

Table S1

Gene list for 3,219 genes whose expression changes at least four fold across development (ANOVA  $p < 0.001$ ).

| Gene ID | mixed annotation (+ indicates sequence confirmation)  |
|---------|---|
|         | + 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  | + * 3e-25 predicted using Genefinder; cDNA EST comes from this * 4e-38 SPC1_HUMAN MICROSOMAL SIGNAL   |
| CG1751  | PEPTIDASE KD SUBUNIT (SPC25) * 3e-38 SPC1_CANFA MICR CG1751 10B17-10C1 dup:1/2 ID:101A12  |
| CG12505 | + unknown * CG12505 LD41905 50F6-50F6 ID:101A2  |
|         | + Ote motor_protein * 1e-174 OTE_DROME OTEFIN otefin - fruit fly (Drosophila melanogaster) * 1e-176 DMOTEDA_2 Ote * * CG5581 LD41911 55C3-55C4 ID:101A4   |
| CG5581  | + BcDNA:LD06837 DNA_replication_factor * Similarity to Human activator KD subunit (SW:AC13_HUMAN); cDNA EST CEESG65F comes from this gene; cDNA EST yk267e6.5 comes from this gene; cDNA EST [RFC] CG6258 LD41983 32D4-32D4 dup:2/2 ID:101B1                  |
| CG6258  |   |
| CG1636  | + unknown * CG1636 LD42063 7D21-7D21 dup:1/2 ID:101B10  |
|         | + Prat enzyme * AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPAT)(aa) * DMPRAT_2 Prat * 1e-55 PUR1_YE [Pribosyltran // PUR_PYR_PR_TRANSFER // ] CG2867 LD42113 84E1-84E1 dup:1/3 ID:101B11     |
| CG2867  |   |
|         | + unknown * zinc finger protein(aa) * maf10(aa) * myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 6(aa) * ALL1 fu [PHD] CG1070 LD42009 84C1-84C3 dup:1/3 ID:101B2   |
| CG1070  |   |
| CG17602 | + unknown * CG17602 LD42024 20A1-20A1 ID:101B4  |
|         | + transcription_factor * 5e-67 putative zinc finger protein * 6e-21 growth factor independence-1B * 4e-21 growth factor independent 1B (potential regulator of CDKN1A, tran * [zf-C2H2 // ZINC_FINGER_C2H2] CG1603 LD42046 43D3-43D3 ID:101B7                 |
| CG1603  |   |
|         | + unknown * similar to * conserved hypothetical protein, family(aa) * Yml080wp(aa) * hypothetical 35.8K protein (fis 5' - Escherichia coli(aa) [UPF0034 // FMN_ENZYMES] CG3645 LD42056 21B5-21B5 ID:101B8   |
| CG3645  |   |
|         | + Dap160 signal_transduction * Dap160 * 0.000000000000000004 * dynamin associated protein isoform Dap160-1 * 5e-08 hum-1 [EPS // EF_HAND // SH3DOMAIN // SH3 // N] CG1099 LD42142 39B1-39B1 ID:101C2  |
| CG1099  |   |
|         | + 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_BP /] CG7392 28E1-28E1 dup:1/3 ID:101C7 |
| CG7392  |   |
|         | + qua actin_binding * qua * QUAI_DROME VILLIN-LIKE PROTEIN QUAIL villin homolog qua * 9e-18 similar to gelsolin; cDNA EST comes from this gene * 3e-71 putative actin-bin [GELS // GELSOLIN] CG6433 LD42165 36C4-36C4 ID:101C8                                |
| CG6433  |   |
| CG15634 | + unknown * CG15634 LD42284 25A4-25A4 ID:101D10   |

CG4036 + unknown \* 5e-28 F09F7.7 gene product \* [NLS\_BP] CG4036 LD42289 32F1-32F1 dup:1/2 ID:101D11

CG9834 + unknown \* F35A5.8 gene product(aa) \* CGI-61 protein(aa) \* 2e-58 F35A5.8 gene product \* 6e-06 antigen 6; AdamAS [NLS\_BP] CG9834 LD42223 56C10-56C11 ID:101D2

CG11596 + EG:39E1.1 unknown \* 5e-33 YNJ2\_YEAST HYPOTHETICAL 45.5 KD PROTEIN IN YPT53-RHO2 INTERGENIC REGION \* /match=(desc:; /ma \* 6e-54 Similarity with yeast hypothetical prote [NLS\_BP] CG11596 LD42227 2B17-2B17 dup:2/2 ID:101D3

+ enzyme \* DMPEROX\_5 Pxd \* 7e-87 PERO\_DROME PEROXIDASE PRECURSOR myeloperoxidase (EC 1.11. \* similar to peroxidase; cDNA EST comes from this gene; \* 4e-93 PERM [MYB\_2 // ANPEROXIDASE // peroxidase // ] CG10211 LD42267 37A1-37A1 ID:101D7

CG10211 + DNA\_binding \* 3e-59 CAC2\_YEAST CHROMATIN ASSEMBLY FACTOR P60 SUBUNIT (CAF-1 KD SUBUNIT) \* 8e-33 HIRA \* 4e-11 YZLL\_CAEEL HYPOTHETICAL 43.1 KD TRP-ASP REPEATS CONTA [GPROTEINB // WD40\_REGION // WD\_REPEATS ] CG12892 LD42270 47A9-47A9 ID:101D8

