

Table S3

genes with two expression peaks

	+ 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	
CG12505	+ unknown * CG12505 LD41905 50F6-50F6 ID:101A2
CG1636	+ unknown * CG1636 LD42063 7D21-7D21 dup:1/2 ID:101B10
CG1070	+ 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
	+ 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	
	+ WD-40-family-member ligand_binding_or_carrier * CELL-CYCLE NUCLEAR AUTOANTIGEN SG2NA (S/G2 NUCLEAR ANTIGEN)(aa) * WD-40-family-member * STRIATIN(aa) * 1e-08 Similarity with hum[GPROTEINBRPT // WD40_REGION // NLS_B /] CG7392 28E1-28E1 dup:1/3 ID:101C7
CG7392	
CG4036	+ unknown * 5e-28 F09F7.7 gene product * [NLS_BP] CG4036 LD42289 32F1-32F1 dup:1/2 ID:101D11
	+ enzyme * 2e-30 5'-nucleotidase (EC 3.1.3.5) - mouse * 2e-31 5' nucleotidase (CD73) 5'-NUCLEOTIDASE PRECURSOR (ECTO-NU * 1e-38 YfkN simila * 2', 3'-cuclic nuc [PHOSPHO_ESTER // 5_nucleotidase // SPAS] CG11883 LD42374 47B1-47B1 dup:2/2 ID:101E4
CG11883	
	+ 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	
	+ 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	
	+ 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 * 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	
	+ unknown * NORBIN(aa) * neurochondrin-2(aa) * BLASTX 1.4E-23 Rattus mRNA for NORBIN, complete cds.(dna) * 2e-76 neurochondrin-1 (AB CG2330 LD42676 83F1-83F1 ID:101F8
CG2330	
	+ 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	
	+ 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

CG18459 + CG18459 54C10-54C10 ID:101H11  
+ 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

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 + structural\_protein \* 7e-07 DR48\_YEAST DDR48 STRESS PROTEIN (DNA DAMAGE-RESPONSIVE PROTEIN 48) (DDR48) (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 + unknown \* putative transposase(aa) \* 3e-05 ORF1 \* 2e-07 putative transposase \* Hermes transposase [AMP\_BINDING]

CG11560 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 + TRAP1 chaperone \* heat shock protein 90(aa) \* Hsp90-related protein TRAP1(aa) \* 2e-55 HS82\_YEAST HEAT SHOCK PROTEIN HSP82 heat shock protein \* 1e-141 similar to heat [HEATSHOCK90 // HSP90] CG3152 LD43460 42B2-42B2 dup:2/2 ID:102C12

CG3152 ID:102C12

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

CG10165 + chaperone \* p58(aa) \* 4e-05 probable membrane protein YLR080w - yeast (Saccharomyces cerevisiae) \* 7e-84 Similarity to Xenopus P58 protein cDNA EST \* 1e-104 man CG6822 LD43551 66D5-66D5 ID:102D10

CG6822 + Rpl215 enzyme \* DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)(aa) \* DMRPRIIA\_2 Rpl215 \* DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT(aa) \* RNA poly [RNA\_POL\_II\_REPEAT] CG1554 LD43558 10C4-10C5 ID:102D12

CG1554 + 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

CG1420

CG17052 + structural\_protein \* 6E-55\* 1e-06 R02F2.4 gene product \* 2e-06 peritrophin \* 7e-35 Gasp CG17052 LD43683 19C1-19C1 dup:1/2 ID:102F1

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

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

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

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

CG6401 + unknown \* 8e-74 GPI3\_YEAST N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN (GLCN \* 6e-92 similar to phosphatidylinositol biosynthetic protein; [Glycos\_transf\_1] CG6401 LD44262 54E7-54E7 ID:103B2

CG9318 + unknown \* multispinning membrane protein (70kD)(aa) \* 1e-107 probable membrane protein YDR107c - yeast (Saccharomyces cerevisiae) \* strong similarity to Sacch CG9318 LD44273 38E3-38E4 ID:103B5

CG10391 + Cyp310a1cytochrome\_P450 \* cytochrome P450(aa) \* DMLCPM Cyt-P450-rBF6-2 \* 2e-29 cytochrome P450 monooxygenase \* 2e-17 similar to cytochrome P450 [EP450II // p450 // P450 // MITP450 // E] CG10391 LD44491 37A3-37A3 ID:103C12

CG15532 + hdc signal\_transduction \* cell cytoplasm ) map\_position:99F6-11 \* 4e-98 hdc protein - fruit fly (Drosophila melanogaster) (Z \* 8e-11 similar to drosophila HCD protein \* 1e-10 CG15532 LD44381 99F-99F3 dup:2/3 ID:103C5

CG11782 + unknown \* tight junction protein (zona occludens 1)(aa) \* TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1)(aa) \* 1e-05 ZO-1 MDCK \* [NLS\_BP] CG11782 LD44404 85B4-85B4 ID:103C6

CG6754 + 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-67C dup:1/2 ID:103C9

CG8625 + 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 ID:103D12

CG6718 + enzyme \* DMANKY\_5 Ank \* calcium-independent phospholipase A2(aa) \* Ca2+-independent phospholipase A2(aa) \* 1e-0 ankyrin ankyrin m [ANK\_REP // ank // ANK\_REP\_REGION] CG6718 LD44515 67C2-67C2 dup:2/2 ID:103D4

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

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

CG3767 + unknown \* /match=(desc;; /match=(desc:(aa) \* 8e-07 hypothetical protein YLR281c - yeast (Saccharomyces cerevisiae) (U ' 7e-10 /match=(desc;; /ma \* 7e-08 RF2\_H [RF-1] CG3767 LD44791 53A2-53A2 ID:103F5

CG7347 + motor\_protein \* 8e-05 myosin heavy chain \* \* [PRO\_RICH] CG7347 LD44887 75B10-75B10 ID:103G1

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

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

CG5502	+ Rpl1 ribosomal_protein * DMRPL1R_2 Rpl1 * 60S RIBOSOMAL PROTEIN L1 (L4)(aa) * PROBABLE 60S RIBOSOMAL 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
CG17686	+ DIP1 RNA_binding * [NLS_BP // DSRBD] CG17686 LD45242 cyto_unknown dup:1/2 ID:104A6
CG17469	+ unknown * 1E-123** CG17469 LD45277 102E2-102E3 dup:2/2 ID:104B4
CG10825	+ unknown * [NLS_BP] CG10825 LD45317 95F1-95F1 ID:104B8
	+ transcription_factor_binding * CHROMATIN ASSEMBLY FACTOR P55 SUBUNIT (CAF-1 P55 SUBUNIT) (DCAF-1)(aa) * SULFUR CONTROLLER-2 (SCON2)(aa) * putative WD-repeat containing prote[WD40_REGION // WD_REPEATS // WD40]
CG1523	CG1523 LD45447 98E4-98E4 ID:104C10
CG9411	+ ion_channel * HISTIDINE-RICH GLYCOPROTEIN PRECURSOR(aa) * histidine-rich protein - Plasmodium lophurae (fragment) hi * [PRO_RICH] CG9411 LD45449 12E8-12E8 ID:104C11
CG8833	+ unknown * R07E5.1 protein (clone R07E5) - Caenorhabditis elegans(aa) * 7e-49 inserted at base Both 5' and 3' ends of P element Inverse PCR * cDNA EST comes fr [PRO_RICH // D111_DOMAIN // NLS_BP] CG8833 LD45361 74B1-74B1 ID:104C2
	+ signal_transduction * Plenty of SH3s; POSH(aa) * 5e-09 hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae) (U1 * 4e-05 DRK_DROME PROTEIN E(SEV)2B (SH2-SH3 A[zf-C3HC4 // ZINC_FINGER_C3HC4 // P67PHO] CG4909 LD45365 54D1-54D1 ID:104C3
CG4909	+ * 5e-70 CY1_YEAST CYTOCHROME C1, HEME PROTEIN PRECURSOR ubiquinol- * 5e-65 similar to cytochrome C1, heme protein; cDNA EST comes * 2e-83 cytochrome c [CYTOCHROME_C1 // CYTOCHROME_C] CG4769 64D3-64D3 dup:1/2 ID:104C4
CG4769	+ unknown * BLASTX 6.9E-07 YJL064W Protein of unknown function(dna) * BLASTX 8.2E-11 G.gallus PR264 mRNA.(dna) * 2e-17 No definition line found * [ZF_CCCH // NLS_BP] CG10084 LD45403 37E5-37E5 dup:2/3 ID:104C7
CG10084	+ transmembrane_receptor * HYPOTHETICAL PROTEIN * cysteine-rich protein (intestinal)(aa) * 4e-09 MLP2_DROME MUSCLE LIM PROTEIN MLP84B muscle L * 4e-18 gene product [LIM_DOMAIN_1 // LIM // LIM_DOMAIN_2 // ] CG4656 LD45536 94E-94E dup:2/2 ID:104D3
CG4656	
CG18638	+ CG18638 36A7-36A7 ID:104D7
	+ cell_adhesion * 2e-09 SLIT_DROME SLIT PROTEIN PRECURSOR slit protein precurs * 2e-06 coded for by C. elegans cDNA yk133e1.5; coded for by C. elegans cDNA yk133d4.5 [LRR] CG17667 LD45603 69E1-69E2 dup:2/2 ID:104E3
CG17667	+ up ligand_binding_or_carrier * DMTRPT_2 up * clot.789(dna) * 1e-112 troponin T - fruit fly (Drosophila melanogaster) * 4e-2 TRT_CAEEL TROPONIN T coded for by C. elegans cDNA yk7 [Troponin // NLS_BP] CG7107 LD45641 12A2-12A4 dup:2/2 ID:104E5
CG7107	
	+ 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
CG1591	+ 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
CG9126	+ enzyme * CHOLINEPHOSPHATE CYTIDYLYLTRANSFERASE (PHOSPHORYLCHOLINE TRANSFERASE) (CT)(aa) * phosphate cytidylyltransferase 1, choline, alpha isoform(aa) * 2e-5 [TONB_DEPENDENT_REC_1 // Cytidylyltransf] CG1049 LD46058 62A6-62A6 dup:2/2 ID:104H10
CG1049	

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

CG10527 + unknown \* farnesoic acid o-methyltransferase(aa) \* 2e-21 farnesoic acid o-methyltransferase farne \* CG10527 LD46156 57B20-57B20 ID:105A6

CG4495 + transporter \* atopy related autoantigen CALC(aa) \* 4e-27 predicted using Genefinder; similar to EF hand (2 domains) \* 2e-9 atopy related autoantigen CALC \* 2e-40 [EF\_HAND // efhand // EF\_HAND\_2] CG4495 LD46238 27E3-27E3 ID:105B3

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

CG6831 + actin\_binding \* talin(aa) \* 7e-11 cytoskeleton assembly control protein SLA2 - yeast (Saccharomyces cerevisiae) \* 8e-08 merlin \* talin [BAND\_41\_1 // Band\_41 // BAND\_41\_3 // PR] CG6831 LD46304 66D6-66D6 dup:1/2 ID:105B9

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

CG3584 + qkr58E-3RNA\_binding \* QKR58E-3(aa) \* qkr58E-3 \* 7e-13 hypothetical protein YLR116w - yeast (Saccharomyces cerevisiae) ( 5e-21 similar to GAP-associated tyrosine phosph [KH-domain // KH\_DOMAIN] CG3584 LD46502 58D7-58D8 ID:105D8

CG6355 + EG:52C10.5 enzyme \* 3e-54 FAB1\_YEAST PROBABLE PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE FAB1 (1-PHOSPHATID \* by content; 1-meth \* 8e-60 similar to FYVE zinc finger; cDN [DEP\_DOMAIN // FYVE\_DOMAIN // FYVE // ZI] CG6355 LD46512 54E9-54E9 dup:2/3 ID:105D9

CG4353 + hep protein\_kinase \* MAP kinase kinase(aa) \* Mkk4 \* hep \* 2e-46 polymyxin B resistance protein PBS2 - yeast (Saccharomyces cerevisiae) [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG4353 LD46661 11D5-11D6 dup:3/3 ID:105E10

CG10053 + unknown \* Weak similarity to Yeast hypothetical protein \* 1e-32 Weak similarity to Yeast hypothetical protein \* \* [D111\_DOMAIN // NLS\_BP] CG10053 LD46678 84C7-84C7 dup:2/2 ID:105E12

CG6896 + cytoskeletal\_structural\_protein \* protein(aa) \* similar to ankyrin motifs; cDNA EST CEMSH89F comes from this gene; cDNA EST CEMSH89R comes from this gene; cDNA E[ANK\_REP // ank // ANK\_REP\_REGION // PRE] CG6896 LD46604 75D2-75D2 dup:2/2 ID:105E5

CG5877 + unknown \* CG5877 13B9-13B9 ID:105F1

CG8505 + structural\_protein \* 6e-14 CUP7\_DROME PUPAL CUTICLE PROTEIN EDG-78 PRECURSOR ecdyson \* 2e-28 CUD4\_LOCM1 ENDOCUTICLE STRUCTURAL GLYCOPROTEIN (ABD-4A) g \* 7e-16 DMEDG78B\_2 [CUTICLE // insect\_cuticle] CG8505 49A3-49A3 ID:105F10

CG4422 + Gdi signal\_transduction \* 1e-135 GDI1\_YEAST SECRETORY PATHWAY GDP DISSOCIATION INHIBITOR G \* GDP dissociation inhibitor - fruit fly (Drosophila melanogaster) \* Guanine nucleo [RABGDIREP // RABGDI // GDI] CG4422 LD46767 30B8-30B9 ID:105F11

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

CG9878 + Tim10 unknown \* small zinc finger-like protein(aa) \* small zinc finger-like protein(aa) \* small zinc finger-like protein(aa) \* 5e-10 hypothetical protein YHR004c-a CG9878 LD46744 57F8-57F8 dup:2/2 ID:105F7

CG12054 + nucleic\_acid\_binding \* 2e-08 SFP1 \* 3e-06 zinc-finger protein Pur-1 - mouse \* 3e-06 MAZ \* 3e-06 serum amyloid A-activating factor SAF-8 [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG12054 LD46863 100B9-100B9 dup:1/2 ID:105G10

CG3305 + structural\_protein \* CG3305 LD46816 39E2-39E2 ID:105G3

CG6092 + Dak1 adenylate\_kinase \* 1e-42 UMPK\_YEAST URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) \* 3e-55 predicted using Genefinder; Similarity to Pig UMP-CMP kin [ADENYLATE\_KINASE // adenylatekinase // ] CG609 LD46840 96F12-96F12 ID:105G6

CG7099 + chaperone \* TFIIC alpha subunit(aa) \* 1e-07 precursor TRG1 protein \* 6e-17 D-ERp60=protein disulphide isomerase isoform/multifunctional endoplasmic retic \* 2e- CG7099 34B6-34B6 ID:105G9

CG6838 + transporter \* 3e-26 GLO3 \* 4e-23 putative ARF1 GTPase activating protein \* 1e-79 YQP4\_CAEEL HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III ( \* 3e-09 ADP- [ArfGap // ZF\_GCS // REVINTRACTNG] CG6838 LD46935 79F2-79F2 ID:105H4

CG5954 + l(3)mbt transcription\_factor \* tumor-supressor(aa) \* DMMBT163 l(3)mbt \* tumor-supressor \* 2e-18 predicted using Genefinder; cDNA EST yk292d9.5 comes from this gen [NLS\_BP] CG5954 LD46950 97F4-97F4 ID:105H7

CG8320 + CG8320 ID:105H9

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

CG16705 + endopeptidase \* DMEAST\_4 ea \* zgr;Try \* SERINE PROTEASE EASTER PRECURSOR(aa) \* 5e-24 PRTC\_MOUSE VITAMIN-K DEPENDENT PROTEIN C PRECURSOR (AUTOPROTHROMBIN IIA) (A[trypsin // CHYMOTRYPSIN // TRYPSIN\_SE] CG16705 LD47115 97D8-97D8 dup:1/2 ID:106A7

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

CG5055 + baz ion\_channel \* BLASTX 4.2E-06 Human super cysteine rich protein mRNA, partial cds.(dna) \* Bazooka protein(aa) \* baz \* 6e-07 similar to lethal(1) discs large-1 tum [PDZ // PRO\_RICH // ATP\_GTP\_A] CG5055 LD47216 15E1-15E5 dup:2/3 ID:106B4

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

CG10595 + motor\_protein \* DMMHC95F Mhc95F \* myosin-A(aa) \* 1e-65 MYS2\_YEAST MYOSIN-2 ISOFORM myosin MYO2 - yeast (Saccharo \* 2e-68 myosin V [myosin\_head // MYOSINHEAVY // ATP\_GTP\_A] CG10595 LD47348 29D1-29D1 ID:106C4

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

+ unknown \* C26E6.5 gene product(aa) \* 1e-36 C9 \* 2e-38 C9 \* [SPRY\_DOMAIN // WD\_REPEATS // GAMMA\_CARB]

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

CG4037 + DNA\_binding \* [NLS\_BP] CG4037 LD47433 49F8-49F9 ID:106D5

+ Gs1 enzyme \* glutamate-ammonia ligase (glutamine synthase)(aa) \* GLUTAMINE SYNTHETASE 2, CYTOPLASMIC (GLUTAMATE--AMMONIA LIGASE 2)(aa) \* predicted using Genefind [GLNA\_1 // gln-synt // GLNA\_ATP] CG2718 LD47536 21B-21B dup:4/4 ID:106E11

CG2718 + 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

CG12759 + signal\_transduction \* 1e-71 YG4C\_YEAST HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 \* 7e-09 Lis1 homolog \* 8e-08 YKY4\_CAEEL HYPOTHETICAL[GPROTEINBRPT // WD40\_REGION // WD\_REPEA]

CG11887 CG11887 LD47515 47B1-47B1 dup:3/3 ID:106E6

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

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

+ peptidase \* VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR(aa) \* Probable serine-type carboxypeptidase (EC 3.4.16.1); Ybr139wp(aa) \* Similarity to Human lysosomal pro [CARBOXYPEPT\_SER\_SER // CARBOXYPEPT\_SER\_] CG4572 LD47549 92B6-92B6 ID:106F2

CG4572 CG13852 + unknown \* CG13852 LD47553 96E1-96E1 ID:106F5

+ 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 10A6-10A6 dup:2/2 ID:106F6

CG1453 + 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

CG5632 + stg protein\_tyrosine\_phosphatase \* DMCDC25\_2 stg \* 3e-21 MPIP\_YEAST M-PHASE INDUCER PHOSPHATASE (MITOSIS INITIATION PROTEIN MIH1) (MITOT \* cdc25 protein - fruit fly (D[Rhodanese // RHODANESE // MPIPHPHTASE] CG1395 LD47579 99A5-99A6 dup:3/3 ID:106F9

CG1395 + motor\_protein \* 2e-11 C15H9.4 gene product \* 8e-43 protein \* protein \* chromosome X open reading frame TEX28 [ANTIFREEZEI] CG1021 LD47668 84A4-84A4 ID:106G10

CG1021 + 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

CG4920 + unknown \* 3e-13 protein phosphatase 1, regulatory subunit FB19 prot \* 7e-13 putative protein phosphatase nuclear targetin subunit \* [NLS\_BP] CG4124 LD47649 21E3-21D3 dup:1/3 ID:106G8

CG4124

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
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
CG4768	+ unknown * [NLS_BP] CG4768 LD47733 15A5-15A6 dup:1/2 ID:106H7
CG4649	+ Sodh-2 enzyme * Sodh-1 * sorbitol dehydrogenase(aa) * 2e-76 DHSO_YEAST SORBITOL DEHYDROGENASE (L-IDITOL 2-DEHYDROGENASE) * 1e-100 similar to sorbitol dehydrogenase [adh_zinc // ADH_ZINC // NAD_BINDING] CG4649 LD47736 86C7-86C7 ID:106H8
CG6692	+ Cp1 endopeptidase * cysteine proteinase cysteine * 1e-99 predicted using Genefinder; similar to cathepsin-like protease; cD * 1e-99 CATL_MOUSE CATHEPSIN L PRECURSOR (MA [THIOL_PROTEASE_CYS // PAPAIN // Peptida] CG6692 50C20-50C20 dup:2/3 ID:107A7
CG18543	+ unknown * CG18543 LD47919 66C12-66C12 ID:107B1
CG11181	+ cup unknown * cup * cup * cup * 1e-113 inserted at base 5' end of P element Inverse PCR [PRO_RICH // NLS_BP] CG11181 LD47924 26F3-26F5 dup:2/2 ID:107B2
CG7899	+ 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
CG3800	+ unknown * 5e-20 YNZ5_YEAST HYPOTHETICAL 17.1 KD PROTEIN IN SIP3-MRPL30 INTERGENIC REGION * 3e-12 RN helicase * 2e-25 cellular nucleic acid binding protein cl [ZF_CCHC // zf-CCHC] CG3800 LD48005 59B6-59B6 ID:107C1
CG1236	+ enzyme * CtBP * Ygl185cp(aa) * C-terminal binding protein(aa) * 5e-31 YN14_YEAST HYPOTHETICAL 38.8 KD PROTEIN IN MET2-SEC2 INTERGENIC REGION [D_2_HYDROXYACID_DH_3 // 2-Hacid_DH] CG1236 LD48009 83C1-83C1 dup:2/2 ID:107C3
CG9362	+ enzyme * MALEYLACETOACETATE ISOMERASE (MAAI)(aa) * glutathione transferase zeta 1(aa) * similar to glutathione S transferase(aa) * 9e-06 glutathione transfer [GST] CG9362 LD48010 85D18-85D18 ID:107C4
CG5026	+ 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
CG3722	+ shg cell_adhesion * DMDACHSOU_2 ds * EPITHELIAL-CADHERIN PRECURSOR (E-CADHERIN) (LIVER CELL ADHESION MOLECULE) (L-CAM)(aa) * DE-cadherin(aa) * DMDEC_1 shg [EGF_1 // EGF_2 // LAM_G_DOMAIN // Cadhe] CG3722 LP01248 57B19-57B20 ID:107D10
CG12237	+ unknown * 8e-24 putative phosphatase * * CG12237 LP01149 18D10-18D10 ID:107D4
CG4837	+ enzyme * 1e-110 ecto-5'-nucleotidase * 1e-109 5' nucleotidase (CD73) 5'-NUCLEOTID * 1e-143 putative 5'-nucleotidase * ecto-5'-nucleotidase [PHOSPHO_ESTER // 5_nucleotidase // 5_NU] CG4837 LP01187 54C7-54C7 ID:107D6
CG12104	+ unknown * 4e-11 protein * protein * CAGF9 * [HMG // HMG_box] CG12104 LP01188 62A-62A ID:107D7
CG6608	+ transporter * 9e-23 probable membrane protein YPR011c - yeast (Saccharomyces cerevisiae) * 2e-07 colt * 2e-39 Similar to mitochondrial carrier protein * 6e-15 bra [mito_carr // MITOCARRIER // MITOCH_CARR] CG6608 LP01207 86C7-86C7 ID:107D8
CG4664	+ CG4664 dup:2/2 ID:107E12



CG1153 + unknown \* CG1153 LP01348 83E2-83E2 dup:2/2 ID:107E8

CG9682 + unknown \* CG9682 LP01629 99E5-99E5 dup:3/4 ID:107F10

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

CG14205 + transmembrane\_receptor \* 2e-08 /match=(desc: \* 6e-55 predicted using Genefinder \* No definition line found \* predicted using Genefinder CG14205 LP01839 18D7-18D7 ID:107G10

CG11650 + Lcp1 structural\_protein \* 9e-53 CLP1\_DROME LARVAL CUTICLE PROTEIN I PRECURSOR cuticle prot \* 1e-35 larval cuticle protein 1, LCP1=Lcp1 gene product {Y allele} miranda \* 4e-53 [CUTICLE // insect\_cuticle] CG11650 LP01670 44C1-44C1 ID:107G

CG17367 + Lnk signal\_transduction \* 3e-08 corkscrew protein 4A \* 5e-61 Pro-rich, PH, SH2 domain-containing signaling mediator \* 9e-63 hypothetical protein [SH2DOMAIN // SH2 // PH\_DOMAIN] CG17367 LP01675 96F7-96F ID:107G3

CG12311 + EG:34F3.7 enzyme \* DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 1(aa) \* BLASTX 2.9E-25 PMT4|Mannosyltransferase (dolichyl phosphate-D-mannose:protein O-D-ma CG12311 LP01681 1C2-1C2 ID:107G4

CG10530 + Lcp65Ag1structural\_protein \* Lcp65Ag1 \* 3e-44 cuticle protein LCP65Ag1 cuticle \* 1e-30 cuticle homolog \* CU15\_MANSE CUTICLE PROTEIN CP14.6 PRECURSOR (MSCP14.6) cut [CUTICLE // insect\_cuticle] CG10530 LP01749 65A-65A ID:107G7

CG12321 + motor\_protein \* 6e-23 ARP5\_YEAST ACTIN-LIKE PROTEIN ARP5 probable nuclear pro \* 2e-12 ACTU\_DROME ACTIN-LIKE PROTEIN 13E actin-related protein \* 6e-11 similar to Act CG12321 LP02120 90E6-90E6 ID:107H11

CG8288 + 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

CG8242 + transcription\_factor \* LIM-domain protein LMP-1(aa) \* 6e-06 LRG1 \* 7e-15 PINCH \* 1e-18 UN97\_CAEEL HOMEBOX PROTEIN UNC-97 contains two LIM domain [LIM\_DOMAIN\_1 // LIM // LIM\_DOMAIN\_2] CG8242 LP02021 52C7-52C7 dup:3/3 ID:107H6

CG18179 + unknown \* CG18179 LP02275 67B-67B ID:108A4

CG13388 + Akap200 signal\_transduction \* [PRO\_RICH // NLS\_BP] CG13388 29C1-29C3 dup:1/2 ID:108A9

CG18317 + unknown \* CG18317 LP02521 22B1-22F3 ID:108B1

CG15818 + ligand\_binding\_or\_carrier \* 9e-14 accessory gland protein Acp29AB \* 1e-07 coded for by C. elegans cDNA CEESH64R; coded for by C. elegans cDNA CEMSH13F; co \* 8e-06 MABA\_MOUSE MA [lectin\_c // C\_TYPE\_LECTIN\_2] CG15818 LP02603 27F6-27F6 ID:108B6

CG10475 + endopeptidase serine proteinase (EC 3.4.21.-) 2 precursor - fruit fly CHYMOTRYPSIN,TRYPSIN\_CATAL, TRYPSIN\_SER,] CG10475 ID:108C1

CG8773 + peptidase \* 1e-109 AAP1\_YEAST ALANINE/ARGININE AMINOPEPTIDASE aminopeptidase \* 1e-121 F49E8.3 gene product \* 1e-175 AMPE\_MOUSE GLUTAMYL AMINOPEPTIDASE (EAP) (AM [ALADIPTASE // Peptidase\_M1 // ZINC\_PROT] CG8773 LP02833 87E5-87E5 ID:108C3

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

CG4799 + ligand\_binding\_or\_carrier \* Pen \* 1e-107 IMA1\_YEAST IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (SERINE-RICH RNA P \* overgrown hematopoietic organs-31 tumor suppressor O [ARM\_REPEAT // Armadillo\_seg] CG4799

LP03126 31A1-31A1 ID:108D10  
 CG13330 + unknown \* [NLS\_BP] CG13330 50B2-50B2 dup:1/2 ID:108D11  
 + Ald enzyme \* plastidic aldolase(aa) \* ALDOLASE-RELATED PROTEIN(aa) \* DMALD\_10 Ald \* 1e-118 similar to Fructose-bisphosphate aldolase class-I; cDNA EST yk252e [glycolytic\_enzy // ALDOLASE\_CLASS\_I // ] CG6058 LP03138 97A6-97A6 dup:4/4 ID:108D12  
 CG6058 + lqf unknown \* EH domain binding protein epsin 2(aa) \* mitotic phosphoprotein 90(aa) \* 1e-31 hypothetical protein YDL161w - yeast (Saccharomyces cerevisiae) \* 1e- [ENTH] CG8532 LP03068 66A-66A3 dup:2/2 ID:108D4  
 CG8532 + protein\_kinase \* DMCDK46\_3 Cdk4/6 \* DMCDK5\_3 Cdk5 \* SNF1A \* DMMAPKIN\_4 rI [LDLRA\_2 // RECEPTOR\_TYR\_KIN\_II // PROTE] CG8250 LP03070 53C10-53C11 ID:108D5  
 CG8250 + enzyme \* hypothetical protein - human(aa) \* putative ubiquitin ligase(aa) \* putative ubiquitin transferase(aa) \* hect-domain-containing protein, containing k [HECT\_DOMAIN // HECT // CYTOCHROME\_C] CG3356 LP03102 60B11-60B11 ID:108D6  
 CG3356 + protein\_kinase \* SERINE/THREONINE-PROTEIN KINASE UNC-51(aa) \* 5e-35 APG1\_YEAST AUTOPHAGY SERINE/THREONINE-PROTEIN KINASE APG1 \* 3e-24 p90 ribosomal S6 kinase \* [PROTEIN\_KINASE\_ST // TYRKINASE // PROTE] CG10967 LP03175 69E1-69E2 dup:2/2 ID:108E3  
 CG10967 + unknown \* predicted using Genefinder; similar to GNS1/SUR4 family; cDNA EST comes from this gene(aa) \* CGI-88 protein(aa) \* 9e-15 SUR4\_YEAST SUR4 PROTEIN (SRE CG5326 LP03255 94B5-94B5 dup:2/2 ID:108E4  
 CG5326 + caup transcription\_factor \* DMCAUP\_2 caup \* 2e-07 CUP9\_YEAST HOMEBOX PROTEIN CUP9 copper homeostasis pro \* CAUP\_DROME HOMEBOX PROTEIN CAUPOLICAN caupo \* 2e-24 IRXH\_[HOMEBOX\_1 // homeobox // HOMEBOX\_2] CG10605 LP03275 69C9-69C11 dup:2/2 ID:108E8  
 CG10605 + 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  
 CG13397 + enzyme \* hydroxysteroid (17-beta) dehydrogenase 4(aa) \* peroxisomal multifunctional beta-oxidation protein; Fox2p(aa) \* ESTRADIOL BETA-DEHYDROGENASE (17-BETA [GDHRDH // adh\_short // ADH\_SHORT // THI] CG3415 LP03478 14B11-14B1 dup:2/2 ID:108F6  
 CG3415 + transcription\_factor \* 3e-09 similar to X box DNA binding protein-1; cDNA EST comes \* 2e-09 X box binding protein-1; XBP \* 8e-11 TREB protein \* 5e-12 hepatocarcinogenesi [B\_ZIP // bZIP // NLS\_BP] CG9415 LP03921 57C3-57C3 dup:2/3 ID:108G12  
 CG9415 + motor\_protein \* 1e-06 TRFA \*\* CG6234 LP04345 87C6-87C6 dup:1/2 ID:108H11  
 CG6234 + structural\_protein \* peritrophin-44(aa) \* peritrophin-48a precursor(aa) \* peritrophin-95 precursor(aa) \* insect intestinal mucin IIM14(aa) CG7290 LP03990 77A-77A ID:108H4  
 CG7290 + unknown \* CG11169 LP04006 60A1-60A2 ID:108H6  
 CG11169 + 6-phosphofructo-2-kinase enzyme \* 6-phosphofructo 2-kinase/fructose 2,6-bisphosphatase long form(aa) \* 1e-105 F26\_YEAST FRUCTOSE-2,6-BISPHOSPHATASE fructose-2,6-bisp \* 1[6PFRUCTKNASE // PGAM // PG\_MUTASE // IG] CG3400 LP04008 18D1-18D1 dup:4/4 ID:108H7  
 CG3400 + kst actin\_binding \* DMBHSPEC kst \* beta-heavy-spectrin(aa) \* SPCA\_DROME SPECTRIN ALPHA CHAIN spectrin alpha chain - fr \* Similar to spectrin beta chain; coded for [SPECTRINPH // spectrin // CH\_DOMAIN // ] CG12008 LP04011 63C5-63D dup:4/5 ID:108H8  
 CG12008 + unknown CG14766 LP04033 ID:108H9  
 CG14766

+ 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  
 CG3628  
 + unknown \* CG9812 LP04417 59D10-59D11 dup:1/2 ID:109A2  
 CG9812  
 + ligand\_binding\_or\_carrier \* ecdysone-induced membrane protein IMP-E3 - fruit fly (*Drosophila melanogaster*)(aa) \* \*  
 CG2723 LP04438 84E6-84E6 ID:109A3  
 CG2723  
 + unknown \* similar to C. elegans CEES08F encoded by GenBank Accession Number \* No definition line found(aa) \* CGI-2' protein(aa) \* CG8031 LP04475 87D9-87D9 ID:109A6  
 CG8031  
 CG10497  
 + CG10497 dup:1/2 ID:109B5  
 + enzyme \* lipoamide dehydrogenase(aa) \* 1e-157 DLDH\_YEAST DIHYDROLIPOAMIDE DEHYDROGENASE PRECURSOR dihydr \* 7e-19 GSHR\_DROME GLUTATHIONE REDUCTASE (GR) (GRAS [HGRDTASE // FADPNR // pyr\_redox // PYRI] CG743( LP04889 75A4-75A4 ID:109B9  
 CG7430  
 + enzyme \* beta-glucosidase(aa) \* cardenolide 16-O-glucosylhydrolase(aa) \* lactase phlorizinhydrolase(aa) \* beta-galactosidase (EC 3.2.1.23) / glycosylceramidase [GLHYDRLASE1 // Glyco\_hydro\_1 // GLYCOSY] CG9701 LP05116 73B5-73B5 ID:109C4  
 CG9701  
 + Neurotactin cell adhesion axon, ocellar nerve, ventral nerve cord CARBOXYLESTERASE\_B\_2, COesterase, ESTERA] CG9704 LP05519 ID:109D11  
 CG9704  
 + sba unknown \* DMTF125\_2 Tf125 \* type I(aa) \* [MBD] CG13598 LP05532 95C9-95C11 ID:109D12  
 CG13598  
 CG7953  
 + BG:DS00941.14 unknown \* CG7953 LP05733 34D4-34D4 dup:2/2 ID:109E10  
 + 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  
 CG9699  
 + enzyme \* MEMBRANE-BOUND ALKALINE PHOSPHATASE PRECURSOR (M-ALP)(aa) \* DMALKPHOS\_2 Aph-4 \* 8e-26 repressible alkaline phosphatase (EC 3.1.3.1) \* 9e-78 alkaline [ALKPHPTASE // alk\_phosphatase] CG5656 LP05865 78D5-78D5 dup:2/2 ID:109F4  
 CG5656  
 CG9795  
 + unknown \* CG9795 LP05867 82A5-82A5 dup:2/2 ID:109F5  
 + unknown \* 6e-35 C09B9.3 gene product \* 5e-16 bestrophin homolog \* 1e-106 vitelliform macular dystrophy (Best disease, bestrophin) \* 2e-48 RFP family member; t [Worm\_family\_8] CG6264 LP05915 85F13-85F14 dup:1/2 ID:109F6  
 CG6264  
 CG5770  
 + unknown \* CG5770 LP06072 55B-55B ID:109G1  
 CG5770  
 CG6968  
 + unknown \* [NLS\_BP] CG6968 LP06178 78D-78D dup:1/3 ID:109G3  
 CG6968  
 CG14681  
 + unknown \* 1e-08 H06A10.1 \* 1E-168\* CG14681 LP06211 86C2-86C2 ID:109G4  
 + Ag5r unknown \* antigen 5-related protein(aa) \* Ag5r \* 1e-156 antigen 5-related \* 6e-33 antigen 5-related protein CG9538 LP06338 12F5-12F5 ID:109G8  
 CG9538  
 + unknown \* coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA/CEMSE18F; coded for by C. elegans cDNA yk [LAMNOPPTDASE // Peptidase\_M17] CG6197 LP06925 50B9-50B9 dup:2/3 ID:109H11  
 CG6197  
 + 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  
 CG7702

