 protein * * [FBOX_DOMAIN] CG3428 LD34623 67B5-67B5 dup:2/2 ID:49E6

+ unknown * predicted using Genefinder(aa) * cDNA EST yk301g10.3 comes from this gene; cDNA EST yk301g10.5 comes
from this gene(aa) * cDNA EST yk321f3.5 comes CG6236 LD34692 90E1-90E1 dup:3/3 ID:49E8

+ 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

+ unknown * apoptosis specific protein(aa) * 1e-05 APG5_YEAST AUTOPHAGY PROTEIN APG5 Apg5 protein - yeast * 6e-
13 apoptosis specific protein homologue * dJ134E1 CG1643 LD34980 7A4-7A4 ID:49F10

+ 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

+ TRICHOHYALIN CG7264 LD34806 ID:49F3

+ DNA_binding * DNA helicase(aa) * HYPOTHETICAL 175.7 KD PROTEIN C05C10.2 IN CHROMOSOME II(aa) * DNA
helicase A; Hcs1p(aa) * hypothetical helicase(aa) [ATP_GTP_A] CG6967 LD34829 53F5-53F6 ID:49F6

+ unknown * P38IP(aa) * Lola-like protein(aa) * GAGA-581 Adf-2 isoform(aa) * 0.000002 [NLS_BP] CG17689 LD34837
70B2-70B2 ID:49F7

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

+ 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

+ motor_protein * HYPOTHETICAL 25.4 KD PROTEIN F53F4.3 IN CHROMOSOME V(aa) * 3e-12 YNO8_YEAST
HYPOTHETICAL 28.4 KD PROTEIN IN RPC8-MFA2 INTERGENIC REGION * 9e-07 kinesin [CAP_GLY_2 // CAP_GLY] CG11242
LD35048 56D9-56D9 dup:2/2 ID:49G2

+ unknown * 1e-146 inserted at base Unknown 5' end of P element Plasmid rescue * * [ZINC_FINGER_C2H2 //

ZINC_FINGER_C2H2_2] CG5580 LD35038 55C4-55C4 ID:49G3

CG9696 + 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

CG1354 + GTP_binding * PTD004(aa) * PUTATIVE GTP-BINDING PROTEIN W08E3.3(aa) * GTP-binding protein - *Methanococcus jannaschii*(aa) * Similar to W08E3.3 putative GTP-binding [GTP1OBG // ATP_GTP_A] CG1354 LD35094 8F10-8F10 dup:2/2 ID:49G5

CG7066 + unknown * 5e-14 Y256_HUMAN HYPOTHETICAL PROTEIN KIA * * CG7066 GH01354 66C5-66C6 ID:54C12

CG3851 + 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

CG4879 + RecQ5 DNA_repair_protein * Recq helicase 5(aa) * Recq helicase 5(aa) * 3e-73 SGS1_YEAST HELICASE SGS1 (HELICASE TPS1) DNA helicase TP * 1e-06 RM62_DROME PUTATIVE ATP-DEPENDENT [helicase_C // HELICASE // DEAD] CG4879 GH01404 70E6-70E7 ID:54D5

CG4013 + Smr transcription_factor * HYPOTHETICAL 113.7 KD PROTEIN C14B9.6 IN CHROMOSOME III(aa) * silencing mediator for retinoid and thyroid hormone receptors(aa) * YCR592 cerevisiae= [myb_DNA-binding // ANTIFREEZEI] CG4013 GH01420 11B16-11B17 ID:54D8

CG8083 + transporter * 4e-71 similar to the NUPC family of transporters * 1e-82 purine-selective Na⁺ nucleoside cotransporter * 2e-82 solute carrier family (sodium-coupled CG8083 GH01486 45A10-45A10 dup:3/3 ID:54E3

CG4563 + enzyme * long-chain-fatty-acid--CoA ligase (fadD-8)(aa) * similar to 4-coumarate-coA ligase; cDNA EST yk455e10.3 comes from this gene; cDNA EST yk455e10.5 c [AMP-binding] CG4563 GH01595 60D2-60D2 ID:54F5

CG18212 + unknown * [NLS_BP] CG18212 GH01770 90C-90C ID:54G11

CG9423 + karyopherin-alpha3 ligand_binding_or_carrier * coded for by *C. elegans* cDNA yk173a10.5; coded for by *C. elegans* cDNA yk96a12.5; coded for by *C. elegans* cDNA cm06h1; coded for by *C. elegans* cDNA CG9423 GH01702 86C3-85D27 ID:54G5

CG1142 + RNA-directed_DNA_polymerase,_group_II_intron_encoded * reverse transcriptase - fruit fly (*Drosophila melanogaster*)(aa) * SPAC3G9.15c; len:230aa; similarity: to YLR051C, Q120 35, unclassified protein, (21 [NLS_BP] CG1142 GH02295 85A1-85A1 ID:55B7

CG6868 + tld metalloendopeptidase DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR ASTACIN,ASX_HYDROXYL, Astacin, CUB, EGF,] CG6868 ID:55D10

CG10579 + Ecdysone-induced protein 63E protein_kinase serine/threonine kinase protein kinase CG10579 GH02721 ID:55D11

CG10238 + 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

CG10039 + unknown * BLASTX 4.5E-06 YDR373W|Protein with similarity to human BDR-1 protein and other calcium binding proteins(dna) * 1e-178 BLASTX 4.5E-06 YDR373W|Protei CG10039 GH02873 24D-24D dup:3/3 ID:55E7

CG9005 + cell_adhesion * 0.00000000000000003 * * CG9005 GH03037 48B1-48B2 dup:2/5 ID:55F7

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

CG10212 + SMC2 DNA_binding * 1e-179 SMC2_YEAST CHROMOSOME SEGREGATION PROTEIN SMC2 (DA-BOX PROTEIN SMC2) * 3e-69 Cap * 1e-136 mitotic chromosome and X-chromosome associated MIX- [ATP_GTP_A] CG10212 GH03364 51D1-51D1 ID:55H8

CG5140 + motor_protein * 8e-08 /motif=(desc: * 7e-11 contains similarity to a C3HC4-class zinc finger * 1e-20 mTRIP * 3e-20 hTRIP [zf-C3HC4 // NLS_BP // ZF_RING] CG5140 GH03577 55B9-55B9 ID:56A7

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

CG9195 + unknown * secretory carrier membrane protein 2(aa) * 1e-43 partial CDS * 4e-54 SCA3_MOUSE SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN * 7e-64 SCA1_HUMAN SEC [PHOSPHOPANTETHEINE] CG9195 GH04264 13D1-13D1 dup:2/2 ID:56G2

CG10308 + CycJ cell_cycle_regulator * CycJ * 4e-11 CG22_YEAST G2/MITOTIC-SPECIFIC CYCLIN cyclin B2 - yeast * cyclin J * 3e-05 Similar to cyclin [cyclin // HELIX_LOOP_HELIX // NLS_BP] CG10308 GH04281 63D2-63D2 ID:56G5

CG3918 + NLS_BP, ZF_CCHC CG3918 ID:56H5

CG11901 + translation_factor * valyl-tRNA synthetase 1(aa) * ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA)(aa) * 1e-41 EF1G_YEAST ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA 1) tr * 7e-83 EF1G [EF1G_domain // EF1G // GST] CG11901 GH04551 99A5-99A5 ID:57A7

CG1746 + enzyme * ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (PROTEIN 9) (SUBUNIT C)(aa) * 5e-12 ATP synthase (EC 3.6.1.-) c chain - Caenorhabditis elegans * 3e- [ATPASE_C // ATPASEC // ATP-synt_C] CG1746 GH04827 100B9-100B9 ID:57C6

CG9804 + enzyme * 4e-16 LIPB_YEAST PROBABLE LIPOATE-PROTEIN LIGASE B PRECURSOR (LIPOATE BIOSYNTHESIS PR * 6e-09 lipoate-protein ligase B * 8e-36 LIPB_ARATH PUTATIVE L [LIPB] CG9804 GH04831 82C1-82C1 ID:57C7

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

CG4571 + unknown * CG4571 GH05034 6D6-6D7 dup:4/4 ID:57E8

CG3312 + CG3312 ID:57H12

CG12749 + Hrb87F RNA_binding * Rbm(aa) * similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST yk474h4.3 comes from this gene; cDNA EST yk505c10.3 comes from [RNP_1 // RBD // rrm] CG12749 GH05625 87F7-87F7 ID:58B2

CG7413 + Rbf cell_cycle_regulator * DMRBFPRTN_2 Rbf * EST comes from the 3' UTR m * 3e-24 similar to retinoblastoma proteins * 1e-84 RBL1_MOUSE RETINOBLASTOMA-LIKE PROTEIN (107 KD RETI CG7413 GH05946 1C2-1C2 ID:58D10

CG7163 + unknown * K10D2.3 gene product(aa) * 3e-14 hypothetical protein YOL102c - yeast (Saccharomyces cerevisiae) * 4e-07 /match=(desc: * 4e-12 The gene is expresse [PAP // ZINC_FINGER_C2H2] CG7163 GH05885 66C11-66C11 dup:1/3 ID:58D3

CG2922 + CG2922 83B4-83B4 dup:3/3 ID:58E11

CG8122 + ion_channel * 5e-06 rhophilin * 8e-18 possesses proline rich domains and has similarity to ankyrin domai * 2e-07 protein co-factor * 9e-08 PDZ domain containing 1 [SH3 // PDZ // PRO_RICH] CG8122 GH06265 50D3-50D3 ID:58F11

CG6098 + Lrr47 actin_binding * LRR47 protein - fruit fly (Drosophila melanogaster)(aa) * DMLRR47_3 Lrr47 * 2e-05 predicted using Genefinder; Similarity to Glucose-repressible alco [LRR // LEURICHRPT] CG6098 GH06740 31E6-31E6 ID:59B11

CG2246 + enzyme * 41-kDa phosphoribosylpyrophosphate synthetase-associated protein(aa) * 3e-48 KPR1_YEAST RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (PHOSPHORIBOSYL PYROPHOSP [Pribosyltran] CG2246 GH07082 100A-100A2 dup:2/4 ID:59C12

CG2469 + transmembrane_receptor * BLASTX 4.3E-09 Mus musculus putative myelin regulatory factor mRNA, partial cds.(dna) * TPR-containing, SH2-binding phosphoprotein(aa) *[TPR_REGION // TPR_REPEAT // TPR // NLS_] CG2469 GH07228 62B4-62B4 dup:4/5 ID:59D12

CG2926 + transcription_factor * putative PHD-type zinc finger(aa) * Atu(aa) * myeloid/lymphoid or mixed-lineage leukemia 2(aa) * ATP-dependent chromatin assembly factor la[zf-C3HC4 // ZINC_FINGER_C3HC4 // PHD //] CG2926 GH07267 83B4-83B4 dup:4/4 ID:59E6

CG7859 + unknown * [NLS_BP] CG7859 GH07769 93D9-93D9 dup:1/2 ID:60A6

CG14967 + 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

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

CG4897 + Rpl7 ribosomal_protein RL7_DROME 60S RIBOSOMAL PROTEIN L7 CG4897 Ribosomal_L30, THIOL_PROTEASE_HIS ID:60C3

CG11808 + unknown * [NLS_BP] CG11808 GH08125 51E9-51E9 dup:1/2 ID:60D4

CG3962 + actin_binding * DMRCPA_X kel * The gene product is related to Drosophila melanogaster ring canel protein.(aa) * 8e-86 kelch protein, long form - fruit fly (Drosophi [BTB // KELCHREPEAT // Kelch] CG3962 GH08610 89E13-89E13 dup:1/3 ID:60G9

CG6315 + fl(2)d unknown * FL(2)D protein(aa) * 1e-08 gene predicted from cDNA with a complete coding sequence * 2e-16 FKBP12 interacting protein * 3e-39 inserted at base Bot [TROPOMYOSIN] CG6315 GH08722 50C12-50C12 dup:3/4 ID:60H8

CG6695 + RNA_binding * 6e-21 predicted using Genefinder; cDNA EST comes from this g * 5e-39 suppressor of white apricot homolog * 5e-39 suppressor of white apricot homolog [NLS_BP] CG6695 GH08943 96A17-96A17 dup:1/3 ID:61C1

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

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

CG12781 + cell_adhesion * 9e-05 tenascin-like protein precursor - fruit fly (Drosophila melanogaster) * 2e-47 C09F9.2 * 5e-06 Ten-m2 * 2e-05 predicted using hexExon; MAL3P2.1 [EGF_1 // EGF_2 // NLS_BP] CG12781 GH10539 59B4-59B4 dup:4/4 ID:62E10