CG12892 + transcription\_factor \* [NLS\_BP] CG17129 LD42420 61C9-61C9 dup:2/2 ID:101E10

CG17129 + osa DNA\_binding \* eyelid(aa) \* eld \* 3e-05 YM42\_YEAST HYPOTHETICAL 162.7 KD PROTEIN IN SIP18-SPT21 INTERGENIC REGION \* 2e-37 coded for by C. elegans cDNA yk7c8.5; co [ARID // PRO\_RICH // ANTIFREEZEI] CG7467 90C-90C dup:4/4 ID:101E12

CG7467 + unknown \* CG5857 LD42327 95C-95C dup:2/2 ID:101E3

CG5857 + 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 + Grip91 cytoskeletal\_structural\_protein \* gamma-tubulin interacting protein(aa) \* gamma-tubulin ring protein Dgrip91(aa) \* 1e-123 spindle pole body protein spindle pole body protein spc98[DEHYDRATASE\_SER\_THR] CG10988 LD42379 12B7-12B7 dup:3/4 ID:101E5

CG10988 + Parg enzyme \* poly(ADP-ribose) glycohydrolase \* 6e-33 cDNA EST comes from this gene; cDNA EST co \* 1e-100 poly(ADP-ribose) glycohydrolase \* 1e-102 poly (ADP-ribos [NLS\_BP // ATP\_GTP\_A] CG2864 LD42380 3F2-3F2 dup:5/5 ID:101E6

CG2864 + BcDNA:LD29892 unknown \* 4e-09 YKT7\_CAEEL HYPOTHETICAL 53.2 KD PROTEIN C07A9.7 IN CHROMOSOME III \* 1e-05 skm-BOP2 \* 8e-52 inserted at base Both 5' and 3' ends of P element I [SET\_DOMAIN] CG8378 48E10-48E10 dup:3/3 ID:101E8

CG8378 + Rep1 enzyme \* Rep1 \* 1e-121 DNA fragmentation factor DREP-1 \* 1e-08 cell death activator CIDE-A \* 4e-09 cell death-inducing DFFA-like effector a c CG8357 48E2-48E2 dup:3/3 ID:101E9

CG8357 + Pi3K21B signal\_transduction \* p60(aa) \* DMPIK57 Pi3K21B \* p60 p \* 2e-08 similar to vav proto-oncogene [PI3KINASEP85 // SH2DOMAIN // SH2] CG2699 LD42724 21B7-21B7 dup:2/2 ID:101F10

CG2699 + Aats-glupro enzyme \* Aats-glupro \* 1e-168 YHI0\_YEAST PUTATIVE PROLYL-TRNA SYNTHETASE YHR020W (PROLINE--TRNA LIGASE) (PRORS \* SYEP\_DROME MULTIFUNCTIONAL AMINOACYL-TRNA S [WHEP-TRS // AA\_TRNA\_LIGASE\_I // tRNA-sy] CG5394 LD42739 95C13-95D1 ID:101F11

CG5394 + 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 + unknown \* CG8121 LD42595 85D9-85D9 ID:101F3