CG8381 + enzyme \* 3e-12 K03C7.1 gene product \* 3e-13 DNA-directed RNA polymerase (EC 2.7.7.6) II large chain - mouse (M12 \* 2e-09 elastic titin \* 8e-10 proline-rich p [ADH\_SHORT] CG8381 LP06813 50E4-50E5 dup:1/2 ID:109H9

CG9453 + serpin \* 2e-44 Similar to serine protease inhibitor \* 6e-55 NEUS\_MOUSE NEUROSERPIN PRECURSOR (PROTEASE INHIBITOR 17) \* 1e-54 protease inhibitor (neuroserpin) [serpin // ER\_TARGET] CG9453 SD01756 42C8-42C8 dup:2/2 ID:113B2 + LanB2 cell\_adhesion \* DMLAMB01\_2 LanB2 \* LAMININ-LIKE PROTEIN C54D1.5 PRECURSOR(aa) \* LAMININ GAMMA-1 CHAIN PRECURSOR (LAMININ B2 CHAIN)(aa) \* 2e-06 putative [ADH\_ZINC // laminin\_B // laminin\_EGF //] CG3322 SD01934 67B-67B ID:113C10

CG3322 + CG4578 dup:2/2 ID:113D11

CG4578 + unknown CG13323 ID:113D4

CG13323 + unknown \* coded for by C. elegans cDNA yk61f1.3; coded for by C. elegans cDNA yk109h8.3; coded for by C. elegans cDNA CEESX42F; coded for by C. elegans cDNA CG8576 SD02002 65F5-65F5 ID:113D5

CG8576 + enzyme \* 5e-16 YM71\_YEAST HYPOTHETICAL OXIDOREDUCTASE IN MRPL44-MTF1 INTERGENIC REGION \* 2e-12 antennal-specific short-chain dehydrogenase/reductase \* 2e-64 [adh\_short\_C2 // GDHRDH // adh\_short //] CG10672 SD02021 64C12-64C12 dup:2/2 ID:113D8

CG10672 + 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

CG9437 + motor\_protein \* contains similarity to ATP synthase subunit B(aa) \* Segregation of mitotic chromosomes (SMC1, yeast human homolog of(aa) \* 1e-124 SMC1\_YEAST CHROMOS [DA\_BOX // NLS\_BP // ATP\_GTP\_A] CG6057 SD02122 95D5-95D5 dup:2/2 ID:113E11

CG6057 + unknown \* UNKNOWN; PRC1(aa) \* protein regulating cytokinesis 1; PRC1 \* [G\_PROTEIN\_GAMMA] CG1655 SD02150 9F5-9F5 ID:113F5

CG1655 + 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

CG17938 + fog unknown \* fog \* FOLDED GASTRULATION PROTEIN PRECURSOR(aa) \* fog \* folded gastrulation (fog) precursor - fruit fly (Drosophila melanogaster) CG9559 SD02223 20A4-20A5 ID:113G3

CG9559 + brk transcription\_factor \* putative transcription factor(aa) \* CG9653 SD02279 7A4-7A4 dup:3/6 ID:113H5

CG9653 + 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 10C5-10C6 ID:113H6

CG1763 + 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 5A8-5A8 dup:1/3 ID:113H7

CG3208 + Prosalpha1 unknown \* endopeptidase multicatalytic endopeptidase ) cell 26S proteasome ) map\_position:54B3-5 \* 20S proteasome subunit alpha1(aa) \* endopeptidase multicatalytic CG18495 SD02332 43F-43F dup:2/2 ID:114A1

CG18495 + enzyme \* LCFACAS3; \* LONG-CHAIN-FATTY-ACID--COA LIGASE (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4)(aa) \* 1e-82 LCF4\_YEAST LONG-CHAIN-FATTY-ACID--COA LIGASE ( [AMP\_BINDING // AMPBINDING // AMP-bindin] CG8732

SD02373 44D4-44D ID:114A6

CG7839 + 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

CG8980 + enzyme\_inhibitor \* nuclear inhibitor of phosphatase-1(aa) \* similar to forkhead-associated (FHA) domains (Pfam: FHA.hmm score: 28.36)(aa) \* NIPP-1, nuclear inhibitor [FHA\_DOMAIN // FHA] CG8980 SD02428 53E10-53E11 ID:114B3

CG9325 + hts actin\_binding \* adducin homolog - fruit fly (Drosophila melanogaster)(aa) \* similar to alpha-adducins(aa) \* DMADDLIKE\_3 hts \* adducin-like(aa) [Aldolase\_II] CG9325 SD02552 56D5-56D6 ID:114C12

CG7434 + Rpl22 ribosomal\_protein Ribosomal protein L22 60S subunit ANTIFREEZEI CG7434 SD02522 ID:114C6

+ Pros26.4 \* Pros26.4 \* 1e-177 PRS4\_YEAST 26S PROTEASE REGULATORY SUBUNIT HOMOLOG (TAT-BINDING HOMOLOG) \* PRS4\_DROME 26S PROTEASE REGULATORY SUBUNIT (P26S4) P [AAA // NLS\_BP // ATP\_GTP\_A] CG5289 95C-95C dup:2/3 ID:114E3

CG5289 + 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 + unknown \* 2e-11 hypothetical protein YLR201c - yeast (Saccharomyces cerevisiae) (U1 \* 1e-39 Unknown gene product \* 1e-21 hypothetical protein \* inserted at ba [CRYSTALLIN\_BETAGAMMA] CG1952 SD02734 43E9-43E9 dup:2/2 ID:114F1

CG1952 + signal\_transduction \* ADP-ribosylation GTPase activating protein(aa) \* differentiation enhancing factor 1(aa) \* 3e-09 hypothetical protein YDR524c - yeast (Sacc[ANK\_REP // GRAM\_POS\_ANCHORING // ArfGap] CG2226 SD02805 44A6-44A6 dup:2/2 ID:114F10

CG2226 + unknown \* 4e-15 MTRP\_MOUSE GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP \* 6e-15 MTRP\_HUMAN GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP \* \* CG8575 SD02746 44D8-44D8 dup:1/2 ID:114F2

CG8575 + unknown \* 8e-31 protein \* \* CG10289 SD02803 65A-65A ID:114F9

CG10289 + Hsf transcription\_factor \* DMHSPHEX\_3 Hsf \* 2e-23 HSF\_YEAST HEAT SHOCK FACTOR PROTEIN (HSF) (HEAT SHOCK TRANSCRIPTION FACTOR) (HST \* HSF\_DROME HEAT SHOCK FACTOR PROTEIN (HSF) [HSFDOMAIN // HSF\_ETS // HSF\_DNA-bind] CG5748 SD02833 55B5-55B5 ID:114G2

CG5748 + Vha16 enzyme \* DMCSUDUC\_5 Vha16 \* VACUOLAR ATP SYNTHASE KD PROTEOLIPID SUBUNIT (DUCTIN)(aa) \* 5e-56 VATL\_YEAST VACUOLAR ATP SYNTHASE KD PROTEOLIPID SUBUNIT \* 1e-53 [VACATPASE // ATP-synt\_C] CG3161 SD02875 42B2-42B2 dup:2/4 ID:114G8

CG3161 + enzyme \* LONG-CHAIN-FATTY-ACID--COA LIGASE (LONG-CHAIN ACYL-COA SYNTHETASE 2) (LACS 2)(aa) \* 1e-83 LCF2\_YEAST LONG-CHAIN-FATTY-ACID--COA LIGASE (LONG-CHAIN A [AMP\_BINDING // AMPBINDING // AMP-binding] CG3961 SD02971 75E2-75E2 ID:114H10

CG3961 + \* predicted using Genefinder; similar to thrombospondin like; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST yk195c9.3 comes [TSP1 // ig // NLS\_BP // tsp\_1 // ATP\_GT] CG2131 39E7-39F1 dup:1/2 ID:115A3

CG2131 + Cyp12a4 cytochrome\_P450 \* CYTOCHROME P450 CYP12A2(aa) \* 3e-17 lanosterol 14-demethylase cytochrome P450 \* 5e-24 cytochrome P450 cytochrome P4 \* 4e-20 YS45\_CAEEL PUTATIVE CYTO [EP450II // p450 // P450 // MITP450 // C] CG6042 SD03227 91F3-91F4 ID:115D8

CG6042 + blow unknown \* 1E-143 blown fuse\* CG1363 SD03683 dup:2/2 ID:116A10.2

CG1363 + unknown CG12004 SD03655 ID:116A6

CG12004

CG18409 + CG18409 SD03761 dup:2/2 ID:116B5.2

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

CG2694 + EG:100G10.8 unknown \* DMC95B7 \* \* by content; by match; LD Drosophila melanogaster...(aa) \* by content; 1-meth CG2694 SD03887 3B5-3B5 dup:1/2 ID:116C11

CG11120 + chaperone \* orf 48(aa) \* NF-180 - sea lamprey(aa) \* 2e-06 strong similarity to the SNF2/RAD54 family of helicases; partial CDS \* K2 [NLS\_BP] CG11120 SD03844 96B8-96B9 dup:2/3 ID:116C3.2

CG10192 + translation\_factor CG10192 SD03848 ID:116C4

CG1902 + CRAL\_TRIO ligand\_binding\_or\_carrier CG1902 SD04017 dup:2/2 ID:116E8

CG10712 + translation\_factor \* 3e-06 Pdd1p Pdd1p thermoph \* \* [chromo // CHROMO\_2] CG10712 79F5-79F5 dup:3/4 ID:116F1

CG9344 + RNA\_binding CG9344 ID:116F8

CG7649 + CG7649 SD04095 dup:2/3 ID:116G1.2

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

+ alpha-Spec actin\_binding \* DMLETHAL\_2 Actn \* DMSPCA\_2 agr;-Spec \* SPECTRIN ALPHA CHAIN(aa) \* 3e-15 USO1\_YEAST INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1 ( [spectrin // SPEC\_REPEAT // EF\_HAND // S] CG1977 SD04436 62B-62B dup:2/7 ID:117C8

CG1977 + G\_protein\_linked\_receptor \* CL3BC(aa) \* protein(aa) \* 4e-20 similar to G-protein coupled receptor protein; cDNA EST \* 2e-14 EMR1\_MOUSE CELL SURFACE GLYCOPROTEIN[7tm\_2 // RECEPTOR\_PKD // GAL\_LLECTIN // ] CG8639 SD04590 44D2-44D2 dup:5/5 ID:117E6

CG8639 + defense/immunity\_protein \* tag7(aa) \* 2e-20 peptidoglycan recognition protein precursor \* 4e-20 TNF superfamily, member (LTB)-like (peptidoglycan recognition \* 2e-19 peptidogl [HTH\_ARAC\_FAMILY\_1] CG4432 SD04722 67A8-67A9 dup:2/2 ID:117F12

CG4432 + CG8151 SD04652 ID:117F3

CG8151 + CG8151 SD04652 ID:117F3

CG6006 + Orct transporter Orct Organic cation transporter 2 CG6006 SD04753 ID:117G9

CG18061 + CG18061 SD04793 ID:117H2

+ unknown \* BLASTX 7.0E-38 YLR386W|Protein of unknown function(dna) \* BLASTX 7.0E-38 YLR386W|Protein of unknown function(dna) \* BLASTX 7.0E-38 YLR386W|Protein o CG5608 SD04925 87C-87C dup:2/2 ID:118A11

CG5608 + no blast hits pioneer protein? CG14800 SD04906 dup:1/2 ID:118A8

CG14800 + lic protein\_kinase (licorn) stress activated MAP kinase kinase 3 [Drosophila melanogaster] PROTEIN\_KINASE\_DOM, PROTEIN\_KINASE\_ST, p] CG12244 SD04985 ID:118B12

CG12244 + Su(z)12 a novel gene that affects zeste, Pc-G and PRE mediated silencing NLS\_BP, PRO\_RICH CG8013 SD04959 ID:118B5

CG8013 + enzyme CG1787 SD05059 ID:118C6

CG1787 + 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 ID:118D10

CG4974 + enzyme \* protease(aa) \* 1e-95 TyB protein - yeast (Saccharomyces cerevisiae) retrotransposon Ty3-2 \* 2e-95 gag, pol anc

CG2485

	env protein precursor * hypothetical [rvt // NLS_BP] CG2485 SD05236 10B1-10B1 dup:4/7 ID:118D11
none	+ none SD05284 ID:118E10
CG12210	+ transporter CG12210 SD05285 dup:2/2 ID:118E11
CG7635	+ unknown stomatin-like protein Band_7, STOMATIN CG7635 SD05291 dup:3/3 ID:118E12
CG5841	+ cytoskeletal_structural_protein homolog of human KIAA1323 protein, similar to ankyrin proteins ANK_REP, ANK_REP_REGION, ZF_RING, ZF_ZZ,] CG5841 SD05267 dup:3/3 ID:118E5
CG17596	+ S6klI protein_kinase ribosomal protein S6 kinase PROTEIN-KINASE-ATP, PROTEIN-KINASE-ST, T] CG17596 SD05277 dup:3/3 ID:118E6
CG8060	+ CG8060 SD05384 dup:2/2 ID:118F10.2
CG7100	+ CadN cell_adhesion * G-cadherin(aa) * CadN * DN-cadherin * 8e-11 contains similarity to multiple cadherin-type repeats [EGF_1 // EGF // EGF_2 // LAM_G_DOMAIN /] CG7100 SD05464 36C8-36D dup:2/2 ID:118G10
CG13907	+ transporter * 1e-14 YNM5_YEAST HYPOTHETICAL 73.8 KD PROTEIN IN SPC98-TOM70 INTERGENIC REGION * 1e-61 /match=(desc:; /ma * 6e-43 K05B2.5 gene product * 3e-26 MOT1_ CG13907 SD05443 61E1-61E1 dup:1/3 ID:118G6
CG5887	+ Fad enzyme * Fad * 1e-51 delta-9 fatty acid desaturase * fatty acid desaturase * 4e-89 predicted using Genefinder; Similarity to Rat acyl-CoA desaturase [Desaturase // FACDDSATRASE] CG5887 SD05462 87C-87C dup:2/5 ID:118G9.2
CG13384	+ transporter putative amino acid transport protein AROMATIC_AA_PERMEASE_2 CG13384 SD05512 dup:2/4 ID:118H7
CG12088	+ enzyme * 3e-31 prolyl 4-hydroxylase alpha subunit * 2e-40 Similarity to Human Prolyl 4-hydroxylase alpha subunit (SW:P4HA_HU * 3e-42 P4H1_MOUSE PROLYL 4-HYDR CG12088 SD05564 99F7-99F7 dup:2/3 ID:119A3.2
CG7795	+ homology to voltage-sensitive calcium channel alpha 1 A and guanine nucleotide exchange factor DC3G CG7795 SD0557 dup:1/2 ID:119A4
CG5721	+ pioneer protein CG5721 SD05591 ID:119A7
CG12473	+ stnB stoned B, mutations affect multivesicular body, nerve terminal, synaptic vesicle Adap_comp_sub, CLATHRINADPT, PRO_RICH CG12473 SD05593 ID:119A9
CG8376	+ transcription_factor CG8376 SD05618 dup:4/5 ID:119B1.2
CG1512	+ cell_cycle_regulator * cullin 2(aa) * 5e-70 CC53_YEAST CELL DIVISION CONTROL PROTEIN (CULLIN A) * 1e-115 LI19_DROME LIN-19 HOMOLOG PROTEIN lin19 protein * 1e-14[CULLIN_2 // NLS_BP // Cullin // CULLIN_] CG1512 SD05653 39E5-39E5 dup:3/3 ID:119B10
CG5105	+ signal_transduction PLAP_MOUSE PHOSPHOLIPASE A-2-ACTIVATING PROTEIN GPROTEINBRPT, WD40, WD40_REGION, WD_REPE] CG5105 SD05646 ID:119B6
CG3696	+ 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 ID:119B7
CG2168	+ 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 // NLS] CG2168 SD05650 101F1-101F1 ID:119B8
CG7821	+ CG7821 SD05678 ID:119C2
CG17452	+ RNAS_binding homology with Drosophila dip1 (disco interacting protein) gene, a new member of the Staufen family of RNA

binding proteins CG17452 SD05690 ID:119C6

CG17437 + signal\_transduction \* AND-1 protein(aa) \* bgr;Cop \* 6e-29 Met30p \* 3e-28 Slimb [GPROTEINBRPT // GPROTEINB // WD40\_REGION] CG17437 3A8-3A8 dup:3/3 ID:119D12.2

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

CG6406 + unknown \* No definition line found(aa) \* \* CG6406 SD05904 54E7-54E7 dup:2/5 ID:119E11.2

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

CG17090 + protein\_kinase similar to serine/threonine kinases PROTEIN\_KINASE\_ATP, PROTEIN\_KINASE\_DOM, ] CG17090 SD0587 dup:4/5 ID:119E6

CG4822 + transporter \* [ABC\_TRANSPORTER // DA\_BOX] CG4822 SD05880 21B-21B dup:6/6 ID:119E7

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

CG13889 + motor\_protein \* 4e-05 unknown \* 5e-06 Similarity with drosophila MSP-300 protein (PIR acc. no. \* 2e-10 rho/rac-interacting citron kinase [PEROXIDASE\_1] CG13889 SD05919 61D4-61D4 ID:119F1

CG10080 + unknown \* protein(aa) \* 4e-83 cDNA EST comes from this gene; cDNA EST co \* CG10080 SD05932 57F5-57F5 dup:2/3 ID:119F2

CG8669 + transcription\_factor \* ATFX(aa) \* leucine-zipper protein(aa) \* 7e-05 Similarity to Human transcription factor ATF-4 (SW:ATF4\_HUMAN); cD \* 3e-09 ATF4\_MOUSE CYCLIC-AMP-DEPE[B\_ZIP // bZIP // BZIP\_BASIC // NLS\_BP] CG8669 39D2-39D2 dup:3/3 ID:119H1

CG1691 + RNA\_binding CG1691 SD07045 dup:1/3 ID:120E7.2

CG18218 + CG18218 SD07272 dup:1/4 ID:120H6.2

CG3140 + adenylate\_kinase CG3140 SD09634 dup:1/2 ID:124A9.2

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

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

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

CG18022 + cytoskeletal\_structural\_protein \* 2e-21 Similarity to N.crassa ADP/ATP carrier protein (SW:ADT\_NEUCR) \* 7e-05 TPCC\_MOUSE TROPONIN C, SLOW SKELETAL AND CARDIAC MUSCLES (TN-C) \* 4e-05 CG18022 SD10992 69B3-69B3 ID:126A10

CG2331 + TER94 endopeptidase \* 8e-87 CC48\_YEAST CELL DIVISION CONTROL PROTEIN cell divisi \* 1E-145\* 1e-118 TER1\_CAEEL TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE HOMOLOG (P97/CDC48 [ENDOLAPTASE // AAA // ATP\_GTP\_A] CG2331 GH01132 46D1-46D1 dup:1/3 ID:30A11

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



+ 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 GH01161 7D14-7D14 ID:30B3  
 + unknown \* No definition line found(aa) \* No definition line found \* H19J13.1 (AL009 \* [CRYSTALLIN\_BETAGAMMA]  
 CG3332 CG3332 GH01206 23E-23E ID:30B7  
 + 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  
 + Mer actin\_binding \* merlin \* 1e-105 coded for by C. elegans cDNA yk167f5.5; coded for by C. elegans cDNA yk130f8.5; \* 1e-  
 135 MERL\_MOUSE MERLIN (SCHWANNOMIN) merlin - mo [Band\_41 // BAND41 // ERM // ERMFAMILY] CG14228 GH01330  
 CG14228 18E1-18E1 ID:30C2  
 + enzyme \* protein kinase C-binding protein RACK7(aa) \* deformed epidermal autoregulatory factor 1(aa) \* No definition line  
 CG1815 found(aa) \* adenovirus E1A binding [PHD] CG1815 GH01331 100D4-100D4 dup:1/2 ID:30C3  
 + Aph-4 enzyme \* alkaline phosphatase(aa) \* 3e-28 repressible alkaline phosphatase (EC 3.1.3.1) \* 4e-95 PPBE\_MOUSE  
 CG1462 ALKALINE PHOSPHATASE, EMBRYONIC PRECURSOR (EAP) e [ALKALINE\_PHOSPHATASE // ALKPHPTASE // ] CG1462  
 GH01338 100B-100B dup:1/2 ID:30C5  
 + protein\_phosphatase \* 3e-41 LAR\_DROME PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (PROTEIN-  
 CG4355 TYROSINE-PHOSPHAT \* 5e-40 similar to protein-tyrosine phosphatase with [Y\_phosphatase // TYR\_PHOSPHATASE\_PTP //]  
 CG4355 GH01353 22A1-22A1 dup:1/3 ID:30C7  
 + BG:DS09217.1 unknown \* 1e-14 predicted using Genefinder; cDNA EST comes from this g \* \* CG13240 GH01660 35D6-35D6  
 CG13240 dup:2/2 ID:30E12  
 + endopeptidase \* 3e-64 cysteine proteinase cysteine \* 2e-56 predicted using Genefinder; similar to cathepsin-like protease;  
 CG4847 cD \* 1e-59 cathepsin K \* 1e-59 cathepsi[THIOL\_PROTEASE\_CYS // PAPAINE // Peptida] CG4847 GH01592 54C9-54C9 dup:3/4  
 CG6210 ID:30E3  
 + unknown \* CG6210 GH01813 68A7-68A7 ID:30G1  
 + endopeptidase \* endothelin converting enzyme-2 - bovine (fragment)(aa) \* endothelin converting enzyme-like 1(aa) \* 7e-30  
 CG14528 similar to Zinc-binding metalloprotease; cD [NEPRILYSIN // PRENYLATION // ZINC\_PROTE] CG14528 GH01940 98F-98F  
 ID:30G10  
 + endopeptidase \* HYPOTHETICAL 37.7 KD PROTEIN C08B11.7 IN CHROMOSOME II(aa) \* DMUBICTHG\_3 Uch \* BRCA1  
 CG8445 associated protein-1 (ubiquitin carboxy-terminal hydrolase)(aa) [UCH // UBCTHYDRLASE // ATP\_GTP\_A] CG8445 GH01941 52F7  
 52F7 ID:30G11  
 + I(2)efl chaperone \* similar to the small heat shock protein (HSP20) family(aa) \* DMHS09\_2 Hsp23 \* DMHSP27G\_3 Hsp27 \*  
 CG4533 HYPOTHETICAL 12.3 KD PROTEIN C14B9.1 IN CHROMOSOME [HSP20 // ACRYSTALLIN] CG4533 GH01960 59F4-59F4  
 ID:30G12  
 + endopeptidase \* DMC9D2 \* 8e-57 serine protease SER4 precursor \* 6e-12 predicted using Genefinder; similar to  
 CG8329 transmembrane receptor (r \* 2e-19 serine protease (BSP) [trypsin // CHYMOTRYPSIN // TRYPSIN\_SER ] CG8329 GH01822 67B-  
 67B ID:30G2  
 CG7415 + unknown \* dipeptidyl peptidase III(aa) \* 1e-109 hypothetical protein YOL057w - yeast (Saccharomyces cerevisiae) \* 1e-105

similar to WD domain, G-beta repeat; CG7415 GH01916 84F14-84F15 dup:1/2 ID:30G7

CG8782 + \* Contains similarity to Pfam domain: (aminotran\_3), Score=462.2, E-value=9.8e-161, N=1(aa) \* ornithine aminotransferase(aa) \* ornithine aminotransferase [aminotran\_3 // AA\_TRANSFER\_CLASS\_3] CG8782 76C1-76C2 dup:2/2 ID:30H4

CG2171 + Tpi enzyme \* Chain A, Does The His12-Lys13 Pair Play A Role In The Adaptation Of Thermophilic Tims To High Temperature ?(aa) \* DMTPIG\_2 Tpi \* TRIOSEPHOSPHATE IS [TIM] CG2171 GH02005 99E-99E dup:1/3 ID:30H5

CG4894 + Ca-alpha1D ion\_channel \* DMCA1\_2 Ca- agr;1D \* calcium channel alpha-1 subunit \* putative L-type calcium channel alpha subunit \* voltage-dependent calcium channel complex alp [NACHANNEL // CACHANNEL // THIOL\_PROTEAS] CG4894 GH02029 35F1-35F3 ID:30H9

CG4791 + structural\_protein \*/match=(desc:; /match=(desc:(aa) \* 2e-21 /match=(desc:; /ma \* 3e-16 CU1A\_TENMO LARVAL CUTICLE PROTEIN A1A (TM-A1A) (TM-LCP A1A) \* 6e-19 DMEDG84A\_3 E [CUTICLE // insect\_cuticle] CG4791 GH02089 31A1-31A1 ID:31A2

CG17814 + unknown CG17814 ID:31A5

CG15387 + CG15387 ID:31A6

CG12182 + BcDNA:GH02340 unknown \* CG12182 GH02340 62F1-62F1 ID:31B5

CG12125 + It has been mapped cytologically to 7E5--6 CG12125 GH02384 ID:31B7

CG4265 + Uch endopeptidase \* DMUBICTHG\_3 Uch \* 3e-19 UBL1\_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE YUH1 (UBIQUITIN THIOLESTERASE) \* 1e-130 UBL\_DROME UBIQUITIN CARBOXYL-TERMIN [UCH // UCH\_1 // UBCTHYDLASE] CG4265 GH02396 23D1-23D1 dup:1/2 ID:31B8

CG8790 + BcDNA:GH02431 \* 2e-48 hypothetical protein YLR348c - yeast (Saccharomyces cerevisiae) (U \* 1e-87 Oxoglutarate/malate carrier protein - Caenorhabditis elegans \* 6e-3 [mito\_carr // MITOCARRIER] CG8790 87E8-87E8 dup:1/2 ID:31C11

CG10888 + Rh3 G\_protein\_linked\_receptor \* OPSIN RH3 (INNER R7 PHOTORECEPTOR CELLS OPSIN)(aa) \* DMRH3A\_3 Rh3 \* OPS3\_DROME OPSIN RH3 (INNER R7 PHOTORECEPTOR CELLS OPSIN) \* 5e-2[GPCRRHODOPSN // OPSIN // G\_PROTEIN\_RECE] CG10888 GH02505 92C5-92C5 dup:2/2 ID:31C6

CG9090 + transporter \* phosphate transporter precursor(aa) \* MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR(aa) \* putative mitochondrial uncoupling protein(aa) \* MITOCH [mito\_carr // MITOCARRIER // RCC1\_2 // M] CG9090 GH02695 56F16-56F16 ID:31D8

CG7364 + BG:DS00797.1 unknown \* unknown protein(aa) \* 1e-113 EMP70 protein precursor - yeast (Saccharomyces cerevisiae) \* Similarity to Yeast endosomal P24A protein (SW:EM70\_YEAST CG7364 GH02822 34D1-34D1 dup:2/2 ID:31E4

CG8611 + BcDNA:GH02833 RNA\_binding \* DMBP45A\_18 Dbp45A \* pit \* 3e-64 DBP7\_YEAST ATP-DEPENDENT RNA HELICASE DBP probable purin \* 1e-58 helicase pitchoune [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

CG3200 + Reg-2 \* RHYTHMICALLY EXPRESSED GENE PROTEIN (DREG-2)(aa) \* Reg-2 \* 4e-16 YM14\_YEAST HYPOTHETICAL 35.3 KD PROTEIN IN POM152-REC114 INTERGENIC REGION \* 1e-157 [Hydrolase // HADHALOGNASE] CG3200 61C-61C dup:4/4 ID:31E8

CG1102 + BEST:GH02921 endopeptidase \* easter(aa) \* DMEAST\_4 ea \* 1e-106 EAST\_DROME SERINE PROTEASE EASTER  
 PRECURSOR serine protein \* 5e-33 KAL\_MOUSE PLASMA KALLIKREIN PRECURSOR (PLASMA P [ANTENNAPEDIA // trypsin  
 // CHYMOTRYPSIN] CG1102 GH02921 82A5-82A5 ID:31F2

CG6446 + Sema-1b unknown \* similar to semaphorin-I \* 4e-93 cDNA EST comes from this gene; cDNA EST \* 2e-81 semaphorin VIb \* 1e-6  
 UNKNOWN semaphorin F homolog [RECEPTOR\_CYTOKINES\_1 // Sema // ATP\_GTP] CG6446 GH03186 54E1-54E2 dup:1/2  
 ID:31G11

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

CG6371 + unknown \* CG6371 GH03388 88C1-88C1 ID:31H11

CG1799 + ras enzyme \* 1e-174 IMH2\_YEAST PROBABLE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP  
 DEHYDROGENASE) \* IMDH\_DROME INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHY [CBS // SNF4\_REP //  
 FMN\_ENZYMES // IMPDH] CG1799 GH03394 9E3-9E4 dup:1/3 ID:31H12

CG11958 + Cnx99A chaperone \* DMCALNEX\_3 Cnx \* 5e-51 CALX\_YEAST CALNEXIN HOMOLOG PRECURSOR calnexin homolog YA \*  
 calnexin \* 1e-117 CALX\_CAEEL CALNEXIN HOMOLOG PRECURSOR hypotheti [CALRETICULIN\_2 // calreticulin // CALRE]  
 CG11958 GH03249 99A7-99A7 dup:1/3 ID:31H2

CG6287 + enzyme \* 3-phosphoglycerate dehydrogenase(aa) \* similar to D-3-Phosphoglycerate dehydrogenase; cDNA EST comes  
 from this gene; cDNA EST comes from this gene; [2-Hacid\_DH // D\_2\_HYDROXYACID\_DH\_1 // A] CG6287 GH03305 32D5-32D5  
 ID:31H4

CG16941 + RNA\_binding \* probable splicing factor Ceprp21 - Caenorhabditis elegans(aa) \* pre-mRNA splicing factor SF3a (120 kDa  
 subunit), similar to S. cerevisiae PRP21(aa) [SURP // ubiquitin // UBIQUITIN // UBIQU] CG16941 GH03554 92C1-92C1 ID:32A12

CG12045 + structural\_protein \* 2e-05 CUP7\_DROME PUPAL CUTICLE PROTEIN EDG-78 PRECURSOR ecdyson \* 8e-06  
 CU26\_ARADI ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 12.6 (ACP 12.6) \* 2e-07 DM [CUTICLE // insect\_cuticle] CG12045  
 GH03728 100B-100B ID:32B12

CG5915 + Rab7 enzyme \* Rab7 \* 6e-61 YPT7\_YEAST GTP-BINDING PROTEIN YPT7 GTP-binding protein Y \* 1e-111 small ras-like  
 GTPase \* 6e-77 similar to ras related protein; cDNA E [ras // ATP\_GTP\_A // RASTRNSFRMNG] CG5915 GH03685 97F1-97F1  
 ID:32B6

CG3799 + BcDNA:GH03693 signal\_transduction \* contains similarity to Src homology domain (SH3) (Pfam: SH3.hmm, score: 50.59)(aa) \*  
 6e-90 contains similarity to Src homology domain [GRF\_DBL // RhoGEF // SH3 // PRO\_RICH //] CG3799 GH03693 73E1-73E1  
 dup:2/2 ID:32B7

CG7738 + CG7738 dup:2/2 ID:32C2

CG8139 + alpha-Man-II enzyme \* LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID  
 ALPHA-MANNOSIDASE)(aa) \* truncated lysosomal acid alpha-mannosidase(aa) [Glyco\_hydro\_38 // NLS\_BP] CG8139 GH03876  
 85D16-85D16 ID:32C7

CG5597 + unknown \* 7e-06 pdb|1BIH|A Chain A, Crystal Structure Of The Insect Immune Protein Hemolin: A New Domain \*  
 HEMO\_HYACE HEMOLIN PRECURSOR (P4 PROTEIN) (HEMOCYT [ig] CG5597 GH04238 60A8-60A8 dup:2/2 ID:32E10

CG8882 + 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

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

CG17259 + enzyme \* PROBABLE SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)(aa) \* SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)(aa) \* seryl-tRNA synthetase(a [tRNA-synt\_2b // TRNASYNTHSER] CG17259 GH04194 23C4-23C5 dup:2/2 ID:32E7

CG3253 + enzyme \* i-beta-1,3-N-acetylglucosaminyltransferase(aa) \* 1e-10 K09C8.4 \* 8e-16 acetylglucosaminyltransferase-like protei

CG5080 \* 5e-24 i-beta-1,3-N-acetylglucosa CG3253 GH04269 60B6-60B6 ID:32F1

+ CG5080 ID:32F10

CG5711 + Arr1 unknown \* PHOSRESTIN II (ARRESTIN A) (ARRESTIN 1)(aa) \* DMARRA\_2 Arr1 \* 1e-75 ARRB\_CAEEL PROBABLE BETA-ARRESTIN coded for by C. elegans \* 6e-74 ARRS\_MOUSE S-A [ARRESTIN // arrestin // ARRESTINS] CG5711 36E-36E dup:8/11 ID:32F7

CG12770 + unknown \* 1e-26 VP28\_YEAST VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS28 \* 3e-40 putative protei

\* 3e-76 inserted at base Both 5' and 3' ends of P elemen CG12770 GH04443 44A4-44A4 ID:32G10

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

CG7727 + Appl unknown \* DMS1C4\_1 Appl \* 2e-25 beta-amyloid homolog apl-1 - Caenorhabditis elegans beta- \* 4e-21 Alzheimer's disease amyloid beta/A4 protein homolog precursor [A4\_EXTRA // A4\_INTRA // AMYLOIDA4 // NL] CG7727 GH04413 1B7-1B8 dup:1/2 ID:32G7