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

CG12727 + unknown * CG12727 GH11189 11F7-11F7 ID:63C5

CG6706 + BcDNA:GH07312 transcription_factor_binding * 3e-09 MGR_DROME METABOTROPIC GLUTAMATE RECEPTOR PRECURSOR (* 4e-62 ZK180.1 gene product * 1e-119 GABA-B1a receptor * 1e-169 [ANF_receptor // 7tm_3 // G_PROTEIN_RECE] CG6706 GH11409 93F6-93F6 dup:2/3 ID:63D7

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

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

CG9354 + ribosomal_protein * ribosomal protein L34(aa) * PROBABLE 60S RIBOSOMAL PROTEIN YIL052C(aa) * ribosomal protein L34(aa) * 1e-47 RL34_AEDAL 60S RIBOSOMAL PROTEIN L34 (L3 NLS_BP, RIBOSOMAL_L34E CG9354 ID:63F9

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

CG4742 + unknown * 1e-10 cDNA EST yk471b2.5 comes from this gene; cDNA EST yk471b2.3 come * * CG4742 GH12140 15A5-15A5 ID:64C2

CG17509 + unknown * androgen-induced prostate proliferative shutoff associated protein(aa) * protein(aa) * 1e-28 unknown * 6e-40 cDNA EST comes from this gene elegan CG17509 GH12788 48E2-48E2 dup:3/3 ID:64H3

+ enzyme * DMYOLK_4 Yp1 * 2e-11 VIT2_DROME VITELLOGENIN II PRECURSOR (YOLK PROTEIN 2) vitel * 1e-29 triacylglycerol lipase (EC 3.1.1.3) precursor, pancreatic - [DOLALLERGEN // TAGLIPASE // ESTERASE //] CG6283 GH13143 100D1-100D1 ID:65C1

CG6283 + 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 + 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

CG5198 + structural_protein * nuclear pore protein; Seh1p(aa) * similar to WD domain, G-beta repeat (2 domains); cDNA EST yk258d4.3 comes from this gene; cDNA EST yk338d5.3 comes [GPROTEINBRPT // WD40] CG8722 GH14024 43F9-43F9 ID:65H2

CG8722 + kek3 cell_adhesion * BDNF / NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (TRKB TYROSINE KINASE) (TRK-B)(aa) * kek1 * 5e-74 KEK1 * 6e-07 coded for by C. elegans cDNA yk132e5.5; [ig // LRR // LRRCT] CG4192 GH14053 35D4-35D4 dup:2/2 ID:65H6

CG4192 + actin_binding * DMRCPA_X kel * protein(aa) * [BTB // KELCHREPEAT // Kelch] CG3571 GH14381 87A-87A dup:2/2 ID:66C6

CG3571 none + none GH14469 ID:66D6

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

+ E(Pc) unknown * 3e-15 YFC4_YEAST HYPOTHETICAL 96.7 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION * enhancer of polycomb * 2e-67 enhancer of polycomb * E(Pc) [NLS_BP] CG7776 GH14582 47F15-47F15 dup:5/6 ID:66E10

CG7776 + 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 + 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 + signal_transduction * 1e-06 fimbriae-associated protein Fap1 * * [NLS_BP] CG11451 GH15349 77E-77E8 dup:1/2 ID:67D9

CG11451 + pn signal_transduction * PRUNE protein(aa) * DMPRUNEG_2 pn * 1e-16 PPX1_YEAST EXOPOLYPHOSPHATASE

CG3461

(METAPHOSPHATASE) exopolyph * PRUNE protein CG3461 GH15456 2E1-2E1 dup:2/2 ID:67E10

CG14895 + protein_kinase * Pak * 2e-89 STE20 * 2e-99 serine/threonine kinase PAK homolog DPAK * 8e-93 similar to serine/threonine-protein kinase [PROTEIN_KINASE_ST // TYRKINASE // pkina] CG14895 GH15507 89C4-89C4 ID:67F10

CG14178 + CG14178 GH15480 ID:67F6

CG11375 + 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

CG14235 + electron_transfer * 5e-23 COXG_YEAST CYTOCHROME C OXIDASE POLYPEPTIDE VIB (AED) cyt * 1e-21 COXG_MOUSE CYTOCHROME C OXIDASE POLYPEPTIDE VIB (AED) * 1e-23 cytochrome c o CG14235 GH15549 18F1-18F1 dup:1/3 ID:67G5

CG9091 + ribosomal_protein * predicted using Genefinder; similar to ribosomal protein L37; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from thi [RIBOSOMAL_L37E // NLS_BP] CG9091 GH15907 13B1-13B1 dup:2/2 ID:68B6

CG8507 + motor_protein * receptor-associated protein(aa) * 9e-14 predicted using Genefinder; Similarity to Human alpha-2-macroglobu * 2e-16 heparin binding protein * 5e-18 CG8507 GH16343 86D1-86D1 dup:3/3 ID:68E5

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

CG9166 + unknown * 5e-07 YM62_CAEEL HYPOTHETICAL 23.2 KD PROTEIN K12H4.2 IN CHROMOSOME III * 5e-09 YBEB_ECOLI HYPOTHETICAL 11.6 KD PROTEIN IN MRDA-PHPB INTERGENIC REGI CG9166 GH16625 61F8-61F8 ID:68G11

CG9630 + RNA_binding * pit * 2e-78 SPB4_YEAST ATP-DEPENDENT RRNA HELICASE SPB4 RNA helicase S * 2e-69 helicase pitchoune * 8e-87 YOQ2_CAEEL PUTATIVE ATP-DEPENDENT RNA HELI [helicase_C // HELICASE // DEAD // NLS_B] CG9630 GH16590 84F-84F ID:68G6

CG9573 + unknown * Ynl288wp(aa) * hypothetical protein(aa) * protein involved in sexual development(aa) * 2e-61 YN28_YEAST HYPOTHETICAL 41.2 KD PROTEIN IN PLC1-SEC21 CG9573 GH18039 29F8-29F8 ID:70B8

CG12138 + * 2e-09 SUR4_YEAST SUR4 PROTEIN (SRE1 PROTEIN) SUR4 protein - yea * 2e-13 predicted using Genefinder; similar to GNS1/SUR4 family; cDNA EST * 3e-12 MU [NLS_BP] CG12138 46C-46C dup:3/4 ID:70C10

CG3314 + Rpl7A * DMRPL7A_2 Rpl7A * 6e-69 RL4A_YEAST 60S RIBOSOMAL PROTEIN L7A-2 (L4-2) (YL5) (RP6) * 1e-132 RL7A_DROME 60S RIBOSOMAL PROTEIN L7A ribosoma * 5e-07 NHP [RIBOSOMAL_L7AE // Ribosomal_L7Ae // L7A] CG3314 6B1-6B1 dup:2/2 ID:70D12

CG4472 + Idgf1 * IDGF1 * 1e-07 probable membrane protein YDR371w - yeast (Saccharomyces cerevisiae) * disc growth factor * 5e-21 CHIT_CAEEL PUTATIVE ENDOCHITINASE co [Glyco_hydro_18] CG4472 36A1-36A1 dup:2/2 ID:70F4

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

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

CG11282 + caps cell_adhesion * DMSLIT_2 sli * tartan protein(aa) * caps * CAPRICIOUS(aa) [LRR // LEURICHRPT // LRRCT] CG11282 GH18689 70A3-70A3 ID:70H8

+ eIF-4a translation_factor * DMEIF4A_3 Eif4a * EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)(aa) * EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) (STIMULATOR FACTOR I KD COMPONENT) [helicase_C // HELICASE // DEAD // DEAD_] CG9075 GH19518 26B1-26B1 dup:3/5 ID:71F5
 CG9075
 + ribosomal_protein Ribosomal protein S28B Ribosomal_S28e CG2998 ID:72A2
 CG2998
 + CG3195 ID:72B11
 CG3195
 + unknown * [PRO_RICH] CG10209 GH20077 51D1-51D1 ID:72C8
 CG10209
 + unknown * predicted using hexExon; MAL3P6.28 Hypothetical protein, len: aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S. CG18042 GH20177 31B1-31B1 ID:72D3
 CG18042
 + 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 86F1-86F1 dup:1/3 ID:72F4
 CG17358
 + unknown * density regulated protein drp1(aa) * 2e-08 YJY4_YEAST HYPOTHETICAL 22.5 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION * 4e-13 hypothetical protein * 8e- [SUI1_2 // NLS_BP] CG9099 GH20858 15B1-15B1 ID:73B7
 CG9099
 + CtBP enzyme * CtBP * C-terminal binding protein CtBP2(aa) * C-terminal binding protein(aa) * similar to the D-isomer specific 2-hdroxyacid dehydrogenases family [2-Hacid_DH] CG7583 GH20987 87D9-87D11 dup:1/2 ID:73C12
 CG7583
 + CG7803 ID:73G3
 CG7803
 + mu2 unknown * mutator 2(aa) * mutator * 4e-06 Pax transcription activation domain interacting protein PTIP * CG1960 GH21591 62B11-62B11 dup:2/2 ID:73H6
 CG1960
 + Rpt4 endopeptidase * 26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED ATPASE DOMAIN PROTEIN 44)(aa) * Pros45 proteosome subunit homolog(aa) * 1e-134 SUG2_YEAST PROB CG3455 GH21618 5E1-5E1 dup:2/2 ID:73H8
 CG3455
 + enzyme * putative exonuclease(aa) * 2e-41 hypothetical protein YOL080c - yeast (Saccharomyces cerevisiae) * 2e-15 /match=(desc;; /ma * 8e-39 predicted using [Exonuclease] CG6833 GH21710 70C12-70C12 dup:1/2 ID:74A8
 CG6833
 + CG6684 dup:2/2 ID:74E3
 CG6684
 + transcription_factor * putative zinc finger protein; Mot2p(aa) * coded for by C. elegans cDNA yk134f9.5; coded for by C. elegans cDNA yk15g6.5; coded for by C. elegans cDN [RBD // rrm // ZF_RING] CG5251 31E1-31E1 ID:75A7
 CG5251
 + unknown * BLASTX 2.0E-06 Theileria parva schizont/sporozoite surface protein gene, partial cds.(dna) * * [NLS_BP] CG12316 GH22749 71B2-71B2 ID:75C3
 CG12316
 + unknown * CG6038 GH23035 71C2-71C2 ID:75G3
 CG6038
 + Hrb27C RNA_binding * DMHRP481_2 Hrb27C * HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1)(aa) * 2e-36 NAB4_YEAST NUCLEAR POLYADENYLATED RNA-BINDING PROTE [RNP_1 // RBD // rrm] CG10377 27C-27C dup:6/8 ID:76B1
 CG10377
 + structural_protein * Ran/TC4-binding nucleopore protein(aa) * RanBP2 protein - mouse (fragment)(aa) * RAN binding protein 2; nucleoporin 358(aa) * HTF9-A protein[GRAM_POS_ANCHORING // zf-RanBP // ZF_RA] CG11856 GH23370 96C4-96C5 dup:2/4 ID:76B5
 CG11856
 + 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

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

CG6359 + transporter * similar to PhoX homologous domain, present in p47phox and p40phox.(aa) * SDP8(aa) * 2e-18 hypothetical protein YOR357c - yeast (Saccharomyces cerev [PX // BEM_DOMAIN] CG6359 87C5-87C5 ID:76D8

CG7628 + transporter * Phosphate Permease(aa) * leukemia virus receptor - human(aa) * 3e-27 YB8I_YEAST PUTATIVE PHOSPHATE-REPRESSIBLE PHOSPHATE PERMEASE YBR29C * 9e-52 Sim [PHO4] CG7628 GH23727 70E3-68A5 ID:76F9

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

CG1866 + transcription_factor * zinc finger protein 37(aa) * hkb * 2e-17 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * 4e-47 zinc finger motif protein [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG8367 GH24215 50E4-50E4 ID:77C11

CG8367 + transcription_factor * DMSUHW_6 su(Hw) * crol * zf43C * 7e-08 zinc finger 30C [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG7101 GH24178 17E1-17E1 ID:77C7

CG7101 + transporter * DMWHITER_2 w * WHITE PROTEIN HOMOLOG(aa) * hypothetical protein * 3e-39 ORF YOL075c [ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG9663 GH24286 25A1-25A1 ID:77D10

CG9663 + Ice endopeptidase * DMICEPROT_2 Ice * 2e-10 ETFB_YEAST PROBABLE ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF) * ICE_DROME CASPASE PRECURSOR (DRICE) drICE pr * [CASPASE_P10 // ICE_p10 // CASPASE_P20 /] CG7788 GH24292 99C4-99C4 ID:77D11