CG8121

+ TH1 unknown \* TH1(aa) \* DMTH1X\_3 TH1 \* potential zinc-finger domains centered at aa and aa 364; kDa protein;  
 CG9984 putative(aa) \* DMTH1X\_3 TH1 CG9984 LD42626 14C4-14C4 ID:101F4  
 + Pabp2 RNA\_binding \* HYPOTHETICAL 29.0 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION(aa) \* DMROX2Y\_3 Rox2 \*  
 CG2163 RNA binding protein(aa) \* 3e-39 Similarity to Bovine Poly-A bind [RNP\_1 // RBD // rrm] CG2163 LD42638 44A7-44A8 ID:101F6  
 + DNA\_binding \* X-linked nuclear protein(aa) \* 8e-36 RA54\_YEAST DNA REPAIR AND RECOMBINATION PROTEIN RAD54  
 RAD5 \* 7e-41 RAD54 \* 1e-145 strong similarity to the SNF2 [helicase\_C // SNF2\_N // NLS\_BP] CG4548 LD42659 96E-96E2  
 CG4548 dup:4/5 ID:101F7  
 + unknown \* NORBIN(aa) \* neurochondrin-2(aa) \* BLASTX 1.4E-23 Rattus mRNA for NORBIN, complete cds.(dna) \* 2e-76  
 CG2330 neurochondrin-1 (AB CG2330 LD42676 83F1-83F1 ID:101F8  
 + enzyme \* 3e-76 alpha esterase \* 1e-40 strong similarity to the type-B carboxylesterase/lipase family e \* 3e-47 pdb|1MAH|A  
 CG9858 Chain A, Fasciculin2 - Mouse Acetyl [TONB\_DEPENDENT\_REC\_1 // ESTERASE // COe] CG9858 LD42723 57F4-57F4 ID:101F9  
 CG15312 + transmembrane\_receptor \* [ig] CG15312 LD42756 9B1-9B1 ID:101G1  
 + Cdic motor\_protein \* Cdic \* cytoplasmic dynein intermediate chain isoform DIC5b(aa) \* cytoplasmic dynein intermediate chain  
 CG18000 isoform DIC3a(aa) \* 3e-83 cytoplasmic dynein CG18000 LD42953 19C1-19C1 dup:1/2 ID:101G10  
 + enzyme \* No definition line found(aa) \* predicted secreted protein(aa) \* 3e-06 predicted secreted protein \* [NLS\_BP]  
 CG1745 CG1745 LD43003 10B15-10B15 dup:1/2 ID:101G12  
 + enzyme \* unknown(aa) \* PROBABLE GMP SYNTHASE (GLUTAMINE-HYDROLYSING) (GLUTAMINE  
 CG9242 AMIDOTRANSFERASE) (GMP SYNTHETASE)(aa) \* guanine-monophosphate synthetase; GM [CPSGATASE // GMP\_synt\_C //  
 ANTSNTHASEII] CG9242 LD42771 39B4-39B4 dup:2/2 ID:101G2  
 + transcription\_factor \* zinc-finger-motif-protein \* 1e-05 Bowel \* 6e-05 predicted using Genefinder; similar to Zinc finger, C2H2  
 CG6791 type (7 \* 5e-14 zinc finger protein - mo[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG6791 87E1-87E1 dup:1/2 ID:101G3  
 + Taf80 signal\_transduction \* 2e-17 TUP1\_YEAST GLUCOSE REPRESSION REGULATORY PROTEIN TUP1 (FLOCCULATION  
 SUPPRESSOR P \* T2D4\_DROME TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUN[GPROTEINBRPT //  
 CG7704 WD40\_REGION // WD\_REPEA] CG7704 LD42828 47C5-47C6 ID:101G5  
 + grp protein\_kinase \* 5e-08 Ssp31 protein kinase \* 2e-54 Ser/Thr kinase \* 5e-13 serine/threonine kinase \* 7e-27 Chk1;  
 CG17161 checkpoint kinase [PROTEIN\_KINASE\_DOM // pkinase] CG17161 LD42896 36A6-36A7 ID:101G7  
 CG5522 + GDP/GTP exchange factor for Ras GRF\_CDC25, PH, PH\_DOMAIN, RasGEF CG5522 dup:1/2 ID:101G8  
 + transporter \* similar to ABC transporters ; ABC transporter transmembrane \* metal resistance protein, similar to multidrug  
 CG7806 resistance proteins and cystic fibrosi [ATP\_GTP\_A2 // ABC\_TRANSPORTER // ABC\_tr] CG7806 LD42916 29A5-29A5 ID:101G9  
 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  
 + cell\_cycle\_regulator \* pombe Cdc5-related protein(aa) \* similar to MYB transforming protein; cDNA EST comes from this  
 gene; cDNA EST comes from this gene; cDNA [MYB\_1 // MYB\_2 // myb\_DNA-binding // MY] CG6905 LD43082 61C1-61C1 dup:2/2  
 CG6905 ID:102A1

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

CG9012 LD43101 13F3-13F3 dup:1/3 ID:102A3  
+ structural\_protein \* 7e-07 DR48\_YEAST DDR48 STRESS PROTEIN (DNA DAMAGE-RESPONSIVE PROTEIN 48) (DDRP  
CG5787 48) (Y \* 7e-07 M84D\_DROME MALE SPECIFIC SPERM PROTEIN MST84DD testis- CG5787 LD43134 33F2-33F2 ID:102A8  
+ unknown \* ecdysone receptor isoform A - fruit fly (Drosophila melanogaster) (fragment)(aa) \* EcR-A=ecdysone receptor

CG8347 isoform melanogaster, Peptide Partial, \* CG8347 LD43136 42A9-42A9 ID:102A9  
+ 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  
CG11330 26F5-26F6 ID:102B11  
+ 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-  
CG6841 75E3 ID:102B12  
+ storage\_protein \* s18 chorion protein(aa) \* GCR protein - fruit fly (Drosophila melanogaster)(aa) \* s19 chorion protein(aa) \*

CG5095 ATP-DEPENDENT RNA HELICASE A (NUCLEAR CG5095 LD43171 15E5-15E5 ID:102B2  
+ 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  
CG7660 ID:102B3  
+ unknown \* 9e-56 cDNA EST comes from this gene; cDNA EST co \* \* [AROMATIC\_AA\_PERMEASE\_2] CG5262 LD43196  
CG5262 77C1-77C1 ID:102B5  
+ unknown \* putative transposase(aa) \* 3e-05 ORF1 \* 2e-07 putative transposase \* Hermes transposase [AMP\_BINDING]

CG11560 CG11560 LD43225 68F3-68F3 ID:102B8  
+ Orc4 DNA\_replication\_factor \* 56-kDa subunit of recognition complex (ORC); Orc4p(aa) \* recognition complex subunit 4-related  
CG2917 protein Orp4p(aa) \* recognition complex, subunit (yea [ATP\_GTP\_A2 // ATP\_GTP\_A] CG2917 LD43280 60D16-60D16 ID:102C1  
+ 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  
CG3152 ID:102C12