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

CG17248 + n-syb transporter \* 2e-21 synaptobrevin isoform B - fruit fly (Drosophila melanogaster) (L142 \* 2e-21 SNB-1; synaptobrevin SNE 1; sy \* 6e-24 SYB2\_MOUSE SYNAPTOBREV1[SYNAPTOBREVN // SYNAPTOBREVIN // synapt] CG17248 GH04664 62A10-62A10 dup:2/2 ID:32H12

CG4070 + Tis11 DNA\_binding \* DTIS11 PROTEIN(aa) \* Tis11 \* 9e-15 hypothetical protein YDR151c - yeast (Saccharomyces cerevisiae) 5e-67 TIScc1 cc1 gene [ZF\_CCCH // zf-CCCH] CG4070 GH04518 11B14-11B16 ID:32H2

CG8206 + unknown \* 4e-07 YN50\_YEAST HYPOTHETICAL 23.5 KD PROTEIN IN RFA2-STB1 INTERGENIC REGION \* 8e-07 A\_TM021B04.14 gene product \* hypothetical protein - fission yea CG8206 GH04557 13E16-13E16 ID:32H3

CG10366 + transcription\_factor \* DMC95B7 \* D19B \* ovo \* DMSRYG1\_25 Sry- dgr; [G\_PROTEIN\_RECEPTOR // zf-C2H2 // ZINC\_F] CG10366 GH04589 37F2-37F2 ID:32H8

CG10233 + signal\_transduction \* 9e-12 hypothetical protein \* unknown \* phosphatidylinositol-4-phosphate 5-kinase isolog \* CG10233 GH04877 83A1-83A1 ID:33B12

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

CG3564 + unknown \* COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (P24A) (RNP21.4)(aa) \* 3e-21 EM24\_YEAST ENDOSOMAL P24B PROTEIN PRECURSOR (24 KD ENDOMEMBRANE PROTE [EMP24\_GP25L] CG3564 GH04989 4C4-4C4 ID:33D2

CG14724 + CoVa enzyme \* 2e-14 COX6\_YEAST CYTOCHROME C OXIDASE POLYPEPTIDE VI PRECURSOR cy \* 6e-81 cytochrome c oxidase subunit Va preprotein melanogaste \* 6e-27 predicted u CG14724 GH05011 86F10-86F11 ID:33D5

CG10472 + endopeptidase \* DMSER2\_7 Ser99Db \* 2e-45 serine proteinase (EC 3.4.21.-) precursor - fruit fly (Drosophila melanogaster) \* 9e-24 similar to peptidase family S1 (tr[trypsin // CHYMOTRYPSIN // TRYPSIN\_SER] CG10472 GH05321 65A2-65A2 dup:2/2 ID:33E11

CG6169 + unknown \* hypothetical PSU1-like protein(aa) \* similar to Bacterial mutT protein; cDNA EST yk352h11.5 comes from this gene; cDNA EST comes from this gene; c [NLS\_BP] CG6169 GH05133 72A1-72A1 dup:6/6 ID:33E3

CG18251 + Msp-300 unknown \* CG18251 GH05169 25C8-25C8 dup:2/2 ID:33E5

CG17246 + Scs-fp enzyme \* succinate dehydrogenase (ubiquinone) (EC 1.3.5.1) flavoprotein precursor, mitochondrial - bovine(aa) \* DMSUCDEHF Scs-fp \* DHSA\_YEAST SUCCINATE DEHY [FADPNR // PNDRDTASEI // FAD\_binding\_2 /] CG17246 GH05404 56D4-56D4 dup:3/3 ID:33F2

CG10151 + unknown \* [GRAM\_POS\_ANCHORING // ATP\_GTP\_A] CG10151 GH05433 51C2-51C2 ID:33F6

CG8740 + BcDNA:GH05582 motor\_protein \* [NLS\_BP] CG8740 GH05582 44E1-44E1 dup:5/6 ID:33G4

CG5867 + BcDNA:GH05536 unknown \* 0.0000002 \* 3e-06 DMRNAPER\_2 anon-3B1.2 \* \* CG5867 GH05588 34A10-34A11 ID:33G5

CG3364 + unknown \* CG3364 GH05668 42D5-42D6 ID:33G9

CG9313 + motor\_protein \* 7e-15 cytoplasmic dynein intermediate chain isoform DIC2b \* 7e-15 similar to the beta transducin family \* 3e-14 cytoplasmic dynein intermediate chain [NLS\_BP // WD40] CG9313 GH05829 57B14-57B14 ID:33H12

CG4757 + BcDNA:GH05741 enzyme \* agr;-Est10 \* 8e-48 alpha esterase \* 6e-46 ACE1\_CAEEL ACETYLCHOLINESTERASE PRECURSOR (ACHE) acetyl \* 3e-54 ACES\_MOUSE ACETYLCHOLINESTERASE PRECURSOR [CARBOXYLESTERASE\_B\_1 // ESTERASE // COE] CG4757 GH05741 86D4-86D5 ID:33H7

CG10142 + peptidase \* ANGIOTENSIN-CONVERTING ENZYME PRECURSOR, TESTIS-SPECIFIC (ACE-T) (DIPEPTIDYL CARBOXYPEPTIDASE I) (KININASE II)(aa) \* metallopeptidase(aa) \* ANGIOTEN [PEPDIPTASEA // Peptidase\_M2 // T2SP\_F] CG10142 GH05754 60E3-60E4 ID:33H9

CG7050 + cell\_adhesion \* neurexin III beta precursor (clone pB794-5) - bovine(aa) \* DMFAT\_2 ft \* CadN \* similar to IG (immunoglobulin) superfamily (17 domains), Low-densi[EGF // PRO\_RICH // laminin\_G // LAM\_G\_D] CG7050 GH05937 94B4-94B4 dup:1/4 ID:34A10

CG3529 + signal\_transduction \* TOM1(aa) \* 2e-17 YHQ8\_YEAST HYPOTHETICAL 64.3 KD PROTEIN IN CDC12-ERP5 INTERGENIC REGION \* 2e-62 weak similarity to yeast hypothetical protein in C [VHS // HRS\_DOMAIN] CG3529 GH05942 67B4-67B4 ID:34A11

CG15900 + unknown \* CG15900 GH05918 41E4-41E4 ID:34A6

CG9528 + unknown \* SEC14 (S. cerevisiae)-like(aa) \* HYPOTHETICAL 84.0 KD PROTEIN T23G5.2 IN CHROMOSOME III(aa) \* 4e-2 pdb|1AUA| Phosphatidylinositol Transfer Protein [CRAL\_TRIO] CG9528 GH05975 26D3-26D4 ID:34B2

CG6639 + endopeptidase \* human factor XII(aa) \* 7e-31 masquerade precursor - fruit fly (Drosophila melanogaster) \* 2e-05 similar to Trypsin \* 5e-25 MCT6\_MOUSE MAST CELL PRO [trypsin // CHYMOTRYPSIN // TRYPSIN\_CATA] CG6639 GH06092 36C2-36C2 ID:34C3

CG7908 + endopeptidase \* 8e-41 kuzbanian \* 1e-93 coded for by C. elegans cDNA yk187d12.5; coded for by C. elegans cDNA

yk187d12.3 \* 1e-143 TNF-alpha converting enzyme (TACE) [DISINTEGRINS\_2 // ADAM\_MEPRO // ZINC\_PR] CG7908 GH06244  
 99D3-99D3 ID:34D2  
 + RpS4 ribosomal\_protein \* DMRPS4\_1 RpS4 \* 1e-113 RS4E\_YEAST 40S RIBOSOMAL PROTEIN S4 (S7) (YS6) (RP5) ribos \*  
 1e-149 RS4\_DROME 40S RIBOSOMAL PROTEIN S4 ribosomal protein S4 - [RIBOSOMAL\_S4E // Ribosomal\_S4e] CG11276  
 CG11276 GH06551 69F2-69F2 ID:34F6  
 + enzyme \* 2e-69 similar to 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1. \* 2e-77 D3HI\_RAT 3  
 HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (HIBADH) \* mm [6PGDHDRGNASE] CG15093 GH06781 55F1-  
 55F1 ID:34G10  
 CG15093  
 CG1163 + RpABC14 CG1163 GH06755 ID:34G8  
 + unknown \* 6e-10 microfilarial chitinase \* microfilarial chitinase \* CHIT\_BRUMA ENDOCHITINASE PRECURSOR (MF1  
 CG14125 ANTIGEN) chitinas \* CG14125 68E3-68E3 dup:2/2 ID:34H10  
 CG12279 + chaperone HEAT SHOCK PROTEIN 67B2 RHODANESE, RHODANESE\_2 CG12279 dup:2/2 ID:34H6  
 CG8547 + DNA\_binding \* [PRENYLATION] CG8547 50F-50F dup:1/3 ID:35A2  
 CG3672 + structural\_protein \* 7e-10 cuticular protein \*\* CG3672 67B2-67B2 dup:1/2 ID:35A3  
 + cytoskeletal\_structural\_protein \* hypothetical protein(aa) \* BRCA1 associated protein(aa) \* HYPOTHETICAL 141.2 KD  
 PROTEIN EEED8.9 IN CHROMOSOME II(aa) \* HYPOTHETI[zf-C3HC4 // SPEC\_REPEAT // ZF\_UBP // ZF] CG5555 GH07062  
 CG5555 91F6-91F7 dup:1/2 ID:35A7  
 CG9921 + unknown \* 6e-05 HSPC010 \* 1e-05 putative protein \* CG9921 GH07174 14B15-14B15 ID:35B4  
 + 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/  
 CG8495 ID:35C1  
 CG18444 + alphaTryunknown \* CG18444 GH07737 47F1-47F1 dup:2/2 ID:35E12  
 + BcDNA:GH07643 endopeptidase \* unknown(aa) \* 1e-59 similar to Zinc-binding metalloprotease; cDNA EST come \* 1e-132  
 CG9761 NEP\_MOUSE NEPRILYSIN (NEUTRAL ENDOPEPTIDASE) (NEP) (ENKE[NEPRILYSIN // ZINC\_PROTEASE // Peptidas] CG976  
 GH07643 82D6-82D7 dup:2/2 ID:35E5  
 + BcDNA:GH07921 RNA\_binding \* homeobox-containing protein Wariai(aa) \* 3e-05 PEP\_DROME ZINC FINGER PROTEIN ON  
 CG8108 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  
 + EG:BACN32G11.6 unknown \* BACN32G11.c \* 1e-53 protein \* BACN32G11.I \* BACN32G11.m [AA\_TRNA\_LIGASE\_I] CG1478:  
 CG14789 GH07929 2B1-2B1 ID:35G12  
 + endopeptidase \* 1e-42 TRYZ\_DROME TRYPSIN ZETA PRECURSOR trypsin-zeta \* 4e-08 coded for by C. elegans cDNA  
 cm04e9; coded for by C. elegans cDNA CESAC59F \* 5e-36 tryp [trypsin // CHYMOTRYPSIN // TRYPSIN\_HIS ] CG7829 GH07957  
 CG7829 99C5-99C5 ID:35H1  
 + unknown \* similar to Protein phosphatase 2C (2 domains); cDNA EST yk279g8.5 comes from this gene(aa) \*  
 CG12091 HYPOTHETICAL 41.2 KD PROTEIN IN ERG7-NMD2 INTERGENIC R CG12091 GH07996 62A6-62A6 ID:35H5  
 CG3223 + unknown \* [UBA // PHOSPHOPANTETHEINE] CG3223 GH08043 84E6-84E6 dup:1/2 ID:35H7

CG8725 + CH4 \* COP9 complex subunit 4(aa) \* COP9 complex homolog subunit DCH4(aa) \* 5e-12 hypothetical protein YDL147w - yeast (*Saccharomyces cerevisiae*) \* 7e-13 [PCI\_DOMAIN // PCI] CG8725 43F8-43F8 dup:1/2 ID:37A9

CG5282 + peptidase \* 1e-34 membrane dipeptidase (EC 3.4.13.19) precursor - mouse \* 4e-35 MDP1\_HUMAN MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DI [Renal\_dipeptase] CG5282 GH09573 77B9-77C1 ID:37B3

CG14899 + unknown \* CGI-101 protein(aa) \* 2e-10 hypothetical protein YDR411c - yeast (*Saccharomyces cerevisiae*) (U \* 5e-79 putative NADH oxidoreductase complex I subunit CG14899 GH09689 89C6-89C6 ID:37C3

CG14290 + unknown \* HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III(aa) \* hypothetical protein(aa) \* CGI-129 protein(aa) \* 3e-25 YGI0\_YEAST HYPOTHETICAL 15.0 K CG14290 GH10244 91D4-91D4 ID:37F9

CG5703 + enzyme \* NADH-UBIQUINONE DEHYDROGENASE KD SUBUNIT PRECURSOR(aa) \* NADH-UBIQUINONE OXIDOREDUCTASE KD SUBUNIT PRECURSOR(aa) \* NADH-UBIQUINONE OXIDOREDUCTASE KD [COMPLEX1\_24K // complex1\_24kD // NLS\_BP] CG5703 16B10-16B10 dup:1/3 ID:37G5

CG6020 + electron\_transfer \* NADH-UBIQUINONE OXIDOREDUCTASE KD SUBUNIT PRECURSOR (COMPLEX I-39KD) (CI-39KD)(aa) \* 9e-70 NUEM\_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE KD SUBUNIT PREC CG6020 GH10437 77C3-77C3 ID:37H12

CG5687 + transporter \* No definition line found(aa) \* sodium-dependent multi-vitamin transporter(aa) \* unknown(aa) \* sodium-dependent multivitamin transporter(aa) [NA\_SOLUTE\_SYMP\_3] CG5687 GH10366 62B10-62B10 ID:37H5

CG6440 + neuropeptide\_hormone \* leucomyosuppressin precursor(aa) \* \* CG6440 GH10451 98B1-98B1 ID:38A1

CG12606 + nAcRbeta-64B ion\_channel \* ACH3\_DROME ACETYLCHOLINE RECEPTOR PROTEIN, BETA-LIKE CHAIN PRECURSOR \* 1e-97 similar to neuronal acetylcholine receptor \* 1e-78 neuronal n[NICOTINICR // neur\_chan // NEUROTR\_ION\_] CG12606 GH10531 64B11-64B11 dup:1/2 ID:38A12

CG10562 + unknown \* /match=(desc;; /match=(desc:(aa) \* 5e-21 /match=(desc;; /ma \* 1e-05 predicted using Genefinder \* No definition line found CG10562 GH10454 96C8-96C8 ID:38A2

CG11963 + enzyme \* 405aa long hypothetical succinyl-CoA synthetase beta chain(aa) \* PROBABLE SUCCINYL-COA LIGASE (GDP-FORMING), BETA-CHAIN PRECURSOR (SUCCINYL-COA SYNT [ligase-CoA] CG11963 GH10480 85C1-85C2 ID:38A5

CG1893 + unknown \* unknown product related to TRA1 protein(aa) \* 3e-07 YJ70\_YEAST HYPOTHETICAL 37.5 KD PROTEIN IN YUH1-URA8 INTERGENIC REGION \* 5e-40 cDNA EST yk383g8. CG1893 GH10494 63B5-63B5 ID:38A7

CG8256 + ligand\_binding\_or\_carrier \* GLYCEROL-3-PHOSPHATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (GPD-M) (GPDH-M)(aa) \* 1e-112 GPDM\_YEAST GLYCEROL-3-PHOSPHATE DEHYDROGENAS[FAD\_G3PDH\_1 // FADG3PDH // FAD\_G3PDH\_2 ] CG8256 GH10595 52D2-52D3 dup:2/2 ID:38B3

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

CG9047 + ligand\_binding\_or\_carrier \* 1e-31 peptidyl-dipeptidase A (EC 3.4.15.1) 67k precursor - fruit fly (*Drosophila me* \* 6e-09 coded for by C. elegans cDNA yk27b10.3; coded for by C. [PRO\_RICH] CG9047 GH10774 60E3-60E3 dup:1/3 ID:38C11

CG14992 + BcDNA:GH10777 protein\_kinase \* 2e-13 KB9S\_YEAST PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR274W \* 7e-69 tyrosine kinase \* 8e-73 YWR1\_CAEEL PUTATIVE TYROSINE-PROTEIN KI[UBA // PROTEIN\_KINASE\_TYR // TYRKINASE ] CG14992 GH10777 64A8-64A9 dup:2/5 ID:38C12

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

CG6910 + unknown \* No definition line found(aa) \* putative protein(aa) \* 5e-71 putative protein \* hypothetical protein CG6910 GH10741 68F7-68F7 dup:1/2 ID:38C7

CG5045 + endopeptidase \* PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP)(aa) \* PUTATIVE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT, MITOCHONDRIAL PRECURSOR (ENDOPEPTIDAS [CLP\_protease // CLP\_PROTEASE\_SER // CLP] CG5045 GH10833 31D10-31D10 ID:38D2

CG7361 + enzyme \* 2e-56 UCRI\_YEAST UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (RIESK \* 2e-60 contains similarity to Rieske iron-sulfur proteins \* [RIESKE\_1 // Rieske // RIESKE // RIESKE\_] CG7361 GH10847 22E1-22E1 ID:38D6

CG7780 + enzyme \* DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)(aa) \* 2e-48 YKU5\_CAEEL HYPOTHETICAL 41.5 KD PROTEIN C07B5.5 IN CHROMOSOM CG7780 GH10876 90D-90D ID:38D8

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

CG1927 + BcDNA:GH11112 unknown \* CG1927 GH11112 62B11-62B11 ID:38F4

CG13830 + receptor \* 7e-29 Contains similarity to Pfam domain: (thyroglobulin\_1), \* 9e-29 testican \* 9e-29 testican - human \* 6e-09 HG2A\_RAT H-2 CLASS II HISTOCOMPATIBIL [thyroglobulin\_1 // THYROGLOBULIN\_1 // k] CG13830 GH11316 94D13-94E dup:1/2 ID:38G11

CG6649 + Ugt35b enzyme \* antennal-enriched UDP-glycosyltransferase melanogas \* 3e-31 similar to UDP-glucuronosyltransferase \* 5e-6. UDB5\_MOUSE UDP-GLUCURONOSYLTRANSFERASE 2B [UDPGT] CG6649 GH11333 86D5-86D5 ID:38H1

CG13095 + endopeptidase \* encodes a-cell barrier activity on alpha factor; Bar1p(aa) \* similar to eukaryotic aspartyl proteases(aa) \* BLASTX 1.4E-29 PEP4|Protease A (PrA) (y [asp // ASP\_PROTEASE // PEPSIN] CG13095 GH11417 29D1-29D1 ID:38H11

CG9319 + enzyme \* HYPOTHETICAL 37.1 KD PROTEIN ZK892.4 IN CHROMOSOME III(aa) \* 3e-53 similar to L-carnitine dehydratase; cDNA EST yk206h7.5 comes from \* 9e-87 alpha-m CG9319 GH11368 38E4-38E4 ID:38H4

CG16858 + vkg cell\_adhesion \* DMINTGRNB\_2 Cg25C \* vkg \* collagen type IV alpha \* 7e-25 Similar to cuticular collagen; F58F6.2 [COLLAGEN\_REP // Collagen // C4] CG16858 GH11516 25C1-25C1 ID:39A7

CG12907 + unknown \* 1E-145\* \* [PRO\_RICH // NLS\_BP] CG12907 GH11521 47A-47A ID:39A8

CG13865 + \* 1e-29 cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes \* 3e-12 conserved hypothetical secreted protein pylori \* putative pylori \* c CG13865 cyto\_unknown dup:3/3 ID:39B1

CG7149 + enzyme \* contains similarity to CDP-alcohol phosphotransferases(aa) \* aminoalcoholphosphotransferase(aa) \* 4e-24 sn-1,2-diacylglycerol cholinephosphotransf [CDP\_ALCOHOL\_P\_TRANSF // CDP\_ALCOHOL\_P\_T] CG7149 GH11618 28C8-28C9 ID:39B5

CG12162 + unknown \* HSPC017(aa) \* 5e-35 YOY9\_CAEEL PUTATIVE UBIQUINONE BIOSYNTHESIS METHYLTRANSFERASE ZK652.9 \* 4e-17 apaG protein \* APAG\_ECOLI APAG PROTEIN apaG prote CG12162 GH11824 83A8-83A9 ID:39C7

CG11796 + unknown \* 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD)(aa) \* 4-hydroxyphenylpyruvate-dioxygenase(aa) \* 1e-139 HPPD\_CAEEL 4-HYDROXYPHENYLPYRUVATE DIOXYGE CG11796 GH11957 77C1-77C1 dup:2/2 ID:39D6



+ unknown \* 2e-12 HNK-1 sulfotransferase HNK-1 sulfotransferase \* 2e-12 HNK-1 sulfotransferase \* [PRO\_RICH] CG14024  
 CG14024 GH11985 25D4-25D5 ID:39D8  
 + unknown \* CG1146 GH12037 62E6-62E6 ID:39D9  
 + EG:115C2.11 unknown \* 2e-37 hypothetical protein YOL133w - yeast (*Saccharomyces cerevisiae*) \* 9e-60 /match=(desc: \* 8e-5( Similarity to yeast hypothetical protein PIR acc [ZF\_RING] CG16982 GH12110 1B10-1B10 dup:2/2 ID:39E4  
 CG16982 + BcDNA:GH12144 unknown \* Contains similarity to Pfam domain: (TPR), Score=38.0, E-value=6.9e-08, N=6(aa) \* weakly similar  
 CG4341 to *E. nidulans* bimA gene product \* \* [TPR\_REGION // TPR\_REPEAT] CG4341 GH12144 21D4-21E dup:3/3 ID:39E7  
 + cher actin\_binding \* contains similarity to the x aa approximate repeats found in human filamin \* filamin, Mueller cell -  
 chicken(aa) \* filamin (actin-binding protein[Filamin // FILAMIN\_REPEAT // GRAM\_POS\_A] CG3937 GH12209 92D1-92D1 dup:2/5  
 CG3937 ID:39F1  
 CG17841 + BcDNA:GH12326 unknown \* CG17841 GH12326 9B14-9B15 dup:2/2 ID:39F7  
 + CBP calcium\_binding \* CBP \* sarcoplasmic calcium-binding protein(aa) \* 1e-161 sarcoplasmic calcium-binding protein \* 4e-23  
 SCP\_PERVT SARCOPLASMIC CALCIUM-BINDING PROTEIN [EF\_HAND // NLS\_BP // efhand // EF\_HAND\_] CG1435 GH1235( 7A4-7A4 ID:39F9  
 CG1435 + enzyme \* antennal-specific short-chain dehydrogenase/reductase(aa) \* 3e-11 YM71\_YEAST HYPOTHETICAL  
 OXIDOREDUCTASE IN MRPL44-MTF1 INTERGENIC REGION \* 7e-08 Si [GDHRDH // adh\_short] CG12466 GH12380 20B1-20B  
 CG12466 dup:1/2 ID:39G1  
 + enzyme \* D-ASPARTATE OXIDASE (DASOX) (DDO)(aa) \* D-AMINO ACID OXIDASE (DAMOX) (DAO) (DAAO)(aa) \*  
 similar to D-amino acid oxidase(aa) \* D-aspartate oxidase i [DAO // FMOXYGENASE // PROTEIN\_KINASE\_AT] CG11236  
 CG11236 GH12548 28E7-28E7 ID:39G11  
 + BcDNA:GH12558 enzyme \* MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) LONG  
 CHAIN ENOYL-COA HYDRATASE ; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE \* s [ECH // 3HCDH //  
 CG4389 ENOYL\_COA\_HYDRATASE] CG4389 GH12558 30B12-30B12 ID:39G12  
 + signal\_transduction \* 1e-115 disc growth factor \* 2e-14 CHIT\_CAEL PUTATIVE ENDOCHITINASE coded for by *C. elegans*  
 CG5154 \* 7e-26 BRP39 protein - mouse BRP39 protein m \* 5e-30 Ch [Glyco\_hydro\_18] CG5154 GH12410 55C9-55C9 ID:39G4  
 + enzyme \* DMC23E12 \* gamma-glutamyltransferase (EC 2.3.2.2) precursor - rat(aa) \* gamma-glutamyl transpeptidase (EC  
 CG4829 2.3.2.2)(aa) \* gamma-glutamyl transpeptida [G\_glu\_transpept] CG4829 GH12430 15A8-15A8 dup:1/2 ID:39G5  
 + metabolism \* 4e-05 epithin \* 7e-06 gp330 precursor \* 4e-05 complement C3b/C4b inactivator (EC 3.4.21.-) precursor -  
 CG3116 African clawed frog > \* 1e-05 yl [LDLRA\_2 // LDLRA\_1] CG3116 GH12701 77F2-77F2 dup:2/3 ID:40A11  
 CG18374 + unknown \* CG18374 GH12641 61A5-61A5 ID:40A2  
 + translation\_factor \* UNKNOWN(aa) \* 7e-86 inserted at base Both 5' and 3' ends of P element Inverse PCR \* eukaryotic  
 CG12131 translation initiation factor eIF3, p35 subunit \* CG12131 GH12681 46C10-46C11 ID:40A7  
 + protein\_phosphatase \* Hop \* DMPPY\_2 PpY-55A \* serine/threonine protein phosphatase PPT1(aa) \* 7e-88 PPT1\_YEAST  
 SERINE/THREONINE PROTEIN PHOSPHATASE T (PPT) [TPR\_REGION // PHOSPHO\_ESTER // STPHPTA] CG8402  
 CG8402 GH12714 85E6-85E6 ID:40B1  
 + peptidase \* 1e-112 APE2\_YEAST AMINOPEPTIDASE II (YSCII) aminopeptidase yscII \* 1e-110 Similarity to Human  
 CG8775 aminopeptidase N (SW:AMPN\_HUMAN); cDNA EST EMB \* 1e-16 [ALADIPTASE // Peptidase\_M1 // ZINC\_PROT] CG8775

GH12821 87E6-87E6 dup:2/2 ID:40B8

CG6742 + signal\_transduction \* centaurin beta 1A(aa) \* BLASTX 1.6E-48 Human mRNA for gene, partial cds.(dna) \* HYPOTHETICAL PROTEIN \* centaurin beta2(aa) [ANK\_REP // ArfGap // GLYCOSYL\_HYDROL\_F5] CG6742 GH12888 94E-94E dup:1/2 ID:40C1

CG12214 + unknown \* 9e-07 PAC2\_YEAST PAC2 PROTEIN PAC2 protein - yeast (Saccharomy \* 3e-46 No definition line found \* 1e-2: tubulin-specific chaperone e cofactor E \* CG12214 GH13040 46F1-46F1 dup:1/2 ID:40C10

CG5506 + unknown \* CG5506 GH13083 75A6-75A6 ID:40C12

CG6306 + unknown \* CG6306 GH12946 17B1-17B1 ID:40C7

CG6575 + Glilectin unknown \* Glilectin \* glilectin(aa) \* 1e-99 Glilectin \* CG6575 GH13232 93F-93F ID:40D12

+ Cyp6w1 cytochrome\_P450 \* Cyp6-like \* 1e-112 CYP6-like microsomal cytochrome P450 \* 2e-45 predicted using Genefinder; similar to cytochrome P450 \* 5e-62 cytochrome P450 3A13 [EP450II // p450 // P450 // MITP450 // C] CG8345 GH13192 42A10-42A10 ID:40D6

CG8345 + translation\_factor \* translation initiation factor eIF3 subunit; Tif35p(aa) \* 7e-28 IF35\_YEAST EUKARYOTIC TRANSLATION INITIATION FACTOR RNA-BINDING SUBUNIT (EIF- \* 6e-34 [RNP\_1 // RBD // rrm] CG10881 GH13208 92E3-92E3 ID:40D8

CG10881 + 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

CG7874 + unknown \* insect intestinal mucin IIM22(aa) \* putative cell surface glycoprotein; Sed1p(aa) \* 71(aa) \* GLYCOPROTEIN X PRECURSOR(aa) CG7874 GH13361 18B6-18B6 dup:2/2 ID:40E12

CG4581 + Thiolaseenzyme \* Thiolase \* thiolase(aa) \* 3e-37 THIL\_YEAST ACETYL-COA ACETYLTRANSFERASE (ACETOACETYL-COA THIOLASE) \* 1e-140 YKA3\_CAEEL HYPOTHETICAL 47.9 KD PROTEIN [thiolase] CG4581 GH13256 60A6-60A6 dup:2/2 ID:40E2

CG9451 + enzyme \* LYSOSOMAL ACID PHOSPHATASE PRECURSOR (LAP)(aa) \* acid phosphatase 2, lysosomal(aa) \* 8e-60 acid phosphatase (EC 3.1.3.2) Acph-1 precursor, lysosomal [HIS\_ACID\_PHOSPHAT\_1 // acid\_phosphat] CG9451 GH13318 76B6-76B6 dup:2/2 ID:40E7

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

CG5903 + unknown \* 6e-06 K02F3.10 gene product \* \* CG5903 GH13386 89B9-89B9 ID:40F3

CG5889 + enzyme \* MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME) (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)(aa) \* malic enzyme(aa) \* 4e-86 MAOX\_YEAST [MALOXRDTASE // malic // ATP\_GTP\_A] CG5889 GH13437 97E11-97F ID:40F4

+ Fpps enzyme \* 8e-80 FPPS\_YEAST FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DI \* farnesyl pyrophosphate synthase melanogas \* 2e-37 predicted [polyprenyl\_synt // POLYPRENYL\_SYNTHET\_1] CG12389 GH13450 47E5-47E6 dup:2/2 ID:40F5

CG12389 + Ela unknown \* [COLLAGEN\_REP] CG7021 GH13458 96B4-96B4 ID:40F7

CG7021 + DNA\_repair\_protein \* 2e-29 CHL1\_YEAST CHL1 PROTEIN CHL1 protein - yeast (Saccharomyce \* 1e-31 /match=(desc;; /ma \* 1e-112 similar to DEAH-type helicase; cDNA EST comes f [PHOSPHOPANTETHEINE] CG4078 GH13485 5B3-5B3 ID:40F8

CG4078 + Pgi enzyme \* glucosephosphate isomerase(aa) \* DMPGIAAAA\_11 \* glucose-6-phosphate isomerase(aa) \* G6PI\_YEAST GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (PHOSPHOGLUCOSE [PGI // P\_GLUCOSE\_ISOMERASE\_1 // P\_GLUCO]

CG8251

CG8251 GH13575 44F9-44F9 ID:40G4

CG3666 + ligand\_binding\_or\_carrier \* TRANSFERRIN PRECURSOR(aa) \* transferrin precursor(aa) \* transferrin precursor(aa) \* transferrin precursor(aa) [PROTEIN\_SPLICING] CG3666 GH13735 52F10-52F10 ID:40H1

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

CG6662 + glutathione\_transferase \* predicted using Genefinder; similar to Glutathione S-transferases.(aa) \* 2e-11 YKJ3\_CAEEL HYPOTHETICAL 42.8 KD PROTEIN C02D5.3 IN CHROMOSOME III \* 7 [GST] CG6662 66D5-66D5 dup:2/2 ID:40H2

CG5461 + bun transcription\_factor \* shortsighted class 2(aa) \* DMSHSA\_5 bun \* shortsighted class \* 2e-07 protein [TSC22] CG5461 GH13775 33E-33E6 ID:40H5

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

CG8721 + Odc1 enzyme \* ornithine decarboxylase(aa) \* ornithine decarboxylase(aa) \* Ornithine decarboxylase; Spe1p(aa) \* ornithine decarboxylase(aa) [ODR\_DC\_2\_1 // ODR\_DC\_2\_2 // Orn\_DAP\_Arg] CG8721 GH13851 43F9-44A1 dup:2/2 ID:41A4

CG10060 + G-alpha65A signal\_transduction \* GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT(aa) \* DMGAS02\_13 G-o agr;65A \* 1e-124 predicted using Genefinder; Similarity to [GPROTEINA // G-alpha // GPROTEINAQ // G] CG10060 GH13864 65D5-65D6 dup:1/2 ID:41A5

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

CG9953 + peptidase \* lysosomal Pro-X carboxypeptidase - like protein(aa) \* similar to alpha/beta hydrolase fold(aa) \* 1e-77 similar to lysosomal carboxypeptidase; cDNA [ESTERASE // abhydrolase] CG9953 GH14014 65D5-65D5 ID:41B7

CG2176 + unknown \* CG2176 GH14263 99E2-99E2 ID:41C11

CG2155 + v enzyme \* DMVERM\_2 v \* VERM\_DROME TRYPTOPHAN 2,3-DIOXYGENASE (TRYPTOPHAN PYRROLASE) (VERMILION PROTEIN) \* 1e-102 T230\_CAEEL PUTATIVE TRYPTOPHAN 2,3-DIOXYGENA CG2155 GH14143 9F13-10A1 ID:41C4

CG3671 + Mvl unknown \* MALVOLIO PROTEIN(aa) \* Mvl \* 7e-42 SMF1\_YEAST TRANSPORTER PROTEIN SMF1/ESP1 vacuolar tran: \* 1e-140 similar to M. musculus transport system membrane [NATRESASSCMP // ATP\_GTP\_A] CG3671 GH14215 93B5-93B7 ID:41C8

CG12239 + unknown \* BLASTX 9.9E-08 Human mRNA for hU1-70K snRNP protein (RNP8).(dna) \* \* [NLS\_BP] CG12239 GH14380 5B8-5B8 ID:41D11

CG3045 + enzyme \* Depressed growth-rate protein; Deg1p(aa) \* PROBABLE PSEUDOURIDYLATE SYNTHASE E02H1.3 (PSEUDOURIDINE SYNTHASE)(aa) \* 6e-54 PUS3\_YEAST PSEUDOURIDYLATE [PseudoU\_synth\_1] CG3045 GH14326 58C5-58C5 dup:2/2 ID:41D5

CG7188 + unknown \* TEGT(aa) \* 3e-31 testis enhanced gene transcript protein \* 3e-29 TEGT \* testis enhanced gene transcript T [UPF0005] CG7188 GH14327 66C6-66C6 ID:41D6

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

CG10664 + enzyme \* cytochrome c oxidase subunit IV(aa) \* CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECURSOR(aa) \* 2e-22

COX4\_MOUSE CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECU CG10664 GH14536 38A8-38A8 dup:2/2 ID:41E11

CG18525 + unknown \* CG18525 GH14439 88E7-88E7 dup:2/2 ID:41E4

CG1552 + unknown \* CG1552 GH14443 10A-10A dup:2/2 ID:41E5

+ unknown \* HNK-1 sulfotransferase(aa) \* 1e-20 HNK-1 sulfotransferase HN \* \* [NLS\_BP] CG4826 GH14503 36A11-36A11 dup:3/3 ID:41E9

CG4826

CG10675 + motor\_protein \* 2e-17 /match=(desc;; /ma \* \* CG10675 GH14673 96C9-96C9 ID:41F11

CG1670 + ligand\_binding\_or\_carrier \* [PBP\_GOBP] CG1670 GH14595 19D2-19D2 ID:41F4