CG7788 + motor_protein * CG7701 GH24272 47C3-47C3 ID:77D8

CG7701 + az2 transcription_factor * zf43C * 2e-09 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * putative zinc finger protein * 3e-09 similar to Zinc finger, C2H2 type (3 do [SERPIN // zf-C2H2 // ZINC_FINGER_C2H2] CG1605 43D3-43D3 dup:3/3 ID:77E5

CG1605 + unknown * 1e-149 inserted at base Unknown 5' end of P element Plasmid rescue * * [NLS_BP] CG7682 GH24605 91A2-91A2 ID:77G5

CG7682 + CG3618 dup:2/2 ID:77H2

CG3618 + unknown * CG11148 GH25014 102F8-102F8 dup:2/2 ID:78B9

CG11148 + Mst57Da unknown * DMMACGP_7 Mst57Dc * 4E-69* CG9074 GH25067 99D1-99D1 ID:78C2

CG9074 + transporter * peroxisomal Ca-dependent solute carrier(aa) * Similarity to N.crassa ADP/ATP carrier protein (SW:ADT_NEUCR)(aa) * 1e-38 probable membrane protein [mito_carr // MITOCARRIER // ADPTRNSLCAS] CG4392 GH25190 69B3-69B3 dup:2/2 ID:78D7

CG4392 + CG3751 dup:1/2 ID:78D9

CG3751 + 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

CG11473 + unknown * hypothetical 43.2 kDa protein(aa) * predicted using Genefinder; Similarity to Yeast hypothetical protein YAE2 (SW:YAE2_YEAST); cDNA EST comes from t CG7011 GH25868 71B3-71B3 dup:2/2 ID:79C6

CG7011 + * CG18316 44A4-44A4 dup:2/3 ID:79F6

CG18316 + da transcription_factor * TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12)

CG5102

(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

CG4694 + her CG4694 her dup:2/2 ID:8-31 cntrlBA4

CG16724 + tra CG16724 tra dup:2/2 ID:8-31 cntrlBA5

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

+ bib transporter * pore-forming protein MIP family(aa) * NEUROGENIC PROTEIN BIG BRAIN(aa) * 1e-07 YFF4_YEAST
HYPOTHETICAL 70.5 KD PROTEIN IN AGP3-DAK3 INTERGENIC REG[MININTRINSICP // MIP // PRO_RICH] CG4722 big brain
30F4-30F5 dup:2/3 ID:8-31 cntrlBB5

CG4722 + cut CG11387 cut dup:2/2 ID:8-31 cntrlBB6

CG11387 + tll steroid_hormone_receptor CG1378 tll dup:2/2 ID:8-31 cntrlBC1

CG1378 + twist transcription_factor CG2956 twist dup:3/5 ID:8-31 cntrlBG3

CG2956 + eve transcription_factor CG2328 eve dup:2/2 ID:8-31 cntrlBH7

CG2328 + apt RNA_binding * apt * apontic * 1e-07 inserted at base 5' end of P element Inverse PCR * tracheae defective protein
[MYB_3] CG5393 apt 59F1-59F1 dup:2/2 ID:8-31 cntrlBH8

CG5393 + 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

CG7977 + Axn signal_transduction * D-Axin(aa) * 6e-15 Axin * 2e-14 axin * 1e-14 Axin [GRK] CG7926 99D5-99D5 dup:1/2 ID:80G2

CG7926 + unknown * CG10965 GH26991 7D21-7D21 ID:80H1

CG10965 + 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

CG15084 + yin transporter * opt1 long(aa) * 8e-17 PTR2_YEAST PEPTIDE TRANSPORTER PTR2 (PEPTIDE PERMEASE PTR2) * 8e-
74 high-affinity peptide transporter * 2e-06 cAMP inducible p [PTR2 // PTR2_1 // PTR2_2] CG2913 GH27264 4A1-4A1 dup:2/2
ID:81B12

CG2913 + CG2968 ID:81C7

CG2968 + 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

CG1227 + * 1e-15 YMB8_YEAST HYPOTHETICAL 43.7 KD PROTEIN IN OST6-PSP2 INTERGENIC REGION * 7e-23 No definition
line found * 2e-19 hypothetical protein * hypothe CG8195 52A13-52A13 ID:81F1

CG8195 + enzyme * threonyl-tRNA synthetase(aa) * threonyl-tRNA synthetase (aa 1-734) * SYTC_CAEEL PROBABLE THREONYL-
TRNA SYNTHETASE, CYTOPLASMIC (THREONINE--TRNA LIG [TRNASYNTHTHR // tRNA-synt_2b // AA_TRNA] CG5353
GH27773 33C1-33C1 ID:81G11

CG5353

CG2865

CG8826 + glakit unknown * Contains similarity to Pfam domain: (PLDc), Score=13.8, E-value=0.2, N=1(aa) * * CG8826 GH27933 23D4-
23D4 ID:82A7

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

CG3644 + bic transcription_factor * BTF3 HOMOLOG EGD1 (GAL4 DNA-BINDING ENHANCER PROTEIN)(aa) * basic transcription factor 3, like 3(aa) * transcription factor BTF3 homolog(aa) * 9e-3 CG3644 GM13744 49D-49D dup:1/2 ID:83B1

CG12740 + ribosomal_protein * 2e-08 predicted using Genefinder; Similarity to Human 60S ribosomal prot * 1e-22 RL28_MOUSE 60S RIBOSOMAL PROTEIN L28 ribosomal protein L * 1e-22 ri CG12740 GM13756 64A3-64A3 ID:83B2

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

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

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

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

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

CG12251 + unknown * CG12251 HL08087 49F11-49F11 ID:83D5

CG9300 + unknown * [SUGAR_TRANSPORT_2] CG9300 76B8-76B8 dup:2/2 ID:83E12

CG17064 + motor_protein * HYPOTHETICAL PROTEIN * PSD-95 binding protein(aa) * 2e-08 PSD-95/SAP90-associated protein-1 * 2e-70 inserted at base Both 5' and 3' ends of P elemen [NLS_BP] CG17064 LD21642 50B1-50B2 dup:3/3 ID:83E2

CG11738 + unknown * conserved protein(aa) * Yor145cp(aa) * cDNA EST comes from this gene(aa) * BLASTX 2.6E-30 YOR145C|Protein of unknown function(dna) CG11738 LD21667 19D1-19D1 dup:3/3 ID:83E3

CG3561 + RNA_binding * atp-dependent, dead box, rna helicase(aa) * PUTATIVE ATP-DEPENDENT RNA HELICASE C13F4.11C(aa) * RNA helicase; Prp28p(aa) * Gene with similaity to [helicase_C // HELICASE // DEAD // ATP_G] CG3561 LD21669 21D2-21D2 dup:2/2 ID:83E4

CG3429 + swa RNA_binding * SWA_DROME SWALLOW PROTEIN gene swallow protein - fruit fl * DMSWAL_3 swa * * [NLS_BP] CG3429 LD21771 5E6-5E7 dup:2/2 ID:83E6

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

CG1587 + Crk signal_transduction * v-crak avian sarcoma virus CT10 oncogene homolog(aa) * CRK protein(aa) * 3e-10 SEM5_CAEEL SEX MUSCLE ABNORMAL PROTEIN sem-5 protein - * 2e-63 CRK_MOU [SH2DOMAIN // SH2 // SH3DOMAIN // SH3] CG1587 LD22148 102A1-102A1 ID:83F5

CG7590 + unknown * CG7590 LD22812 68B1-68B1 ID:83G11

CG3938 + CycE cell_cycle_regulator * DMRNACE_2 CycE * 4e-20 CGS5_YEAST S-PHASE ENTRY CYCLIN cyclin B5 - yeast (Sacc *

CG1E_DROME G1/S-SPECIFIC CYCLIN E cyclin E type I - frui * 5e-37 c [cyclin // CYCLINS // ATP_GTP_A] CG3938 LD22682 35D5-35D6 dup:2/2 ID:83G5

CG5884 + par-6 ion_channel * PAR-6(aa) * PAR-6(aa) * PAR-6(aa) * dJ850H21.2 (novel protein containing a PDZ (DHR, GLGF) domain)(aa) [PDZ // ATP_GTP_A] CG5884 LD22757 16C5-16C5 ID:83G6

CG14030 + protein_kinase mitotic checkpoint control protein kinase B-like PROTEIN_KINASE_ATP CG14030 LD22858 dup:1/2 ID:83H1

CG1800 + RNA_binding double-stranded binding protein DSRBD CG1800 LD23072 dup:3/4 ID:83H11

+ zf30C transcription_factor * leukemia/lymphoma related factor cLRF(aa) * zf30C * 4e-17 YJF6_YEAST HYPOTHETICAL 98.9 KD ZINC FINGER PROTEIN IN BTN1-PEP8 INTERGENIC REG * zinc f[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG3998 LD23102 30D1-30D1 ID:83H12

CG3998 + MRG15 DNA_binding * MRG15(aa) * MORF-related gene 15(aa) * 4e-19 hypothetical protein YPR023c - yeast (Saccharomyces cerevisiae) * 4e-10 predicted using Genefinder; cDN [NLS_BP] CG6363 LD22902 88E9-88E10 dup:2/2 ID:83H4

CG6363 + B4 unknown * No definition line found(aa) * No definition line found * 1e-16 inserted at base 5' end of P element Inverse PCR

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

CG6686 + unknown * IgE autoantigen(aa) * drosocrystallin(aa) * hypoxia associated factor(aa) * BLASTX 2.4E-18 Homo sapiens mRNA for IgE autoantigen.(dna) [NLS_BP] CG6686 LD23187 33B9-33B9 ID:84A6

CG10777 + RNA_binding * RNA helicase (DEAD box)(aa) * DMHELI_2 me31B * DMRM62RH_2 Rm62 * PUTATIVE ATP-DEPENDENT RNA HELICASE P62(aa) [helicase_C // HELICASE // DEAD // DEAD_] CG10777 LD23203 7C8-7C8 ID:84A7

CG7946 + unknown CG7946 ID:84A8

CG9791 + RNA_binding * 4e-55 SUV3_YEAST MITOCHONDRIAL ATP-DEPENDENT RNA HELICASE SUV3 PRECURSOR * 1e-151 Similarity to Yeast ATP-dependent RNA helicase (SW:SUV3_YEAST); cD [helicase_C] CG9791 LD23445 82A5-82A5 ID:84B12

CG2221 + * Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST CG2221 9B14-9B14 dup:3/3 ID:84B2

+ 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 ID:84B6

CG15442 + unknown NLS_BP CG6712 LD23405 dup:2/2 ID:84B8

CG6712 + metastasis-associated-1-like-protein unknown * metastasis associated gene 1-like 1(aa) * 3e-74 similar to metastasis-associated protein mta-1 (GB:U0 * 1e-128 metastasis associat[ELM2 // myb_DNA-binding // zf-C2H2 // Z] CG2244 LD24461 83B6-83B6 ID:84C10

CG2244 + pcm enzyme * pacman protein(aa) * enzyme exoribonuclease, -3) map_position:18C1-4 * BLASTX 2.9E-53 Mus musculus mRNA for DhM2 protein, complete cds.(dna) * 3e- CG3291 LD24464 18D1-18D1 dup:2/6 ID:84C11

CG3291 + La RNA_binding * LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)(aa) * La * LUPUS LA PROTEIN (SJOGREN SYNDROME TYPE B ANTIGEN (SS-B)) (LA RIBONUCL [RNP_1 // RBD // rrm // NLS_BP // LUPUSL] CG10922 LD24519 38C7-38C7 ID:84C12

CG10922 + TflIB transcription_factor * TflIB * 3e-43 TF2B_YEAST TRANSCRIPTION INITIATION FACTOR IIB (TflIB) (TRANSCRIPTION FACTOR E) * 1e-174 TF2B_DROME TRANSCRIPTION INITIATION FACTOR I[TIFACTORIIB // transcript_fac2 // TflIB] CG5193

CG5193

LD24035 33D1-33D1 ID:84C6

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

CG5971 + DNA_replication_factor * replication control protein 1(aa) * CDC6 protein(aa) * 7e-31 CC6_YEAST CELL DIVISION CONTROL PROTEIN cell division * 3e-30 recognition complex subu [AAA // ATP_GTP_A] CG5971 LD25083 66D-66D ID:84D11

CG2446 + 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' ends of P element Inverse PCR * CG2446 LD24866 10D4-10D5 dup:2/2 ID:84D4

+ enzyme * 1e-171 CTP synthase (EC 6.3.4.2) URA8 - yeast (*Saccharomyces cerevisiae*) * 1e-147 similar to CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP * [GATase // GATASE_TYPE_I]) CG6854 LD25005 71B2-71B2 dup:2/6 ID:84D5