CG10165 + unknown \* CG10165 LD43293 37F1-37F1 ID:102C2  
+ motor\_protein \* 7e-10 NUF1\_YEAST NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110) \* 2e-14

CG5740 nonmuscle myosin-II heavy chain \* 1e-10 Similarity to Human endosoma CG5740 LD43488 94A-96C1 dup:2/2 ID:102D1  
+ chaperone \* p58(aa) \* 4e-05 probable membrane protein YLR080w - yeast (Saccharomyces cerevisiae) \* 7e-84 Similarity to

CG6822 Xenopus P58 protein cDNA EST \* 1e-104 man CG6822 LD43551 66D5-66D5 ID:102D10  
+ RplI215 enzyme \* DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)(aa) \* DMRPRIIA\_2 RplI215 \*  
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT(aa) \* RNA poly [RNA\_POL\_II\_REPEAT] CG1554 LD43558 10C4-  
CG1554 10C5 ID:102D12

CG4867 + unknown \* 1e-21 BC10\_HUMAN BLADDER CANCER KD PROTEIN 10kD protein \* 1E-136\* CG4867 LD43519 64E-64E

ID:102D3

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

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

CG4497 + unknown \* [GRAM\_POS\_ANCHORING] CG4497 LD43863 27E4-27E4 ID:102F12

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

CG4702 + unknown \* CG4702 LD43816 88A1-88A1 ID:102F9

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

CG18677 + unknown \* protein kinase cAMP-dependent protein kinase ) unlocalised cAMP-dependent protein kinase ) map\_position:77F \*\* CG18677 LD43873 77E8-77E8 ID:102G2

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

CG9031 + BG:BACR48E02.4 cell\_adhesion \* Ras suppressor protein 1(aa) \* 3e-07 adenylate cyclase \* 3e-06 CHAO\_DROME CHAOPTIN PRECURSOR (PHOTORECEPTOR CELL-SPECIFIC MEMBRANE PROTEIN) \* 3e-63 [LRR // LEURICHRPT] CG9031 LD43891 36E3-36E3 ID:102G5

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

CG17184 + motor\_protein \* ARFAPTIN 1(aa) \* 3e-36 YL87\_CAEEL HYPOTHETICAL 35.0 KD PROTEIN F54C8.7 IN CHROMOSOME III \* 2e-82 por1 \* AFP2\_HUMAN ARFAPTIN (POR1 PROTEIN) arfaptin CG17184 LD44124 86D8-86D8 dup:2/2 ID:102H10

CG7129 + signal\_transduction \* 3e-07 hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae) (U1 \* 3e-08 YKA7\_CAEEL HYPOTHETICAL 39.7 KD PROTEIN IN CHROMOSOME III \* 2e-1[P67PHOX // SH3DOMAIN // SH3 // PRO\_RICH] CG7129 LD44138 90F7-90F7 ID:102H11

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

CG9874 + Tbp transcription\_factor \* Tbp \* TRANSCRIPTION INITIATION FACTOR TFIID (TATA-BOX FACTOR) (TATA SEQUENCE-BINDING PROTEIN) (TBP) (TATA-BOX BINDING PROTEIN)(aa) \* 4e-80 TF2D\_YEAS [TFIID // TIFACTORIID // TBP] CG9874 LD44083 57F8-57F8 dup:1/2 ID:102H7

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

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

CG11005 + enzyme \* 3alpha-hydroxysteroid dehydrogenase (B-specific) (EC 1.1.1.50) - Pseudomonas sp. (strain \* DMGLUTAC\_9 Glt \* DMADHA1\_9 Adh \* DMSCU scu [adh\_short\_C2 // GDHRDH // adh\_short // ] CG11005 LD44221 83B6-83B6 ID:103A10