+ ribosomal\_protein \* similar to Ribosomal protein L7Ae; cDNA EST comes from this gene(aa) \* 2e-18 NHP2\_YEAST HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN hi \* 2e-27 similar [Ribosomal\_L7Ae // L7ARS6FAMILY // NUCLE] CG5258

CG5258 GH14757 70F6-70F6 ID:41G10

+ endopeptidase \* DMSER2\_7 Ser99Db \* 1e-57 serine proteinase (EC 3.4.21.-) precursor - fruit fly (Drosophila melanogast \* 1e-15 KAL\_MOUSE PLASMA KALLIKREIN PRECURSOR [trypsin // CHYMOTRYPSIN // TRYPSIN\_CATA] CG3088 GH14734 67B9-67B9 ID:41G7

CG3088

+ unknown \* 3e-06 LBM\_DROME LATE BLOOMER PROTEIN late bloomer me \* 4e-08 lbm \* \* [transmembrane4 // TMFOU // TM4\_2] CG12840 GH14950 42E2-42E2 ID:41H10

CG12840

+ enzyme \* Yjr105wp(aa) \* Similarity to Human adenosine kinase cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cD [PFKB\_KINASES\_2 // ADENOKINASE // pfkB] CG11255 GH14845 69F2-69F2 ID:41H4

CG11255

+ Cyp6g1 cytochrome\_P450 \* CYP6-like microsomal cytochrome P450 \* 1e-33 YRV5\_CAEEL PUTATIVE CYTOCHROME P450 T10B9.5 IN CHROMOSOME II \* 1e-59 cytochrome P450 3A11 - mouse c[EP450II // p450 // P450 // MITP450 // C] CG8453

CG8453 GH14851 48F1-48F1 dup:2/4 ID:41H5

+ BG:DS00797.2 unknown \* 6e-38 YMY9\_YEAST HYPOTHETICAL 34.0 KD PROTEIN IN CTF13-YPK2 INTERGENIC REGION \* 3e-35 putative protein \* AAPC\_PENCL POSSIBLE AOSPORY-ASSOCIATED PR CG9008 GH14910 34D1-34D1 ID:41H8

CG9008

+ metabolism \* similar to glutamate synthase; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA ES comes from this gene; cDNA EST comes from thi [ADXRDTASE // FADPNR // PNDRDTASEII] CG9674 GH14941 73C-73C2 dup:4/5 ID:41H9

CG9674

+ enzyme \* stromal cell-derived factor 2(aa) \* 2e-09 PMT6\_YEAST DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE \* 7e-07 /match=(desc;; /ma \* 3e-47 cont CG11999 GH15022 83A4-83A4 ID:42A4

CG11999

+ enzyme \* DMUBCD2\_2 UbcD2 \* similar to Ubiquitin-conjugating enzymes; cDNA EST comes from this gene(aa) \* ubiquitin conjugating enzyme(aa) \* 6e-12 UBCC\_YEAST [CRYSTALLIN\_BETAGAMMA // UQ\_con // UBIQU] CG7220 GH15032 47B7-47B7 ID:42A5

CG7220

+ enzyme \* Adh-Finnegan(aa) \* fat body protein 2(aa) \* development-specific 25K protein - flesh fly (Sarcophaga peregrina)(aa) \* 7e-09 YM71\_YEAST HYPOTHETICAL [adh\_short // ADH\_SHORT // adh\_short\_C] CG4842 GH15220 72F1-72F1 ID:42B10

CG4842

+ signal\_transduction \* predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDN/ EST comes from this gene; cDNA EST comes from thi [ArfGap // ZF\_GCS // REVINTRACTNG] CG8243 GH15285 44F9-44F9 ID:42C5

CG8243

	+ signal_transduction * serine/threonine kinase with Dbl- and pleckstrin homology domains(aa) * actin-filament binding protein Frabin(aa) * 5e-12 ROM1_YEAST RHO1 GDP-GTP E [GRF_DBL // RhoGEF // PRO_RICH // NLS_BP] CG8606 LD21492 65F2-65F2 ID:43A5
CG8606	
CG3510	+ CycB cell_cycle_regulator G2/MITOTIC-SPECIFIC CYCLIN B CYCLINS, cyclin CG3510 dup:2/4 ID:43B3
	+ 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 // TGF_BETA_2]
CG1901	CG1901 102D1-102D1 dup:2/2 ID:43C8
CG12124	+ enzyme * [NLS_BP] CG12124 LD23314 8D5-8D5 dup:4/4 ID:43E11
	+ 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 * 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	+ CG5926 dup:2/2 ID:43E9
	+ Bub3 signal_transduction * WD-40 repeat protein(aa) * 7e-49 YET7_YEAST HYPOTHETICAL 40.5 KD TRP-ASP REPEATS CONTAINING PROTEIN IN NUP157-PDH * 7e-72 predicted using Genefinder [GPROTEINBRPT // WD40_REGION // WD_REPEA]
CG7581	CG7581 LD23540 99B-99B ID:43F6
	+ 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	
	+ dbp unknown * DMDRIBBLE dbp * dribble(aa) * 9e-98 YCF9_YEAST HYPOTHETICAL 37.2 KD PROTEIN IN CHA1-PRD1 INTERGENIC REGION * 5e-88 similar to human REV interacting CG4258 LD24634 21E3-21E3 ID:43G5
CG4258	
	+ 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
CG4735	
	+ 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 LD24746 86A2-86A3 ID:43G7
CG4029	
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	
CG9967	+ CG9967 LD25280 dup:1/2 ID:43H7
	+ enzyme homology to NADPH-ferrihemoprotein reductase and NADPH-cytochrome P450 reductase FAD_binding, FLAVODOXIN, FPNCR, PHEHYDRX] CG13667 LD25514 dup:2/2 ID:44A6
CG13667	
CG12129	+ RNA binding homology to human CGI-18 protein KH-domain CG12129 LD25546 ID:44A7
CG8572	+ unknown * 9e-61 inserted at base Both 5' and 3' ends of P element Inverse PCR * * [SAM_DOMAIN] CG8572 LD26045

65F5-65F5 dup:2/2 ID:44C6

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

CG6319 + 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

CG1109 + 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

CG18622 + CHROMO\_2, chromo CG18622 LD26416 dup:2/3 ID:44D9

CG8856 + Sr-CII cell\_adhesion Scavenger receptor class C, type II MAM, MAM\_2, SOMATOMEDIN\_B, Somatomedin\_B] CG8856 LD26673 dup:3/3 ID:44E10

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

+ transmembrane\_receptor \* protein(aa) \* 4e-12 gene flightless-I protein - fruit fly (*Drosophila melanogaster*) ( \* 2e-14 Ras-binding protein SUR-8 leuc \* 2e-12 RSU1[LRR // CNMP\_BINDING\_3 // LEURICHRPT // ] CG6860 LD26544 36C1-36C1 dup:2/2 ID:44E7

CG6860

CG16928 + CG16928 dup:3/3 ID:44E9

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

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

CG10923 + Klp67A motor\_protein kinesin family protein 3B ATP\_GTP\_A, KINESINHEAVY, KINESIN\_MOTOR\_D] CG10923 LD27326 dup:2/2 ID:44H12

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

+ 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

CG9446

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

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

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

+ 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

CG14650

CG9933 + Weak homology to SNF2 family (CHD1 subfamily) chromodomain protein [*Arabidopsis thaliana*] CHROMO\_2 CG9933

LD28372 dup:5/5 ID:45E9  
+ Doa protein\_kinase \* PROTEIN KINASE DOA (PROTEIN DARKENER OF APRICOT)(aa) \* DMDOA\_2 Doa \* 2e-60 ORF YLL019c \* 1e-127 Similarity to Drosophila Doa kinase (PIR Acc. No. cD [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM]  
CG1658 CG1658 98F-98F2 dup:3/3 ID:45F12  
+ EG:66A1.2 transcription\_factor\_binding \* map\_position:4C6 \* map\_position:4C6 \* map\_position:4C6 \* by match; 1-mat  
CG12179 CG12179 LD28429 4C6-4C7 ID:45F3  
CG4300 + unknown spermine synthase SAM\_BIND CG4300 LD28457 ID:45F5  
+ unknown \* 7e-10 /match=(desc: \* 9e-10 K10D2.3 gene product \* 1e-10 The gene is expressed ubiquitously.; The protein \*  
CG1091 1e-09 caffeine-induced death protein >g [PAP\_ASSOCIATED // PAP\_CORE // PAP // AA] CG1091 84C1-84C1 dup:3/3 ID:45F7  
+ chaperone \* 1e-07 STI1\_YEAST HEAT SHOCK PROTEIN STI1 stress-induced protein \* 1e-08 Hsp70/Hsp90 organizing  
protein homolog \* 1e-54 similar to TPR Domain (2 doma [RNP\_1 // TPR\_REGION // TPR\_REPEAT // TP] CG2947 3F6-3F6  
CG2947 dup:3/4 ID:45F9  
CG12000 + CG12000 ID:45G11  
CG2890 + CG2890 dup:2/3 ID:45H3  
+ phtf unknown \* supported by Genscan and several ESTs: and \* 3e-12 supported by Genscan and several ESTs: (NID:g2 \* \*  
CG3268 CG3268 42C3-42C3 dup:1/2 ID:46B11  
CG7414 + CG7414 79A4-79A4 dup:2/2 ID:46B6  
+ unknown \* MA3(aa) \* 3e-70 apoptosis protein MA-3 - mouse apoptosis-i \* 1e-69 nuclear protein H731 - human nuclear  
CG10990 antigen H731 \* nuclear antigen H731-like pr [RCC1\_2 // NLS\_BP] CG10990 12B8-12B8 ID:46B7  
+ unknown \* 1e-07 ADRP\_MOUSE ADIPOSE DIFFERENTIATION-RELATED PROTEIN (ADRP) \* \* [ATP\_GTP\_A] CG9057  
CG9057 13A11-13A11 dup:2/2 ID:46D11  
CG5991 + enzyme PHOSPHATIDYLSERINE DECARBOXYLASE PROENZYME CG5991 ID:46D2  
CG8073 + enzyme CG8073 ID:46D3  
CG2034 + CG2034 ID:46D4  
+ transcription\_factor \* host cell factor C1 (VP16-accessory protein)(aa) \* HOST CELL FACTOR C1 (HCF) (VP16  
CG1710 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF)(aa) \* host cell factor 2(a CG1710 LD29768 102B3-102B3 dup:3/3 ID:46E3  
+ transporter \* ATP-DEPENDENT RNA HELICASE GLH-1(aa) \* 1e-08 EAST\_DROME SERINE PROTEASE EASTER  
CG3820 PRECURSOR serine protein \* 6e-22 similar to nucleoporin; cDNA EST com CG3820 LD29808 59B4-59B4 dup:3/4 ID:46E7  
CG9107 + CG9107 LD29822 dup:3/3 ID:46E8  
+ enzyme \* (novel PUTATIVE protein similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8)(aa) \* 1e-  
CG4263 32 RLR1\_YEAST RLR1 PROTEIN RLR1 protei [NLS\_BP] CG4263 LD29940 22C3-22C3 dup:3/3 ID:46F10  
CG14459 + none none CG14459 LD29969 ID:46F11  
+ protein\_phosphatase regulatory subunit B' of serine-threonine protein phosphatase 2A ANTIFREEZEI, B56 CG7913  
CG7913 LD29902 dup:1/3 ID:46F5  
+ RhoGEF3 signal\_transduction RHO guanyl-nucleotide exchange factor ATP\_GTP\_A, GRF\_DBL, RhoGEF, SH3 CG1225  
CG1225 LD29915 dup:1/2 ID:46F8

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

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

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

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

CG4968 + unknown \* predicted using Genefinder; cDNA EST comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA CG4968 LD30683 31D6-31D6 ID:47C3

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

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

CG3409 + transporter \* DMC103B4 \* 8e-09 YNM5\_YEAST HYPOTHETICAL 73.8 KD PROTEIN IN SPC98-TOM70 INTERGENIC REGION \* 3e-37 /match=(desc;; /ma \* 2e-24 similar to the monocarb CG3409 LD30953 42C6-42C1 ID:47D9

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

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

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

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

CG8440 + signal\_transduction CG8440 ID:47F8

CG1530 + unknown CG1530 ID:47H2

CG6199 + 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

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

CG1487 + 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



CG5203 + CHIP chaperone \* defined colon cancer antigen 7(aa) \* carboxy terminus of Hsp70-interacting protein(aa) \* 3e-09 hypothetical protein YOR007c - yeast (Saccharomyces c [TPR\_REGION // TPR\_REPEAT // TPR] CG5203 LD32251 33D1-33D1 ID:48B6

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

CG8435 + 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

CG8975 + 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

CG15893 + 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

CG4455 + BG:DS09218.3 chaperone \* 8e-19 ERP5\_CAEEL PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR \* 4e-21 protein disulfide isomerase-related protein \* 9e-21 ERP5\_RAT PROBABLE PRO CG4455 LD33101 35F10-35F10 dup:2/3 ID:48F10

CG4262 + elav RNA\_binding \* DMELAVK\_2 elav \* 1e-16 polyadenylate-binding protein \* ELAV\_DROME ELAV PROTEIN (EMBRYONIC LETHAL ABNORMAL VISUAL PROTEIN) \* 1e-58 Similar to the hu [RNP\_1 // RBD // HUDSXL RNA // rrm] CG4262 LD33076 1B5-1B5 ID:48F5

CG10938 + ProsMA5 endopeptidase \* 9e-71 PRCZ\_YEAST PROTEASOME COMPONENT PUP2 (MACROPAIN SUBUNIT PUP2) (PROTEINASE YSCE \* 1e-137 PRCZ\_DROME PROTEASOME PSMA5 SUBUNIT (MULTICATALYTIC EN [PROTEASOME\_PROTEASE // PROTEASOME\_A // ] CG10938 LD33318 54C1-54C1 ID:48G11

CG3350 + transcription\_factor \* transcription factor-like protein beta(aa) \* 4e-09 No definition line found \* 3e-43 transcription factor like protein \* 3e-10 WS basic-helix-loop-h[HLH // HELIX\_LOOP\_HELIX // HELIX\_LOOP\_H] CG3350 LD33275 97F6-97F6 ID:48G9

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

CG12369 + Lac cell\_adhesion \* DMLACH\_2 Lac \* LACH\_DROME LACHESIN PRECURSOR lachesin melanoga \* 2e-16 predicted protei 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

CG5793 + unknown \* 5-oxo-1,2,5-tricarboxylic-3-penten acid decarboxylase/isomer(aa) \* 3e-26 YNQ8\_YEAST HYPOTHETICAL 28.8 KD PROTEIN IN PSD1-SKO1 INTERGENIC REGION \* 9e CG5793 LD33646 95F1-95F1 ID:49A1

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

	+ enzyme * 2e-60 COXX_YEAST CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR * 5e-94 heme / farnesyltransferase * 4e-46 putative heme A:farnesyltransferase [COX10_ctaB_cyoE // COX10_CTAB_CYOE] CG5037 LD33876 31D9-31D9 dup:3/3 ID:49B6
CG5037	
CG1913	+ CG1913 dup:6/7 ID:49B9
	+ 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
CG7654	
	+ peptidase * PROBABLE CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)(aa) * leucine aminopeptidase(aa) * PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III( [LAMNOPPTDASE // RCC1_2 // Peptidase_M17] CG7340 LD34492 87D7-88E1 ID:49D12
CG7340	
	+ 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
CG4050	
	+ motor_protein * 7e-09 by content; 1-meth * 2e-07 homeotic most like HMPB_DROME: homeotic proboscipedia protein * 9e-07 Williams-Beuren syndrome deletion transcript [PHD // NLS_BP // ATP_GTP_A] CG8677 LD34730 39C1-39C1 dup:5/5 ID:49E1
CG8677	
	+ 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
CG12130	
	+ 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
CG6563	
	+ 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
CG6236	
	+ 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
CG6967	
	+ motor_protein * HYPOTHETICAL 25.4 KD PROTEIN F53F4.3 IN CHROMOSOME V(aa) * 3e-12 YNO8_YEAST HYPOTHETICAL 28.4 KD PROTEIN IN RPC8-MFA2 INTERGENIC REGION * 9e-07 kine [CAP_GLY_2 // CAP_GLY] CG11242 LD35048 56D9-56D9 dup:2/2 ID:49G2
CG11242	
	+ 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
CG1354	
	+ signal_transduction * vasodilator-stimulated phosphoprotein(aa) * 3e-09 Abl substrate ena (enabled) - fruit fly (Drosophila melanogaster) * 3e-08 neural variant mena+ pr [RANBP1_WASP // CYTOCHROME_C] CG10155 GH01083 51C2-51C2 dup:1/4 ID:54A10
CG10155	
	+ ligand_binding_or_carrier * 2e-05 odorant-binding protein Rpal2' palmaru ** [PBP_GOBP] CG13421 GH01026 57A6-57A6 ID:54A2
CG13421	
	+ enzyme * 2e-18 pdb 1GKY  Guanylate Kinase (E.C.2.7.4.8) Complex With Guanosine Monophosphate * 2e-70 Camguk * 2e-67 LIN2_CAEEL LIN-2 PROTEIN LIN-2A * 5e-97 D [Guanylate_kin // GUANYLATE_KINASE_1 // ] CG13219 GH01140 47D7-47D7
CG13219	

ID:54B3

CG11400 + unknown \* CG11400 GH01142 54A-54A ID:54B4

CG17926 + unknown \* [NLS\_BP] CG17926 GH01154 66D6-66D7 ID:54B7

+ enzyme \* 7e-52 acyl-coenzyme A oxidase \* 1e-120 similar to ACYL-COENZYME A OXIDASE, PEROXISOMAL (EC 1.3.3.6 (PALM \* 1e-125 peroxisomal acyl-CoA oxidase \* 1e CG9707 GH01226 57D11-57D11 dup:1/3 ID:54C1

CG9707

CG7066 + unknown \* 5e-14 Y256\_HUMAN HYPOTHETICAL PROTEIN KIA \* \* CG7066 GH01354 66C5-66C6 ID:54C12

+ syt transporter \* similar to synaptotagmin(aa) \* SYNAPTOTAGMIN (P65)(aa) \* 2e-09 probable membrane protein YOR086c - yeast (*Saccharomyces cerevisiae*) \* 3e-49 SYT1\_CAE [C2\_DOMAIN\_1 // SYNAPTOTAGMIN // C2 // C2] CG3139 GH01240 23B1-23B2 dup:1/4 ID:54C2

CG3139

+ BcDNA:GH07485 enzyme \* 3e-55 CAO\_YEAST ACYL-COENZYME A OXIDASE (ACYL-COA OXIDASE) ac \* 1e-130 Similarity 1 Rat Acyl-CoA oxidase I (SW:CAO1\_RAT); cDNA EST EMBL: \* 1e-145 p CG5009 GH01266 54E8-54E8 dup:1/2 ID:54C6

CG5009

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

CG11142

+ transcription\_factor \* CROL BETA(aa) \* 2e-08 AZF1\_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin \* 6e-09 CROL GAMMA \* 2e-09 similar to Zinc finger, C2H2 type (4 doma[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG12071 GH01388 100B-100B ID:54D4

CG12071

+ 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

CG4879

CG1545 + unknown \* CG1545 GH01560 10A-10A dup:2/2 ID:54E10

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

CG8083

+ endopeptidase \* DMSER2\_7 Ser99Db \* 7e-70 serine proteinase (EC 3.4.21.-) precursor - fruit fly (*Drosophila melanogaster*) \* 1e-11 similar to peptidase family S1 (tryp[trypsin // CHYMOTRYPSIN // TRYPSIN\_SER ] CG6483 GH01508 65A2-65A2 dup:2/2 ID:54E6

CG6483

+ protein\_kinase \* protein kinase(aa) \* PUTATIVE SERINE/THREONINE-PROTEIN KINASE C01C4.3 IN CHROMOSOME X(aa) \* 5e-17 SNF1\_YEAST CARBON CATABOLITE DEREPRESSING PROTEIN[PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG4945 GH01572 53C7-53C7 dup:3/4 ID:54F3

CG4945

+ 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

CG9423

CG11446 + unknown \* CG11446 GH01717 2A3-2A3 ID:54G6

+ enzyme \* alkaline phosphatase(aa) \* MEMBRANE-BOUND ALKALINE PHOSPHATASE PRECURSOR (M-ALP)(aa) \* DMALKPHOS\_2 Aph-4 \* intestinal alkaline phosphatase VII; IAP [ALKALINE\_PHOSPHATASE // ALKPHPTASE // ] CG3290 GH01891 58C7-58C7 ID:54H10

CG3290

+ enzyme \* ODO1\_YEAST 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (ALPHA-KETOGLUTAR \* Similar to 2-oxoglutarate dehydrogenase; coded for by *C. elegans* [E1\_dehydrog] CG11661 73D6-73D7 dup:3/7

CG11661

ID:54H3  
+ HLHmbetatranscription\_factor \* 1e-108 helix-loop-helix protein m-beta - fruit fly (Drosophila melanogaster) \* 2e-10 lin-22 \* 3e-20  
CG14548 HES1\_MOUSE TRANSCRIPTION FACTOR HES-1 (HAIRY[HLH // HELIX\_LOOP\_HELIX // HELIX\_LOOP\_H] CG14548 GH01842  
96F10-96F10 ID:54H5  
+ Eno enzyme \* DMENOLAS\_2 Eno \* 1e-154 phosphopyruvate hydratase (EC 4.2.1.11) - yeast (Saccharomyces cerevisiae) >g  
CG17654 ENO\_DROME ENOLASE (2-PHOSPHOGLYCERATE DEHYD [ENOLASE // enolase] CG17654 GH01942 22F3-22F3 ID:55A2  
+ \* MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM-SENSITIVE MYC  
INOSITOL MONOPHOSPHATASE A1)(aa) \* 2e-41 hypothetical p [inositol\_P // INOSPHPTASE // IMP\_1 // ] CG9391 78C7-78C7  
dup:2/2 ID:55B1  
CG9391  
CG2657 + ion\_channel glutamate receptor, delta-2 subunit-like SBP\_GLUR CG2657 GH02344 ID:55B12  
CG17506 + unknown smilarity to indora CG17506 GH02266 ID:55B6  
+ RNA-directed\_DNA\_polymerase,\_group\_II\_intron\_encoded \* reverse transcriptase - fruit fly (Drosophila melanogaster)(aa)  
SPAC3G9.15c; len:230aa; similarity: to YLR051C, Q120 35, unclassified protein, (21 [NLS\_BP] CG1142 GH02295 85A1-85A1  
CG1142 ID:55B7  
+ enzyme \* DMPGMII\_3 agr;-Man-II \* alpha-mannosidase(aa) \* alpha-mannosidase (EC 3.2.1.24) precursor - human(aa) \*  
CG9466 LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANN [Glyco\_hydro\_38] CG9466 GH02475 29F1-29F1 ID:55C11  
+ transporter \* DMWHITER\_2 w \* ORF YOL075c(aa) \* putative protei(aa) \* 6e-69 WHIT\_DROME WHITE PROTEIN white  
CG9664 protein - fruit fly (Droso [ATP\_GTP\_A2 // ABC\_tran // DA\_BOX // ATP] CG9664 GH02377 25A1-25A1 ID:55C2  
+ LanB1 cell\_adhesion \* DMLAMB01\_2 LanB2 \* LanB1 \* LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN)(aa) \*  
LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN)(aa) [laminin\_EGF // EGF\_1 // EGFLAMININ // L] CG7123 GH0245  
CG7123 28D-28D ID:55C7  
CG7506 + unknown \* 2e-07 cDNA EST comes from this gene; cDNA EST co \* \* CG7506 GH02466 66A7-66A7 ID:55C9  
+ unknown \* 9E-36\* 7e-34 cDNA EST comes from this gene; cDNA EST co \* 3e-59 cytoplasmic protein Ndr1 \* 2e-60 RTP  
CG15668 nickel-specific inductio CG15668 GH02495 57E8-57E dup:2/4 ID:55D1  
+ tld metalloendopeptidase DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR ASTACIN,ASX\_HYDROXYL  
CG6868 Astacin, CUB, EGF,] CG6868 ID:55D10  
CG10579 + Ecdysone-induced protein 63E protein\_kinase serine/threonine kinase protein kinase CG10579 GH02721 ID:55D11  
+ cell\_adhesion \* 1e-180 odd Oz product \* 8e-31 similar to tenascin \* 1e-107 Ten-m4 \* 1e-101 (mouse DOC4 LIKE protein)  
CG2578 [NLS\_BP] CG2578 GH02628 11B1-11B1 ID:55D3  
CG7366 + unknown \* CG7366 GH02649 67E7-67E7 ID:55D4  
CG1537 + unknown \* CG1537 GH02938 10A-10A dup:2/2 ID:55E12  
+ EG:100G10.2 unknown \* by motif; 1-match\_description=ATP/GTP-binding site motif A (P-loop).; by match; 2-  
CG2681 match\_accession=SPTRE...(aa) \* by motif; \* 2e-10 seven-in-absentia CG2681 GH02982 3B5-3B5 ID:55F2  
CG18249 + unknown \* CG18249 GH03003 84F5-84F5 ID:55F4  
CG16772 + unknown \* CG16772 GH03035 38B1-38B1 ID:55F6  
CG15855 + Eip63F-1ligand\_binding\_or\_carrier \* Eip63F-1 \* 2e-74 E631\_DROME CALCIUM-BINDING PROTEIN E63-1 calcium-binding pr \*

3e-17 similar to EF-hand calcium binding proteins; most similar to ca CG15855 GH03109 63F7-63F7 ID:55G4

CG10382 + wrapper cell\_adhesion \* wrapper protein(aa) \* 9e-17 predicted protein contains a large number of Ig superfamily repeat \* 2e-16 NCA1\_MOUSE NEURAL CELL ADHESION MOLECULE, LAR [ig] CG10382 GH03113 58D6-58D6 ID:55G5

CG4008 + und peptidase \* 1e-107 AMP2\_YEAST METHIONINE AMINOPEPTIDASE (METAP 2) (PEPTIDASE M 2) (U \* methionine aminopeptidase \* 1e-38 Similarity to Rat initiation factor ass [Peptidase\_M24 // MAPEPTIDASE] CG4008 GH03119 30D1-30D1 ID:55G6

CG3390 + enzyme \* 3e-37 FOLE\_YEAST PUTATIVE FOLYLPOLYGLUTAMATE SYNTHASE (FOLYLPOLY-GAMMA-GLUTAMATE SYNT \* 3e-43 FOLC\_CAEEL PUTATIVE FOLYLPOLYGLUTAMATE SYNTHASE (FOLYL [Mur\_ligase] CG3390 GH03216 25C5-25C5 dup:1/3 ID:55G9

CG8128 + DNA\_repair\_protein \* putative antisense basic fibroblast growth factor(aa) \* antisense basic fibroblast growth factor B(aa) \* 4e-30 GFG\_RAT PROTEIN GFG antisense basic f [MUTT // mutT // MUTTDOMAIN] CG8128 GH03273 13E13-13E14 ID:55H3

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

CG14617 + unknown \* 0.00000002\* 0.00000002\* CG14617 GH03511 19F6-20A1 ID:56A1

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

CG10509 + unknown \* 2e-20 coded for by C. elegans cDNA yk173c12.5 \* 3e-11 unknown protein \* contains similarity to Physcomitrella patens glyceraldehyde 3-phosphate dehy CG10509 GH03649 57D3-57D4 dup:1/2 ID:56B3

CG18358 + unknown \* CG18358 GH03717 15A3-15A3 ID:56B7

CG3523 + BcDNA:GH07626 enzyme \* p270(aa) \* Similar to polyketide synthase.(aa) \* FK506 polyketide synthase(aa) \* [adh\_zinc // Thioesterase // ACP\_DOMAIN ] CG3523 GH03816 23D-23D dup:4/9 ID:56C9

CG3481 + Adh storage\_protein \* DMADHA1\_9 Adh \* 3e-06 FOX2\_YEAST PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL \* 1e-145 alcohol dehydrogenase (EC 1.1.1.1[ALCDHDRGNASE // GDHRDH // adh\_short // ] CG3481 GH03875 35B3-35B3 dup:4/6 ID:56D5

CG18210 + unknown \* CG18210 GH04075 13C5-13C5 dup:2/2 ID:56E10

CG17977 + unknown \* CG17977 GH04104 44A3-44A3 ID:56F1

CG1809 + enzyme \* alkaline phosphatase(aa) \* soluble alkaline phosphatase(aa) \* 1e-27 repressible alkaline phosphatase (EC 3.1.3.1) \* 2e-96 alkaline phosphatase (EC [ALKALINE\_PHOSPHATASE // ALKPHPTASE // ] CG1809 GH04113 45F3-45F3 ID:56F2

CG8993 + \* DMC132E8 \* similar to thioredoxin(aa) \* thioredoxin - Chloroflexus aurantiacus(aa) \* 4e-15 TRX1\_YEAST THIOREDOXIN I (TR-I) thioredoxin I - yeast (Sa [THIOREDOXIN // THIOREDOXIN\_2 // thioered] CG8993 62E-62E ID:56G3

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

CG11425 + enzyme \* 4e-08 probable membrane protein YDR284c - yeast (Saccharomyces cerevisiae) \* 2e-40 wunen \* 1e-20 YSX3\_CAEEL HYPOTHETICAL 39.0 KD PROTEIN T28D9.3 IN [PA\_PHOSPHATASE] CG11425 GH04282 79E4-79E4 ID:56G6

CG6866	+ RNA_binding * DOUBLE STRANDED RNA BINDING PROTEIN A (XLRBPA)(aa) * TAR (HIV) RNA-binding protein 2(aa) *
CG18609	TAR (HIV) RNA binding protein 2(aa) * 1e-05 contains simi [dsrm // DSRBD] CG6866 GH04468 34B6-34B6 dup:1/2 ID:57A1
CG12955	+ unknown * CG18609 GH04567 55E10-55E10 ID:57A10
CG3714	+ ligand_binding_or_carrier * 3e-07 similar to agrin and follistatin; egf-like repeats * 2e-08 FSA_MOUSE FOLLISTATIN
CG10342	PRECURSOR (FS) (ACTIVIN-BINDING PROTEIN) * 9e-08 follistatin [kaza] CG12955 GH04473 51E9-51E9 ID:57A2
	+ enzyme * putative nicotinate phosphoribosyltransferase(aa) * 1e-169 putative nicotinate phosphoribosyltransferase *
	hypothetical protein * similar to nicotin CG3714 25E1-25E1 dup:2/3 ID:57A8
	+ npf signal_transduction * neuropeptide F(aa) ** CG10342 GH04563 89D5-89D5 ID:57A9
	+ enzyme * DMALKPHOS_2 Aph-4 * 7e-27 PPB_YEAST REPRESSIBLE ALKALINE PHOSPHATASE PRECURSOR al * 2e-
CG5150	86 alkaline phosphatase * 1e-100 PPBT_MOUSE ALKALINE PHOSPHAT [ALKPHPTASE // alk_phosphatase] CG5150 GH04681
	64E-64E ID:57B10
	+ cell_adhesion * Kallmann syndrome KAL product - quail(aa) * 3e-18 similar to WAP-type (Whey Acidic Protein) 'four-disulfid
CG6173	core', F * 4e-29 Kallmann syndrome prote [wap // 4_DISULFIDE_CORE // 4DISULPHCORE] CG6173 GH04611 95E1-95E1
	ID:57B4
	+ RNA_binding * 2e-05 coded for by C. elegans cDNA yk102b7.3; coded for by C. elegans cDNA yk124e5.3; * 6e-05
CG6995	ROG_MOUSE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (H [RBD // rrm // NLS_BP] CG6995 GH04738 96B1-
	96B2 dup:3/5 ID:57C1
CG5497	+ unknown * 2e-23 predicted using Genefinder; cDNA EST yk414f4.5 comes from this g * 9e-27 HSPC007 * CG5497
CG7515	GH04861 55E4-55E4 ID:57C12
	+ CG7515 GH04814 ID:57C5
CG17544	+ enzyme * Similar to acyl-coenzyme A oxidase; coded for by C. elegans cDNA yk133e10.5(aa) * ACYL-COENZYME A
CG4571	OXIDASE PXP-2 (ACYL-COA OXIDASE)(aa) * ACYL-COENZY CG17544 GH04872 37E1-37E1 dup:3/3 ID:57D3
	+ unknown * CG4571 GH05034 6D6-6D7 dup:4/4 ID:57E8
CG2096	+ flw protein_phosphatase * phosphoprotein phosphatase (EC 3.1.3.16) gamma-2 - human(aa) * Similarity to Human
	serine/threonine protein phosphatase PP1B (SW:PP1B_HUMAN);[PHOSPHO_ESTER // STPHPTASE // SER_THR_] CG2096
	GH05039 9C1-9C1 dup:2/2 ID:57E9
CG6016	+ enzyme * predicted using Genefinder; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST
CG3312	yk199c3.5 comes from this gene; cDNA EST yk199c3 [CDP_ALCOHOL_P_TRANSF // CDP_ALCOHOL_P_T] CG6016 GH05229
CG14008	50B1-50B1 dup:1/2 ID:57G4
	+ CG3312 ID:57H12
	+ unknown * 1E-109** CG14008 GH05437 25F3-25F3 ID:57H8
CG9808	+ BcDNA:GH12504 transmembrane_receptor * 3e-07 microtubule binding protein D-CLIP-190 * 1e-06 DYNA_MOUSE DYNACTIN
CG5783	KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP- * 1e-06 DYNA_HUMAN CG9808 GH05455 85B3-85B4
CG4402	dup:3/4 ID:57H9
	+ unknown * 3e-07 hypothetical protein ** CG5783 GH05617 36E6-36E6 ID:58A12
	+ enzyme * lysyl oxidase-like 2(aa) * 8e-09 Similarity to Human M130 antigen cDNA EST * 1e-103 lysyl oxidase-related protei