CG6854 + furrowed selectin C_TYPE_LLECTIN_1, lectin_c CG1500 LD25020 ID:84D7

CG1500 + transcription_factor CG10267 dup:2/2 ID:84E4

CG10267 + unknown * p52 pro-apototic protein(aa) * * CG8470 13F1-13F1 dup:3/3 ID:84E6

CG8470 + endopeptidase * Tat-binding protein-1(aa) * 1e-112 AFG2_YEAST AFG2 PROTEIN valosin-containing protein homolo * 1e-60 smallminded * 3e-97 TER1_CAEEL TRANSITIONAL END [AAA // ATP_GTP_A] CG5776 LD25466 33F2-33F2 ID:84G1

CG5776 + Gbeta13Fsignal_transduction * HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V(aa) * Miller-Dieker lissencephaly gene(aa) * HYPOTHETICAL WD-REPEAT[GPROTEINBRPT // GPROTEINB // WD40_REGIO] CG10545 LD25526 13F5-13F5 ID:84G4

CG10545 + unknown CG13345 dup:2/3 ID:84H11

CG13345 + RNA_binding * DMMLE_2 mle * protein(aa) * PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE C04H5.6(aa) * PR22_YEAST PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 PRP [DEAH_ATP_HELICASE // HELICASE // ATP_GT] CG10689 LD25692 37C1-37C1 ID:84H6

CG10689 + numb unknown * NUMB PROTEIN(aa) * DMNUMB_2 numb * 3e-42 similar to Phosphotyrosine interaction domain (PTB/PID).; cDNA EST * 8e-67 m-Numb [PTB_DOMAIN // PID // NLS_BP // ATP_GTP_] CG3779 LD25907 30B5-30B6 dup:1/3 ID:85A11

CG3779 + * [NLS_BP] CG17159 cyto_unknown dup:2/3 ID:85A4

CG17159 + transcription_factor * zinc finger protein(aa) * ZINC FINGER PROTEIN 184(aa) * protein(aa) * [zf-C2H2 // ZINC_FINGER_C2H2_2] CG5135 LD25880 86D8-86D8 dup:3/3 ID:85A9

CG5135 + Pros45 endopeptidase * Ug * 1e-157 PRS8_YEAST 26S PROTEASE REGULATORY SUBUNIT HOMOLOG (SUG1 PROTEIN) (CIM3 PROTE * Pros45 proteosome subunit homolog * 1e-176 similar to AT [AAA // ATP_GTP_A] CG1489 LD26005 19F2-19F2 ID:85B12

CG1489 + glu DNA_binding * 1e-123 hypothetical protein YLR086w - yeast (*Saccharomyces cerevisiae*) (* 2e-34 Cap * 1e-100 Similarity with the yeast chromosome segregation prot[ATP_GTP_A2 // DA_BOX // NLS_BP // ATP_G] CG11397 LD25919 36A7-36A7 dup:3/3 ID:85B2

CG11397 + Tsc1 cell_cycle Tuberous Sclerosis Complex 1 tumor-suppressor gene. also gigas, rocky. regulates cell size and cell cycle ATPASE_ALPHA_BETA, NLS_BP CG6147 LD25933 dup:2/2 ID:85B5

CG6147 + unknown * unknown(aa) * 5e-26 hypothetical protein YDR214w - yeast (*Saccharomyces cerevisiae*) * 9e-55 cDNA EST CEMSC45R comes from this gene; cDNA EST yk436a5 CG1416 LD25951 39F1-39F1 dup:2/2 ID:85B7

CG1416

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

CG18145 + unknown * mitochondrial and cytoplasmic fumarase (fumarate hydralase); Fum1p * FUMARATE HYDRATASE, MITOCHONDRIAL PRECURSOR (FUMARASE) * Contains similarity to CG18145 31B-31B dup:2/2 ID:85C2

CG9591 + unknown * 2e-12 inserted at base 5' end of P element Inverse PCR * * CG9591 LD26057 87F8-87F8 dup:2/2 ID:85C4

CG7109 + mts protein_phosphatase microtubule star Ser/Thr protein phosphatase CG7109 LD26077 dup:2/2 ID:85C5

CG16989 + EG:34F3.4 unknown * /match=(desc;; /ma * * CG16989 LD26306 1C2-1C2 ID:85D12

+ EG:30B8.3 ligand_binding_or_carrier * /match=(desc;; /match=(desc:(aa) * 1e-171 62D9.a * 1e-11 cellular retinaldehyde-binding protein; CRALBP * 1e-11 retinaldehyde-binding protein C [CRETINALDHBP // CRAL_TRIO] CG3191 LD26231 2F1-2F1 dup:2/2 ID:85D2

CG3191

CG1868 + unknown * [SET_DOMAIN // CYTOCHROME_C] CG1868 LD26240 45F4-45F4 ID:85D4

+ unknown * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST yk266f8.5 comes from this gene; cDNA EST yk28 [NLS_BP] CG8312 LD26277 85E-85E dup:2/2 ID:85D8

CG8312

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

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

+ motor_protein * 7e-07 No definition line found * 1e-15 ATRX protein * 2e-15 X-linked nuclear protein * 6e-06 putative protein [NLS_BP // CYTOCHROME_C] CG8290 48D7-48D8 dup:3/3 ID:85E2

CG8290 + CRAG ligand_binding_or_carrier * CRAG protein * 1e-145 contains similarity to human MAP kinase-activating death domain * 1e-120 protein * 3e-16 Rab3 GDP/GTP exchange protein [DENN_DOMAIN // CYTOCHROME_C] CG12737 LD26363 7F4-7F4 dup:6/6 ID:85E3

CG12737

+ 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

CG3726

+ 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

CG8352

+ enzyme * farnesyltransferase, CAAX box, alpha(aa) * 2e-35 RAM2_YEAST PROTEIN FARNESYLTRANSFERASE ALPHA SUBUNIT (CAAX FARNESYLTRANSFERASE A * 4e-58 Similar to [PPTA] CG2976 LD26412 25B-25B dup:2/2 ID:85E8

CG2976

+ 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

CG2158

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

CG17018

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

+ 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 16D4-16D5 ID:85F5

CG6474

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

CG9925

CG11371 + BcDNA:LD26519 ligand_binding_or_carrier * 1e-126 inserted at base Both 5' and 3' ends of P element Inverse PCR * * [NLS_BP] CG11371 LD26519 21A5-21A5 dup:3/4 ID:85F7

CG2107 + enzyme * similar to the carnitine/choline acetyltransferase family(aa) * DMCACTTR_3 Cha * carnitine palmitoyltransferase II precursor(aa) * 7e-57 carnitine [RAS_GTPASE_ACTIV_2 // Carn_acyltransf /] CG2107 LD26545 63B1-63B1 dup:3/3 ID:85F9

CG4057 + signal_transduction * 4e-09 protein * spermatogenesis associated PD1 * [PRO_RICH // IG_MHC] CG4057 LD26757 60B7-60B8 ID:85G11

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

CG7824 + 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

CG10274 + protein_kinase * 1e-07 probable membrane protein YDL146w - yeast (Saccharomyces cerevisiae) * 3e-09 hypothetical protein * [SH3] CG2258 LD26707 7D9-7D9 dup:1/3 ID:85G7

CG2258 + protein_phosphatase * 3e-11 PVH1_YEAST PROTEIN-TYROSINE PHOSPHATASE YVH1 (PTPASE YVH1) * 3e-14 puckered protein * 9e-19 Similar to protein-tyrosine phosphatase * [DSPc // TYR_PHOSPHATASE_DUAL // TYR_PHO] CG6238 LD26729 98F1-98F1 dup:1/4 ID:85G9

CG6238 + unknown * 1e-35 YNU1_YEAST HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION * 1e-118

CG9351 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 + transcription_factor ZINC_FINGER_C2H2, ZINC_FINGER_C2H2_2, zf] CG10016 LD26791 dup:2/2 ID:85H2

CG10016 + * 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 + unknown * 6e-11 hypothetical protein * hypothetical protein * YG73_SYNY3 HYPOTHETICAL TRNA/RRNA

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

+ 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 + RNA_binding * 2e-14 predicted using Genefinder; Similarity to Arabidopsis DNA-damage-r * 8e-43 splicing factor (45kD);

CG17540 SPF 45kDa splicing factor; SPF * 2e-17 D111 [D111_DOMAIN] CG17540 LD27025 cyto_unknown ID:86A12

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

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

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

+ bcd transcription_factor * DNA-binding-protein,transcription-factor(aa) * DMBCDG_3 bcd * 1e-125 bcd protein * 8e-52

CG1034 homeotic protein bicoid - fruit fly (Drosophila ps[RNP_1 // HOMEBOX_1 // homeobox // HOME] CG1034 LD27003 84D1-84D1

dup:1/2 ID:86A8
 + cell_cycle_regulator * protein(aa) * HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III(aa) * 5e-05
 USF2_MOUSE UPSTREAM STIMULATORY FACTOR (UPSTREAM TRANSCRIPT[HLH // HELIX_LOOP_HELIX_2 // NLS_BP]
 CG18362 CG18362 LD27073 39D1-39D2 dup:3/4 ID:86B10
 CG7843 + arsenate resistance protein ARS2 CG7843 LD27090 dup:2/2 ID:86B12
 + peptidase * insulin-regulated membrane aminopeptidase IRAP(aa) * LEUKOTRIENE A-4 HYDROLASE (LTA-4
 HYDROLASE) (LEUKOTRIENE A(4) HYDROLASE)(aa) * LEUKOTRIENE A-4 [ALADIPTASE // Peptidase_M1 // ZINC_PROT]
 CG10602 CG10602 LD27070 37B4-37B5 ID:86B9
 + dnk enzyme * 1e-145 deoxynucleoside kinase * 2e-31 DCK_MOUSE DEOXYCYTIDINE KINASE (DCK) deoxycytidine kina *
 CG5452 1e-49 thymidine kinase * 2e-30 DCK_RAT DEOXYCYTIDINE [ATP_GTP_A] CG5452 94A3-94A3 dup:2/2 ID:86C1
 + enzyme * Drosophila melanogaster P lethal line Drosophila melanogaster genomic Sequence recovered from 5' end of P
 element, genomic survey sequence(dna) * IS [tRNA-synt_1 // AA_TRNA_LIGASE_I // TRNA] CG11471 LD27166 79E2-79E2
 CG11471 dup:1/2 ID:86C7
 + fidipidine cytoskeletal_structural_protein homology to sarcolemmal-associated protein (SLAP-2) [Homo sapiens] and latent
 CG7773 nuclear antigen [Kaposi's sarcoma-associated herpesvirus] NLS_BP CG7773 LD27169 dup:2/2 ID:86C8
 + dco protein_kinase * serin/threonin-kinase(aa) * dbt * Ckl agr; * DMDG2CD5_3 for [PROTEIN_KINASE_ST //
 CG2048 PROTEIN_KINASE_DOM] CG2048 LD27173 100B-100B ID:86C9
 CG9028 + unknown * 2e-15 inserted at base 5' end of P element Inverse PCR * CG9028 LD27194 70C8-70C9 dup:2/2 ID:86D1
 CG6005 + NLS_BP CG6005 LD27322 dup:2/2 ID:86D10
 + pescadillo [Homo sapiens] (widely expressed in embryogenesis of zebrafish, high in liver) BRCT, BRCT_DOMAIN,
 CG4364 NLS_BP CG4364 LD27336 dup:2/2 ID:86D12
 CG7396 + unknown * [PPASE // NLS_BP] CG7396 LD27215 71E1-71E1 dup:2/2 ID:86D3
 + unknown * F56C9.10 gene product(aa) * 9e-22 Strong similarity to F21B7.33 from A. thaliana BAC EST * CG1905
 CG1905 LD27278 10E6-10F1 dup:2/5 ID:86D7
 + transporter * 2e-14 aquaporin * 5e-22 BIB_DROME NEUROGENIC PROTEIN BIG BRAIN bib protein - frui * 6e-22 similar to
 CG7777 MIP transmembrane protein; cDNA EST yk459g7.3 c [MINTRINSICP // MIP] CG7777 LD27313 47F13-47F13 ID:86D9
 + 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
 CG13298 ID:86E10
 + UbcD4 enzyme * 3e-33 UBC1_YEAST UBIQUITIN-CONJUGATING ENZYME E2-24 KD (UBIQUITIN-PROTEIN LIGASE) (UBI
 * 1e-107 ubiquitin conjugating enzyme * 7e-54 contains simila [UBA // UBIQUITIN_CONJUGAT // UQ_con //] CG8284 LD27480
 CG8284 67B12-67B12 dup:2/2 ID:86E11
 + poly-U-binding-splicing-factor RNA_binding * siah binding protein 1(aa) * 4e-13 PABP_YEAST POLYADENYLATE-BINDING
 PROTEIN, CYTOPLASMIC AND NUCLEAR (PABP) (ARS CO * 3e-14 polyadenylate-bind[RNP_1 // RBD // rrm] CG12085
 CG12085 LD27486 62A4-62A4 dup:2/2 ID:86E12
 + Similar to a hydrophilic protein that is peripherally associated with the late Golgi in yeast. Homology to uncharacterized
 CG3338 proteins in Arabidopsis, h CG3338 LD27356 dup:3/3 ID:86E2