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

+ unknown \* putative centromere protein(aa) \* HYPOTHETICAL 75.7 KD PROTEIN T10F2.3 IN CHROMOSOME III(aa) \* 6e-12 SMT4\_YEAST SMT4 PROTEIN SMT4 protein - yeast ( CG10107 LD44235 65C3-65C3 dup:1/2 ID:103A12  
 CG10107  
 CG4229 + unknown \* CG4229 LD44179 77A1-77A1 ID:103A2  
 + signal\_transduction \* Taf80 \* katanin p80 subunit(aa) \* 5e-07 YCW2\_YEAST HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN CPR4-SSK2 \* 4e-09 transcription ini[GPROTEINBRPT // GPROTEINB // WD40\_REGIO]  
 CG9910 CG9910 LD44201 14B11-14B11 ID:103A6  
 + signal\_transduction \* PACSIN(aa) \* 3e-07 hypothetical protein YFR024c-a - yeast (Saccharomyces cerevisiae) \* 7e-08 Cortactin \* 1e-52 weakly similar to surface[FCH // CDC15\_NT // P67PHOX // SH3DOMAIN] CG15694 LD44220 92F13-92F13 dup:2/2 ID:103A9  
 CG15694  
 CG1503 + unknown \* CG1503 LD44327 19E7-19E7 ID:103B10  
 + unknown \* 8e-74 GPI3\_YEAST N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN (GLCN \* 6e-92 similar to phosphatidylinositol biosynthetic protein; [Glycos\_transf\_1] CG6401 LD44262 54E7-54E7 ID:103B2  
 CG6401  
 + unknown \* multispreading membrane protein (70kD)(aa) \* 1e-107 probable membrane protein YDR107c - yeast (Saccharomyces cerevisiae) \* strong similarity to Sacch CG9318 LD44273 38E3-38E4 ID:103B5  
 CG9318  
 + enzyme \* isopeptidase T(aa) \* 3e-68 UBPE\_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (UBIQUITIN THIOLESTERASE 14) \* 1e-125 Similar to ubiquitin carboxyl-term [UBA // UCH\_2\_1 // UCH\_2\_2 // UCH\_2\_3 //] CG12082 LD44295 63B10-63B11 ID:103B7  
 CG12082  
 CG3995 + unknown \* [NLS\_BP] CG3995 89E12-89E12 dup:2/2 ID:103B9  
 + CycA cell\_cycle\_regulator \* cell cycle regulator cyclin ) map\_position:68E1-2 \* DMCYCA\_3 CycA \* G2/MITOTIC-SPECIFIC CYCLIN A(aa) \* 2e-27 CG23\_YEAST G2/MITOTIC-SPECIFIC[cyclin // HELIX\_LOOP\_HELIX // CYCLINS] CG5940 LD44443 68D4-68D4 dup:2/2 ID:103C10  
 CG5940  
 + 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  
 CG10391  
 + pav motor\_protein \* 7e-35 YGW6\_YEAST PUTATIVE KINESIN-LIKE PROTEIN YGL216W hypoth \* PAV-KLP protein \* 5e-91 Similar to kinesin-like protein; coded for by C. elegans cDN [kinesin // KINESIN\_MOTOR\_DOMAIN1 // KIN] CG1258 64B4-64B4 dup:1/2 ID:103C2  
 CG1258  
 CG9241 + function\_unknown \* Cdc23(aa) \* \* [NLS\_BP] CG9241 LD44370 39B4-39B4 dup:1/2 ID:103C3  
 + chaperone \* 5e-33 Similarity to Xenopus P58 protein cDNA EST \* 3e-78 GP36b glycoprotein \* 3e-83 coded for by C. elegans cDNA yk74e11.5; coded for by C. elegans CG5510 95E3-95E3 dup:2/2 ID:103C4  
 CG5510  
 + 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  
 CG15532  
 + 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  
 CG11782  
 + 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  
 CG6754  
 CG4316 + Sb endopeptidase \* trypsin-like serine protease(aa) \* DMSTUBBLE\_1 Sb \* masquerade precursor - fruit fly (Drosophila