\* 5e-99 lysyl oxidase homolog [SCAVENGER\_RECEPTOR // Lysyl\_oxidase // ] CG4402 GH05569 58A2-58A2 ID:58A8  
 + RNA\_binding \* No definition line found(aa) \* qrk58E-3 \* KEP1(aa) \* 8e-05 hypothetical protein YLR116w - yeast  
 (Saccharomyces cerevisiae) ( [KH\_DOMAIN] CG9337 GH05725 38F1-38F1 ID:58B8  
 + \* muscle-specific serine kinase 1; MSK1(aa) \* PROTEIN KINASE DSK1 (DIS1-SUPPRESSING PROTEIN KINASE)(aa) \*  
 hypothetical protein - Caenorhabditis elegans [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG9085 79E2-79E2 dup:1/3  
 ID:58C1  
 + sm RNA\_binding \* DMSMOOTH\_2 sm \* 4e-20 homologous to human hnRNP L \* 5e-22 DMSMOOTH\_2 sm \* [RBD] CG9218  
 GH05823 56D11-56E1 dup:1/2 ID:58C12  
 + CG7296 GH05801 ID:58C6  
 + unknown \* gene product(aa) \* 6e-19 gene product \* 2e-23 JWA protein \* JM4 CG10373 GH05842 37A4-37A4 ID:58D2  
 + unknown \* K10D2.3 gene product(aa) \* 3e-14 hypothetical protein YOL102c - yeast (Saccharomyces cerevisiae) \* 4e-07  
 /match=(desc: \* 4e-12 The gene is expressed [PAP // ZINC\_FINGER\_C2H2] CG7163 GH05885 66C11-66C11 dup:1/3 ID:58D3  
 + CG2922 83B4-83B4 dup:3/3 ID:58E11  
 + enzyme \* acid phosphatase (EC 3.1.3.2) Acph-1 precursor, lysosomal - fruit fly (Drosophila melanogaster)(aa) \* acid  
 phosphatase-1(aa) \* PUTATIVE ACID PHOSPH [acid\_phosphat] CG6656 GH06011 93F-93F dup:3/3 ID:58E4  
 + CG12612 GH06062 dup:2/2 ID:58E6  
 + Zw enzyme \* 1e-129 glucose-6-phosphate dehydrogenase (ZWF1) (EC 1.1.1.49) \* glucose-6-phosphate 1-dehydrogenase (E  
 1.1.1.49) - fruit fly (Drosophila mela \* 1e- [G6PD // G6PDHDRGNASE // G6P\_DEHYDROGENA] CG12529 GH06084 18D12-18D1:  
 dup:3/3 ID:58E7  
 + protein\_kinase \* Mlc-k \* Lk6 \* DMRSK\_2 S6kII \* DMDAKT1\_2 Akt1 [PROTEIN\_KINASE\_ST // TYRKINASE // PROTE]  
 CG11221 GH06138 27A2-27A2 ID:58F2  
 + unknown \* predicted using Genefinder; cDNA EST yk268h6.5 comes from this gene; cDNA EST yk465f2.5 comes from this  
 gene; cDNA EST yk393g7.5 comes from this gene CG10512 GH06154 78C3-78C4 ID:58F3  
 + unknown \* [PFKB\_KINASES\_1] CG18494 GH06208 32A1-32A1 ID:58F8  
 + EG:BACN32G11.3 unknown \* BACN32G11.f \* 1e-29 L130\_HUMAN KD LEUCINE-RICH PROTEIN (LRP 130) (GP130) le \*  
 leucine-rich protein - human leucine-rich protein sa \* BACN32G11.I CG14786 GH06301 2B1-2B1 ID:58G4  
 + signal\_transduction \* 1e-20 YMH2\_YEAST HYPOTHETICAL 171.1 KD PROTEIN IN YL16A-DAK1 INTERGENIC REGION  
 2e-07 SY65\_DROME SYNAPTOTAGMIN (P65) synaptotagmin - fruit fly ( \* [C2 // C2\_DOMAIN\_2] CG6643 GH06342 96A-96A  
 dup:1/2 ID:58G6  
 + \* 2e-19 /match=(desc:; /ma \* 2e-06 No definition line found \* C29F7.1 \* cDNA EST yk381e5.3 comes from this gene  
 CG10550 96C8-96C8 dup:1/4 ID:58G9  
 + \* [G\_PROTEIN\_RECEPTOR] CG5571 77B6-77B6 dup:1/2 ID:58H1  
 + unknown \* CG4377 GH06474 58A3-58A3 ID:58H6  
 + stil unknown \* 1e-171 STAND STILL (Y \* 1e-173 stil \* \* [NLS\_BP] CG8592 GH06596 49B2-49B2 ID:59A10  
 CG8430  
 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  
 + Scp2 ligand\_binding\_or\_carrier \* 6e-95 calcium-binding protein Cex C \* 1e-15 YSO6\_CAEEL HYPOTHETICAL CALCIUM-BINDING PROTEIN F56D1.6 IN CHROMOSOME II \* 2e-33 calexcitin \* 7[EF\_HAND // EF\_HAND\_2 // ATP\_GTP\_A] CG14904  
 CG14904 GH06666 92A1-89D4 dup:2/4 ID:59B6  
 + enzyme \* 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  
 CG2246 + \* VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE KD SUBUNIT) (VAA3-1)(aa) \* H+-transporting ATPase (EC 3.6.1.35), vacuolar, A chain, VA68 type - [ATP-synt\_ab // ATP-synt\_ab\_C // ATPASE\_] CG3762 34A4-34A4 dup:1/2 ID:59C4  
 CG3762 + 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  
 CG2469 + unknown \* CG4682 GH07323 94D10-94D10 dup:2/2 ID:59E10  
 CG4682 + defense/immunity\_protein \* 2e-33 peptidoglycan recognition protein precursor \* 7e-37 TNF superfamily, member (LTB)-like (peptidoglycan recognition \* 1e-33 peptidoglycan recogn CG8577 GH07464 44D8-44D8 ID:59F11  
 CG8577 + unknown \* Mob1p-like protein; Mob2p(aa) \* partial CDS(aa) \* cDNA EST yk373c2.5 comes from this gene; cDNA EST yk361f7.5 comes from this gene(aa) \* putative m CG11712 GH07469 68C5-68C5 dup:2/2 ID:59F12  
 CG11712 + cell\_adhesion \* 6e-06 CYAA\_YEAST ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) 1e-10 leucine-rich motif (LRR) protein homology to interleukin rec [LRR // LEURICHRPT // PRO\_RICH // CYTOCH] CG15151 GH07373 36E-36E ID:59F3  
 CG15151 + unknown \* CG10912 GH07575 55B2-55B2 ID:59G12  
 CG10912 + Ets65A transcription\_factor \* ETS domain transcription factor PET-1(aa) \* Friend leukemia virus integration 1(aa) \* contains strong similarity to ETS domains and \* DNA-BINDING [ETS\_DOMAIN\_1 // HSF\_ETS // ETSDOMAIN //] CG7018 GH07491 65A3-65A3 ID:59G3  
 CG7018 + unknown \* [NLS\_BP] CG7859 GH07769 93D9-93D9 dup:1/2 ID:60A6  
 CG7859 + unknown \* protein(aa) \* \* CG11877 GH07807 99A1-99A1 dup:2/3 ID:60A8  
 CG11877 + enzyme \* 9e-10 contains similarity to enoyl-CoA hydratases/isomerases Score=59 \* 2e-38 D3D2\_MOUSE 3,2-TRANS-ENOYL-COA ISOMERASE, MITOCHONDRIAL PRECURSOR (DOD [ECH] CG4592 GH07905 33A1-33A1 dup:1/2 ID:60B11  
 CG4592 + BG:DS00941.11 unknown \* AAs(aa) \* AAs(aa) \* CG16887 GH07914 34D4-34D4 dup:2/3 ID:60B12  
 CG16887 + unknown \* CG17124 GH07856 32A4-32A4 dup:1/2 ID:60B6  
 CG17124 + transporter \* 8e-07 predicted using Genefinder; cDNA EST yk416g4.5 comes from this g \* 2e-05 hypothetical protein - rabbi ORF might exte \* CG4526 GH08173 73A3-73A4 dup:3/6 ID:60D10  
 CG4526 + endopeptidase \* 2e-24 STUB\_DROME SERINE PROTEINASE STUBBLE (STUBBLE-STUBBLOID PROTEIN) \* 2e-16 MCT7\_MOUSE MAST CELL PROTEASE PRECURSOR (MMCP-7) (TRYPTASE) \* 6e-17 F [trypsin // TRYPSIN\_CATAL] CG9377 GH08193 34B6-34B6 dup:1/2 ID:60D12  
 CG9377



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

CG5888 + BG:DS02780.1 cell\_adhesion \* Toll protein(aa) \* 9e-05 cell-surface molecule connectin - fruit fly (Drosophila melanogaster) \* 2e-06 predicted using Genefinder; Similarity to Dr [LRR] CG5888 GH08155 35F12-36A1 dup:1/2 ID:60D6

CG7096 + unknown \* hypothetical protein(aa) \* DMRNAPER\_2 anon-3B1.2 \* 2e-08 0.9-kb RNA transcript \* 7e-10 DMRNAPER\_2 anon-3B1.2 CG7096 GH08336 93B5-93B5 dup:3/3 ID:60E10

CG16727 + transporter \* DMORCT2\_2 Orct \* putative organic cation transporter(aa) \* 5e-40 Similarity to Rat organic cation transporter cDNA EST \* 1e-39 OCTN3 [sugar\_tr] CG16727 GH08275 94D3-94D3 dup:2/2 ID:60E3

CG8460 + unknown \* A\_IG002N01.31 gene product(aa) \* No definition line found(aa) \* C44C1.2 gene product \* CG8460 GH08401 28F1-28F1 ID:60F5

CG10830 + ion\_channel \* 1e-35 VM106R.1 \* 2e-06 (novel protein similar to and mouse, worm an \* similar to TNF-alpha induced Protein B12 \* similar to human tumor necrosis fac CG10830 GH08630 93A2-93A2 dup:1/2 ID:60G10

CG9342 + ligand\_binding\_or\_carrier \* microsomal triglyceride transfer protein large subunit precursor(aa) \* 1e-51 MTP\_MOUSE MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN, LARGE SUBUNIT PRECU [MYB\_1 // ATP\_GTP\_A] CG9342 GH08556 38F4-38F4 dup:1/3 ID:60G5

CG5248 + loco signal\_transduction \* regulator of G-protein signalling LOCO C2(aa) \* 6e-08 YTN3\_CAEEL HYPOTHETICAL 33.0 KD PROTEIN C29H12.3 IN CHROMOSOME II (U \* 6e-43 RGSE\_MOUSE REGULA [GRK // RGS // NLS\_BP] CG5248 GH08607 94B11-94C1 dup:1/3 ID:60G8

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

CG17336 + Lcch3 ion\_channel \* Lcch3 \* GAB3\_DROME GAMMA-AMINOBUTYRIC-ACID RECEPTOR BETA-LIKE SUBUNIT PRECURSOR (GABA(A) \* 1e-109 similar to GABA receptor \* 1e-112 GAB3\_MOUSE GAMM [neur\_chan // NEUROTR\_ION\_CHANNEL // NRI] CG17336 GH08705 13F13-13F13 ID:60H3

CG3966 + ninaA chaperone \* DMNINAA\_7 ninaA \* PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, RHODOPSIN SPECIFIC ISOZYME PRECURSOR (PPIASE) (ROTAMASE)(aa) \* 4e-44 cyclophilin-related prot [pro\_isomerase // CSA\_PPIASE\_1 // CSA\_PP] CG3966 GH08867 21D3-21D3 dup:1/3 ID:61A11

CG9246 + unknown \* hypothetical protein(aa) \* cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST yk317d5.5 comes fro [NLS\_BP] CG9246 GH08927 39B3-39B3 dup:1/2 ID:61B10

CG4608 + bnl signal\_transduction \* FGF homolog(aa) \* bnl \* 3e-09 LET-756 protein \* 3e-14 fibroblast growth factor fibro [HBGFFGF // FGF // IL1HBGF] CG4608 GH08887 92B3-94E1 dup:3/3 ID:61B2

CG11790 + chaperone \* 1e-13 gene product \* 1e-09 disulfide-like protein prote \* [THIOREDOXIN\_2] CG11790 GH08893 96B15-96B15 dup:1/2 ID:61B4

CG12024 + signal\_transduction \* 5e-25 BAW protein \*\* [NLS\_BP] CG12024 GH08896 62E3-62E3 dup:1/2 ID:61B6

CG1208 + transporter \* Ser89E \* Glut1; \* 5e-38 YB91\_YEAST PROBABLE METABOLITE TRANSPORT PROTEIN YBR241C \* 4e-31 GTRL\_DROME GLUCOSE TRANSPORTER-LIKE PROTEIN glucose transp[HELIX\_LOOP\_HELIX // SUGRTRNSPORT // SUG] CG1208 GH09052 83C4-83C4 dup:1/2 ID:61C10

CG17524 + enzyme \* DMGST\_3 GstD1 \* 7e-09 probable membrane protein YLL060c - yeast (Saccharomyces cerevisiae) \* 7e-45 unknown \* 3e-16 GTT1\_MOUSE GLUTATHIONE S-TRANSFER [GST] CG17524 GH09055 55C9-55C9 dup:1/2 ID:61C11

CG11232 + unknown \* CG11232 GH08969 102F8-102F8 ID:61C4

CG8947 + 26/29kD-proteinase \* 26,29kDa proteinase(aa) \* 8e-61 cysteine proteinase cysteine \* 1e-56 predicted using Genefinder; similar to cathepsin-like protease; cD \* 2e-61 cath [THIOL\_PROTEASE\_CYS // PAPAINE // Peptidase] CG8947 70C9-70C9 dup:1/2 ID:61C5

CG18452 + scro transcription\_factor (scarecrow) homeobox protein Nkx2-1 homeobox CG18452 GH09166 dup:2/3 ID:61D10

+ unknown \* 5e-07 YNK8\_YEAST HYPOTHETICAL 30.7 KD PROTEIN IN CYB5-LEU4 INTERGENIC REGION \* 4e-46 T07F12.1 gene product \* 3e-09 Y33K\_HUMAN HYPOTHETICAL 33.4 KD P [UBA // SH3] CG13604 GH09153 97F1-97F1 dup:2/4 ID:61D8

CG13604 none

+ none GH09355 ID:61F3

CG4302 CG11051 + CG4302 CG11051 GH09393 ID:61F9

+ Pp1alpha-96A protein\_phosphatase \* DMPP113C\_2 Pp1-13C \* 1e-153 PP12\_YEAST SERINE/THREONINE PROTEIN PHOSPHATASE PP1-2 pho \* PP11\_DROME SERINE/THREONINE PROTEIN PHOSPHATASE ALPHA-[PHOSPHO\_ESTER // STPHPTASE // SER\_THR\_] CG6593 GH09488 96A5-96A5 ID:61G3

CG6593 + signal\_transduction \* agrin(aa) \* 8e-33 similar to agrin and follistatin; egf-like repeats \* 4e-13 FSA\_MOUSE FOLLISTATIN PRECURSOR (FS) (ACTIVIN-BINDING PROTEIN) \* 4e-13 [kazal] CG7159 GH09510 66C12-66C12 ID:61G5

CG7159 + cell\_adhesion \* 6e-05 similar to the protein kinase domain of myosin light chain kinases \* 6e-05 myosin light chain kinase isoform \* 5e-05 KMLS\_CHICK MYOSIN LIGHT C CG5699 GH09541 62C3-62C3 dup:2/3 ID:61G9

CG5699 + G-alpha47A signal\_transduction GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT (CLASS-I) >gi|

CG2204 ATP\_GTP\_A, G-alpha, GPROTEINA, GPROTEINA] CG2204 GH09771 dup:3/4 ID:61H10

CG7448 + transporter \* DMORCT2\_2 Orct \* 5e-13 putative organic cation transporter \* 4e-09 similar to C. elegans protein and to rat synaptic vesicle protein (PIR:S3 \* 2e-13 CG7448 GH09791 79B2-79B2 dup:1/2 ID:61H11

CG7448 + transcription\_factor \* 3e-05 HUNB\_TRICA HUNCHBACK PROTEIN hunchback \* 2e-06 DMHBG\_10 hb \* Hunchback protein \* [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG9932 GH09733 34A-34A dup:1/2 ID:61H6

CG9932 + alpha-Man-I enzyme mannosyl-oligosaccharide 1,2-alpha-mannosidase GLYHDRLASE47 CG17809 GH09743 dup:1/2 ID:61H7

CG17809 + unknown \* /match=(desc;; /match=(desc:(aa) \* 3e-38 /match=(desc;; /ma \* 4e-07 predicted using Genefinder \* cDNA EST yk381e5.3 comes from this gene CG11892 GH09761 96C7-96C7 dup:1/2 ID:61H9

CG11892 + cytochrome\_P450 CG17875 GH09824 dup:1/3 ID:62A2

CG17875 + unknown \* CG18550 GH09841 88E1-88E1 ID:62A3

CG18550 + unknown \* CG11462 GH09844 5C2-5C2 ID:62A4

CG11462 + \* neural precursor cell expressed developmentally downregulated Nedd9(aa) \* 1e-37 Crk-associated substrate \* 6e-36 enhancer of filamentation Crk-assoc [SH3DOMAIN // SH3] CG1212 61A4-61A5 dup:2/4 ID:62B1

CG1212 + ligand\_binding\_or\_carrier \* 2e-68 62D9.a \* 4e-10 cellular retinaldehyde-binding protein; CRALBP \* 2e-15 alpha tocopherol transfer protein \* 1e-15 TTPA\_RAT ALPHA-TOCOPHEROL TRAN [CRETINALDHBP // CRAL\_TRIO] CG3823 GH10083 5E1-5E1 ID:62B11

CG3823 + \* APOLIPOPROTEIN D PRECURSOR(aa) \* 7e-13 APD\_MOUSE APOLIPOPROTEIN D PRECURSOR apolipoprotein D \* 2e-16 apolipoprotein D APOLIPOPROTEIN D P \* 2e-17 APD [lipocalin // LIPOCALIN] CG4604 49F7-49F7 dup:2/2 ID:62B12

CG4604 + enzyme \* alpha-L-fucosidase(aa) \* fucosidase, alpha-L- 1, tissue(aa) \* 8e-28 hypothetical protein YIL106w - yeast

CG6128

(Saccharomyces cerevisiae) \* 4e-73 FUCO\_CAE [Alpha\_L\_fucos // GLHYDRLASE29] CG6128 GH09976 68C4-68C5 ID:62B4  
 + metabolism \* NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (COMPLEX I-SGDH) (CI-SGDH)(aa) \* NADH dehydrogenase (ubiquinone) beta subcomplex, (16kD, SGD) CG9762 GH10129 68F5-68F5 ID:62C1  
 + unknown \* DMRHO\_2 ve \* RHOMBOID PROTEIN (VEINLET PROTEIN)(aa) \* 5e-32 similar to transmembrane of D. melanogaster rhomboid protein \* 9e-28 UNKNOWN rhomboid-re CG1697 GH10260 10C6-10C6 dup:1/7 ID:62C10  
 + NetB cell\_adhesion \* extracellular extracellular ) map\_position:12F1 \* NetB \* 1e-170 NETB\_DROME NETRIN-B PRECURSOR Netrin-B melanog \* 3e-67 UNC6\_CAEEL UNC-6 PROTEIN P[ laminin\_EGF // EGFLAMININ // EGF\_LAM // ] CG10521 GH10173 12F1-12F3 dup:1/2 ID:62C5  
 + transmembrane\_receptor \* 2e-09 /match=(desc: \* 2e-52 YP84\_CAEEL HYPOTHETICAL 90.9 KD PROTEIN C08B11.4 IN CHROMOSOME II \* predicted using Genefinder \* cDNA EST comes from thi CG3106 GH10201 8F2-8F2 ID:62C6  
 + enzyme \* protein(aa) \* CG9164 GH10344 13C5-13C5 ID:62D5  
 + cell\_cycle\_regulator \* 1e-35 RAS1\_YEAST RAS-LIKE PROTEIN GTP-binding protein RAS1 \* 5e-32 RAS3\_DROME RAS-LIKE PROTEIN (ROUGHENED PROTEIN) transfo \* 3e-35 RASL\_CAEEL RAS-L[PRENYLATION // ras // ATP\_GTP\_A // RAST] CG1081 GH10361 83B3-83B3 ID:62D7  
 + unknown \* 4e-05 c431H6.1.2 (PUTATIVE novel protein) (PUTATIVE isoform 2) s \* c431H6.1.1 (PUTATIVE novel protein) (isoform 1) \* c431H6.1.3 (PUTATIVE novel prot CG17238 GH10365 87E1-87E1 dup:2/2 ID:62D8  
 + 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  
 + unknown \* 2e-05 No definition line found \* 4e-16 type II membrane protein \* 1E-175\* [SAP\_B // ER\_TARGET] CG12918 GH10427 46D7-46D7 dup:2/2 ID:62E2  
 + unknown \* 4e-07 inserted at base Both 5' and 3' ends of P element Inverse PCR \* [BTB] CG13917 GH10468 62A8-62A dup:3/3 ID:62E3  
 + unknown \* 3e-61 F38A5.1 gene product \* 1e-40 putative protein \* CG16979 GH10640 71D3-71D3 ID:62F11  
 + \* [PRENYLATION] CG10433 57F3-57F3 dup:4/5 ID:62F12  
 + ligand\_binding\_or\_carrier \* 2e-16 alpha tocopherol transfer protein \* 1e-15 TTPA\_RAT ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TTP) al \* tocopherol (alpha) transfer protein (ata [CRAL\_TRIO] CG13848 GH10582 96E1-96E1 ID:62F2  
 + transcription\_factor \* CG2267 100A2-100A2 dup:2/2 ID:62F6  
 + acj6 DNA\_binding \* DMIPOU\_2 acj6 \* POU domain transcription factor(aa) \* INHIBITORY POU PROTEIN (I-POU) (ABNORMAL CHEMOSENSORY JUMP PROTEIN)(aa) \* 1e-152 PP12\_YEAST SE [HOMEBOX\_1 // homeobox // HOMEBOX\_ // ] CG9151 GH10637 13C1-13C4 ID:62F9  
 + none GH10751 ID:62G7  
 + cell\_adhesion \* DMARTAN\_7 trn \* kek1 \* tartan protein(aa) \* 5e-16 CYAA\_YEAST ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) [LRR // LEURICHRPT // LRRCT] CG11280 GH10871 69F5-69F5 ID:62H10  
 + motor\_protein \* CG7029 GH10817 94C8-94D dup:2/5 ID:62H3  
 + enzyme \* intermediate chain 1(aa) \* nm23-H7(aa) \* NUCLEOSIDE DIPHOSPHATE KINASE (NDK) (NDP KINASE)(aa) \* 1e-06 type nucleoside diphosphate kinase NM23-H6 CG8362 GH10857 85E4-85E4 ID:62H9

CG18662 + unknown \* CG18662 GH10940 29F7-29F7 ID:63A8  
+ function\_unknown \* galactokinase 2(aa) \* 2e-45 GAL1\_YEAST GALACTOKINASE galactokinase (EC 2.7.1.6) - yea \* 5e-35  
Similar to galactokinase \* 2e-65 galactose kinase [GHMP\_kinases // GALCTOKINASE // GHMP\_KI] CG5288 GH11113 66E6-66E  
CG5288 ID:63B10  
+ transcription\_factor \* 9e-06 TBP-like factor \* 9e-06 TATA box binding protein-related factor \* CG9879 GH11020 23A3-23A  
CG9879 ID:63B2  
+ enzyme \* 1e-09 URE2\_YEAST URE2 PROTEIN glutathione transferase homolog U \* 4e-78 glutathione transferase (EC  
CG10091 2.5.1.18) D1 - fruit fly (Drosophila melanogaste [GST] CG10091 GH11034 87B12-87B12 ID:63B3  
+ enzyme \* Ac76E \* 5e-56 adenylyl cyclase 76E \* 2e-45 Similar to guanylate cyclase \* 2e-54 adenylyl cyclase type I  
CG5712 [GUANYLATE\_CYCLASES // guanylate\_cyc // ] CG5712 GH11267 62D3-62D4 ID:63C10  
+ Rack1 signal\_transduction \* Rack1 \* GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN  
CG7111 (RECEPTOR OF ACTIVATED PROTEIN KINASE C HOMOLOG)(aa) \* 3e-89 GBLP\_YEAS[GPROTEINBRPT // WD40\_REGION //  
WD\_REPEA] CG7111 GH11320 28D2-28D2 dup:2/3 ID:63C12  
+ EG:100G10.4 enzyme \* by content; by match; 2-match\_description=4-NITROPHENYLPHOSPHATASE.; 2-match...(aa) \*  
CG2680 BLASTX 8.9E-14 PHO13|4-Nitrophenylphosphatase(dna) \* 1e-20 4- CG2680 GH11163 3B5-3B5 ID:63C4  
CG12727 + unknown \* CG12727 GH11189 11F7-11F7 ID:63C5  
+ transcription\_factor \* scrt \* Similarity to Drosophila scratch neuronal zinc-finger transcription factor \* 9e-05 RIM1 \* 7e-73  
CG12605 neuron specific zinc finger transcription[zf-C2H2 // ZINC\_FINGER\_C2H2 // ATP\_GTP\_] CG12605 GH11439 64A1-64A1 ID:63D10  
+ ion\_channel \* ATP-regulated potassium channel brain, Peptide Partial, \* G PROTEIN-ACTIVATED INWARD RECTIFIER  
POTASSIUM CHANNEL (GIRK3) (POTASSIUM CHANNEL, INWARDL [CHANNEL\_PORE\_K // IRK] CG4370 GH11459 97D1-  
CG4370 97D1 ID:63D11  
+ porin ion\_channel \* DMMITPORN\_2 porin \* 1e-24 porin - yeast (Saccharomyces cerevisiae) outer mitochondri \* 1e-162 voltage  
dependent anion-selective channel \* 2e-55 code [Euk\_porin // EUKARYTPORIN // EUKARYOTIC] CG6647 GH11331 32B3-32B4  
CG6647 dup:2/3 ID:63D2  
+ srp transcription\_factor \* GATA factor(aa) \* DMGATAFAC\_2 srp \* 3e-12 GAT1\_YEAST GAT1 PROTEIN probable membrane  
protein YFL02 \* 2e-18 ELT1\_CAEEL TRANSCRIPTION FACTOR[GATAZNFINGER // LECTIN\_LEGUME\_BETA // G] CG3992  
CG3992 GH11649 89B3-89B4 dup:2/5 ID:63F10  
+ Cbp53E calcium\_binding \* DMCALB32A\_2 Cbp53E \* calbindin 2, (29kD, calretinin)(aa) \* CALRETININ (CR)(aa) \* CALBINDIN-  
CG6702 32(aa) [EF\_HAND // effhand // EF\_HAND\_2] CG6702 GH11671 53E7-53E10 ID:63F12  
+ receptor \* 5e-05 LIRP\_LOCM1 LIRP PRECURSOR (LOCUSTA INSULIN-RELATED PEPTIDE) \* \* [INSULIN // Insulin //  
CG8167 NLS\_BP] CG8167 GH11579 67C-67C ID:63F4  
CG16959 + unknown \* [EGF\_2] CG16959 GH11627 71B2-71B2 dup:2/2 ID:63F7  
+ ribosomal\_protein \* ribosomal protein L34(aa) \* PROBABLE 60S RIBOSOMAL PROTEIN YIL052C(aa) \* ribosomal protein  
CG9354 L34(aa) \* 1e-47 RL34\_AEDAL 60S RIBOSOMAL PROTEIN L34 (L3 NLS\_BP, RIBOSOMAL\_L34E CG9354 ID:63F9  
+ endopeptidase \* similar to the M13 or zinc metalloprotease family of peptidases(aa) \* endothelin converting enzyme 1(aa) \*  
CG9505 endothelin converting enzyme-2 - bovine [ZINC\_PROTEASE // Peptidase\_M13] CG9505 GH11680 28D1-28D1 ID:63G3  
CG18107 + unknown \* 1e-10 immune induced protein \* 0.000000000002\* 1E-141\* CG18107 GH11719 55C9-55C9 ID:63G6

CG8759	+ Nacalpaunknown * 4e-13 EGD2_YEAST EGD2 PROTEIN EGD2 protein - yeast (Saccharomyc * 5e-73 alpha NAC * 1e-34 alph
none	NAC/1.9.2. protein alpha-NAC, non-musc * 1e-34 Nasce CG8759 GH11940 49C2-49C2 dup:2/2 ID:63H12
	+ none GH11889 ID:63H7
CG1449	+ zfh2 transcription_factor * ZINC-FINGER PROTEIN (ZINC-FINGER HOMEODOMAIN PROTEIN 2)(aa) * DMZFH2_2 zfh2 * 7e-40 Contains similarity to Pfam domain: (zf-C2H2), Score=[HOMEBOX_1 // homeobox // ZF_MATRIN // ] CG1449 GH11902 102C1-102C3 dup:2/2 ID:63H9
	+ gbb signal_transduction * DM60AP * 60A PROTEIN PRECURSOR(aa) * 9e-17 contains similarity to the TGF-beta family of growth factors e * 3e-52 BMP7_MOUSE BONE MORPHOGENETIC PROT [TGFb_propeptide] CG5562 GH12092 60A5-60A5 ID:64B10
CG5562	+ bnb unknown * DMBNBR_2 bnb * 1e-148 BNB_DROME BANGLES AND BEADS PROTEIN bangles and * GAP-43-related protein - fruit fly (Drosophila melanogaster) * bnb gene prod CG7088 GH12078 17D6-17D6 ID:64B8
CG7088	+ unknown * 1e-10 cDNA EST yk471b2.5 comes from this gene; cDNA EST yk471b2.3 come ** CG4742 GH12140 15A5-15A5 ID:64C2
CG4742	+ emc transcription_factor * DNA-binding protein inhibitor Id-1H - human(aa) * EXTRA-MACROCHAETAE PROTEIN(aa) * DMEC3_3 emc * 7e-78 extramacrochaetae protein - fruit fly[HELIX_LOOP_HELIX // HELIX_LOOP_HELIX_2] CG1007 GH12170 61D1-61D2 dup:1/2 ID:64C5
CG1007	+ endopeptidase * DMEAST_4 ea * DMSNAKE_2 snk * 2e-28 SNAK_DROME SERINE PROTEASE SNAKE PRECURSOR serine proteina * 3e-18 similar to peptidase family S1 (trypsin famil [trypsin // CHYMOTRYPSIN // TRYPSIN_SER ] CG6367 GH12385 17B3-17B4 ID:64D10
CG6367	+ cell_adhesion CG5291 GH12331 dup:2/3 ID:64D5
CG5291	+ enzyme * DMPAH Hn * 1e-114 phenylalanine hydroxylase * 1e-117 tryptophan hydroxylase * 1e-149 TR5H_MOUSE TRYPTOPHAN 5-MONOOXYGENASE (TRYPTOPHAN 5-HYDROXYLASE [FYWHYDRXLASE // bioplerin_H // BIOPTERI] CG9122 GH12537 61F3-61F3 ID:64F2
CG9122	+ unknown * [PRO_RICH] CG14821 GH12583 65D5-65D5 ID:64F7
CG14821	+ signal_transduction * Ras-binding protein SUR-8(aa) * 4e-25 adenylate cyclase * 9e-32 gene flightless-I protein - fruit fly (Drosophila melanogaster) ( * 1e-152 Ras-bindi [LRR // LEURICHRPT] CG5407 GH12617 90A6-92E12 ID:64F8
CG5407	+ enzyme * diacylglycerol kinase(aa) * 2e-30 diacylglycerol kinase (EC 2.7.1.107) - fruit fly (Drosophila melanogaster) * 1e-57 alpha diacylglycerol kinase; a [DAG_PE_BINDING_DOMAIN // RA // C1 // DA] CG5875 GH12677 95D1-97F1 dup:2/5 ID:64G5
CG5875	+ transporter * protein:Na+/H+ antiporter(aa) * cdu2(aa) * cdu2 cd * CG10806 GH12682 27C-27C ID:64G6
CG10806	+ Snap transporter * Snap * soluble NSF attachment protein(aa) * 3e-40 transport vesicle fusion protein SEC17 - yeast (Saccharomyces cerevisiae) * 1e-73 coded for by C. [NSFATTACHMNT] CG6625 GH12751 77B3-77B3 dup:1/2 ID:64G9
CG6625	+ 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
CG17509	+ transcription_factor_binding * coded for by C. elegans cDNA yk131g12.5(aa) * Rack1 * transcription initiation factor IID-associated protein, 80K - fruit fly (Drosophil[WD40_REGION // BEACH_DOMAIN // IG_MHC /] CG6734 GH12955 33B10-33B11 ID:65A8
CG6734	+ structural_protein * 9e-09 cuticle protein LCP65Ac cuticle p * 2e-11 CUD4_LOCFMI ENDOCUTICLE STRUCTURAL
CG8511	

GLYCOPROTEIN (ABD-4A) g \* 1e-10 Lcp65Ac \* cuticle homolog [CUTICLE // insect\_cuticle] CG8511 GH12964 49A3-49A3 ID:65A9  
 + protein\_kinase \* serine/threonine kinase(aa) \* predicted using Genefinder; Similarity to Arabidopsis serine/threonine protein kinase (PIR Acc. No. cDNA EST comes from [PROTEIN\_KINASE\_ST // TYRKINASE // PROTE] CG6114 GH13047 72A5-72B1 ID:65B6  
 CG6114  
 CG6123 + unknown \* [NLS\_BP] CG6123 GH13094 17A7-17A7 ID:65B9  
 CG18065 + unknown \* CG18065 GH13245 57A8-57A8 ID:65C11  
 CG14889 + structural\_protein \* [COLLAGEN\_REP // Collagen] CG14889 GH13492 92A1-92A1 dup:1/2 ID:65D11  
 + sax transmembrane\_receptor \* DMTVP\_2 tkv \* DMBKR4A\_2 sax \* 9e-13 NRK1\_YEAST SERINE/THREONINE-PROTEIN KINASE NRK1 (N-RICH KINASE 1) \* receptor protein serine/threonine [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG1891 GH13369 43E18-43E18 dup:2/2 ID:65D2  
 CG1891  
 CG13784 + unknown \* CG13784 GH13387 27E4-27E5 ID:65D3  
 CG17108 + \* cdc2MsC(aa) \* cdc2MsC \* CG17108 32A-32A dup:4/4 ID:65E10  
 + cytoskeletal\_structural\_protein \* 2e-47 dystrophin \* 1e-117 unnamed protein product \* 1e-143 dystrobrevin dystrobrevin \* 1e-143 dystrobrevin B [ZF\_ZZ // ZZ // CYTOCHROME\_C] CG8529 GH13689 49A6-49A7 dup:2/2 ID:65E12  
 CG8529 + transporter \* HYPOTHETICAL 48.6 KD PROTEIN IN CHROMOSOME II(aa) \* DMORCT2\_2 Orct \* solute carrier family (organic cation transporter), member 1(aa) \* 1e-42 putative [sugar\_tr] CG7342 GH13557 92A11-94D3 dup:2/2 ID:65E3  
 CG7342 + structural\_protein \* 8e-30 YLS5\_CAEEL HYPOTHETICAL 55.1 KD PROTEIN F09G8.5 IN CHROMOSOME III \* 2e-07 B7 \* 6e-36 chromosome open reading frame 28.3 KD PROTEIN C21OR \* 8e- [LRR] CG14995 GH13848 64A7-64A8 dup:3/3 ID:65F12  
 CG14995 + unknown \* similar to Arabidopsis thaliana male sterility protein \* 3e-52 /match=(desc;; /ma \* 3e-32 male sterility 2-like protein \* 3e-54 DMC103B4 CG1441 GH13752 46C5-46C5 ID:65F4  
 CG1441 + BcDNA:GH06032 transporter \* DSERCA\_2 Ca-P60A \* 1e-158 ATC6\_YEAST PROBABLE CALCIUM-TRANSPORTING ATPASE hypoth \* Similarity to Yeast E1-E2 ATPase YEL031W (SW:YED1\_YEAST); cDNA E[COF\_2 // CATATPASE // E1-E2\_ATPase] CG6230 GH13756 32D4-32D4 dup:2/2 ID:65F6  
 CG6230 + unknown \* 9e-05 glucose transport protein homolog - Caenorhabditis elegans \* 2e-14 protein \* 2e-14 transporter-like protein p87 \* predicted using Genefinder; [sugar\_tr] CG3690 GH13765 1D1-1D1 ID:65F8  
 CG3690 + signal\_transduction \* cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; CG8683 GH13975 28E5-28E6 dup:2/3 ID:65G12  
 CG8683 + enzyme \* putative dehydrogenase(aa) \* GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE REDUCTASE) (HPR) (GDH) (HYDROXYPYRUVATE DEHYDROGENASE) (GLYOXYL [D\_2\_HYDROXYACID\_DH\_3 // 2-Hacid\_DH] CG9331 GH13879 38E9-38E9 ID:65G4  
 CG9331 + endopeptidase \* mas \* Ser5 \* Tequila \* zgr;Try [trypsin // CHYMOTRYPSIN // TRYPSIN\_SER] CG11912 GH13929 21B7-21B8 ID:65G7  
 CG11912 + Cyp6a2 cytochrome\_P450 \* PUTATIVE CYTOCHROME P450 T10B9.7 IN CHROMOSOME II(aa) \* DMCYP6A2A\_5 Cyp6a2 \* CYP6A2 \* 3e-43 similar to cytochrome P450 [EP450II // MITP450 // CYTOCHROME\_P450 /] CG9438 GH13965 42C5-42C5 ID:65G9  
 CG9438