+ unknown * 8e-15 YKK3_CAEEL HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III >g *
 CG10795 YJ05_CAEEL HYPOTHETICAL 85.1 KD NUCLEASE C41D11.5 simila * CG10795 LD27358 57D11-57D11 dup:2/2 ID:86E3
 CG5868 + CG5868 dup:2/2 ID:86E9
 CG6066 + unknown * O1(aa) * 2e-31 predicted protein of unknown function thal * * [NLS_BP] CG6066 LD27582 97E8-97E8 ID:86F10
 + Ptpmeg protein_phosphatase * BLASTX 5.3E-20 Human protein-tyrosine phosphatase mRNA, complete cds.(dna) * merlin(aa)
 CG1228 * DMPTPM_2 Ptp69D * protein tyrosine phosphatase, n[TYR_PHOSPHATASE_PTP // ERMFAMILY // Y_p] CG1228 LD27491 61C1-61C1 dup:3/3 ID:86F2
 + Cdk8 protein_kinase * Cdk8(aa) * 3e-67 cyclin-dependent kinase chain SRB10 - yeast (Saccharomyces cerevisiae) * Cdk8 *
 CG10572 1e-127 Similarity to Human cell division protein ki [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG10572 LD27520 69D3-69D3 ID:86F4
 CG11278 + transporter * 8e-11 syntaxin * 3e-17 hypothetical protein * 2e-17 syntaxin * 1e-19 inserted at base 5' end of P element Inverse PCR [T_SNARE // Syntaxin] CG11278 LD27581 69F2-69F2 ID:86F9
 + protein_phosphatase * PROTEIN PHOSPHATASE 2C GAMMA ISOFORM (PP2C-GAMMA) (FIBROBLAST GROWTH
 CG10417 FACTOR INDUCIBLE PROTEIN 13) (FIN13)(aa) * PROTEIN PHOSPHATASE 2C GAMMA ISOFORM [PP2C_1 // PP2C // PP2C_2] CG10417 LD27655 41D1-41D1 ID:86G1
 + transmembrane_receptor * contains similarity to M. musculus patched * 1e-21 No definition line found * [PEROXIDASE_1
 CG2019 // 5TM_BOX // NLS_BP] CG2019 LD27661 83C4-83C4 dup:3/4 ID:86G4
 + CkIIalpha protein_kinase * 1e-103 KC21_YEAST CASEIN KINASE II, ALPHA CHAIN (CK II) casein ki * KC2A_DROME
 CG17520 CASEIN KINASE II, ALPHA CHAIN (CK II) casein kina * 1e-151 KC2A_CAE[PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG17520 LD27706 cyto_unknown ID:86G9
 + transcription_factor * CROL ALPHA(aa) * zinc finger protein 207(aa) * predicted using Genefinder; similar to Zinc finger,
 CG17912 C2H2 type; cDNA EST comes from this gene; cDNA E CG17912 LD27810 36A7-36A8 dup:3/3 ID:86H6
 CG9680 + RNA_binding CG9680 ID:86H8
 + GAP signal_transduction * Cdc42 GTPase-activating protein(aa) * Rga1p (Dbm1p)(aa) * DMC23E12 * ABR protein -
 CG10538 human(aa) [RHO_GAP // RhoGAP // SH3] CG10538 LD27836 38A-38A dup:2/3 ID:86H9
 + zimp nucleic_acid_binding * map_position:45A4-8 * Zimp-A(aa) * 2e-19 NFI1_YEAST NFI1 PROTEIN NFI1 protein - yeast
 CG8068 (Saccharom * 6e-43 cDNA EST comes from this gene; cDNA EST co CG8068 LD27861 45A13-45B1 dup:1/5 ID:87A1
 + protein_phosphatase * 7e-33 protein-tyrosine phosphatase; PTPase; MPTP-MEG2 * 1e-32 protein tyrosine phosphatase,
 CG3102 non-receptor type * 7e-40 protein-tyrosine-phosphatase ([G_PROTEIN_RECEPTOR // CRAL_TRIO] CG3102 LD27988 8F2-8F2 ID:87A10
 + Rad23 DNA_repair_protein * DHR23(aa) * 2e-30 UV excision repair protein UV exci * 9e-05 ubiquitin / ribosomal protein S27a -
 CG1836 fruit fly (Drosophila melanogaster) * 4e-38 Simila [UBA // ubiquitin // UBIQUITIN_2] CG1836 102A8-102A8 dup:1/3 ID:87A11
 + ion_channel * similar to S. cerevisiae HAP4 transcriptional activator (SP:HAP4_YEAST, similar to regulatory domain of PI3-
 CG1976 kinase P85-alpha subunit (phosphatidylin [PDZ] CG1976 LD28013 100F1-100F2 ID:87A12
 + sl enzyme * 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) gamma-D - fruit fly (Drosophila
 CG4200 melanogaster)(aa) * DMCS_2 sl * phospholipa [PHPHLIPASEC // SH2DOMAIN // C2 // PIPLC] CG4200 LD27939 14B18-14C1

ID:87A7

+ 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 + actin_binding CG9924 LD28030 dup:2/2 ID:87B2

CG9924 + 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 cyto_unknown ID:87B8

CG17454 + unknown * 1e-21 protein * [ZINC_FINGER_C3HC4] CG2218 LD28173 99F6-99F6 ID:87C11

CG2218 + 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 + cell_adhesion CG15427 LD28224 dup:1/2 ID:87D1

CG15427 + unknown * 5e-29 candidate adaptor protein CED-6 * 8e-05 m-Numb * 2e-07 E2a-Pbx1-associated protein * 3e-05 JIP-1 related protein [PTB_DOMAIN // PID] CG11804 LD28347 45D7-45D8 ID:87D10

CG11804 + 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 + sn actin_binding * singed protein - fruit fly (Drosophila melanogaster)(aa) * DMSING2_2 sn * SING_DROME SINGED PROTEIN singed * 2e-96 FASC_MOUSE FASCIN fascin - mouse CG1536 LD28250 7D2-7D2 ID:87D3

CG1536 + signal_transduction transducin (beta) like 1 protein GPROTEINBRPT, WD40 CG7275 LD28275 dup:2/3 ID:87D5

CG7275 + unknown * 2e-20 protein * CG13777 LD28289 27D3-27D4 dup:3/5 ID:87D7

CG13777 + enzyme * DMUBCD1_2 eff * ben * UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN)(aa) * ubiquitin-conjugating enzym [UBIQUITIN_CONJUGAT // UQ_con // UBIQUIT] CG4443 LD28310 14F2-14F2 ID:87D8

CG4443 + unknown * CG7168 LD28404 90F1-90F1 dup:2/2 ID:87E8

CG7168 + G_protein_linked_receptor * Dfz2(aa) * 1e-32 transmembrane receptor * 2e-60 transmembrane receptor * 1e-43 frizzled (Drosophila) homolog frizzled homo [Fz // FRIZZLED] CG4626 LD28410 6F5-6F5 dup:2/2 ID:87E9

CG4626 + CG16798 dup:2/3 ID:87F12

CG16798

CG6961	+ RNA_binding * dJ222E13.3.2 (PUTATIVE partial isoform 2)(aa) * DMBNBR_2 bnb * CG6961 LD28479 17D5-17D5 dup:3/4 ID:87F6
CG10627	+ CG10627 ID:87F7
CG3634	+ CG3634 LD28488 dup:1/2 ID:87F8
	+ 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 // ANTIFREEZEI]
CG11486	CG11486 63F4-63F4 dup:1/6 ID:87G3
CG10346	+ chaperone * CG10346 37A4-37A4 dup:1/3 ID:87G7
	+ Qm ribosomal_protein 60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) RIBOSOMAL_L10E, Ribosomal_L10e
CG17521	CG17521 ID:87H3
CG12134	+ CG12134 ID:87H4
CG6407	+ signal_transduction CG6407 dup:3/3 ID:87H5
CG17033	+ CG17033 ID:87H8
CG1218	+ CG1218 ID:87H9
CG1542	+ CG1542 ID:88A10
	+ unknown * rap55(aa) * 2e-07 SCD6_YEAST SCD6 PROTEIN SCD6 protein - yeast (Saccharom * 2e-19 predicted using Genefinder; cDNA EST yk343c12.5 comes from this * CG10686 69C3-69C3 dup:1/3 ID:88A5
CG10686	
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	
CG9216	+ unknown * [NLS_BP] CG9216 14A6-14A8 ID:88B5
CG18041	+ CG18041 ID:88B6
CG12081	+ unknown CG12081 ID:88C3
CG12132	+ unknown * 7e-30 C34G6.1 gene product * CG12132 8D8-8D8 dup:1/3 ID:88C6
CG11177	+ CG11177 ID:88C8
	+ unknown * 4e-08 cDNA EST CEMSE83F comes from this gene; cDNA EST comes * * CG10217 95B7-95B8 dup:2/4 ID:88D6
CG10217	
CG8116	+ unknown * 1e-108 inserted at base 3' end of P element Inverse PCR * * CG8116 85B2-85B2 dup:1/2 ID:88D7
	+ Ugt enzyme * Ugt * UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)(aa) * 8e-19 KRE5_YEAST KILLER TOXIN-RESISTANCE PROTEIN PRECURSOR * coded for by [NLS_BP] CG6850 79E3-79E3 dup:5/7 ID:88D8
CG6850	
CG7407	+ CG7407 dup:1/2 ID:88D9
CG13849	+ unknown CG13849 dup:2/2 ID:88E12
CG7162	+ ligand_binding_or_carrier * protein kinase sgg39 (EC 2.7.1.-) (clone pNB39) - fruit fly (Drosophila melanogaster)(aa) *

thyroid hormone receptor interactor 2(aa) * peroxisome [PRO_RICH] CG7162 78E5-78E6 dup:5/5 ID:88E7

CG7483 + RNA_binding CG7483 ID:88F1

CG2051 + 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

+ BcDNA:GH02636 transporter * 1e-134 putative open reading frame * 1e-133 P protein * 2e-30 arsA * P protein, truncated

CG2831 CG2831 26D1-26D1 dup:1/4 ID:88G1

CG17138 + CG17138 dup:2/2 ID:88G10

CG16901 + CG16901 ID:88G12

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

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

CG3180

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

+ Ef1alpha48D ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (50 KD FEMALE-SPECIFIC PROTEIN ATP_GTP_A, EFACITOR_GTP, ELONGATNFCT, GTP] CG8280 dup:2/2 ID:89B10

CG8280

CG10428 + RCC1_2, SAM_BIND CG10428 dup:3/5 ID:89B11

CG17678 + CG17678 dup:2/2 ID:89B3

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

CG12121

CG12269 + unknown LD29726 89B6

+ enzyme * coded for by C. elegans cDNA yk4d2.3; coded for by C. elegans cDNA yk4d2.5; coded for by C. elegans cDNA yk109a1.5; similar to protein tyrosine phos [PHOSPHOPANTETHEINE // PDZ // PRO_RICH] CG16757 62E7-62E7 dup:5/6 ID:89B7

CG16757

+ 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

CG6779

dup:2/2 ID:89B9

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

CG9450 + tud involved in pole cell determination NLS-BP, TUDOR CG9450 LD29866 dup:2/2 ID:89C11

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/SYNAPTOBREVIN 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

CG7022 + unknown * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST yk228b12.5 comes from this gene; cDNA EST yk273g2.5 comes from this gene; cD CG7022 LD30146 61B1-61B1 dup:2/3 ID:89F1

CG5788 + UbcD10 enzyme (Ubiquitin conjugating enzyme 10) similar to ubiquitin conjugating enzymes [Caenorhabditis elegans] UBIQUITIN_CONJUGAT, UBIQUITIN_CONJUGAT_2] CG5788 LD30207 dup:3/3 ID:89F12