melanogaster)(aa) \* plasminogen activator, tiss[trypsin // CHYMOTRYPSIN // TRYPSIN\_SER ] CG4316 LD44584 89B9-89B9  
 dup:3/3 ID:103D10  
 + 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  
 CG8625 + SPT4 enzyme \* 3e-13 SPT4\_YEAST TRANSCRIPTION INITIATION PROTEIN SPT4 SPT4 pro \* 6e-30 contains similarity to  
 CG12372 Saccharomyces cerevisiae Spt4 \* 7e-39 unknown \* 1e-39 CG12372 LD44495 49B5-49B5 ID:103D2  
 + enzyme \* DMANKY\_5 Ank \* calcium-independent phospholipase A2(aa) \* Ca2+-independent phospholipase A2(aa) \* 1e-08  
 CG6718 ankyrin ankyrin m [ANK\_REP // ank // ANK\_REP\_REGION] CG6718 LD44515 67C2-67C2 dup:2/2 ID:103D4  
 + unknown \* 1e-12 YKK4\_CAEEL HYPOTHETICAL 30.2 KD PROTEIN C02F5.4 IN CHROMOSOME III \* \* [NLS\_BP] CG9018  
 CG9018 LD44521 62D3-62D3 dup:2/2 ID:103D5  
 + motor\_protein \* CLIP-190 \* 6e-05 microtubule binding protein D-CLIP-190 \* 3e-05 myosin \* 4e-06 ORF 73, contains large  
 CG8621 complex repeat CR sarcoma-associated herpesv CG8621 LD44526 65E6-65E6 dup:2/2 ID:103D6  
 + unknown \* 4e-14 YZG1\_CAEEL HYPOTHETICAL 28.7 KD PROTEIN F13E6.1 IN CHROMOSOME X \* 1e-13 D52 \* 7e-20  
 CG5174 tumor protein D52-like hD54+ins2 isoform \* 3e-14 CSPP28 CG5174 LD44733 55C11-55C11 dup:3/3 ID:103E10  
 + unknown \* F1N21.18(aa) \* HYPOTHETICAL 51.8 KD PROTEIN ZK632.11 IN CHROMOSOME III(aa) \* \* [ZF\_CCHC //  
 CG4622 PRO\_RICH // zf-CCHC // NLS\_B] CG4622 LD44757 60D5-60D5 dup:3/3 ID:103E12  
 + DNA\_binding \* 4e-06 probable finger protein YOL054w - yeast (Saccharomyces cerevisiae) \* 5e-22 contains similarity to  
 CG13605 C3HC4-class zinc finger eleg \* 1e-06 peroxis [zf-C3HC4] CG13605 LD44641 95D10-95D10 dup:2/2 ID:103E3  
 + sut1 transporter \* metabolite transport protein(aa) \* membrane transporter like protein(aa) \* ERD6 protein(aa) \* solute carrier  
 family (facilitated glucose transport[SUGRTRANSPORT // SUGAR\_TRANSPORT\_2 // su] CG8714 LD44652 44A4-44A4 dup:4/4  
 CG8714 ID:103E4  
 CG5422 + RNA\_binding CG5422 dup:2/2 ID:103E5  
 + unknown \* 7E-80\* 4e-29 inserted at base Both 5' and 3' ends of P element Inverse PCR \* [ATP\_GTP\_A] CG11104 LD44686  
 CG11104 12B8-12B8 dup:2/2 ID:103E6  
 CG7832 + unknown \* [NLS\_BP // ANTIFREEZEI] CG7832 LD44696 88C10-88C10 dup:3/3 ID:103E7  
 + unknown \* HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME II(aa) \* 1e-19 hypothetical protein  
 CG7530 YDR492w - yeast (Saccharomyces cerevisiae) (U \* 5e-26 C43G2 CG7530 LD44720 88D2-88D2 dup:3/3 ID:103E8  
 + Rab8 cell\_cycle\_regulator \* Rab8 \* rab8(aa) \* rab1(aa) \* 4e-55 SEC4\_YEAST RAS-RELATED PROTEIN SEC4 GTP-binding  
 CG8287 protein SE [SIGMA54\_INTERACT\_1 // PRENYLATION // ra] CG8287 LD44762 76D5-76D5 ID:103F1  
 + unknown \* 5e-08 No definition line found \* 5e-16 PSD-95/SAP90-associated protein-2 \* 1e-16 PSD-95 binding protein \* 1e-  
 CG8390 171 inserted at base Unknown 5' end of [NLS\_BP] CG8390 LD44824 41E5-41E5 ID:103F11  
 + unknown \* /match=(desc:; /match=(desc:(aa) \* 8e-07 hypothetical protein YLR281c - yeast (Saccharomyces cerevisiae) (U \*  
 CG3767 7e-10 /match=(desc:; /ma \* 7e-08 RF2\_H [RF-1] CG3767 LD44791 53A2-53A2 ID:103F5  
 CG17260 + nucleic\_acid\_binding \* [ZF\_RING] CG17260 LD44813 23C5-23C5 ID:103F8  
 + unknown \* BLASTX 4.0E-27 YER156C|Protein of unknown function(dna) \* HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-  
 CG11980 NCB1 INTERGENIC REGION(aa) \* 6e-60 similar to Yeast h CG11980 LD44814 85C3-85C3 dup:2/2 ID:103F9

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

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

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

CG8571 + smid endopeptidase \* DMSMMIN\_2 smallminded \* smallminded(aa) \* 3e-68 AFG2\_YEAST AFG2 PROTEIN valosin-containing protein homolo \* smallminded [ENDOLAPTASE // AAA // ATP\_GTP\_A] CG8571 65F5-65F6 dup:2/2 ID:103G2

CG1635 + unknown \* weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase \* acyl-CoA thioesterase(aa) \* contains weak similarity to rat cytosolic acyl CG1635 LD44914 100D2-100D2 ID:103G3

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

CG10622 + enzyme \* hypothetical protein(aa) \* 3e-93 SUCB\_YEAST PROBABLE SUCCINYL-COA LIGASE (GDP-FORMING), BETA-CHAIN PRECURSOR (SU \* 1e-134 SCB2\_CAEEL PROBABLE SUCCI [SUCCINYL\_COA\_LIG\_3 // ligase-CoA] CG10622 LD44970 64E-64E ID:103G7

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

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

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

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

CG3060 + cell\_cycle\_regulator \* hypothetical protein(aa) \* 8e-23 hypothetical protein YLR127c - yeast (Saccharomyces cerevisiae) \* 3e-05 LI19\_DROME LIN-19 HOMOLOG PROTEIN lin19 pro [CULLIN\_2] CG3060 60A14-60A14 dup:2/3 ID:103H3

CG17149 + enzyme \* protein(aa) \* 3e-07 FMS1\_YEAST FMS1 PROTEIN FMS1 protein - yeast (Saccharom \* 6e-12 Cs protein [ADXRDASE // NAD\_BINDING] CG17149 LD45081 77A4-77A4 ID:103H4

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

CG4875 + receptor \* 1e-07 weak similarity with quinone oxidoreductase; cDNA EST \* 2e-12 CGRP-receptor component protein; CGRP-RCP \* 1e-13 CGRP-receptor component protei CG4875 LD45115 15B1-15B1 ID:103H8

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

CG12225 + SPT6 structural\_protein \* 3e-79 SPT6\_YEAST TRANSCRIPTION INITIATION PROTEIN SPT6 SPT6 pro \* EMB5\_CAEEL EMB-5 PROTEIN emb-5 protein - Caenorhabditis e \* Supt6h \* similar to e [S1] CG12225 LD45251 5E1-5E1 dup:3/5 ID:104A10