CG11427 + rb chaperone \* beta3 \* Beta3 protein(aa) \* 2e-50 beta-adaptin protein \* 2e-78 cDNA EST yk288h5.5 comes from this gene; cDNA EST yk288f1.5 comes CG11427 GH14079 4C4-4C4 ID:66A1

CG5939 + Prm motor\_protein \* DMSTPMY\_2 Prm \* 7e-13 integrin homolog - yeast (Saccharomyces cerevisiae) \* MYSP\_DROME PARAMYOSIN, LONG FORM paramyosin, standard - f \* 1e-179 Sili [NLS\_BP] CG5939 GH14085 66D-66D ID:66A3

CG1009 + peptidase \* ALANINE/ARGININE AMINOPEPTIDASE(aa) \* HYPOTHETICAL ZINC AMINOPEPTIDASE YIL137C(aa) \* protein(aa) \* aminopeptidase-like protein(aa) [ALADIPTASE // Peptidase\_M1 // ZINC\_PROT] CG1009 GH14158 62A5-62A5 dup:1/2 ID:66B1

CG9665 + unknown \* 2e-05 CU19\_LOCF1 CUTICLE PROTEIN (LM-19) (LM-ACP 19) Lm-ACP1 \*\* [GRAM\_POS\_ANCHORING // insect\_cuticle] CG9665 GH14349 73D-73D6 ID:66C3

CG3571 + actin\_binding \* DMRCPA\_X kel \* protein(aa) \* [BTB // KELCHREPEAT // Kelch] CG3571 GH14381 87A-87A dup:2/2 ID:66C6

CG9813 + unknown \* [ATPASE\_ALPHA\_BETA] CG9813 GH14502 87E8-87E9 dup:1/2 ID:66D11

CG14723 + ion\_channel \* 7e-59 DrosGluCl \* 1e-48 Contains similarity to Pfam domain: (neur\_chan), Score=39 \* 7e-67 glycine receptor subunit alpha \* 8e-68 glycine receptor al [neur\_chan // NEUROTR\_ION\_CHANNEL // NRI] CG14723 GH14445 86F9-86F9 ID:66D

CG7084 + transporter \* DMORCT2\_2 Orct \* organic cation transporter(aa) \* Similarity to Rat organic cation transporter cDNA EST comes from this gene; cDNA EST comes from [sugar\_tr] CG7084 GH14589 94A11-96D1 dup:2/2 ID:66E11

CG7503 + Con cell\_adhesion \* DMCONNECTN\_1 Con \* 1e-180 cell-surface molecule connectin - fruit fly (Drosophila melanogaster) \* 3e-15 coded for by C. elegans cDNA yk132e5.5; coded [LRR // LRRCT] CG7503 GH14524 64C6-64C7 dup:2/2 ID:66E2

CG9321 + unknown \* [ATP\_GTP\_A] CG9321 GH14542 29E4-29E4 dup:3/3 ID:66E4

CG9469 + unknown \* [PRO\_RICH // NLS\_BP // ATP\_GTP\_A] CG9469 GH14660 42E1-42E1 dup:2/3 ID:66F10

CG18255 + A(225) unknown \* bt \* MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (MLCK) (CONTAINS: TELOKIN)(aa) \* CG18255 GH14667 52D14-52D15 dup:3/3 ID:66F11

CG10149 + Rpn6 endopeptidase \* 26S proteasome subunit p44.5(aa) \* BLASTX 3.9E-25 YDL097C|Protein of unknown function(dna) \* 2e-90 hypothetical protein YDL097c - yeast (Saccharomyc [PCI\_DOMAIN // PCI] CG10149 GH14689 51C2-51C2 ID:66F12

CG10226 + transporter \* 8e-59 MDL1\_YEAST ATP-DEPENDENT PERMEASE MDL1 MDL1 protein - y \* MDR5\_DROME MULTIDRUG RESISTANCE PROTEIN HOMOLOG (P-GLYCOPROTEIN 65) \* similar to mu [ATP\_GTP\_A2 // ABC\_TRANSPORTER // ABC\_tr] CG10226 GH14758 65A7-65A7 ID:66G7

CG1814 + unknown \* hypothetical protein(aa) \* similar to human 5'-nucleotidase \* Unknown(aa) \* 6e-46 similar to human 5'-nucleotidase CG1814 GH14884 45F4-45F4 ID:66H7

CG8285 + boss G\_protein\_linked\_receptor \* DMBRSEVM\_5 boss \* BOSS\_DROME BRIDE OF SEVENLESS PROTEIN PRECURSOR (X558 \* 4e-06 CELF35-1 \* 2e-07 Unknown gene product CG8285 GH14887 96F9-96F9 dup:2/2 ID:66H8

CG8212 + endopeptidase \* Ypl125wp(aa) \* possible RanBP7-importin-beta-Cse1p superfamily(aa) \* 1e-36 hypothetical protein YPL125w - yeast (Saccharomyces cerevisiae) ( \* 1e-[trypsin // CHYMOTRYPSIN // IBN\_NT // TR] CG8212 GH15020 52C-52C dup:1/2 ID:67A11

CG15512 + unknown \* CG15512 GH14951 99C7-99C7 dup:2/4 ID:67A3

CG3285 + transporter \* 1e-09 myo-inositol transporter \* 5e-13 GTRL\_DROME GLUCOSE TRANSPORTER-LIKE PROTEIN glucose transpo \* 1e-08 Similar to sugar transporter; coded for b [N4\_MTASE // SUGRTRNSPORT // SUGAR\_TRANS] CG3285 GH15136

25A1-25A1 ID:67B12

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

CG3066 + endopeptidase \* PROCLOTTING ENZYME PRECURSOR(aa) \* DMEAST\_4 ea \* 6e-67 EAST\_DROME SERINE PROTEASE EASTER PRECURSOR serine protein \* 3e-29 anticoagulant protein C [trypsin // CHYMOTRYPSIN // TRYPSIN\_SER CG3066 GH15156 85B1-85B1 dup:2/5 ID:67C3

CG5455 + transcription\_factor \* cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene cDNA EST comes from this gene; cDNA EST yk270e3.3 come [HELIX\_LOOP\_HELIX // LIPASE\_SER] CG5455 GH15286 97B2-97B2 dup:2/3 ID:67D4

CG12284 + th apoptosis\_inhibitor \* DMDIAP1X\_3 th \* APOPTOSIS INHIBITOR (INHIBITOR OF APOPTOSIS 1) (DIAP1) (THREAD PROTEIN)(aa) \* 2e-05 similar to Zinc finger, C3HC4 type (RIN[zf-C3HC4 // BIR // BIR\_REPEAT // BIR\_RE] CG12284 GH15335 72D1-72D1 dup:2/3 ID:67D8

CG11451 + signal\_transduction \* 1e-06 fimbriae-associated protein Fap1 \*\* [NLS\_BP] CG11451 GH15349 77E-77E8 dup:1/2 ID:67D9

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

CG12142 + unknown \* [TMFOUR] CG12142 GH15469 42E-42E ID:67F2

CG14178 + CG14178 GH15480 ID:67F6

CG13356 + enzyme \* antennal-specific short-chain dehydrogenase/reductase(aa) \* 1e-22 YM71\_YEAST HYPOTHETICAL OXIDOREDUCTASE IN MRPL44-MTF1 INTERGENIC REGION \* 1e-13 si [GDHRDH // adh\_short] CG13356 20B1-20B1 dup:1/2 ID:67G2

CG2225 + unknown \* CG2225 GH15653 39E5-39E ID:67H2

CG7105 + unknown \* [FLAGELLA\_BB\_ROD] CG7105 GH15664 28D3-28D3 ID:67H3

CG11316 + signal\_transduction \* SH3P18-like WASP associated protein(aa) \* 35K proline-rich protein xlan4 - African clawed frog(aa) \* p85SPR(aa) \* 9e-07 YHA2\_YEAST HYPOTHETICAL 51. [P67PHOX // SH3DOMAIN // SH3] CG11316 GH15696 100A7-100B dup:3/5 ID:67H5

CG12184 + EG:66A1.3 unknown \* by match; LD Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone 5prime.; 1-match\_species=Drosophil...(aa) \* map\_position:4 [PRO\_RICH] CG12184 GH15731 4C6-4C6 dup:1/2 ID:67H9

CG7742 + unknown \* [TBC // RAB\_GAP] CG7742 GH15768 25C9-25C9 ID:68A4

CG6105 + enzyme \* F1F0-ATP synthase g subunit(aa) \* 9e-14 ATPN\_CAEEL PUTATIVE ATP SYNTHASE G CHAIN, MITOCHONDRIAL \* 3e-24 F1F0-type ATP synthase subunit g \* 4e-25 AT CG6105 GH15786 32C5-32C5 dup:1/2 ID:68A6

CG7580 + metabolism \* 7e-06 UCRQ\_HUMAN UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN \* 7e-10 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 9.5K pr CG7580 GH15942 74C3-74C3 ID:68B10

CG2736 + transmembrane\_receptor \* DMEMP\_3 emp \* DMCD362\_2 croquemort \* 9e-18 epithelial membrane protein - fruit fly (Drosophila melanogaster) \* 8e-15 mLGP85/LIMP II [CD36] CG2736 GH15894 60E7-60E7 ID:68B4

CG12558 + endopeptidase \* [TRYPSIN\_CATAL] CG12558 GH15905 98E3-98E3 ID:68B5

CG7002 + Hml cell\_adhesion \* HEMOCYTIN PRECURSOR (HUMORAL LECTIN)(aa) \* 3e-13 neurexin IV \* 9e-15 similar to EGF-like



domain, Fibrinogen beta and gamma chains, C-te \* 1e-145 o[LDLRA\_2 // vwd // EGF\_1 // EGF\_2 // CTC] CG7002 GH15913 70C4-70C4 dup:2/3 ID:68B8

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

+ enzyme \* DMACOASYN\_2 AcCoAS \* 6e-96 ACS1\_YEAST ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE 1) (ACYL-ACTIVATI \* 1e-81 acetyl-CoA synthetase - fruit fly [AMP-binding] CG6432 GH15945 98B1-98B1 dup:1/2 ID:68C1

CG6432 + ion\_channel \* DMARD1\_2 nAcR bgr;-64B \* nicotinic acetylcholine receptor alpha subunit(aa) \* DMALSR\_4 nAcR agr;-96A; \* 9e-63 similar to neuronal acetylcholine rec [NICOTINICR // neur\_chan // NEUROTR\_ION\_] CG8109 GH16126 18C3-18C3 ID:68C7

CG8109 + BG:DS03431.1 neurotransmitter\_transporter \* 1e-101 neurotransmitter transporter \* 2e-86 similar to the sodium:neurotransmitter symporter family (SNF) \* 1e-104 NTGL\_MOUSE SODIUM-[NANEUSMPORT // NA\_NEUROTRAN\_SYMP\_3 // S] CG15279 GH16161 35B7-35B7 ID:68D1

CG15279 + cell\_adhesion \* 7e-56 strong similarity to rat integral membrane glycoprotein GP120 precursor (SP:P116 \* 4e-18 protein \* 1e-95 GP21\_RAT INTEGRAL MEMBRANE GLYCOPROTE CG7897 GH16206 41F-41F dup:4/6 ID:68D5

CG7897 + \* ZRP protein(aa) \* 4e-10 hypothetical protein YDR299w - yeast (Saccharomyces cerevisiae) (U \* 3e-26 ZRP protein \* 2e-10 inserted at base Both 5' and [NLS\_BP] CG11188 27A1-27A1 dup:2/2 ID:68D6

CG11188 + unknown \* 5e-08 myosin phosphatase, target subunit (A \* 1e-07 PP1M M21 subunit=protein phosphatase 1M kda regulator; subunit \* myosin phosphatase, target subu CG5600 GH16214 72D3-72D4 dup:2/4 ID:68D7

CG5600 + transporter \* predicted using Genefinder; Similarity to E.coli long-chain-fatty-acid-CoA ligase cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA CG17999 GH16244 57B7-57B7 ID:68D9

CG17999 + Anxb11 actin\_binding \* annexin IV(aa) \* ANNEXIN IV (LIPOCORTIN IV) (36 KD ZYMOGEN GRANULE MEMBRANE ASSOCIATED PROTEIN) (ZAP36)(aa) \* DMANNIX AnnIX \* annexin max4(aa) [ANNEXINVI // ANNEXINIV // ANNEXIN // an] CG9968 GH16395 14C5-14C6 dup:3/3 ID:68E11

CG9968 + Cyp4g15 cytochrome\_P450 \* Cyp4e2 \* CYTOCHROME P450 4C1 (CYPIVC1)(aa) \* 2e-13 CP51\_YEAST CYTOCHROME P450 (CYPL1) (P450-L1A1) (STEROL 14-ALPHA DEMETHYLASE) \* 1E-151 [EP450II // p450 // P450 // CYTOCHROME\_P] CG11715 GH16320 10B15-10B17 dup:2/2 ID:68E2

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

CG18111 + endopeptidase \* chymotrypsin-like serine protease(aa) \* TRYPSIN DELTA PRECURSOR(aa) \* DMEAST\_4 ea \* Ser6 [trypsin // CHYMOTRYPSIN // TRYPSIN\_CATA] CG9672 GH16384 15A2-15A2 dup:2/2 ID:68E9

CG9672 + CG15068 GH16622 ID:68G10

CG15068 + 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

CG9166 + 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

CG9630 + ligand\_binding\_or\_carrier \* FGF intracellular binding protein(aa) \* FGF-1 intracellular binding protein \* CG8660 GH16593 76D3-76D3 ID:68G7

CG8660

CG11910	+ * DMWHEELER_2 18w * DMCOP10_2 chp * 1e-20 leucine-rich motif (LRR) protein homology to interleukin receptor cy * 2e-16 coded for by C. elegans cDNA yk [LRR] CG11910 96D2-96D2 dup:2/2 ID:68G8
CG6320	+ enzyme * Similar to calcium channel subunit; coded for by C. elegans cDNA yk19b1.5; coded for by C. elegans cDNA yk47a5.3; coded for by C. elegans cDNA yk47a [Ca_channel_B // SH3 // ATP_GTP_A] CG6320 GH16612 32D5-32D5 ID:68G9
CG11341	+ CG11341 ID:68H10
CG15426	+ cell_adhesion * 4e-11 LAR_DROME PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (PROTEIN-TYROSINE-PHOSPHAT * 1e-09 predicted protein contains a large number of Ig super [ig] CG15426 GH16705 24E1-24E3 dup:2/2 ID:68H5
chimera	+ chimera GH16723 ID:68H7
CG4230	+ unknown * CG4230 GH16729 25C-25C ID:68H8
CG7560	+ enzyme * methylenetetrahydrofolate reductase(aa) * 5e-09 YGM5_YEAST HYPOTHETICAL 68.5 KD PROTEIN IN SCS3-SUP44 INTERGENIC REGION * 2e-14 methylenetetrahydro CG7560 GH18008 68C2-68C2 ID:70A11
CG3663	+ unknown * conserved hypothetical protein(aa) * CGI-111 protein(aa) * predicted using Genefinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOL [Isochorismatase // ATP_GTP_A] CG3663 GH17932 60D10-60D10 dup:1/3 ID:70A3
CG17223	+ unknown * hypothetical protein(aa) * 3e-09 hypothetical protein * 3e-91 inserted at base Both 5' and 3' ends of P element Inverse PCR * CG17223 GH17972 23C4-23C4 ID:70A7
CG17603	+ Taf250 transcription_factor * Taf250 * 3e-49 T145_YEAST TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUNIT (TBP-ASSOCIATED * transcription factor * 5e-34 cDNA EST comes from this[BROMODOMAIN_2 // NLS_BP // BROMODOMAIN_] CG17603 GH17990 84A2-84C4 ID:70A9
CG14994	+ Gad1 enzyme * DCE_DROME GLUTAMATE DECARBOXYLASE (GAD) glutamate decarbo * 1e-163 predicted using Genefinder; similar to Pyridoxal-dependent decar * 1e-169 67kD g [DDC_GAD_HDC_YDC // pyridoxal_deC] CG14994 GH18029 64A5-64A7 ID:70B5
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
CG14813	+ deltaCOPligand_binding_or_carrier * 7e-29 COPD_YEAST COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) * /motif=(desc;; /ma * 1e-103 COPD_CAEEL PROBABLE COATOMER DELTA SUBUNIT (D [ATP_GTP_A] CG14813 GH18123 2B12-2B13 ID:70C8
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
CG9520	+ unknown CG9520 dup:5/5 ID:70E7
CG11842	+ endopeptidase * serine protease 18D(aa) * 4e-36 SNAK_DROME SERINE PROTEASE SNAKE PRECURSOR serine proteina * 2e-15 similar to peptidase family S1 (trypsin family) * [trypsin // CHYMOTRYPSIN // TRYPSIN_SER ] CG11842 GH1860 98F10-98F10 ID:70G11
CG5955	+ enzyme * F08F3.4 gene product(aa) * 2e-06 GALX_YEAST UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) / ALDOSE 1-EPIMERASE (MUTA * 4e-84 F08F3.4 gene product * 2e- CG5955 GH18546 77C2-77C2 ID:70G5
CG12339	+ unknown * [NLS_BP] CG12339 GH18573 47B11-47B11 dup:1/2 ID:70G7

+ Cyp28a5 cytochrome\_P450 \* CYP6A2(aa) \* cytochrome P450 monooxygenase CYP28A1(aa) \* 6e-37 YS24\_CAEEL PUTATIV  
 CYTOCHROME P450 IN CHROMOSOME II \* 5e-40 cytochrome P450 3A[EP450II // p450 // P450 // EGF\_2 // MIT] CG8864  
 CG8864 GH18601 34E2-34E2 dup:1/2 ID:70G9  
 CG15891 + unknown \* CG15891 GH18658 5E1-5E1 ID:70H6  
 + enzyme \* 1e-09 ATPK\_CAEEL PUTATIVE ATP SYNTHASE F CHAIN, MITOCHONDRIAL \* 3e-10 ATPK\_MOUSE ATP  
 CG4692 SYNTHASE F CHAIN, MITOCHONDRIAL \* 2e-08 F1Fo-ATPase synthase f CG4692 GH18886 60D8-60D8 dup:1/2 ID:71A7  
 CG15772 + unknown \* 1E-141\*\* CG15772 GH18971 5B3-5B4 ID:71B2  
 + transmembrane\_receptor \* DMEMP\_3 emp \* 3e-53 epithelial membrane protein - fruit fly (Drosophila melanogaster) \* 5e-24  
 CG3829 predicted using Genefinder; similar to CD36 family; cD [CD36] CG3829 GH19047 60E8-60E8 ID:71B9  
 CG13124 + unknown \* 1E-135\*\* CG13124 GH19095 33A1-33A1 dup:1/2 ID:71C3  
 + transporter \* 7e-08 product highly similar to metabolite transport proteins \*\* [SUGAR\_TRANSPORT\_2 // sugar\_tr] CG6640  
 CG6640 GH19118 67C10-67C10 ID:71C5  
 + enzyme \* 3e-07 alpha-actinin-2 associated LIM protein \* 9e-08 actinin-associated LIM protein \* 4e-08 CL36\_RAT LIM  
 CG6416 PROTEIN CLP36 LIM protein - rat \* alpha-act [PDZ] CG6416 GH19182 66D9-66D ID:71D2  
 + BcDNA:GH02439 unknown \* 1e-59 cDNA EST comes from this gene; cDNA EST co \* 7e-33 cytoplasmic protein Ndr1 \* 5e-32  
 CG2082 RTP nickel-specific inductio \* 2e-25 development-related p CG2082 GH19206 83C-83C dup:2/2 ID:71D3  
 + endopeptidase \* DMSNAKE\_2 snk \* gd \* Tequila \* zgr;Try [trypsin // CHYMOTRYPSIN // TRYPSIN\_HIS ] CG9649  
 CG9649 GH19262 88B3-88B3 ID:71D8  
 + transmembrane\_receptor \* patched (Drosophila) homolog(aa) \* PATCHED PROTEIN HOMOLOG (PTC1) (PTC)(aa) \* simil:  
 to drosophila membrane protein PATCHED \* 1e-26 probable m[PHOSPHOPANTETHEINE // 5TM\_BOX] CG11212 GH19449  
 CG11212 42A10-42A10 dup:2/2 ID:71E10  
 CG7224 + unknown \* CG7224 GH19363 30C1-30C1 dup:3/3 ID:71E4  
 CG15386 + unknown \* 1E-132\*\* CG15386 GH19557 23D1-23D1 ID:71F10  
 + peptidase \* PROBABLE 55.1 KD PEPTIDASE C12B10.05(aa) \* Xaa-Pro dipeptidase; peptidase D; prolidase;  
 imidodipeptidase; proline dipeptidase(aa) \* 2e-59 YEQ8\_YEAST [Peptidase\_M24 // MAPEPTIDASE] CG9581 GH19483 19C1-  
 CG9581 19C1 ID:71F2  
 + metabolism \* HYPOTHETICAL 143.2 KD PROTEIN C14B9.8 IN CHROMOSOME III(aa) \* phosphorylase kinase, alpha  
 (liver), glycogen storage disease IX(aa) \* PHOSPHORYLASE B [PRENYLATION // PHOSPHOPANTETHEINE] CG7766 GH19532  
 CG7766 8C13-8C14 dup:1/2 ID:71F8  
 CG4679 + unknown \* CG4679 GH19550 49F14-49F15 ID:71F9  
 + peptidase \* 3e-78 aminopeptidase yscII \* 9e-93 Similarity to Human aminopeptidase N (SW:AMPN\_HUMAN); cDNA EST  
 EMB \* 1e-102 AMPN\_MOUSE AMINOPEPTIDASE N (MICROSOM [ALADIPTASE // Peptidase\_M1 // ZINC\_PROT] CG5839  
 CG5839 GH19677 93F4-93F6 dup:3/7 ID:71G10  
 + transporter \* unknown(aa) \* anon-100EF-D3 \* 1e-20 Similarity to Salmonella sodium/proline symporter (SW:PUTP\_SALTY)  
 CG2196 \* 1e-33 sodium iodide symporter [SSF // NA\_SOLUTE\_SYMP\_3] CG2196 GH19680 100E2-100E3 ID:71G12  
 CG3282 + transcription\_factor \* 3e-30 zinc finger motif protein \* 6e-09 contains multiple of strong similarity to C2H2-type zinc fingers

(PS:PS00 \* 4e-25 zinc finger pro[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG3282 GH19637 57B16-57B16 dup:1/2 ID:71G6  
+ peptidase \* 1e-100 aminopeptidase yscII \* 1e-112 Similarity to Human aminopeptidase N (SW:AMPN\_HUMAN); cDNA EST  
EMB \* 1e-165 AMPE\_MOUSE GLUTAMYL AMINOPEPTIDASE [ALADIPTASE // NUCLEASE\_NON\_SPEC // Pept] CG8774  
CG8774 GH19688 87E5-87E5 ID:71H1  
CG17485 + CG17485 GH19718 ID:71H3  
+ Eaat2 neurotransmitter\_transporter \* EXCITATORY AMINO ACID TRANSPORTER (SEAT1)(aa) \* glutamate transporter  
2B(aa) \* CeGlt-2(aa) \* predicted using Genefinder; Similar[SDF // EDTRANSPORT // NA\_DICARBOXYL\_SYMP] CG3159 GH19729  
CG3159 21D1-21D1 dup:2/4 ID:71H5  
+ enzyme \* putative ribitol dehydrogenase(aa) \* coded for by C. elegans cDNA CEESL70F; similar to protochlorophyllide  
CG11200 oxidoreductases(aa) \* CGI-82 protein(aa) [GDHRDH // adh\_short] CG11200 GH19857 56F17-56F17 ID:72A6  
+ transporter \* Similarity to sugar transporters(aa) \* DMORCT2\_2 Orct \* 2e-08 HXT5\_YEAST PROBABLE GLUCOSE  
CG6126 TRANSPORTER HXT5 hexose trans \* 3e-90 putative organic ca [SUGAR\_TRANSPORT\_1 // sugar\_tr] CG6126 89B13-89B13  
dup:1/4 ID:72A7  
+ endopeptidase \* neuropsin(aa) \* TRYPSIN BETA PRECURSOR(aa) \* zgr;Try \* 4e-27 TRYA\_DROME TRYPSIN ALPHA  
CG1497 PRECURSOR trypsin-like proteinase ( [trypsin // CHYMOTRYPSIN // TRYPSIN\_HIS ] CG1497 GH20003 19F1-19F1 ID:72B8  
+ peptidase \* 1e-30 YHT2\_YEAST HYPOTHETICAL 49.8 KD PROTEIN IN ACT3-YCK1 INTERGENIC REGION  
CG8560 PRECURSOR \* 7e-06 carboxypeptidase precursor \* 4e-52 similar to zinc ca [CRBOXYPTASEA // Zn\_carbOpept] CG8560  
GH20109 65F7-65F8 ID:72C10  
+ Hs2st enzyme \* DMSD\_2 Sd \* SEGREGATION DISTORTER PROTEIN(aa) \* 2e-74 cDNA EST yk273d10.3 comes from this  
CG10234 gene; cDNA EST yk273d10.5 come \* 1e-101 heparan sulfate 2- CG10234 GH20044 37E3-37E3 ID:72C3  
CG12375 + unknown \* 1e-05 hypothetical protein \* [lactamase\_B] CG12375 GH20064 28E-28E ID:72C5  
CG10209 + unknown \* [PRO\_RICH] CG10209 GH20077 51D1-51D1 ID:72C8  
+ enzyme \* polyketide synthase(aa) \* 1e-68 CEM1\_YEAST SYNTHASE HOMOLOG (BETA-KETOACYL-ACP \* 1e-69 similar  
to beta-ketoacyl synthase \* 3e-92 putative 3-oxoacyl [B\_KETOACYL\_SYNTHASE // PPTA // ketoacyl] CG12170 GH20093 83B6-  
CG12170 83B6 ID:72C9  
+ GI transcription\_factor \* DMGLASS\_8 gl \* GLAS\_DROME GLASS PROTEIN finger protein glass - fruit fly \* 3e-19 similar to  
zinc finger protein \* 3e-30 zinc finger type transcrip[ZINC\_FINGER\_C2H2 // zf-C2H2 // ZINC\_FIN] CG7672 GH20219 91A-91A2  
CG7672 ID:72D10  
+ transporter \* BLASTX 2.0E-28 Human sodium iodide symporter mRNA, complete cds.(dna) \* 4e-36 unknown \* 2e-17  
CG7720 Similarity to Salmonella sodium/proline symporter (SW: [NA\_SOLUTE\_SYMP\_3] CG7720 GH20226 93F9-91C7 ID:72D11  
+ chaperone \* contains similarity to mouse DRPLA protein \* 3e-21 BCL2-associated athanogene 2; BAG-2 (AF09 \* 8e-16  
CG7945 contains similarity to mouse DRPLA protein ele CG7945 76A1-76A1 ID:72D12  
+ unknown \* 1e-39 /match=(desc;; /ma \* 3e-06 F20D6.5 gene product \* predicted using Genefinder \* cDNA EST yk381e5.3  
CG10514 comes from this gene [NLS\_BP] CG10514 GH20308 96C7-96C7 dup:2/2 ID:72E7  
+ Myosin-heavy-chain-like motor\_protein \* nonmuscle myosin II heavy chain A(aa) \* nonmuscle myosin heavy chain-A(aa) \*  
myosin heavy chain nonmuscle form A - human(aa) \* 2e-97 m[myosin\_head // IQ // MYOSINHEAVY] CG10218 GH20309 89B7-  
CG10218 89B7 dup:4/4 ID:72E8

CG17822 + transcription\_factor CG17822 GH20378 ID:72F5

CG15688 + unknown \* CG15688 GH20388 92F4-92F5 ID:72F7

CG12089 + unknown \* 7e-07 beaten path precursor \* 9e-09 beat \* \* CG12089 GH20456 98D1-98D1 ID:72G2

CG18020 + projectin [Drosophila melanogaster] CG18020 ID:72G5

CG5797 + unknown CG5797 dup:1/3 ID:72G9

CG8981 + unknown \* [BRCT\_DOMAIN // BRCT] CG8981 GH20709 48D1-48D1 ID:72H11

+ transporter \* putative methyltransferase(aa) \* 6e-05 probable membrane protein YDR198c - yeast (Saccharomyces cerevisiae) \* 2e-09 putative methyltransferase \* F21 [ATP\_GTP\_A2 // ABC\_TRANSPORTER // ABC\_tr] CG7955 GH20617 62A-62A ID:72H3

CG7955

CG10408 + enzyme CG10408 ID:72H5

CG17111 + unknown \* CG17111 GH20645 94D13-94D13 ID:72H6

+ enzyme \* Similar to glycogenin.(aa) \* GLYCOGENIN(aa) \* 1e-27 GLG2\_YEAST GLYCOGEN SYNTHESIS INITIATOR PROTEIN GLG2 hy \* 7e-67 Similar to glycogenin. CG9480 GH20752 57C7-57C7 dup:1/2 ID:73A3

CG9480 + structural\_protein \* 4e-07 CUP8\_DROME PUPAL CUTICLE PROTEIN EDG-84 PRECURSOR ecdyson \* 3e-08 CU19\_LOCM1 CUTICLE PROTEIN (LM-19) (LM-ACP 19) Lm-ACP1 \* 5e-09 DMEDG84A\_3 Ed [CUTICLE // PRO\_RICH // insect\_cuticle] CG6305 GH20904 50C9-50C11 ID:73B10

CG6305

CG17736 + unknown \* CG17736 GH20919 76E2-76E2 ID:73B12

+ Vha68 enzyme \* VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE KD SUBUNIT) (VAA3-1)(aa) \* encodes a protein with three (ABC) that is spliced to yield the extei [ATP-synt\_ab // ATP-synt\_ab\_C // ATPASE\_] CG12403 GH21132 34A-34A ID:73D11

CG12403

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

+ transporter \* 2e-28 YG5F\_YEAST PUTATIVE MITOCHONDRIAL CARRIER YGR257C hypot \* 1e-52 YQ51\_CAEEL PUTATIVE MITOCHONDRIAL CARRIER C16C10.1 (Z \* 1e-53 mitochondrial ca [mito\_carr // MITOCH\_CARRIER] CG14208 GH21048 18D8-18D8 ID:73D5

CG14208

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

+ enzyme \* 5e-12 GLO2\_YEAST HYDROXYACYLGLUTATHIONE HYDROLASE ISOZYME (GLYOXALASE II) (GLX II) \* 2e-62 cDNA EST yk301h4.5 comes from this gene; cDNA EST yk301h4 [lactamase\_B // NLS\_BP // ATP\_GTP\_A] CG9026 GH21160 47F7-47F7 dup:3/3 ID:73E3

CG9026

+ DNA\_binding \* cDNA EST yk384f3.5 comes from this gene; cDNA EST comes from this gene; cDNA EST yk287a1.5 come from this gene(aa) \* 5e-30 YE06\_YEAST HYPOTHETICAL [ATP\_GTP\_A] CG6204 GH21168 95E5-95E5 dup:2/2 ID:73E5

CG6204 + ligand\_binding\_or\_carrier \* MAP-kinase activating death domain(aa) \* Rab3 GDP/GTP exchange protein(aa) \* regulator of presynaptic activity(aa) \* 3e-12 CRAG protein [DENN\_DOMAIN // PRO\_RICH // ATP\_GTP\_A] CG5627 GH21304 13A12-13B1 ID:73F8

CG5627

CG7803 + CG7803 ID:73G3

+ Acp1 structural\_protein \* Acp1 \* ADULT CUTICLE PROTEIN PRECURSOR (DACP-1)(aa) \* cuticle protein=Dacp-1 melanogaster, Peptide, \* CG7216 GH21504 28C3-28C3 dup:1/2 ID:73G8

CG7216

CG1960 + mu2 unknown \* mutator 2(aa) \* mutator \* 4e-06 Pax transcription activation domain interacting protein PTIP \* CG1960 GH21591 62B11-62B11 dup:2/2 ID:73H6

CG12355 + unknown \* 2e-07 /match=(desc: \* 3e-08 MPV1\_MOUSE MPV17 PROTEIN mpv17 protein - mouse \* 1e-07 MpV17 transgene, murine homolog, glomerulosclerosis \* 1e-06 PMP2\_ CG12355 GH21685 75F9-75F9 ID:74A4

CG3091 + ligand\_binding\_or\_carrier \* 4e-59 62D9.a \* 1e-09 cellular retinaldehyde-binding protein; CRALBP \* 3e-14 tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with \* 3e- [CRAL\_TRIO] CG3091 GH21689 2F1-2F1 ID:74A6

CG6156 + motor\_protein \* mutated in colorectal cancers(aa) \* 3e-05 myosin heavy chain, MHC CCl4-cirrhotic liver fat-storing cell I \* 2e-06 DMMHC\_2 Mhc \* myosin heavy chain I CG6156 GH21874 88F1-88F1 dup:2/2 ID:74B12