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

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

CG4488 + protein_kinase CG4488 ID:89H8

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

CG7456 + unknown * hypothetical protein(aa) * 2e-19 probable membrane protein YPR105c - yeast (Saccharomyces cerevisiae) * 2e-40 contains similarity to Arabidopsis me CG7456 LD35507 31E4-31E4 dup:2/2 ID:95B1

CG1057 + unknown * Similarity to Yeast SOH-1 protein * CGI-125 protein(aa) * 2e-19 YB78_YEAST HYPOTHETICAL 35.9 KD PROTEIN IN PCS60-ABD1 INTERGENIC REGION CG1057 LD35644 82D2-82D2 ID:95B11

CG9764 + actin_binding * erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)(aa) * DMP41A_4 cora * 2e-55 product of alternative splicing; homologue to membra [BAND_41_1 // Band_41 // BAND41 // BAND_] CG9764 LD35542 89A1-89A1 ID:95B4

CG5456 + unknown * CG5456 LD35728 94A3-94A3 ID:95C10

+ RNA_binding * splicing factor (CC1.3)(aa) * 5e-12 polyadenylated RNA-binding protein PUB1 - yeast (Saccharomyces cerevisiae) >g * 7e-11 RNA-binding protein * 1e-1 [RNP_1 // RBD // rrm // NLS_BP] CG11266 LD35730 27D-27D3 dup:1/2 ID:95C11
 CG11266
 + 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
 CG6376
 + unknown * beclin 1(aa) * 2e-30 hypothetical protein YPL120w - yeast (Saccharomyces cerevisiae) (* 2e-35 T19E7.3 gene product * 3e-20 Bcl-2-interacting protei CG5429 LD35669 95D5-95D5 dup:1/2 ID:95C2
 CG5429
 + 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
 CG4621
 CG7705
 + unknown * CG7705 LD35690 91B7-91B8 ID:95C5
 + CycC cell_cycle_regulator * DMCYCLCG_2 CycC * cyclin C(aa) * cyclin C protein(aa) * cyclin C(aa) CG7281 LD35705 88D8-88D8 dup:3/3 ID:95C8
 CG7281
 + Arp66B cytoskeletal_structural_protein * DMACTR66B_2 Arp66B * 1e-126 ARP3_YEAST ACTIN-LIKE PROTEIN ARP3 actin homolog YJR065 * ARP3_DROME ACTIN-LIKE PROTEIN (ACTIN-LIKE PROTEIN 66B) (ACTIN [ACTINS_ACT_LIKE // actin] CG7558 LD35711 66B8-66B8 ID:95C9
 CG7558
 + CDC45L DNA_replication_factor * CDC45L * 2e-31 Cdc45p: assembles into a complex with Cdc46p/Mcm5p * CDC45L * 1e-30 predicted using Genefinder; cDNA EST yk307h3.3 comes from this ge CG3658 LD35753 1E1-1E1 ID:95D1
 CG3658
 + 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
 CG3735
 + 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
 CG9425
 + EG:114E2.2 * MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT)(aa) * MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT)(aa) * by content; by mat [THIOLASE_3 // HLH // HELIX_LOOP_HELIX_2] CG2856 3F2-3F2 dup:2/2 ID:95D2
 CG2856
 + Rad51 DNA_repair_protein * DMDMRBA_1 Rad51 * 2e-97 RA51_YEAST DNA REPAIR PROTEIN RAD51 RAD51 protein - yeast * 1e-176 RA51_DROME DNA REPAIR PROTEIN RAD51 HOMOLOG (RECA PROTEIN [HHH // RECA_1 // RECA_2 // ATP_GTP_A] CG7948 LD35801 99D5-99D6 ID:95D3
 CG7948
 + Bub1 enzyme * Bub1 * 4e-75 hypothetical protein YLR419w - yeast (Saccharomyces cerevisiae) (U * DDX9_CAEEL PROBABLE ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HEL [PROTEIN_KINASE_ST // pkinase // PROTEIN] CG7838 LD35813 42A1-42A1 ID:95D5
 CG7838
 + 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
 CG3287
 + 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
 CG1708
 CG15435
 + nucleic_acid_binding * [ZINC_FINGER_C2H2 // ZINC_FINGER_C2H2_2] CG15435 LD35850 24F5-24F5 ID:95D9

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

CG11837 + unknown * dimethylase(aa) * 2e-97 DIM1_YEAST DIMETHYLADENOSINE TRANSFERASE (S-ADENOSYLMETHIONINE-6-N', N'-ADENOSY * 4e-99 YQN1_CAEEL HYPOTHETICAL 34.1 KD PROT [RrnaAD // RRNA_A_DIMETH // SAM_BIND] CG11837 LD35950 98F9-98F9 dup:2/2 ID:95E6

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[GPTEINBRPT // 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

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

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

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

CG11055 + unknown * hormone-sensitive lipase testicular isoform(aa) * 1e-07 similar to the 'GDxG' family of lipolytic enzymes * 4e-83 hormone-sensitive lipase * 2e-85 I [ESTERASE] CG11055 LD36294 56F15-56F15 ID:95H7

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

CG8806 + unknown * bromodeoxyuridine-sensitive transcript protein - chicken(aa) * 1e-13 hypothetical protein YLR193c - yeast (*Saccharomyces cerevisiae*) (U1 * 1e-13 sim CG8806 LD36516 45D5-45D5 dup:2/2 ID:96A12

CG11798 + transcription_factor * zinc finger protein - mouse (fragment)(aa) * 6e-05 probable transcription factor YPL230w - yeast (*Saccharomyces cerevisiae*) * 2e-05 stripe[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG11798 LD36410 51E3-51E4 dup:1/4 ID:96A3

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

CG9403 + transcription_factor * ZINC FINGER PROTEIN GLI4 (NEURAL SPECIFIC DNA BINDING PROTEIN XGLI4) (XGLI-4)(aa) * 4e-07 YJF6_YEAST HYPOTHETICAL 98.9 KD ZINC FINGER PROTE[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG9403 LD36562 42B2-42B2 dup:1/2 ID:96B3

CG3480 + EG:86E4.4 signal_transduction * /match=(desc;; /match=(desc;; /match=(de * 2e-25 lin-9 protein - *Caenorhabditis elegans* * 8e-21 protein * 4e-07 inserted at base Both 5' and 3' ends CG3480 LD36606 2B16-2B16 ID:96B7

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

CG1275 + electron_transfer * 2e-36 C561_CAEEL PUTATIVE CYTOCHROME B561 (CYTOCHROME B-561) hy * 6e-37 cytochrome B561 * 4e-39 C561_HUMAN CYTOCHROME B561 (CYTOCHROME B-561) cytoch CG1275 LD36721 62D4-62D5 dup:1/2 ID:96C1

CG4612 + RNA_binding * Poly(A) binding protein, cytoplasmic and nuclear; Pab1p(aa) * POLYADENYLATE-BINDING PROTEIN (POLY(A) BINDING PROTEIN) (PABP)(aa) * polyadenylate bin [RNP_1 // RBD // rrm] CG4612 LD36772 60D4-60D4 ID:96C3

CG7012 + unknown * 2e-08 YHC6_CAEEL HYPOTHETICAL 81.4 KD PROTEIN ZC434.6 IN CHROMOSOME I PRECURSOR * 3e-53 Y253_HUMAN HYPOTHETICAL PROTEIN KIA * * CG7012 LD36812 96B2-96B3 ID:96C4

CG6395 + 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

CG13929 + unknown * Yor240wp(aa) * hypothetical protein(aa) * * 1e-56 probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae) [MET_TRANS // SAM_BIND] CG13929 LD36863 62A10-62A10 ID:96C9

CG4831 + motor_protein * Mklp1 * kinesin motor protein KIFC3(aa) * 2e-20 NUF1_YEAST NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110) * 4e-30 microtubule binding prote [kinesin // KINESIN_MOTOR_DOMAIN1 // KIN] CG4831 LD36932 32E4-32E4 ID:96D1

CG5785 + 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

CG3082 + l(2)k09913 unknown * 1e-22 inserted at base Both 5' and 3' ends of P element Inverse PCR * * CG3082 LD36990 59C3-59C3 dup:2/2 ID:96D4

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

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

CG9749 + Abi signal_transduction * Abl tyrosine kinase-interacting protein(aa) * 9e-07 YFJ4_YEAST HYPOTHETICAL 40.4 KD PROTEIN IN PES4-HIS2 INTERGENIC REGION * 2e-05 DRK_DRO[AA_TRANSFER_CLASS_2 // P67PHOX // SH3DO] CG9749 LD37010 88A10-88A10 dup:2/2 ID:96D8

CG7015 + unknown * 1e-111 protein * 1e-114 UNR_RAT UNR PROTEIN probable unr protein - rat * unknown [COLD_SHOCK // CSD] CG7015 LD37025 66C13-66C13 dup:2/4 ID:96D9

CG6144 + unknown * predicted using Genefinder(aa) * * CG6144 LD37206 31E4-31E4 dup:2/2 ID:96E12

CG10009 + 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

CG4898 + Tm1 actin_binding * TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL TROPOMYOSIN)(aa) * DMTMII_2 Tm1 * 1e-10 NUF1_YEAST NUF1 PROTEIN (SPINDLE POLY B[Tropomyosin // TROPOMYOSIN // PRO_RICH] CG4898 LD37158 88E10-88E11 dup:4/4 ID:96E7

CG8705 + pnut cytoskeletal_structural_protein * pnut * PEANUT PROTEIN(aa) * 3e-82 cell division cycle protein * 1e-134 CDC10 [GTP_CDC // NLS_BP // ATP_GTP_A] CG8705 LD37170 44B3-44B4 dup:2/2 ID:96E9

CG13601 + unknown * 7e-08 No definition line found * * CG13601 LD37258 95C-95C ID:96F10

CG8825 + unknown * 3e-18 Contains similarity to Pfam domain: (PLDc), Score=13.8, * * CG8825 LD37277 23D4-23D4 ID:96F12

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

+ endopeptidase * 5e-26 QRI7_YEAST PUTATIVE PROTEASE QRI7 QRI7 protein - yeast * 5e-42 similar to O-sialoglycoprotein endopeptidase; cDNA EST * 8e-52 putative sialogl [OSIALOPTASE // Peptidase_M22] CG14231 LD37221 18E1-18E1 ID:96F4

CG14231 + fs(1)K10DNA_binding * regulatory protein K10, oocyte-specific - fruit fly (*Drosophila melanogaster*)(aa) * DMK10G_4 fs(1)K10 * 4e-58 K10_DROME DNA-BINDING PROTEIN K10 * 62 [PRO_RICH] CG3218 LD37240 2F1-2F1 ID:96F7

CG3218 + enzyme * BLASTX 2.5E-12 FMS1|Protein with similarity to *Candida albicans* corticosteroid-binding protein CBP1(dna) * l(2)37Cs * Fms1p(aa) * 1e-12 FMS1_YEAST F [NAD_BINDING] CG8032 LD37279 85A11-85A11 dup:1/2 ID:96G1

CG8032 + 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 + unknown * C06G3.9 gene product(aa) * protein(aa) * 3e-45 C06G3.9 gene product [NLS_BP] CG1104 LD37409 84C1-84C1 dup:2/2 ID:96G12

CG1104 + function_unknown * 2e-05 hypothetical protein YDL115c - yeast (*Saccharomyces cerevisiae*) * 5e-09 hypothetical protein * 2e-43 inserted at base 5' end of P element Inve CG10528 LD37329 38A-38A4 dup:1/3 ID:96G3

CG10528 + transcription_factor * DMGLASS_8 gl * 8e-07 Adr1p * 4e-25 CF2_DROME CHORION TRANSCRIPTION FACTOR CF2, ISOFORMS I AND II * 5e-22 similar to Zinc finger, C2H2 type (5 domai[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG4424 LD37349 92C3-92C3 ID:96G5

CG4424 + unknown * No definition line found(aa) * 3e-40 hypothetical protein YER007c-a - yeast (*Saccharomyces cerevisiae*) * 3e-58 No definition line found * 3e-39 hypo CG5941 LD37358 5D1-5D1 ID:96G7

CG5941 + EG:EG0007.10 unknown * by content; * 1e-92 by content; 1-meth * 1E-94* CG4865 LD37360 4B1-4B1 ID:96G8

CG4865 + ion_channel * outer membrane protein(aa) * The gene product is related to adenylyl cyclase.(aa) * 1e-18 DLG1_DROME LETHAL(1)DISCS LARGE-1 TUMOR SUPPRESSOR PROTEIN [PDZ] CG5462 LD37377 100B1-97B9 dup:1/3 ID:96G9