CG5739 + unknown \* [NLS\_BP] CG5739 LD45253 31B2-31B2 ID:104A11



CG17686 + DIP1 RNA\_binding \* [NLS\_BP // DSRBD] CG17686 LD45242 cyto\_unknown dup:1/2 ID:104A6  
+ unknown \* short of similarity to human transforming protein (tre) \* similar to human (TRE) transforming protein \*

CG5916 Ypl249cp(aa) \* pollux(aa) [TBC // RAB\_GAP] CG5916 LD45246 89B9-89B9 ID:104A9

CG17469 + unknown \* 1E-123\* \* CG17469 LD45277 102E2-102E3 dup:2/2 ID:104B4  
+ endopeptidase \* energy-dependent regulator of proteolysis(aa) \* 9e-61 YB77\_YEAST HYPOTHETICAL 57.9 KD PROTEIN  
IN PDB1-ABD1 INTERGENIC REGION \* 1e-104 Similarity to [AAA // ATP\_GTP\_A] CG4538 LD45279 92B9-92B9 dup:3/3  
ID:104B5

CG4538 + EG:34F3.8 transporter \* /match=(desc;; /match=(desc;; /match=(desc;; /match=(desc;; /motif=(desc;; the EST /match=(desc;;  
CG7359 /match=(desc;; /match=(desc;; /match=(desc;; /mot [SYNAPTOBREVN // synaptobrevin] CG7359 LD45288 1C2-1C2 ID:104B6  
+ snf RNA\_binding \* DMD25SNRN\_2 snf \* U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) (SEX  
DETERMINATION PROTEIN SNF)(aa) \* 3e-05 YIS9\_YEAST HYPOTHETICAL 12.8 [RNP\_1 // RBD // rrm] CG4528 LD45302 4F1-  
4F2 dup:3/3 ID:104B7

CG4528

CG10825 + unknown \* [NLS\_BP] CG10825 LD45317 95F1-95F1 ID:104B8  
+ unknown \* fruit fly STS clone T7(dna) \* PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE  
CG7217 SPOT 71B)(aa) \* PEROXISOMAL MEMBRANE PROTEIN PMP20(aa) \* [AhpC-TSA] CG7217 LD45324 90E-90E dup:2/2 ID:104B9  
+ 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  
+ ion\_channel \* HISTIDINE-RICH GLYCOPROTEIN PRECURSOR(aa) \* histidine-rich protein - Plasmodium lophurae  
CG9411 (fragment) hi \* [PRO\_RICH] CG9411 LD45449 12E8-12E8 ID:104C11  
+ neur DNA\_binding \* finger protein neuralized - fruit fly (Drosophila melanogaster)(aa) \* DMC3HC4ZF\_2 neur \* 3e-89 coded for  
CG11988 by C. elegans cDNA yk27g3.5; coded for by C [zf-C3HC4 // ZF\_RING] CG11988 LD45505 85C4-85C5 dup:1/2 ID:104C12  
+ unknown \* R07E5.1 protein (clone R07E5) - Caenorhabditis elegans(aa) \* 7e-49 inserted at base Both 5' and 3' ends of P  
CG8833 element Inverse PCR \* cDNA EST comes fr [PRO\_RICH // D111\_DOMAIN // NLS\_BP] CG8833 LD45361 74B1-74B1 ID:104C2  
+ signal\_transduction \* Plenty of SH3s; POSH(aa) \* 5e-09 hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae)  
(U1 \* 4e-05 DRK\_DROME PROTEIN E(SEV)2B (SH2-SH3 A[zf-C3HC4 // ZINC\_FINGER\_C3HC4 // P67PHO] CG4909 LD45365  
CG4909 54D1-54D1 ID:104C3  
+ \* 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  
CG4769 ID:104C4  
+ unknown \* BLASTX 6.9E-07 YJL064W|Protein of unknown function(dna) \* BLASTX 8.2E-11 G.gallus PR264 mRNA.(dna) \*  
CG10084 2e-17 No definition line found \* [ZF\_CCCH // NLS\_BP] CG10084 LD45403 37E5-37E5 dup:2/3 ID:104C7

CG1780 + Idgf4 signal\_transduction imaginal disc growth factor 4 Glyco\_hydro\_18 CG1780 ID:104D10  
+ 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 LD45535  
CG4656 94E-94E dup:2/2 ID:104D3

CG13425 + bl RNA\_binding \* hnRNP-K protein(aa) \* 1e-05 YB83\_YEAST HYPOTHETICAL 45.8 KD PROTEIN IN PCS60-ABD1

INTERGENIC REGION \* 4e-05 unknown \* 9e-32 coded for by C. elegans CG13425 LD45549 57B1-57B1 dup:2/2 ID:104D5

CG18638 + CG18638 36A7-36A7 ID:104D7

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

CG18426 + cell\_adhesion \* 2e-09 SLIT\_DROME SLIT PROTEIN PRECURSOR slit protein precursor \* 2e-06 coded for by C. elegans

CG17667 cDNA yk133e1.5; coded for by C. elegans cDNA yk133d4.5 [LRR] CG17667 LD45603 69E1-69E2 dup:2/2 ID:104E3