CG5539 + unknown \* POLYPOSIS LOCUS PROTEIN (TB2 PROTEIN)(aa) \* pathogenicity protein(aa) \* 2e-09 YSV4\_CAEEL HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III (U CG5539 GH21788 60A2-60A2 ID:74B2

CG3560 + metabolism \* 3601, 14-kDa protein subunit of reductase complex(aa) \* ubiquinol-cytochrome c reductase binding protein(aa) \* UBIQUINOL-CYTOCHROME C REDUCTASE COMP CG3560 GH21854 14B12-14B12 ID:74B9

CG7135 + unknown \* /match=(desc;; /match=(desc:(aa) \* 4e-77 /match=(desc;; /ma \* 7e-06 No definition line found \* No definition line found CG7135 GH21891 16F7-16F7 dup:1/2 ID:74C3

CG10947 + \* hypothetical protein(aa) \* 3e-07 hypothetical protein \* \* CG10947 38C9-38C9 dup:2/2 ID:74C6

CG1640 + enzyme \* 7e-97 ALAM\_YEAST PUTATIVE ALANINE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (GLUTAMIC \* 1e-159 Similar to alanine aminotransferase; coded for by C. [aminotran\_1 // ACCSYNTHASE] CG1640 GH21936 11E9-11E10 dup:2/3 ID:74C8

CG5449 + receptor \* 3e-10 tolloid related-1 \* 5e-17 similar to CUB domain (2 domains), Low-density lipoprotein recepto \* 8e-15 BMP1\_MOUSE BONE MORPHOGENETIC PROTEIN PRE [LDLRA\_2 // CUB // ldl\_recept\_a // PRO\_R] CG5449 GH21941 94A3-94A3 ID:74C9

CG10949 + transcription\_factor \* TRANSCRIPTION FACTOR ADF-1 (ADH DISTAL FACTOR 1)(aa) \* DMADF1A\_2 Adf1 \* 3e-07 cDNA EST comes from this gene; cDNA EST yk319a3.5 come [NLS\_BP // ATP\_GTP\_A] CG10949 GH22016 38C9-38C9 ID:74D3

CG10693 + CG10693 GH22026 ID:74D5

CG17046 + kls unknown \* klarsicht protein(aa) \* 8e-06 protein \* hypothetical protein \* protein [NLS\_BP // SUGAR\_TRANSPORT\_1] CG17046 GH22034 61C3-61C7 dup:5/6 ID:74D8

CG7365 + enzyme \* phospholipase B(aa) \* similar to phospholipase precursor; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this ge [LIPASE\_GDSL\_SER // LIPASE\_GDSL // Lipas] CG7365 GH22081 76F3-76F3 dup:2/2 ID:74E2

CG4096 + endopeptidase \* ADAMTS-1(aa) \* 1e-86 Weak similarity to Eimeria thrombospondin (PIR Acc. No. c \* 1e-102 secretory protein containing thrombospondin motifs \* 2e-74 a [TSP1 // ADAM\_MEPRO // RECEPTOR\_CYTOKINE] CG4096 GH22104 5B1-5B1 dup:3/3 ID:74E6

CG2233 + unknown \* CG2233 GH22123 7D5-7D5 dup:5/5 ID:74E8

CG17800 + cell\_adhesion \* Down syndrome cell adhesion molecule(aa) \* 3e-66 neuroglian \* 1e-58 predicted protein contains a large number of Ig superfamily repeat \* 2e-39 PTPT9 [ig // PRO\_RICH // fn3] CG17800 GH22207 43B1-43B2 dup:3/4 ID:74F3

CG7565 + chitinase \* dJ73M23.3 \* 1E-137\* 9e-06 chitinase protein precursor \* similar to similar to [EGF\_2] CG7565 GH22222 66B6-66B6 ID:74F4

CG11737 + unknown \* 3e-24 K02G10.3 gene product \* \* CG11737 GH22337 85A5-85A5 ID:74G2

CG8920 + BcDNA:LD21403 unknown \* unknown \* 1e-06 tudor repeat associator with PCTAIRE \* [TUDOR] CG8920 GH22439 57A-57A dup:2/2 ID:74G9

CG6335 + enzyme \* histidyl tRNA synthetase - Caenorhabditis elegans(aa) \* HISTIDYL-TRNA SYNTHETASE HOMOLOG (HISTIDINE-TRNA LIGASE HOMOLOG) (HISRS)(aa) \* HISTIDYL-TRN [WHEP-TRS // tRNA-synt\_2b // AA\_TRNA\_LIG] CG6335 GH22474 17B5-17B5 ID:74H5

CG3902 + acyl-CoA\_dehydrogenase \* Similar to acyl-CoA dehydrogenase; coded for by C. elegans cDNA yk122b9.5(aa) \* acyl-Coenzyme A dehydrogenase, short/branched chain prec[Acyl-CoA\_dh // ACYL\_COA\_DH\_1 // ACYL\_CO] CG3902 GH22479 75E2 75E2 dup:2/2 ID:74H6

CG3241 + msl-2 DNA\_binding \* male-specific lethal-2(aa) \* DMDNAMEL2\_2 msl-2 \* MSL2\_DROME MALE-SPECIFIC LETHAL-2 PROTEIN RING finger prote \* 3e-38 male-specific lethal-2 [ZINC\_FINGER\_C3HC4 // PRO\_RICH // NLS\_BP] CG3241 GH22488 25A3-25A3 ID:74H7

CG5001 + \* DnaJ-1 \* heat shock protein dnaJ homolog - human(aa) \* similar to DNAJ protein; cDNA EST comes from this gene; cDN, EST comes from this gene; cDNA E CG5001 ID:75A5

CG8596 + unknown \* C25E10.5 gene product(aa) \* 7e-38 weak similarity to two short of multi-drug resistance proteins \* No definition line found \* Similarity to multidr CG8596 GH22722 65F3-65F3 ID:75B11

CG7277 + enzyme \* PUTATIVE UBIQUINONE BIOSYNTHESIS MONOOXYGENASE COQ6(aa) \* CGI-10 protein(aa) \* UbiH-like protein(aa) \* COQ6 monooxygenase; Coq6p(aa) [UBIH // Monooxygenase // RINGMONOXGNASE] CG7277 GH22740 25E6-25E6 ID:75C2

CG8991 + transcription\_factor \* [PRO\_RICH] CG8991 GH22790 48C-48C ID:75C6

CG1479 + bt protein\_kinase \* projectin - fruit fly (Drosophila melanogaster)(aa) \* bt \* similar to Fibronectin type III domain (31 domains), IG (immunoglobulin) superfam[ig // PROTEIN\_KINASE\_ST // FNTYPEIII //] CG1479 GH22863 102D6-102E1 dup:1/2 ID:75D11

CG10561 + enzyme \* l(2)37Cs \* Cs protein \* 2e-19 No definition line found \* 4e-15 protein [NAD\_BINDING] CG10561 GH22841 37C1-37C1 dup:2/2 ID:75D3

CG3330 + unknown \* CG3330 GH22851 97F8-97F8 ID:75D7

CG3770 + unknown CG3770 dup:2/2 ID:75E10

CG11388 + unknown \* CG11388 GH22974 60B1-60B1 dup:2/2 ID:75E11

CG5441 + dei transcription\_factor \* DMDELILAH\_2 dei \* HELIX-LOOP-HELIX PROTEIN DELILAH(aa) \* 2e-08 ATH2\_MOUSE ATONAL PROTEIN HOMOLOG (HELIX-LOOP-HELIX PROTEIN MATH-2) (MATH2) ( \* 6e[HLH // HELIX\_LOOP\_HELIX // HELIX\_LOOP\_H] CG5441 GH22991 100A5-100A5 ID:75F3

CG6038 + unknown \* CG6038 GH23035 71C2-71C2 ID:75G3

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

CG11023 + unknown \* hypothetical protein gs1.1.27.1(aa) \* 6e-26 hypothetical protein YPL020c - yeast (Saccharomyces cerevisiae) ( \* 1e-29 YRW3\_CAEEL HYPOTHETICAL 75.7 K CG11023 GH23213 21A3-21A3 dup:1/2 ID:75H9

CG3868 + signal\_transduction \* 2e-07 antifreeze glycopeptide AFGP polypeptide precursor \* \* CG3868 GH23259 70D7-70D7 ID:76A

CG12283 + kek1 cell\_adhesion \* KEK1(aa) \* kek1 \* 2e-11 Simiarity to Rat insulin-like growth factor binding protein comple \* 1e-17 leucine

rich-repeat protein [ig // LRR // LEURICHRPT // LRRCT] CG12283 GH23277 34A-34A dup:1/2 ID:76A7

CG8723 + enzyme \* coded for by C. elegans cDNA yk61f5.5; coded for by C. elegans cDNA yk40b3.5; coded for by C. elegans cDNA yk129d12.5; coded for by C. elegans cDNA [CPSASE\_2 // Carboxyl\_trans // CPSase\_L\_] CG8723 GH23405 43F8-43F9 dup:3/4 ID:76B12

CG10383 + unknown \* cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST yk270e3.3 come CG10383 GH23377 37A4-37A4 ID:76B6

CG1193 + cytoskeletal\_structural\_protein \* p60 katanin(aa) \* katanin p60 subunit(aa) \* 4e-42 CC48\_YEAST CELL DIVISION CONTROL PROTEIN cell divisi \* 3e-43 transitional endoplasmic reticulum A [AAA // NLS\_BP // ATP\_GTP\_A] CG1193 GH23455 83C-83C ID:76C7

CG8896 + 18w cell\_adhesion \* DMWHEELER\_2 18w \* 5e-15 CYAA\_YEAST ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE (ADENYLYL CYCLASE) \* leucine-rich motif (LRR) protein homology to int CG8896 GH23463 56F9-56F9 dup:1/4 ID:76C9

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

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

CG1848 + protein\_kinase \* LIM actin binding protein (limatin)(aa) \* Xlimk1(aa) \* 1e-18 protein kinase D \* 4e-12 PINCH [LIM\_DOMAIN\_1 // PROTEIN\_KINASE\_DOM // L] CG1848 GH23615 11B10-11B12 dup:2/2 ID:76E5

CG9519 + enzyme \* DMGLDY01\_11 Gld \* 1e-101 DHGL\_DROME GLUCOSE DEHYDROGENASE (ACCEPTOR) PRECURSOR glu \* 6e-68 similar to choline dehydrogenase; cDNA EST yk346d5.5 come [GMC\_oxred // GMC\_OXRED\_2] CG9519 13A1-13A1 dup:2/2 ID:76E9

CG9027 + enzyme \* 1e-31 pdb|1SDY|A Saccharomyces cerevisiae Saccharomyces cerevisiae \* 1e-34 SODC\_DROME SUPEROXIDE DISMUTASE (CU-ZN) superoxide dismuta \* 5e-38 SODE\_C [CUZNDISMTASE // SOD\_CU\_ZN\_1 // SOD\_CU\_Z] CG9027 47F6-47F7 ID:76F8

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

CG6467 + endopeptidase \* mas \* DMSER1\_2 Ser99Dc \* 7e-61 serine proteinase (EC 3.4.21.-) precursor - fruit fly (Drosophila melanogast \* 2e-29 EL2\_MOUSE ELASTASE PRECURSOR pan [trypsin // CHYMOTRYPSIN // TRYPSIN\_SER] CG6467 GH23808 65A2-65A2 ID:76G10

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

CG11455 + unknown \* 1e-05 NIPM\_BOVIN NADH-UBIQUINONE OXIDOREDUCTASE KD SUBUNIT (COMPLEX I-15 KD) (CI-15 \*\* CG11455 GH23780 21B2-21B2 ID:76G6

CG6424 + BcDNA:GH05095 motor\_protein \* 8e-34 protein \* [NLS\_BP] CG6424 GH23788 54E3-54E4 dup:1/3 ID:76G9

CG9780 + unknown \* [ABC\_TRANSPORTER] CG9780 GH23891 82A4-82A4 ID:76H12

CG11448 + EG:132E8.4 motor\_protein \* DMC132E8 \* 4e-06 USO1\_YEAST INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1 ( \* melanog \* 2e-31 similar to coiled coil domains; cDNA EST yk302g12.5 com CG11448 GH23825 2A3-2A3 ID:76H2

CG1963 + Pcd enzyme \* Pcd \* 5e-40 pterin-4a-carbinolamine dehydratase \* 1e-24 similar to 4a-carbinolamine dehydratases \* 4e-22 pterin-4-alpha-carbinolamine dehydratase (E [RIBOSOMAL\_L23 // Pterin\_4a] CG1963 GH23826 99C1-99C1 dup:1/2 ID:76H3



CG3403 + unknown \* HYPOTHETICAL 30.5 KD PROTEIN C30A5.3 IN CHROMOSOME III(aa) \* CGI-95 protein(aa) \* 2e-10 MOB1\_YEAST MOB1 PROTEIN (MPS1 BINDER 1) \* 9e-09 putative mit CG3403 GH23829 42C6-42C6 ID:76H4

CG8866 + protein\_kinase \* DMSTPK Pk61C \* DMFUSED\_2 fu \* similar to the CDF-1/PDGF receptor family of tyrosine protein kinases(aa) \* DMRSK\_2 S6klI [PROTEIN\_KINASE\_ST // TYRKINASE // PROTE] CG8866 GH23955 85D8-85D9 ID:77A4

CG2555 + structural\_protein \* 4e-11 cuticle protein LCP65Ac cuticle p \* 3e-13 CLP1\_HELAM LARVAL CUTICLE PROTEIN PRECURSOR larval cut \* 5e-13 Lcp65Ac \* CU16\_MANSE LARVAL CUTICLE [CUTICLE // insect\_cuticle] CG2555 GH23965 11B10-11B10 ID:77A6

CG5942 + brm DNA\_binding \* DMBRAPRO\_6 brm \* 1e-180 STH1\_YEAST NUCLEAR PROTEIN STH1/NPS1 nuclear protein STH \* BRM\_DROME HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN) transc \* pred [SNF2\_N] CG5942 GH23970 72C1-72C1 ID:77A7

CG4288 + transporter \* EAT-4(aa) \* 2e-55 Na(+)-dependent inorganic phosphate cotransporter mela \* 4e-92 EAT-4 \* 1e-57 NPT1\_MOUSE RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT CG4288 GH23975 92E8-92E8 ID:77A9

CG16932 + motor\_protein \* epidermal growth factor pathway substrate 15(aa) \* involved in signaling by the epidermal growth factor receptor; Method: conceptual translation su [EPS // EF\_HAND // effhand // EF\_HAND\_2] CG16932 60D14-60D15 dup:2/4 ID:77B5

CG8367 + 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

CG3187 + unknown \* 5e-11 HST2\_YEAST HST2 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 2) \* 1e-09 SIR2 \* 1e-48 similar to SIR; cDNA EST yk300f10.3 comes from this gene \* 3e-49 u CG3187 GH24142 5A12-5A12 ID:77C5

CG9663 + 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

CG7788 + lce endopeptidase \* DMICEPROT\_2 lce \* 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

CG14032 + Cyp4ac1 cytochrome\_P450 \* 2e-75 /motif=(desc;; /ma \* 3e-80 similar to Cytochrome P450 \* 1e-54 cytochrome P450 Cyp4a - mouse \* 2E-56 [EP450II // p450 // P450 // MITP450 // C] CG14032 GH24257 25D2-25D2 ID:77D4

CG1605 + 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

CG6922 + unknown \* 6e-43 COX11 (AA 1-277) \* 2e-44 cDNA EST comes from this gene; cDNA EST co \* 1e-124 protein \* 3e-51 component involved in Haem biosynthesis americana CG6922 GH24534 25E6-25E6 ID:77F11

CG12268 + enzyme \* DMC103B4 \* 1e-05 LYS2\_YEAST AMINOADIPATE-SEMIALDEHYDE DEHYDROGENASE LARGE SUBUNIT (ALPHA-AMINOADI \* 2e-53 /match=(desc;; /ma \* 4e-75 similar to Arab [HELIX\_LOOP\_HELIX] CG12268 GH24480 95C13-95C13 ID:77F5

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

CG6745 + unknown \* Yor243cp(aa) \* 2e-79 YO43\_YEAST HYPOTHETICAL 77.0 KD PROTEIN IN HES1-SEC63 INTERGENIC REGION \* 3e-35 YQ4B\_CAEEL HYPOTHETICAL 64.6 KD PROTEIN IN CHRO [UPF0024 // NLS\_BP] CG6745 GH24787 66D4-

66D4 ID:77H10

CG10731 + unknown \* 4e-14 weak similarity to Bos taurus mitochondrial ATP synthase coupling factor B (SP \* 1e-11 unknown \* 8e-06 ATPW\_BOVIN ATP SYNTHASE COUPLING FACTOR CG10731 GH24822 52F3-52F3 ID:77H11

CG9176 + ion\_channel \* DMCNGCHAN\_2 Cng \* cyclic nucleotide-gated ion channel LCNG1(aa) \* cyclic nucleotide gated channel alpha 3(aa) \* cyclic nucleotide-gated channel(aa) [cNMP\_binding // CNMP\_BINDING\_1 // CHANN] CG9176 GH24752 13C5-13C5 dup:2/3 ID:77H7

CG5813 + chif cell\_cycle\_regulator \* activator of S phase kinase(aa) \* map\_position:35F11-36A2 \* BLASTX 8.0E-09 Lytechinus variegatus Endo16 homolog (LvEndo16) mRNA, partial cds.(dna) \* [GRAM\_POS\_ANCHORING // NLS\_BP] CG5813 GH25089 35F9-35F10 dup:1/2 ID:78C4

CG14026 + tkv signal\_transduction \* DMTVP\_2 tkv \* transmembrane receptor type I transforming growth factor beta receptor ) plasma membrane plasma membrane ) map\_position:25D6 \* 2E-5[PROTEIN\_KINASE\_DOM // pkinase // TGFB\_R] CG14026 25C10-25D dup:4/7 ID:78D11

CG8444 + CG8444 ID:78D12

CG9441 + Pu enzyme \* 4e-52 GCH1\_YEAST GTP CYCLOHYDROLASE I (GTP-CH-I) GTP cyclohyd \* 1e-133 GCH1\_DROME GTP CYCLOHYDROLASE I (GTP-CH-I) (PUNCH PROTEIN) \* 2e-67 GCH1\_CAEEL [GTP\_cyclohydrol // GTP\_CYCLOHYDROL\_1\_1 ] CG9441 GH25630 57C5-57C6 dup:3/3 ID:78H12

CG2677 + EG:100G10.3 translation\_factor \* by match; 1-match\_description=TRANSLATION INITIATION FACTOR EIF-2B BETA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).; 1-match\_species=RATTUS NORVEGICUS [IF-2B] CG2677 GH25592 3B5-3B5 ID:78H7

CG9155 + Myo61F motor\_protein \* Myo61F \* Myo31DF \* 1e-143 YMZ9\_YEAST HYPOTHETICAL MYOSIN-LIKE PROTEIN IN ILV2-ADE1 INTERGENIC REGION \* myosin IB - fruit fly (Drosophila melanoga[myosin\_head // IQ // MYOSINHEAVY // ATP] CG9155 GH2560 62B4-62B4 dup:3/3 ID:78H8

CG14653 + unknown \* 1E-59\* \* CG14653 GH25780 82D5-82D5 ID:79B5

CG13503 + unknown \* 1E-112\* \* [PRO\_RICH] CG13503 GH25793 58C2-58C2 dup:1/2 ID:79B7

CG5186 + transcription\_factor \* 7e-05 host cell factor \* inserted at base 5' end of P element Inverse PCR \* similar to human host cell factor \* YC81\_CAEEL HYPOTHETICAL 143.1 KD PR CG5186 GH26048 55C13-55C13 dup:2/2 ID:79D11

CG8888 + enzyme \* 1e-09 BACR37P7.d \* 8e-25 strong similarity to the insect-type alcohol/ribitol dehydrogenase family \* 2e-27 cis-retinol androgen dehydrogenase \* 2e-3 [adh\_short] CG8888 GH26015 48E4-48E6 ID:79D8

CG9848 + unknown \* 3e-09 probable membrane protein YPR028w - yeast (Saccharomyces cerevisiae) \* 4e-46 YSV4\_CAEEL HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III [PRO\_RICH] CG9848 GH26090 59B4-59B6 dup:4/4 ID:79E9

CG10842 + Cyp4p1 cytochrome\_P450 \* predicted using Genefinder; similar to cytochrome P450(aa) \* DMCYP4D2\_12 Cyp4d2 \* Cyp4p1 \* cytochrome P450 (CYP4M2) - tobacco hornworm(aa) [EP450II // p450 // MITP450] CG10842 45C-45C dup:3/6 ID:79F11

CG7227 + transmembrane\_receptor \* DMCD362\_2 croquemort \* 2e-55 D-CD36 protein - fruit fly (Drosophila melanogaster) \* 1e-21 predicted using Genefinder; similar to CD36 family; cDNA E [CD36] CG7227 GH26133 30C1-30C1 dup:3/3 ID:79F4

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

CG9007 + transcription\_factor \* determined by GENSCAN prediction and spliced EST; match to EST \* 5e-09 YK09\_YEAST HYPOTHETICAL 85.5 KD PROTEIN IN SAP190-SPO14 INTERGENIC REGIO[SET\_DOMAIN // SET // PHD // NLS\_BP] CG9007

GH26152 70C9-70C10 dup:2/2 ID:79F7  
 + enzyme \* PROBABLE ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT BETA PRECURSOR (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH)(aa) \* NAD+-specific iso [isodh] CG6439 GH26270 93F14-93F14 ID:79G10  
 CG6439  
 CG6836 + unknown \* CG6836 GH26215 75E6-75E6 ID:79G4  
 CG17012 + Caenorhabditis elegans 'similar to peptidase family S1 (trypsin family)' EMBL:U58751 CG17012 ID:79G7  
 CG7300 + unknown \* CG7300 GH26358 32A-32A ID:79H9  
 CG4694 + her CG4694 her dup:2/2 ID:8-31 cntrlBA4  
 + bib transporter \* pore-forming protein MIP family(aa) \* NEUROGENIC PROTEIN BIG BRAIN(aa) \* 1e-07 YFF4\_YEAST HYPOTHETICAL 70.5 KD PROTEIN IN AGP3-DAK3 INTERGENIC REG[MINTRINSICP // MIP // PRO\_RICH] CG4722 big brain 30F4-30F5 dup:2/3 ID:8-31 cntrlBB5  
 CG4722 + pnt transcription\_factor \* DMPOINT2A\_2 pnt \* PNT2\_DROME ETS-LIKE PROTEIN POINTED P2 (D-ETS-2) gene po \* 3e-12 contains similarity to DNA-binding domain of[HSF\_ETS // ETSDOMAIN // Ets // ETS\_DOMA] CG17077 pnt-p1 94E12-94F1 dup:4/7 ID:8-31 cntrlBC10  
 CG17077  
 CG6496 + pdf CG6496 pdf dup:2/2 ID:8-31 cntrlBC11  
 CG17348 + drl CG17348 drl dup:2/2 ID:8-31 cntrlBC8  
 CG4354 + slbo CG4354 slbo dup:2/2 ID:8-31 cntrlBD9  
 CG4889 + Wg signal\_transduction CG4889 Wg dup:2/2 ID:8-31 cntrlBE8  
 CG9885 + dpp signal\_transduction CG9885 dpp dup:2/2 ID:8-31 cntrlBE9  
 + tup transcription\_factor \* isl \* LIM homeobox protein(aa) \* LIM homeobox protein \* 4e-30 CeLIM-7 contains similarity to L [LIM\_DOMAIN\_1 // HOMEBOX\_1 // homeobox ] CG10619 islet 37B5-37B5 dup:3/3 ID:8-31 cntrlBF7  
 CG10619  
 CG10325 + abdA transcription\_factor CG10325 abdA dup:4/4 ID:8-31 cntrlBH1  
 + 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 + dMEF2 \* DMMEF2\_2 Mef2 \* myocyte enhancer-binding factor 2(aa) \* 5e-07 RLM1\_YEAST TRANSCRIPTION FACTOR RLM RLM1 protein - yea \* myocyte-specific enhancer f CG1429 dup:1/8 ID:8-99Cntrl IE7  
 CG1429  
 CG6845 + \* 2e-12 cDNA EST yk452h4.3 comes from this gene; cDNA EST yk452h4.5 comes \* \* CG6845 61A-61A dup:1/2 ID:80A8  
 CG18253 + unknown \* CG18253 GH26442 82D5-82D5 ID:80A9  
 + unknown \* DMANO66DB\_2 anon-66Db \* ANON-66Db protein \* 5e-08 similar to PDZ domain (Also known as DHR or GLGF \* 5e-10 hypothetical protein CG5989 GH26459 68C1-68C1 ID:80B2  
 CG5989  
 CG8154 + unknown \* [NLS\_BP] CG8154 GH26521 67C2-67C2 ID:80B9  
 + endopeptidase \* similar to neprilysin and other zinc proteases(aa) \* 7e-05 YKL7\_YEAST 24.1 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION \* 3e-29 similar to Zinc-bindin [NEPRILYSIN // PRENYLATION // ZINC\_PROTE] CG8358 GH26575 85E4-85E4 ID:80C1  
 CG8358  
 CG10483 + unknown \* polytropic murine leukemia virus receptor SYG1(aa) \* 3e-32 SYG1\_YEAST SYG1 PROTEIN SYG1 protein - yeast (Saccharomy \* 1e-150 predicted using Genefin [CRYSTALLIN\_BETAGAMMA] CG10483 GH26628 64F5-64F5 ID:80C8

CG5261 + enzyme \* dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) precursor - Arabidopsis thaliana (fragment)(aa) \* Dihydrolipoamide acetyltransferase component (E [LIPOYL // 2-oxoacid\_dh // biotin\_lipoyl] CG5261 27F7-27F7 ID:80D4

CG11353 + unknown \* HYPOTHETICAL 90.9 KD PROTEIN C08B11.4 IN CHROMOSOME II(aa) \* weak similarity to nodulation protein (probable sugar acetylase) (Swiss Prot accessio CG11353 GH26735 64B13-64B14 dup:3/3 ID:80E2

CG8603 + motor\_protein \* APXL(aa) \* 2e-23 APXL \* 2e-23 apical protein, Xenopus laevis-like \* [PRO\_RICH] CG8603 GH26744 50F1 50F6 dup:4/4 ID:80E4

CG11466 + Cyp9f2 cytochrome\_P450 \* CYP9 cytochrome P450(aa) \* 3e-18 CYP6A2 \* 2e-10 similar to cytochrome P450 \* 5e-16 cytochrome P450 3A11 - mouse cytochrome P-45 [EP450II // p450] CG11466 GH26796 87B14-87B14 ID:80F2

CG7675 + enzyme \* CGI-82 protein(aa) \* 1e-16 YM71\_YEAST HYPOTHETICAL OXIDOREDUCTASE IN MRPL44-MTF1 INTERGENIC REGION \* 0.000000000002\* 6e-42 predicted using Genefinde [GDHRDH // adh\_short] CG7675 GH26851 91A2-91A2 dup:2/4 ID:80F8

CG7321 + transporter \* protein(aa) \* BLASTX 3.6E-09 Plasmodium falciparum protein gene, complete cds.(dna) \* rab3 effector(aa) \* 4e-11 SY65\_DROME SYNAPTOTAGMIN (P65) syna [C2 // C2\_DOMAIN\_2 // PDZ] CG7321 GH26867 90C7-90C7 ID:80F9

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

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

CG2092 + scra actin\_binding \* DMANILLIN\_2 Ani \* anillin - fruit fly (Drosophila melanogaster) \* 5e-26 predicted using Genefinder; similar to PH (pleckstrin homology) do \* DMANILL [PH // PRO\_RICH // PH\_DOMAIN] CG2092 GH27072 43E3-43E3 ID:80H10

CG15433 + unknown \* hypothetical protein(aa) \* hypothetical protein YPL086c - yeast (Saccharomyces cerevisiae) ( \* Similarity to Yeas LPG22P protein cDNA EST EMBL:T0 \* CG15433 GH27091 26A1-26A1 ID:80H11

CG8012 + unknown \* CG8012 GH26995 67E7-67E7 ID:80H3

CG18138 + unknown \* CG18138 GH27024 65E5-65E5 ID:80H4

CG2358 + BcDNA:GM04682 endopeptidase \* MICROSOMAL SIGNAL PEPTIDASE KD SUBUNIT (SPC18)(aa) \* signal peptidase complex kDa subunit(aa) \* SPC 21-kDa-like(aa) \* 2e-36 SC11\_YEAST SIGNAL SEQUE [Peptidase\_S26 // SIGNALPTASE // SPASE\_I] CG2358 GH27340 84C4-84C4 ID:81C9

CG8733 + Cyp305a1cytochrome\_P450 \* CYTOCHROME P450 76C4(aa) \* cytochrome P450 epoxxygenase(aa) \* cinnamate 4-hydroxylase(aa) \* Cytochrome P-450 2A14(aa) [EP450II // p450 // P450 // MITP450 // B] CG8733 GH27419 76D3-76D3 ID:81D5

CG9431 + cell\_adhesion \* DMARTAN\_7 trn \* 4e-35 KEK1 \* 3e-06 contains similarity to leucine-rich repeats (LRR) \* 8e-12 neurogenic extracellular slit protein [ig // LRR // LRRCT] CG9431 GH27420 34A10-34A10 ID:81D6

CG4841 + unknown \* [NLS\_BP] CG4841 GH27425 36A11-36A11 ID:81D7

CG6503 + CG6503 dup:2/2 ID:81E12

CG5534 + enzyme \* 1e-43 CCR4\_YEAST GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL EFFECTOR (C \* 2e-07 ANGEL \* 3e-86 predicted using Genefinder; Similarity CG5534 GH27503 95E6-95E6 dup:2/2 ID:81E4

CG11595 + unknown \* CG11595 GH27568 12D5-12D5 dup:2/2 ID:81E9

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

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

CG15360 + unknown \* CG15360 GH27779 22B3-22B3 ID:81H1

CG17272 + \* caltractin (20kD calcium-binding protein)(aa) \* Calmodulin; Cmd1p(aa) \* 7e-09 CALM\_YEAST CALMODULIN calmodulin yeast (Saccharomyces cere \* 1e-09 C [EF\_HAND\_2] CG17272 92F13-92F13 dup:2/2 ID:81H6

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

CG10630 + RNA\_binding \* CG10630 GH28067 64E-64E ID:82B10

CG7816 + unknown \* 2e-19 YIC3\_YEAST HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION \* 4e-37 cDNA EST comes from this gene; cDNA EST co \* 3e-39 KE4 \* 1e-38 CG7816 GH28072 99C7-99C7 dup:2/2 ID:82B11

+ transcription\_factor \* hepatocyte nuclear factor alpha(aa) \* Contains similarity to Pfam domain: (homeobox), Score=20.5, N=1(aa) \* onecut 2(aa) \* coded for by C. elegans [homeobox // HOMEBOX\_2 // NLS\_BP] CG1922 GH28062 102C6-102C6 ID:82B9

CG1922 + ligand\_binding\_or\_carrier \* 16k antigen precursor - nematode (Onchocerca volvulus)(aa) \* phosphatidylethanolamine bindin protein Ovd1 - nematode (Onchocerca volvulus) (fragmen [BPB] CG6180 33F2-33F2 dup:1/2 ID:82C12

CG6180 + transporter \* chromaffin granule ATPase II homolog(aa) \* ATC3\_YEAST PROBABLE CALCIUM-TRANSPORTING ATPASE (ENDOPLASMIC RETICULUM CA2+-AT \* 9e-12 OBA5\_DROME PUTAT [ATPASE\_E1\_E2 // CATATPASE // NLS\_BP // CG17034 GH28327 50A9-50A9 ID:82C4

CG17034 + endopeptidase \* DMSTUBBLE\_1 Sb \* 7e-07 T2D4\_YEAST TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUNIT (TAFII-90) \* 2e-26 EAST\_DROME SERINE PROTEASE EASTER PRECURSOR se [trypsin // CHYMOTRYPSIN // TRYPSIN\_SEF ] CG1773 GH28342 46A3-46A3 ID:82C7

CG1773 + unknown \* CGI-05 protein(aa) \* 7e-23 YQT5\_CAEEL HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III (U \* 1e-65 432aa long hypothetical protein \* conserved [UPF0004] CG6550 GH28477 54C1-54C1 ID:82D10

CG6550 + AcCoAS enzyme \* DMACOASYN\_2 AcCoAS \* 1e-154 ACS2\_YEAST ACETYL-COENZYME A SYNTHETASE (ACETATE--CO/ LIGASE 2) (ACYL-ACTIVAT \* acetyl-CoA synthetase - fruit fly (Droso [AMP\_BINDING // AMPBINDING // AMP-bindin] CG9390 78C7-78C7 ID:82D4

CG9390 + unknown \* 6e-20 /match=(desc:; /ma \* \* CG6908 GH28576 86F1-86F1 dup:2/2 ID:82E7

CG6908 + igl ligand\_binding\_or\_carrier \* ligand binding or carrier calmodulin binding ) map\_position:51E \* 6e-51 growth-associated protein GAP-43 homolog=igloo-L melanogas \* 6e-53 igl \* gro [IQ] CG18285 GH28577 51A4-51E7 dup:2/2 ID:82E8

CG18285 + Rh5 G\_protein\_linked\_receptor \* Rh5 \* DMNKDTACH\_2 Takr86C \* OPSIN RH4 (INNER R7 PHOTORECEPTOR CELLS OPSIN)(aa) \* short wavelength-sensitive opsin; ultraviolet-sensi[GPCRRHODOPSN // OPSIN // G\_PROTEIN\_RECE] CG5279 GH28578 33B10-33B10 dup:2/2 ID:82E9

CG5279 + unknown \* protein(aa) \* 5e-16 SSM4\_YEAST SSM4 PROTEIN SSM4 protein - yeast (Saccharomy \* 2e-08 predicted using Genefinder \* 2e-37 putative protein [PRO\_RICH] CG1317 GH28722 62E-62E ID:82F10

CG1317 + Chd64 actin\_binding \* DMMP20\_6 Mp20 \* predicted using Genefinder; Similarity to Human SM22 smooth muscle protein (SW:SM2H\_HUMAN); cDNA EST comes from this gene; cDNA EST [SM22CALPONIN // CH] CG14996 GH28730 64A9-64A9 dup:2/2 ID:82F12

CG14996 + Snap25 synaptosome-associated\_protein Synapse protein 25 CG17884 GH28821 ID:82G10

CG17884 + lat DNA\_replication\_factor \* recognition complex subunit mela \* 8e-92 recognition complex subunit \* 9e-95 recognition comple