CG5462 + 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 + enzyme * protein(aa) * 3e-37 PAN2_YEAST PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN2 (PAB1P-DEPE * 4e-59 YPO4_CAEEL HYPOTHETICAL 127.2 KD PROTEIN [UCH_2_3 // Exonuclease] CG8232 LD37466 44F9-44F11 dup:1/4 ID:96H2

CG8232 + 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 + yps unknown * yps * Y-box protein(aa) * Y box protein(aa) * 1e-74 Y-box protein [COLD_SHOCK // COLDSHOCK // CSD // NLS_B] CG5654 LD37574 68F4-68F4 dup:3/5 ID:96H8

CG5654 + * 2e-14 cDNA EST yk448c11.3 comes from this gene; cDNA EST com * * CG10978 83C-83C dup:2/4 ID:97A5

CG10978

CG12878	+ unknown * 6e-10 MLN * 1e-41 I(3)rL203 I(3)rL203 inserted at base 5' end of P element Inverse PCR * CG12878 LD37788 98A8-98A8 dup:2/2 ID:97B3
CG2669	+ unknown * [NLS_BP] CG2669 LD38047 83A4-83A5 ID:97C12
CG13089	+ unknown * member of major facilitator superfamily; Cdc91p(aa) * 6e-41 CC91_YEAST CELL DIVISION CONTROL PROTEIN cell divisio * 4e-13 similar to cell division c CG13089 LD37974 29D1-29D1 ID:97C4
CG14442	+ unknown * 7e-05 unknown * * [MIP // NLS_BP] CG14442 LD38069 6C7-6C8 dup:2/3 ID:97D2
CG4639	+ transcription_factor * Cys2/His2 zinc finger protein(aa) * ovo * fruit fly STS clone SP6(dna) * zinc finger protein NY-REN-21 antigen(aa) [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG4639 LD38072 94E-94E ID:97D4
CG8928	+ unknown * CG8928 LD38104 13F14-13F14 ID:97D7
CG5109	+ transcription_factor * DMPLYCMB_2 Pcl * BLASTX 2.1E-16 element DNA-binding protein(dna) * polycomblake nuclear protein [PHD // PRO_RICH] CG5109 LD38218 55B5-55B7 dup:3/3 ID:97E2
CG8892	+ unknown * 1e-18 hypothetical protein YDR330w - yeast (Saccharomyces cerevisiae) (U * 3e-35 protein * 1e-24 ubiquitin regulatory domain protein * 1E-111 [UX_DOMAIN] CG8892 LD38226 25B-25B9 dup:2/2 ID:97E3
CG17170	+ su(f) DNA_binding * 2e-47 RN14_YEAST MRNA 3'-END PROCESSING PROTEIN RNA14 RNA14 p * SUF_DROME SUPPRESSOR OF FORKED PROTEIN gene su(f) protein * cleavage stimulation fa [NLS_BP] CG17170 LD38348 cyto_unknown ID:97F2
CG11417	+ EG:8D8.4unknown * /match=(desc:(aa) * 5e-48 hypothetical protein YDR365c - yeast (Saccharomyces cerevisiae) (U * 6e-34 cDNA EST comes from this gene * 4e-60 hypothet [NLS_BP] CG11417 LD38432 2A2-2A2 dup:2/2 ID:97F9
CG1078	+ unknown * 5e-10 FIP1_YEAST FIP1 PROTEIN FIP1 protein - yeast (Saccharom * 3e-16 contains similarity to S. cerevisiae FIP1 * 2e-13 YAAA_SCHPO HYPOTHETICAL 37.3 [PRO_RICH // NLS_BP] CG1078 LD38592 82C2-82C2 dup:1/3 ID:97G11
CG8180	+ unknown * 1E-178 * * [ANTIFREEZEI] CG8180 LD38554 52A4-52A4 dup:1/2 ID:97G8
CG6773	+ BcDNA:LD03471 transcription_factor_binding * SEC13-RELATED PROTEIN(aa) * cytoplasmic protein involved in release of transport vesicles from the ER; Sec13p(aa) * PROTEIN TRANSPORT PROTEIN SEC13([WD40_REGION // WD40] CG6773 LD38669 94F1-94F1 ID:97H2
CG4645	+ unknown * dJ167A19.1 (novel protein)(aa) * No definition line found(aa) * 2e-14 No definition line found * No definition line found CG4645 LD38670 11D1-11D1 ID:97H3
CG3221	+ motor_protein * 3e-05 unknown protein IT1 * * CG3221 LD38682 57B15-57B15 ID:97H5
CG7986	+ transcription_factor * hypothetical protein(aa) * 1e-19 YFJ1_YEAST HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION * 3e-69 No definition line found * 3e-24 un [ATP_GTP_A] CG7986 LD38705 66B13-66B13 ID:97H7
CG6701	+ DNA_binding * 7e-32 NAM7_YEAST NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT * 1e-27 nonsense-mediated mRNA decay trans-acting factor * 2[ZINC_FINGER_C2H2 // PRO_RICH // ATP_GTP] CG6701 LD38709 50C21-50C22 dup:2/2 ID:97H8
CG5924	+ unknown * weak similarity to ATP/GTP-binding site motif A * 2e-40 weak similarity to ATP/GTP-binding site motif A elega * 1e-63 POM1 chabaudi * [ATP_GTP_A] CG5924 LD38710 33A1-33A1 dup:1/2 ID:97H9
CG8793	+ unknown * protein(aa) * 3e-30 F46F11.9 gene product * CG8793 LD38816 76B11-76C1 ID:98A10
CG14224	+ ubiquitin * 2e-11 ubiquitin-like protein DSK2 - yeast (Saccharomyces cerevisiae) * 1e-76 similar to Ubiquitin family; cDNA

EST comes from this * 1E-61* 1e-58 pu [UBA // ubiquitin // UBIQUITIN_2] CG14224 LD38919 18D13-18D13 dup:3/4 ID:98B11
+ BcDNA:GH07910 protein_kinase * 7e-22 CC5_YEAST CELL CYCLE PROTEIN KINASE CDC5/MSD2 protein ki * 3e-12 p90
ribosomal S6 kinase * 1e-121 YKT3_CAEEL PUTATIVE SERINE/THREONINE-[PFKB_KINASES_1 // PROTEIN_KINASE_ST //]

CG2829 CG2829 LD38852 3F4-3F6 dup:5/6 ID:98B2
+ Psi RNA_binding * Psi * PSI=P element somatic inhibitor Peptide, * 1E-176* 3e-37 similar to RNA binding protein [KH-domain
// PFKB_KINASES_1 // KH_DOMAI] CG8912 LD38872 53D14-53D14 dup:1/2 ID:98B5

CG8912 + RasGAP signal_transduction * RasGap protein(aa) * 2e-16 BUD2_YEAST INHIBITORY REGULATOR PROTEIN BUD2/CLA2
GTPase- * RasGap protein * 1e-40 similar to GTPase-activating p[RAS_GTPASE_ACTIV_2 // SH2DOMAIN // C2 /] CG9209

CG9209 LD38909 14A1-14A1 dup:1/2 ID:98B8
+ 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
+ transcription_factor_binding * Ydr324cp(aa) * 1e-25 hypothetical protein YDR324c - yeast (Saccharomyces cerevisiae) (U *
3e-29 hypothetical protein * 7e-05 DMENHSPA_3 gro [WD40_REGION] CG5018 LD39110 72D11-72D12 ID:98C8

CG5018 CG18533 LD39166 ID:98D1
+ CG18533 LD39166 ID:98D1

CG18533 + transcription_factor * 0.00000000006* 9e-25 YMB4_CAEEL HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN
CHROMOSOME III * 4e-13 TIF1 protein - mouse TIF1 isoform Pepti * 8e-24 brai [NHL] CG1624 LD39167 43C5-43C7 ID:98D2

CG1624 + unknown * 5e-40 prediabetic NOD sera-reactive autoantigen muscul * 5e-10 IVR-like protein * IVR-like protein *
[TPR_REGION // TPR_REPEAT] CG14444 LD39177 6C1-6C1 dup:3/3 ID:98D4

CG14444 CG14764 LD39211 43F6-43F6 ID:98D5
+ unknown * CG14764 LD39211 43F6-43F6 ID:98D5

CG14764 + unknown * CGI-25 protein(aa) * Unknown protein(aa) * 5e-61 R05G6.4 gene product * [NLS_BP] CG6179 LD39230 17A10-
17A10 ID:98D7

CG6179 + sta ribosomal_protein * 6e-69 NABA_YEAST 40S RIBOSOMAL PROTEIN SA HOMOLOG A (NUCLEIC ACID-BINDING
PROTEIN NAB1 * 1e-143 RSP4_DROME 40S RIBOSOMAL PROTEIN SA (P40) (STUBARIST RIBOSOMALS2,
RIBOSOMAL_S2_1 CG14792 ID:98D8

CG14792 + enzyme * 9e-41 /match=(desc;; /ma * 5e-35 cDNA EST comes from this gene; cDNA EST co * 9e-06 Ubc84D * contains
similarity to ubiquitin-conjugatin enzymes (Pf [UQ_con // UBIQUITIN_CONJUGAT_2] CG4502 LD39243 27E4-27E4 ID:98D9

CG4502 + unknown * nucleotide binding protein (E.coli MinD like)(aa) * putative nucleotide binding protein(aa) * 7e-82 NB35_YEAST
NBP35 PROTEIN NBP35 protein - yeast CG17904 LD39271 36A7-36A7 dup:2/2 ID:98E2

CG17904 CG6425 LD39291 97C3-97C3 dup:2/2 ID:98E3
+ unknown * CG6425 LD39291 97C3-97C3 dup:2/2 ID:98E3

CG6425 + unknown * 9e-16 lamin B receptor LAMIN B RECEPTOR (INTEGRAL NUCLEAR ENVEL * 8e-19 ERG3_NEUCR C-14
STEROL REDUCTASE (STEROL C14-REDUCTASE) C * integral nuclear CG17952 57F10-57F10 dup:4/4 ID:98E6

CG17952 + asf1 cell_cycle_regulator * involved in silencing; Asf1p(aa) * Similarity with yeast anti-silencing protein I (Swiss Prot accession
number cDNA EST comes from this gene; cDNA CG9383 LD39377 76C1-76C1 dup:2/2 ID:98E8

CG9383 + ial protein_kinase * Ipl1/aur serine/threonine kinase(aa) * 2e-68 IPL1_YEAST SERINE/THREONINE-PROTEIN KINASE IPL1
probable * 1e-75 protein kinase (EC 2.7.1.37) aurora - [PROTEIN_KINASE_ST // TYRKINASE // PROTE] CG6620 32B4-32B4
dup:4/5 ID:98E9

CG6620 CG4699
+ unknown * inserted at base Both 5' and 3' ends of P element Inverse PCR * 6e-68 inserted at base Both 5' and 3' ends of P

element Inverse PCR * [AA_TRNA_LIGASE_I // NLS_BP] CG4699 LD39557 89A-89A dup:9/11 ID:98F10
 + DNA_binding * 2e-15 YJ89_YEAST HYPOTHETICAL 85.0 KD PROTEIN IN STE24-ATP2 INTERGENIC REGION * 8e-26
 Similarity to Human XE169 protein (SW:XE169_HUMAN); cDNA EST E [ARID // PRO_RICH // NLS_BP] CG3654 LD39559 67B5-
 67B5 dup:3/3 ID:98F11
 CG3654
 CG1896 + unknown * [NLS_BP] CG1896 LD39576 100E2-100E2 dup:2/2 ID:98F12
 + protein_kinase * ZC581.9 gene product(aa) * 4e-40 SCY1_YEAST SCY1 PROTEIN SCY1 protein - yeast (Saccharom * 8e-
 26 ZC581.9 gene product * 3e-05 putative serine/threon [PROTEIN_KINASE_DOM // pkinase] CG1951 LD39455 98F-98F dup:2/2
 ID:98F2
 CG1951
 + Pitslre protein_kinase * DMPITSLRE_3 Pitslre * protein_kinase(aa) * 2e-60 PHO85 * 1e-123 YP62_CAEEL PUTATIVE
 SERINE/THREONINE-PROTEIN KINASE IN CHROMOSOME II >g [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM]
 CG4268 LD39519 77E5-77E dup:3/3 ID:98F6
 CG4268
 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
 100F5-100F5 dup:3/3 ID:98F9
 CG2050
 + 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
 ID:98G12
 CG5720
 + unknown * weak similarity to C. elegans predicted protein C33G8.2(aa) * HYPOTHETICAL PROTEIN * 7e-15 weak
 similarity to C. elegans predicted protein C33G8.2 * CG9723 LD39612 14F5-14F6 ID:98G3
 CG9723
 + Abl protein_kinase * DMTKABL3_2 Abl * Dsrc41(aa) * TYROSINE-PROTEIN KINASE DASH/ABL(aa) * 2e-16 SPK1_YEAST
 PROTEIN KINASE SPK1 (SERINE-PROTEIN KINASE 1) [SH2DOMAIN // SH3DOMAIN // PRO_RICH // P] CG4032 LD39618
 77A3-73B1 ID:98G4
 CG4032
 + unknown * 3e-21 hypothetical protein YOR289w - yeast (Saccharomyces cerevisiae) * 1e-43 R166.3 * 3e-45 unknown
 protein * Y810_METJA HYPOTHETICAL PROTEIN hypo CG5902 97F1-97F1 dup:1/6 ID:98G6
 CG5902
 + transporter * minidisks(aa) * 3e-26 MUP1_YEAST HIGH AFFINITY METHIONINE PERMEASE methionine * 1e-110
 Similarity to Human membrane protein E16 (SW:E16_HUMAN); cDNA [aa_permeases // AMINO_ACID_PERMEASE_2] CG12317
 LD39658 33B12-33B13 ID:98G7
 CG12317
 + 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
 ID:98G8
 CG2712
 + PRL-1 protein_phosphatase * PRL-1 * 4e-06 phosphoprotein phosphatase * 1e-100 putative prenylated protein tyrosine
 phosphatase PRL-1 melanogaste * 3e-44 Similar to protein-tyro [PRENYLATION // TYR_PHOSPHATASE_2] CG4993 LD39844
 35F6-35F6 ID:98H11
 CG4993
 CG10944 + RpS6 ribosomal_protein 40S RIBOSOMAL PROTEIN S6 NLS_BP, RIBOSOMAL_S6E CG10944 ID:98H3
 CG14646 + unknown * 2e-20 predicted using Genefinder; cDNA EST comes from this g * * CG14646 LD39811 82B2-82B3 ID:98H8

CG10057 + enzyme * protein(aa) * 3e-83 predicted using Genefinder; Similarity in 3' end to Human * 5e-16 TTL_BOVIN TUBULIN--
TYROSINE LIGASE (TTL) * similar to tubulin [ZF_MATRIN // NLS_BP] CG10057 LD39904 96B19-96B20 dup:2/2 ID:99A1

CG6222 + su(s) RNA_binding * DMSUSG_16 su(s) * su(s) homolog; similar to Drosophila melanogaster suppressor of sable (su(s)) pro *
DMSUSG_16 su(s) * SUS_DROME SUPPRESSOR OF SAB [NLS_BP] CG6222 LD39941 1B10-1B10 dup:2/3 ID:99A10

CG4654 + Dp transcription_factor * DMDPRTF_2 Dp * transcription factor * 6e-59 similar to transcription factor DP-1; cDNA EST comes
f * 5e-72 TDP1_MOUSE TRANSCRIPTION FACTOR DP-1 (E2F CG4654 LD39905 49F13-49F13 dup:2/2 ID:99A2

CG3303 + enzyme * putative serine protease-like protein(aa) * weakly similar to human placental protein precursor
(SP:PP11_HUMAN)(aa) * placental protein (serine pro CG3303 LD39912 89A13-89B1 ID:99A3

CG8247 + unknown * 4e-31 SRYA_DROME SERENDIPITY LOCUS ALPHA PROTEIN serendipity (sr * 4e-32 Drosophila simulans
serendipity * 4e-33 DMSRYG1_16 Sry-&agr; CG8247 LD39926 44F9-44F9 ID:99A5

CG6542 + BcDNA:LD23181 protein_phosphatase * 1e-41 inserted at base Both 5' and 3' ends of P element Inverse PCR * *
[TYR_PHOSPHATASE_1] CG6542 LD39930 54C1-54C3 ID:99A6

CG5850 + unknown * HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I(aa) * 5e-24 YK31_YEAST
HYPOTHETICAL 48.8 KD PROTEIN IN TRK2-MRS4 INTERGENIC REGION * 1e-41 c [FKBP_PPIASE_1] CG5850 LD39938
30F2-30F2 dup:2/2 ID:99A8

CG12734 + motor_protein * 8e-22 putative * 4e-19 microtubule binding protein D-CLIP-190 * 3e-36 predicted using Genefinder * 1e-10
rho/rac-interacting citron kinase [SPEC_REPEAT // NLS_BP // CYTOCHROME_C] CG12734 LD40094 63B13-63B13 dup:2/2
ID:99B10

CG4586 + enzyme * 2e-45 acyl-coenzyme A oxidase * 1e-100 Similarity to Rat Acyl-CoA oxidase I (SW:CAO1_RAT); cDNA EST
EMBL: * 1e-116 peroxisomal acyl-CoA oxidase * 1e CG4586 LD40103 6E4-6E4 ID:99B12

CG12701 + transcription_factor * BLASTX 5.2E-13 Mus musculus glutamine repeat protein-1 mRNA, complete cds.(dna) * BLASTX
1.1E-08 FLO11|Cell surface flocculin(dna) * 7e-09[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG12701 LD40013 18F2-18F2
dup:5/5 ID:99B5

CG10565 + 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

CG5212 + Pli unknown * Pelle associated protein Pellino * 1e-100 F25B4.2 gene product * Pli * CG5212 LD40134 95C7-95C9 ID:99C1

CG6584 + unknown * 5e-24 YCD3_YEAST HYPOTHETICAL 19.3 KD PROTEIN IN STE50 5'REGION * 1e-25 YL56_CAEEL
HYPOTHETICAL 17.2 KD PROTEIN F44E2.6 IN CHROMOSOME III * 1e-21 co [CYTOCHROME_C // IG_MHC] CG6584
LD40260 86C7-86C7 ID:99C11

CG12941 + 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

CG9104 + * similar to S. cerevisiae nitrogen permease regulator * G21 protein(aa) * homologous to yeast nitrogen permease
(candidate tumor suppressor)(aa) * 3e CG9104 15A11-15B1 dup:1/2 ID:99C3

CG9866 + unknown * CG9866 LD40170 22E-22E ID:99C4

CG3157 + gammaTub23C cytoskeletal_structural_protein * similar to Tubulin (2 domains); cDNA EST CEMSG51F comes from this

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

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

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

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

CG1490 + CG13840 LD40283 ID:99D4

CG13840 + 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 + transcription_factor * Yjr119cp(aa) * XE169 PROTEIN (SMCX PROTEIN)(aa) * T17H7.10(aa) * JUMONJI PROTEIN(aa) [ARID // PHD] CG9088 LD40310 26B1-26B1 dup:2/2 ID:99D7

CG9088 + Rfc40 DNA_replication_factor * 3e-99 RFC4_YEAST ACTIVATOR KD SUBUNIT (REPLICATION FACTOR C KD SUBUNIT) * AC14_DROME ACTIVATOR KD SUBUNIT (REPLICATION FACTOR C KD SUBUNIT) (A1 * 1 [ATP_GTP_A] CG14999 LD40483 64A10-64A10 dup:2/2 ID:99E11

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

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

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

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

CG2982 + M(2)21ABenzyme * 1e-88 METK_YEAST S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE 1) * 1e-142 METK_DROME S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE [ADOMET_SYNTHETASE_1 // ADOMET_SYNTHETAS] CG2674 LD40460 21B-21B dup:2/2 ID:99E9

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

CG6987 + for unknown * CGMP-DEPENDENT PROTEIN KINASE, ISOZYME FORMS T1/T3 (CGK) (PROTEIN FORAGING)(aa) * * CG10033 LD40611 25B1-25B1 dup:3/4 ID:99F10

CG10033

+ 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 similarity 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
 + BcDNA:LD34343 enzyme * 1e-111 SCS1 product=suppressor of chaperonin sixty-1 cerevisi * 1e-152 similar to RTS1 PROTEIN (SCS1 PROTEIN) * 1e-149 protein phosphatase 2A subuni CG5643 LD40774 98A3-98A3 dup:2/3 ID:99G11
 CG5643
 + 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
 + 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
 CG5589
 + transporter * CGI-19 protein(aa) * 5e-07 probable membrane protein YPL244c - yeast (Saccharomyces cerevisiae) * 7e-83 No definition line found * 2e-40 putative pr CG7853 LD40702 73E4-73E4 ID:99G5
 CG7853
 + unknown * HYPOTHETICAL 50.0 KD PROTEIN K07E8.7 IN CHROMOSOME IV(aa) * DRAP deaminase; Rib2p(aa) * 1e-72 RIB2_YEAST DRAP DEAMINASE RIB2 protein - yeast (Saccha [PseudoU_synth_2 // PSI_RLU // NLS_BP] CG6187 LD40728 31E3-31E3 ID:99G8
 CG6187
 + enzyme * Yjr084wp(aa) * acyl-protein thioesterase(aa) * 1e-22 probable membrane protein YLR118c - yeast (Saccharomyces cerevisiae) * 3e-67 YPI7_CAEEL HYPOTH [TNF_1] CG7351 LD40777 68C10-68C10 dup:2/3 ID:99H1
 CG7351
 + unknown * 7e-41 SS72_YEAST SSU72 PROTEIN hypothetical protein YNL222w - * 7e-57 coded for by C. elegans cDNA yk10c10.3; coded for by C. elegans cDNA yk37e8.3; CG14216 LD40846 18D12-18D12 ID:99H10
 CG14216
 + * BLASTX 2.3E-13 TRA1|Homolog of human TR-AP which associates with a domain of c-Myc essential for cellular transformation(dna) * predicted using Gen [PI3_4_KINASE_3] CG2905 41A1-41A1 ID:99H3
 CG2905
 + DNA_repair_protein * DMDNAPOLD_2 DNAPol- dgr; * DNA polymerase zeta subunit; Rev3p(aa) * 1e-152 DPOZ_YEAST DNA POLYMERASE ZETA CATALYTIC SUBUNIT DNA-dire * 2e-69 DPOD_D[DNAPOLB // DNA_POLYMERASE_B // DNA_pol_] CG1925 LD40801 43E16-43E17 ID:99H4
 CG1925
 CG1404
 + enzyme CG1404 ID:99H5

CG8176	+ motor_protein * * similar to S. pombe phosphoprotein * BLASTX 2.1E-09 P.falciparum merozoite surface antigen (MSA-2) gene, complete cds.(dna) * BLASTX 5.7E-22 Homo [ZINC_PROTEASE] CG8176 LD40806 86C1-85D23 dup:3/3 ID:99H6
CG1250	+ sec23 unknown * COPII protein, homolog of s. cerevisiae SEC23p(aa) * SC23_YEAST PROTEIN TRANSPORT PROTEIN SEC23 protein transpo * S23A_MOUSE PROTEIN TRANSPORT PRO CG1250 LD40826 83B6-83B6 dup:3/4 ID:99H8
CG14709	+ transporter CG14709 LD21507 ID:Farhad's BA11
CG7873	+ protein_kinase CG7873 Src42 dup:2/3 ID:Farhad's BB12
CG7664	+ CG7664 AP-4 dup:3/5 ID:Path + Ctrl1 + kras110
CG10520	+ tub unknown * DMTUBE_3 tub * TUBE PROTEIN(aa) * 3e-76 TUBE_DROVI TUBE PROTEIN tube protein * tube protein - fruit fly (Drosophila melanogaster) CG10520 tube 82B2-82B2 dup:3/4 ID:Path + Ctrl1 + kras17
CG3619	+ cell_adhesion CG3619 Delta dup:2/4 ID:Path + Ctrl1 + kras195
CG5848	+ cytoskeletal_structural_protein CG5848 cactus dup:3/4 ID:Path + Ctrl1 + kras198
CG4257	+ Stat92E DNA_binding * Stat92E * STAT_DROME SIGNAL TRANSDUCER AND TRANSCRIPTION ACTIVATOR (MARELLE PROTEIN) (D-S * 6e-08 similar to SH2 domain; cDNA EST yk354e12.5 comes [STAT // SH2] CG4257 STAT 95C4-95C4 dup:3/6 ID:Path + Ctrl1 + kras243
CG3936	+ N transmembrane_receptor * cell adhesion cell adhesion) plasma membrane plasma membrane) map_position:3C7 * NEUROGENIC LOCUS NOTCH PROTEIN PRECURSOR[ANK_REP // EGFBLOOD // EGF_1 // EGF //] CG3936 Notch 3C7-3C9 dup:2/4 ID:Path + Ctrl1 + kras248
CG7524	+ protein_kinase CG7524 Src64 dup:3/3 ID:Path + Ctrl1 + kras302
CG8049	+ protein_kinase CG8049 Tec29 dup:3/3 ID:Path + Ctrl1 + kras350