CG4088

associated protein p81 \* 2e-92 inserted at base Bot [NLS\_BP // ATP\_GTP\_A] CG4088 GH28787 49F10-49F10 dup:1/2 ID:82G4  
 CG17676|unknown|CT39055 + CG17676|unknown|CT39055 ID:82H3  
 + unknown \* 5e-05 XIAP associated factor-1 (ZAP-1) \* 6e-09 SINA\_DROME DEVELOPMENTAL PROTEIN SEVEN IN  
 CG16745 ABSENTIA devel \* 1e-07 seven-in-absentia protein homologue- [ZF\_TRAF] CG16745 GH28844 63B5-63B5 ID:82H4  
 + bic transcription\_factor \* BTF3 HOMOLOG EGD1 (GAL4 DNA-BINDING ENHANCER PROTEIN)(aa) \* basic transcription  
 CG3644 factor 3, like 3(aa) \* transcription factor BTF3 homolog(aa) \* 9e-3 CG3644 GM13744 49D-49D dup:1/2 ID:83B1  
 + protein\_phosphatase \* 4e-11 PVH1\_YEAST PROTEIN-TYROSINE PHOSPHATASE YVH1 (PTPASE YVH1) \* 5e-22  
 CG14080 puckered protein \* 3e-32 Similar to protein-tyrosine phosphatase \* 1e-26 DU [DSPc] CG14080 GM13896 75F5-75F5 ID:83B6  
 + Gr enzyme \* 4e-59 glutathione reductase \* GSHR\_DROME GLUTATHIONE REDUCTASE (GR) (GRASE) glutathione \* 1e-12  
 TRXB\_CAEEL PROBABLE THIOREDOXIN REDUCTASE Similar t [HGRDTASE // FADPNR // pyr\_redox // PYRI] CG2151  
 GM14215 7D18-7D18 ID:83C1  
 CG2151  
 CG6544 + fau unknown \* CG6544 HL07933 86C4-86C4 dup:1/2 ID:83C11  
 + unknown \* CUTICLE PROTEIN (BC-NCP1)(aa) \* BLASTX 1.2E-10 Theileria parva schizont/sporozyte surface protein gene  
 CG8736 partial cds.(dna) \* CG8736 HL08183 44D-44D ID:83D10  
 CG7671 + chaperone \* 6e-06 C09G9.2 \*\* [WD40\_REGION // WD40] CG7671 LD21432 91A-91A ID:83D12  
 + Phas1 translation\_factor \* 2e-16 PHAS-II \* 4e-16 eukaryotic translation initiation factor 4E binding protein \* 1e-14 insulin-  
 CG8846 stimulated phosphoprotein PHAS-I - rat PHAS-I \* in CG8846 HL08053 25A3-25A3 ID:83D4  
 CG9578 + CG9578 ID:83D8  
 + motor\_protein \* HYPOTHETICAL PROTEIN \* PSD-95 binding protein(aa) \* 2e-08 PSD-95/SAP90-associated protein-1 \* 2e-  
 CG17064 70 inserted at base Both 5' and 3' ends of P elemen [NLS\_BP] CG17064 LD21642 50B1-50B2 dup:3/3 ID:83E2  
 + RNA\_binding \* atp-dependent, dead box, rna helicase(aa) \* PUTATIVE ATP-DEPENDENT RNA HELICASE C13F4.11C(a  
 \* RNA helicase; Prp28p(aa) \* Gene with similaity to [helicase\_C // HELICASE // DEAD // ATP\_G] CG3561 LD21669 21D2-21D2  
 CG3561 dup:2/2 ID:83E4  
 + swa RNA\_binding \* SWA\_DROME SWALLOW PROTEIN gene swallow protein - fruit fl \* DMSWAL\_3 swa \* \* [NLS\_BP]  
 CG3429 CG3429 LD21771 5E6-5E7 dup:2/2 ID:83E6  
 + Cyp4e2 cytochrome\_P450 \* cytochrome P450 - fruit fly (Drosophila melanogaster) (fragment)(aa) \* Cyp4e2 \* Cyp4e3 \* 2e-12  
 ERG5\_YEAST CYTOCHROME P450 (C-22 STEROL DESATURASE) [EP450II // p450 // P450 // MITP450 // B] CG2060 LD22157  
 CG2060 44C1-44C1 ID:83F6  
 + 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  
 CG3938 35D5-35D6 dup:2/2 ID:83G5  
 + par-6 ion\_channel \* PAR-6(aa) \* PAR-6(aa) \* PAR-6(aa) \* dJ850H21.2 (novel protein containing a PDZ (DHR, GLGF)  
 CG5884 domain)(aa) [PDZ // ATP\_GTP\_A] CG5884 LD22757 16C5-16C5 ID:83G6  
 + cell\_adhesion \* DMFAT\_2 ft \* 7e-55 adherin \* 3e-43 Similarity to Drosophila Cadherin-related tumor suppressor precurs \* 1e-  
 CG7805 58 seven-pass transmembrane receptor prec [CADHERIN // cadherin // CADHERIN\_2] CG7805 LD23052 99C6-99C6 ID:83H9  
 + motor\_protein \* DNA segment, single copy, probe pH4 (transforming sequence, thyroid-1,(aa) \* 1e-07 microtubule binding  
 CG6664 protein D-CLIP-190 \* 1e-20 YRU4\_CAEEL HYPOTHE CG6664 LD23434 73E2-73E3 dup:2/2 ID:84B11

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

CG10922 + 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

CG11964 + unknown \* dJ633O20.1 (similar to Bos taurus P14)(aa) \* M01E11.2(aa) \* 1e-84 dJ633O20.1 (similar to Bos taurus P14) \*  
7e-20 P14 CG11964 LD23493 85C2-85C2 ID:84C3

CG11403 + DNA\_repair\_protein CG11403 LD24267 dup:2/2 ID:84C8

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

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

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

CG2275 + Jra transcription\_factor \* DMJUN\_2 Jra \* 1e-139 AP1\_DROME TRANSCRIPTION FACTOR JUN (DJUN) (DJRA) (JUN-  
RELATED ANTIGEN) (AP-1) >g \* 1e-07 similar to BZIP protein; cDNA[LEUZIPPRJUN // B\_ZIP // bZIP // BZIP\_BA] CG2275  
LD25202 46E2-46E2 dup:2/2 ID:84E7

CG3297 + mnd transporter \* minidisks(aa) \* 1e-23 MUP1\_YEAST HIGH AFFINITY METHIONINE PERMEASE methionine \* 1e-105 stror  
similarity to Schistosoma amino acid permease \* 1e-120 [aa\_permeases // AMINO\_ACID\_PERMEASE\_2] CG3297 LD25378 71A2  
71A3 ID:84F8

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

CG10689 + 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

CG17159 + \* [NLS\_BP] CG17159 cyto\_unknown dup:2/3 ID:85A4

CG9509 + enzyme \* glucose dehydrogenase (acceptor) (EC 1.1.99.10) - fruit fly (Drosophila melanogaster) (fragment)(aa) \*  
DMGLDY01\_11 Gld \* putative benzyl alcohol deh [GMC\_OXRED\_1 // GMC\_oxred // GMC\_OXRED\_2] CG9509 LD25803 13A1-  
13A1 ID:85A6

CG5135 + 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

CG8525 + enzyme \* 7e-52 DEOC\_CAEEL PUTATIVE DEOXYRIBOSE-PHOSPHATE ALDOLASE  
(PHOSPHODEOXYRIBOALDOLASE) ( \* 9e-69 CGI-26 protein \* 1e-26 2-deoxyribose 5-phosphate aldol CG8525 LD25963 49A4-  
49A5 ID:85B10

CG12894 + Cyp49a1 cytochrome\_P450 \* 7e-16 lanosterol 14-demethylase cytochrome P450 \* 2e-24 cytochrome P450 cytochrome P4 \* 4e-  
23 YS45\_CAEEL PUTATIVE CYTOCHROME P450 ZK177.5 IN CHROMOS [EP450II // p450 // P450 // MITP450 // C] CG12894  
LD25993 47A7-47A7 ID:85B11

CG6147 + 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

CG10621 + unknown CG10621 dup:1/4 ID:85C9  
+ EG:34F3.1 signal\_transduction \* /match=(desc;; /ma \* 2e-27 similar to PH (pleckstrin homology) domain; cDNA EST c \* 8e-06 Y053\_HUMAN HYPOTHETICAL PROTEIN KIAA \* 7e-09 KRAC\_DICDI RA [PH // PHOSPHOPANTETHEINE // PH\_DOMAIN]

CG12467 CG12467 LD26268 1C2-1C3 ID:85D7

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

CG10609 + Or83b signal\_transduction (Odorant receptor 83b ) olfactory receptor CG10609 LD26485 ID:85F4

CG9925 + unknown \* [PRO\_RICH] CG9925 LD26515 88A4-88A4 dup:2/3 ID:85F6  
+ BcDNA:LD26519 ligand\_binding\_or\_carrier \* 1e-126 inserted at base Both 5' and 3' ends of P element Inverse PCR \* \* [NLS\_BF]

CG11371 CG11371 LD26519 21A5-21A5 dup:3/4 ID:85F7  
+ enzyme \* Similar to carbonic anhydrase; coded for by C. elegans cDNA yk72d10.3; coded for by C. elegans cDNA yk119b1.3; coded for by C. elegans cDNA cm18b8; [carb\_anhydrase] CG6906 LD26647 68F7-68F7 dup:2/2 ID:85G2

CG6906 + exu RNA\_binding \* Exuperantia (exu) protein - fruit fly (Drosophila melanogaster)(aa) \* exu \* 1e-158 exuperantia protein - fruit fly (Drosophila virilis) \* exu [LECTIN\_LEGUME\_BETA] CG8994 LD26657 57B2-57B2 ID:85G4

CG8994 + 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 + unknown \* [NLS\_BP] CG9188 LD26930 27C7-27C7 ID:86A2

CG9188 + chaperone DnaJ homolog 2 DNAJPROTEIN CG9828 LD27049 dup:2/2 ID:86B6

CG9828 + 140up unknown \* RP140-upstream(aa) \* DMDMRP3\_7 140up \* hypothetical 30K protein (DmRP140 5' - fruit fly (Drosophila melanogaster)(aa) \* CG9852 LD27182 88A10-88A10 ID:86C11

CG9852 + Mcr enzyme\_inhibitor \* ovomacroglobulin, ovostatin(aa) \* complement C3-Q2(aa) \* COMPLEMENT C3-1 (CONTAINS: C3A ANAPHYLATOXIN)(aa) \* 3e-83 similar to Alpha-2-macroglobulin [LDLRA\_2 // RNP\_1 // A2M // ldl\_recept\_a] CG7586 LD27113 28E3-28E3 ID:86C4

CG7586 + 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 dup:1/2 ID:86C7

CG11471 + fidipidine cytoskeletal\_structural\_protein homology to sarcolemmal-associated protein (SLAP-2) [Homo sapiens] and latent nuclear antigen [Kaposi's sarcoma-associated herpesvirus] NLS\_BP CG7773 LD27169 dup:2/2 ID:86C8

CG7773 + pescadillo [Homo sapiens] (widely expressed in embryogenesis of zebrafish, high in liver) BRCT, BRCT\_DOMAIN, NLS\_BP

CG4364 CG4364 LD27336 dup:2/2 ID:86D12

CG4790 + unknown \* CG4790 LD27288 5C8-5C9 ID:86D8  
+ 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 67B12-67B12 dup:2/2 ID:86E11

CG8284 + Aats-pheenzyme \* 8e-84 mitochondrial phenylalanyl-tRNA synthetase alpha subunit precursor \* 1e-125 phenylalanine-tRNA synthetase \* phenylalanyl tRNA synthetase \* Aat [AA\_TRNA\_LIGASE\_II\_1 // AA\_TRNA\_LIGASE\_I] CG13348 LD27389 50C20-50C20 dup:2/2 ID:86E6

CG13348



CG8531	+ chaperone * 9e-13 XDJ1 protein - yeast (Saccharomyces cerevisiae) Xdj1p: H * 4e-09 DNJ1_DROME DNAJ PROTEIN HOMOLOG (DROJ1) droj1 * 1e-46 contains strong similar [DnaJ // DNAJ_2] CG8531 LD27406 50E9-50E9 dup:2/2 ID:86E7
CG5868	+ CG5868 dup:2/2 ID:86E9
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
CG10120	+ metabolism * MALATE OXIDOREDUCTASE, CHLOROPLAST (MALIC ENZYME) (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)(aa) * malic enzyme 1, soluble(aa) * MALATE OXIDOREDUCT [MALIC_ENZYMES // MALOXRDTASE // malic] CG10120 LD27718 87C9-87D dup:1/3 ID:86G10
CG17520	+ Ckl1alpha protein_kinase * 1e-103 KC21_YEAST CASEIN KINASE II, ALPHA CHAIN (CK II) casein ki * KC2A_DROME CASEIN KINASE II, ALPHA CHAIN (CK II) casein kina * 1e-151 KC2A_CAE[PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG17520 LD27706 cyto_unknown ID:86G9
CG12030	+ enzyme GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE Epimerase CG12030 LD27852 dup:2/2 ID:86H11
CG10538	+ GAP signal_transduction * Cdc42 GTPase-activating protein(aa) * Rga1p (Dbm1p)(aa) * DMC23E12 * ABR protein - human(a: [RHO_GAP // RhoGAP // SH3] CG10538 LD27836 38A-38A dup:2/3 ID:86H9
CG8068	+ zimp nucleic_acid_binding * map_position:45A4-8 * Zimp-A(aa) * 2e-19 NFI1_YEAST NFI1 PROTEIN NFI1 protein - yeast (Saccharom * 6e-43 cDNA EST comes from this gene; cDNA EST co CG8068 LD27861 45A13-45B1 dup:1/5 ID:87A1
CG4491	+ noc transcription_factor * zinc finger protein nocA - fruit fly (Drosophila melanogaster) (L1 * DMNOVA_3 noc * * [zf-C2H2 // ZINC_FINGER_C2H2_2] CG4491 LD28078 35A4-35A4 ID:87B10
CG9924	+ actin_binding CG9924 LD28030 dup:2/2 ID:87B2
CG5809	+ CaBP1 chaperone protein disulfide isomerase ER_TARGET, THIOREDOXIN CG5809 LD28038 dup:2/2 ID:87B5
CG2218	+ unknown * 1e-21 protein * * [ZINC_FINGER_C3HC4] CG2218 LD28173 99F6-99F6 ID:87C11
CG4500	+ BG:DS05899.1 enzyme * protein(aa) * fadD15(aa) * putative long chain fatty acid coA ligase(aa) * protein(aa) [AMP-binding] CG4500 LD28132 34E4-34E4 ID:87C8
CG15427	+ cell_adhesion CG15427 LD28224 dup:1/2 ID:87D1
CG1536	+ 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
CG2054	+ Cht2 enzyme * chitinase(aa) * 4e-66 chitinase * 3e-53 CHIT_CAEEL PUTATIVE ENDOCHITINASE coded for by C. elegans * 8e-60 BRP39 protein - mouse BRP39 protein m [CHITINASE_18 // Glyco_hydro_18] CG2054 LD28264 62B1-62B1 ID:87D4
CG7275	+ signal_transduction transducin (beta) like 1 protein GPROTEINBRPT, WD40 CG7275 LD28275 dup:2/3 ID:87D5
CG9741	+ Dhod enzyme * DMDHORO_3 Dhod * 2e-10 PYRD_YEAST DIHYDROOROTATE DEHYDROGENASE (DIHYDROOROTATE OXIDASE) (DHODEHASE) * dihydroorotate oxidase (EC 1.3.3.1), mitochond [FMN_ENZYMES // DHODEHASE_1 // DHodehase] CG9741 LD28427 85A10-85A10 dup:2/2 ID:87E10
CG7168	+ unknown * CG7168 LD28404 90F1-90F1 dup:2/2 ID:87E8
CG16798	+ CG16798 dup:2/3 ID:87F12
CG3634	+ CG3634 LD28488 dup:1/2 ID:87F8
CG10346	+ chaperone * CG10346 37A4-37A4 dup:1/3 ID:87G7

CG12134	+ CG12134 ID:87H4
CG6407	+ signal_transduction CG6407 dup:3/3 ID:87H5
CG17870	+ unknown CG17870 dup:3/4 ID:87H7
CG3876	+ unknown CG3876 ID:88A4
CG10686	+ 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
CG14207	+ chaperone * 1e-14 embryonal lethal (2)13-1 (el(2)13-1) - fruit fly (Drosophila melanogaster) * 4e-41 similar to small heat shock protein HSP20 family * 1e-12 CR [HSP20 // ACRYSTALLIN] CG14207 18D8-18D8 dup:3/4 ID:88B12
CG17927	+ Mhc motor_protein Myosin heavy chain CG17927 ID:88B3
CG1826	+ unknown * contains similarity to a BR-C/TTK domain(aa) * 5e-10 kelch protein, long form - fruit fly (Drosophila melanogaste * 7e-12 Kelch motif containing [BTB // PROTEIN_SPLICING // NLS_BP] CG1826 9E2-9E2 dup:2/2 ID:88B4
CG9216	+ unknown * [NLS_BP] CG9216 14A6-14A8 ID:88B5
CG12081	+ unknown CG12081 ID:88C3
CG12132	+ unknown * 7e-30 C34G6.1 gene product * CG12132 8D8-8D8 dup:1/3 ID:88C6
CG7291	+ * EPIDIDYMAL SECRETORY PROTEIN E1 PRECURSOR (CE1)(aa) * 4e-22 epididymal secretory protein * 9e-23 EP1_HUMAN EPIDIDYMAL SECRETORY PROTEIN E1 PRECURSOR CG7291 22B8-22B8 dup:2/3 ID:88D3
CG10217	+ unknown * 4e-08 cDNA EST CEMSE83F comes from this gene; cDNA EST comes * * CG10217 95B7-95B8 dup:2/4 ID:88D6
CG6850	+ Ugt enzyme * Ugt * UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)(aa) * 8e-19 KRE5_YEAST KILLER TOXIN-RESISTANCE PROTEIN PRECURSOR * coded for by [NLS_BP] CG6850 79E3-79E3 dup:5/7 ID:88D8
CG7407	+ CG7407 dup:1/2 ID:88D9
CG13849	+ unknown CG13849 dup:2/2 ID:88E12
CG2831	+ BcDNA:GH02636 transporter * 1e-134 putative open reading frame * 1e-133 P protein * 2e-30 arsA * P protein, truncated CG2831 26D1-26D1 dup:1/4 ID:88G1
CG17138	+ CG17138 dup:2/2 ID:88G10
CG3180	+ Rpl140 enzyme * polymerase (RNA) II (DNA directed) polypeptide B (140kD)(aa) * DNA-DIRECTED RNA POLYMERASE SUBUNIT B'(aa) * second largest subunit of RNA polymerase [RNA_pol_B // RNA_POL_BETA] CG3180 88A10-88A11 dup:2/3 ID:88G9
CG8280	+ Ef1alpha48D ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (50 KD FEMALE-SPECIFIC PROTEIN ATP_GTP_A, EFACOR_GTP, ELONGATNFCT, GTP] CG8280 dup:2/2 ID:89B10
CG17678	+ CG17678 dup:2/2 ID:89B3
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
CG7065	+ unknown * [NLS_BP] CG7065 LD35502 8C17-8C17 ID:95A12
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  
 + actin\_binding \* erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)(aa) \* DMP41A\_4 cora \* 2e-55 product c  
 CG9764 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  
 CG3658 + 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  
 + EG:114E2.2 \* MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT)(aa) \* MAX BINDING PROTEIN MNT  
 (ROX PROTEIN) (MYC ANTAGONIST MNT)(aa) \* by content; by mat [THIOLASE\_3 // HLH // HELIX\_LOOP\_HELIX\_2] CG2856  
 CG2856 3F2-3F2 dup:2/2 ID:95D2  
 CG15435 + nucleic\_acid\_binding \* [ZINC\_FINGER\_C2H2 // ZINC\_FINGER\_C2H2\_2] CG15435 LD35850 24F5-24F5 ID:95D9  
 + protein\_kinase \* DMRNASTK\_2 mnb \* protein kinase Dyrk1B(aa) \* MNB(aa) \* SRPK1(aa) [PROTEIN\_KINASE\_ST //  
 CG8174 PROTEIN\_KINASE\_DOM] CG8174 LD35909 51F11-51F11 dup:3/3 ID:95E3  
 + unknown \* dimethylase(aa) \* 2e-97 DIM1\_YEAST DIMETHYLADENOSINE TRANSFERASE (S-ADENOSYLMETHIONINE-  
 CG11837 6-N', N'-ADENOSY \* 4e-99 YQN1\_CAEEL HYPOTHETICAL 34.1 KD PROT [RrnaAD // RRNA\_A\_DIMETH // SAM\_BIND] CG11837  
 LD35950 98F9-98F9 dup:2/2 ID:95E6  
 + Hsp67Bb chaperone \* DMHGS2\_7 Hsp67Bb \* 1e-14 hypothetical protein YOR285w - yeast (Saccharomyces cerevisiae) \* 5e-6  
 CG4456 HS6B\_DROME HEAT SHOCK PROTEIN 67B2 heat shock prot [Rhodanese // RHODANESE] CG4456 LD36162 67B1-67B1  
 ID:95G6  
 CG11658 + unknown \* DY3.6(aa) \* \* CG11658 LD36342 71C2-71C2 dup:2/2 ID:95H11  
 + unknown \* HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III(aa) \* similar to Zinc finger, C3HC4 type  
 CG15814 (RING finger); cDNA EST EMBL:D7 \* [zf-C3HC4 // ZF\_RING] CG15814 16D6-16D6 dup:3/3 ID:95H12  
 + unknown \* hormone-sensitive lipase testicular isoform(aa) \* 1e-07 similar to the 'GDxG' family of lipolytic enzymes \* 4e-83  
 CG11055 hormone-sensitive lipase \* 2e-85 I [ESTERASE] CG11055 LD36294 56F15-56F15 ID:95H7  
 + DNA\_binding \* 3e-05 HP1\_DROME HETEROCHROMATIN PROTEIN (HP1) (NONHISTONE CHROMOSOMAL PROTEIN  
 CG8289 C1A9 \* 6e-06 similar to 'chromo' (CHRromatin Organization MOdifier) do [chromo // CHROMO\_2 // NLS\_BP] CG8289 LD36501  
 16B10-16B10 ID:96A10  
 + 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  
 CG11798 ID:96A3  
 + chaperone \* FKBP54(aa) \* 2e-11 FKBP\_YEAST FK506-BINDING PROTEIN (FKBP) (PEPTIDYL-PROLYL CIS-TRANS  
 ISOMERASE) (P \* 3e-08 FKB2\_DROME KD FK506-BINDING PROTEIN (FK [TPR\_REGION // FKBP\_PPIASE\_2 // FKBP\_PPI]  
 CG5482 CG5482 LD36412 55E5-55E5 ID:96A4  
 CG1918 + \* [PHOSPHOPANTETHEINE // ANTIFREEZEI] CG1918 43F4-43F4 ID:96A9  
 + 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  
 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-2 protein \* 4e-07 inserted at base Both 5' and 3' ends CG3480 LD36606 2B16-2B16 ID:96B7

CG6394 + enzyme \* GLY7(aa) \* 1e-165 GLY7 \* 1e-104 polypeptide GalNAc transferase-T1 \* 1e-103 PAGT\_HUMAN POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACE [RICIN\_B\_LLECTIN // GLYC\_TRANS // Glycos\_] CG6394 LD36616 17B4-17B4 dup:1/2 ID:96B8

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

CG2858 + \* similar to Arabidopsis thaliana male sterility protein \* 4e-47 /match=(desc;; /ma \* 6e-30 male sterility 2-like protein \* 4e-49 DMC103B4 CG2858 60E5-60E5 dup:1/2 ID:96C7

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

CG11642 + unknown TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN)(aa) NLS\_BP CG11642 LD36954 dup:2/2 ID:96D3

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

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 // CSC CG7015 LD37025 66C13-66C13 dup:2/4 ID:96D9

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

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

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

CG1438 + Cyp4c3 cytochrome\_P450 \* DMCYP4D2\_12 Cyp4d2 \* 1e-14 ERG5\_YEAST CYTOCHROME P450 (C-22 STEROL DESATURASE) \* 1e-109 cytochrome P450 cytochrome P4 \* 1e-101 similar to Cytoc[EP450II // P450 // MITP450 // BP450 // ] CG1438 LD37233 100B-100B2 dup:2/3 ID:96F5

CG5941 + 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

CG8232 + 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

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

CG12220 + ribosomal\_protein \* 4e-06 RM32\_YEAST MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32 PRECURSOR (YML32) \* 2e 12 YLA1\_CAEEL HYPOTHETICAL 19.1 KD PROTEIN C30C11.1 IN CHROMOSOME II [NLS\_BP] CG12220 LD37925 100C-100C ID:97C1

CG2669 + unknown \* [NLS\_BP] CG2669 LD38047 83A4-83A5 ID:97C12

+ enzyme \* 1e-171 SYMC\_YEAST METHIONYL-TRNA SYNTHETASE, CYTOPLASMIC (METHIONINE--TRNA LIGASE) (ME \* 1e-08 SYEP\_DROME MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [tRNA-synt\_1 // TRNASYNTHMET // WHEP-TRS] CG15100 LD37969 55F3-55F4 ID:97C3

CG14442 + unknown \* 7e-05 unknown \* \* [MIP // NLS\_BP] CG14442 LD38069 6C7-6C8 dup:2/3 ID:97D2

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

CG2921 + unknown \* hypothetical protein(aa) \* Hrt2p(aa) \* F31D4.2(aa) \* hypothetical protein(aa) CG2921 LD38241 58C1-58C1 dup:2/2 ID:97E5

CG5486 + Ubp64E endopeptidase \* DMUBP\_2 Ubp64E \* 9e-55 UBPF\_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (UBIQUITIN THIOLESTERASE \* UBPE\_DROME UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [UCH\_2\_1 // UCH\_2\_2 // UCH\_2\_3 // UCH-1 ] CG5486 LD38333 64E13-66A5 ID:97F1

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

CG7004 + enzyme \* BLASTX 1.3E-13 Bos taurus phosphatidylinositol 4-kinase mRNA, complete cds.(dna) \* 1e-29 PIK1\_YEAST PHOSPHATIDYLINOSITOL 4-KINASE PIK1 (PI4-KINASE) [PI3\_4\_KINASE\_1 // PI3\_PI4\_kinase // PI3] CG7004 LD38593 61B3-61B3 dup:3/3 ID:97G12

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

CG9086 + unknown \* ubiquitin-protein ligase E3-alpha(aa) \* similar to S. cerevisiae ubiquitin-protein ligase E3 component \* ubiquitin-protein ligase e3 componen n-rec CG9086 LD38820 15B5-15C1 dup:1/3 ID:98A11

CG8912 + 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

CG8483 + unknown \* HYPOTHETICAL 35.0 KD PROTEIN F48E8.1 IN CHROMOSOME III(aa) \* Similar to plant PR-1 class of pathogen related proteins; Pry3p(aa) \* sol i antigen(aa [SCP\_AG5\_PR1\_SC7\_2 // V5TPXLIKE // V5ALL] CG8483 LD39025 87E2-87E3 ID:98C2

CG6678 + chromatin\_binding \* hypothetical protein - human (fragment)(aa) \* UVB-resistance protein UVR8(aa) \* 8e-06 RCC\_YEAST

REGULATOR OF CHROMOSOME CONDENSATION (PRP20 [RCC1 // RCC1\_2 // GRF\_RCC // RCCNDNSATI] CG6678 LD3906 93F10-93F10 dup:2/2 ID:98C4

CG6292 + CycT cell\_cycle\_regulator \* CycT \* cyclin T; positive elongation transcription factor b cyclin subunit(aa) \* 4e-23 YL34\_CAEEL HYPOTHETICAL 53.6 KD PROTEIN F44B9.4 IN CHROMOSOM [NLS\_BP] CG6292 LD39065 74D2-74D3 dup:1/5 ID:98C5

CG5018 + transcription\_factor\_binding \* Ydr324cp(aa) \* 1e-25 hypothetical protein YDR324c - yeast (Saccharomyces cerevisiae) (U \* 3e-29 hypothetical protein \* 7e-05 DMENHSPA\_3 gro [WD40\_REGION] CG5018 LD39110 72D11-72D12 ID:98C8

CG18533 + CG18533 LD39166 ID:98D1

CG14444 + 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

CG8355 + sli cell\_adhesion \* DMSLIT\_2 sli \* slit protein(aa) \* 2e-35 contains similarity to multiple EGF-like domains \* neurogenic extracellular slit protein [LRR // LRRNT // EGF\_1 // EGF // LEURICH] CG8355 LD39407 52D4-52D7 dup:2/2 ID:98E11

CG17904 + 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

CG6620 + 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

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

CG5194 + unknown \* CG5194 LD39537 66F1-66F1 ID:98F8

CG9723 + 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

CG5902 + 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

CG12317 + 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

CG4993 + 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

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

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

CG2198 + Ama cell\_adhesion \* DMAMA\_5 Ama \* Immunoglobulin-C2-type-domain protein \* 1e-15 hemicentin precursor \* 3e-19 cell

adhesion molecule (AA - 681) is 1st base in codon) [ig] CG2198 LD39923 84D1-84D1 ID:99A4

CG8247 + unknown \* 4e-31 SRYA\_DROME SERENDIPITY LOCUS ALPHA PROTEIN serendipity (sr \* 4e-32 Drosophila simulans serendipity \* 4e-33 DMSRYG1\_16 Sry- $\Delta$ ; CG8247 LD39926 44F9-44F9 ID:99A5

CG8602 + transporter \* conserved hypothetical protein(aa) \* 8e-14 conserved hypothetical protein \* 7e-40 inserted at base 5' end of P element Inverse PCR \* [sugar\_tr] CG8602 LD39967 65F2-65F2 ID:99B1

CG5938 + unknown \* W06E11.6 gene product(aa) \* BRX protein(aa) \* W06E11.5 gene product CG5938 LD40095 97F5-97F5 dup:2/2 ID:99B11

CG1726 + unknown CG1726 LD40039 ID:99B7

CG12869 + enzyme \* 5e-30 gliotactin precursor - fruit fly (Drosophila melanogaster) \* 8e-15 similar to carboxyesterase \* 7e-37 ESTN\_MOUSE LIVER CARBOXYLESTERASE PRECUR [COesterase] CG12869 LD40049 51B4-51B4 ID:99B8

CG9335 + unknown \* CG9335 LD40063 38F1-38F1 ID:99B9

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

+ 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

CG6584

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

+ 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

+ transporter \* 1e-120 similar to serine/threonine dehydratases (Pfam: S\_T\_dehydratase.hmm, score: \* 1e-153 tetracycline transporter-like protein \* 5e-28 tetracycli [SUGAR\_TRANSPORT\_1 // TCRTETA // sugar\_t] CG11537 LD40292 63B10-63B10 ID:99D5

CG11537

+ 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

+ enzyme \* ubiquitin-conjugating enzyme E2-32k(aa) \* 2e-33 UBC7\_YEAST UBIQUITIN-CONJUGATING ENZYME E2-18 KI (UBIQUITIN-PROTEIN LIGASE) (UBI \* 3e-24 UBC6\_DROME [UBIQUITIN\_CONJUGAT // UQ\_con // UBIQUIT] CG7656 LD40324 71D4-71E1 dup:3/3 ID:99D8

CG7656

+ 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

+ 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

CG9633

ID:99E5

+ 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 + enzyme \* 3-KETOACYL-COA THIOLASE MITOCHONDRIAL (BETA-KETOTHIOLASE) (ACETYL-COA ACYLTRANSFERASE) (MITOCHONDRIAL 3-OXOACYL-COA THIOLASE)(aa) \* 8e-54 pdb|1AFW|A [thiolase // THIOLASE\_1 // THIOLASE\_2 //] CG4600 LD40538 33A1-33A1 dup:1/2 ID:99F6

CG4600 + unknown \* predicted using Genefinder; similar to Acetyltransferase (GNAT) family (2 domains); cDNA EST yk466g5.3 come from this gene; cDNA EST yk255h7.3 come [Acetyltransf] CG1969 LD40766 99C1-99C1 ID:99G10

CG1969 + 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 + unknown \* hypothetical protein(aa) \* 6e-71 inserted at base Both 5' and 3' ends of P element Inverse PCR \* [NLS\_BP] CG2162 LD40717 63B4-63B5 dup:2/2 ID:99G7

CG2162 + transporter CG14709 LD21507 ID:Farhad's BA11

CG14709 + protein\_kinase CG7873 Src42 dup:2/3 ID:Farhad's BB12

CG7873 + CG17682 LP04696 ID:Farhad's BB8

CG17682 + unknown \* 0.0000000007\* 4e-10 0.9-kb RNA transcript \* CG2016 ck01170 82E7-82E7 dup:2/3 ID:Farhad's BD11

CG2016 + W unknown \* W \* HEAD INVOLUTION DEFECTIVE PROTEIN (WRINKLED PROTEIN)(aa) \* 1e-148 W \* 6E-99 CG5123 ck02091 75C-75C2 dup:2/4 ID:Farhad's BE10

CG5123 + nucleic\_acid\_binding \* protein(aa) \* 2e-23 F28F5.2 gene product \* zinc-finger domain-containing protein \* LIM domain only LIM domain only s [LIM\_DOMAIN\_1 // LIM // LIM\_DOMAIN\_2 //] CG1055 ck02463 82D5-82D6 ID:Farhad's BE12

CG1055 + structural\_protein \* 70kD peroxisomal integral membrane protein(aa) \* similar to kD peroxisomal membrane protein (PMP70), an ATP-binding transport protein(aa) \* 1e-19 CG12703 ck01606 18F1-18F1 ID:Farhad's BE5

CG12703 + unknown \* BLASTX 5.8E-08 Mouse proteolipid protein variant DM-20 mRNA, complete cds.(dna) \* 2e-21 M6A\_MOUSE MEMBRANE GLYCOPROTEIN M6-A membrane glycoprote \* 3 [Myelin\_PLP] CG7540 ck01837 78D7-78D8 ID:Farhad's BE8

CG7540 + enzyme CG9503 ck02694 ID:Farhad's BF1

CG9503 + unknown CG4859 dMMP dup:2/2 ID:Path + Ctrl1 + kras160

CG4859 + cell\_adhesion CG3619 Delta dup:2/4 ID:Path + Ctrl1 + kras195

CG3619 + transcription\_factor CG6794 dif dup:3/3 ID:Path + Ctrl1 + kras210

CG6794 + CG12763 Dipteracin dup:2/3 ID:Path + Ctrl1 + kras244

CG12763 + N transmembrane\_receptor \* cell adhesion cell adhesion ) plasma membrane plasma membrane ) map\_position:3C7 \* NEUROGENIC LOCUS NOTCH PROTEIN PRECURSOR[ANK\_REP // EGF BLOOD // EGF\_1 // EGF //] CG3936 Notch 3C7-3C9 dup:2/4 ID:Path + Ctrl1 + kras248

CG3936 + CG7939 RP49 dup:3/3 ID:Path + Ctrl1 + kras60

CG7939