CG4619 + unknown \* CG4619 LD45607 30F1-30F1 dup:2/2 ID:104E4

+ up ligand\_binding\_or\_carrier \* DMTROPT\_2 up \* clot.789(dna)\* 1e-112 troponin T - fruit fly (Drosophila melanogaster) \* 4e-28 TRT\_CAEEL TROPONIN T coded for by C. elegans cDNA yk7 [Troponin // NLS\_BP] CG7107 LD45641 12A2-12A4 dup:2/2 ID:104E5

CG7107 ID:104E5

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

+ 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 \* symplekin(aa) \* 6e-19 contains weak similarity to human microtubule-vesicle linker CL \* symplekin \* BLASTX

CG2097 1.6E-16 Human symplekin mRNA, partial cds [NLS\_BP] CG2097 LD45768 83C1-83C1 ID:104F6

+ unknown \* partner of Ral-binding protein 1(aa) \* 3e-09 PAN1\_YEAST PAN1 PROTEIN poly(A)-specific ribonuclease (EC \* CG6192 6e-06 PAST-1 \* 3e-05 contain EF-hand-like c [EPS // PRO\_RICH // EF\_HAND\_2] CG6192 LD45769 32D3-32D4 ID:104F7

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

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

+ enzyme \* 1e-07 BET4\_YEAST TYPE II PROTEINS GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT (TYPE II PRO \* CG3073 9e-11 similar to the protein prenyltransferase alpha subuni [PPTA] CG3073 LD45906 2F1-2F1 ID:104G2

+ unknown \* forkhead (Drosophila) homolog (rhabdomyosarcoma)(aa) \* forkhead protein FKHR(aa) \* myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila [Fork\_head // FORKHEAD // FORK\_HEAD\_3] CG3143 LD45950 88A8-88A9 ID:104G8

CG3143 + enzyme \* CHOLINEPHOSPHATE CYTIDYLYLTRANSFERASE (PHOSPHORYLCHOLINE TRANSFERASE) (CT)(aa) \* phosphate cytidyltransferase 1, choline, alpha isoform(aa) \* 2e-5 [TONB\_DEPENDENT\_REC\_1 // Cytidylyltransf] CG1049 LD46058 62A6-62A6 dup:2/2 ID:104H10

CG1049 + enzyme \* BLASTX 7.5E-52 FUM1|Fumarate hydratase (fumarase) (mitochondrial and cytoplasmic), converts L-malate to fumarate as part of the TCA cycle(dna) \* fum [DCRYSTALLIN // FUMRATELYASE // FUMARATE] CG4094 LD46083 6C7-6C7 ID:104H12

CG4094 + 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

CG7108 + transporter \* cystic fibrosis transmembrane conductance regulator(aa) \* DMMDR49\_2 Mdr49 \* canalicular multispecific organic anion transporter (ABC superfamily)(a[ATP\_GTP\_A2 // ABC\_TRANSPORTER // ABC\_tr] CG7627 LD46040 29B2-29B2

CG7627

dup:2/4 ID:104H4  
 + ash2 transcription\_factor \* ash2 \* trithorax protein ASH2 \* 6e-83 Y17G7B.2a \* 1e-134 similar to Drosophila ash2  
 CG6677 [SPRY\_DOMAIN // NLS\_BP] CG6677 LD46053 96A17-96A17 ID:104H8  
 CG10916 + unknown \* CG10916 LD46221 55B9-55B9 dup:2/2 ID:105A10  
 + BG:DS00004.12 unknown \* hypothetical 23.1kd-like protein(aa) \* 2e-17 YBF7\_YEAST HYPOTHETICAL 23.1 KD PROTEIN IN  
 CG1307 SHP1-PTC3 INTERGENIC REGION \* 9e-15 No definition line found CG1307 LD46144 84C4-84C4 ID:105A4  
 + unknown \* farnesoic acid o-methyltransferase(aa) \* 2e-21 farnesoic acid o-methyltransferase farne \* CG10527 LD46156  
 CG10527 57B20-57B20 ID:105A6  
 + DNA\_binding \* 2e-19 blastopia polyprotein - fruit fly (Drosophila melanogaster) \* 4e-53 neural plakophilin related arm-repeat  
 CG17484 protein \* 1e-56 neural plakophilin-r [ARM\_REPEAT // Armadillo\_seg] CG17484 41A1-41A1 dup:1/2 ID:105A8  
 + alien endopeptidase \* COP9 complex homolog subunit DCH2(aa) \* alien \* COP9 complex subunit 2(aa) \* thyroid receptor  
 CG9556 interacting protein 15(aa) CG9556 LD46201 29F8-29F8 ID:105A9  
 CG4949 + unknown \* [ATP\_GTP\_A] CG4949 LD46305 15D1-15D1 ID:105B10  
 + transporter \* atopy related autoantigen CALC(aa) \* 4e-27 predicted using Genefinder; similar to EF hand (2 domains) \* 2e-91  
 CG4495 atopy related autoantigen CALC \* 2e-40 [EF\_HAND // efhand // EF\_HAND\_2] CG4495 LD46238 27E3-27E3 ID:105B3  
 + nucleic\_acid\_binding \* 3e-05 YNN6\_YEAST HYPOTHETICAL 49.4 KD PROTEIN IN NAM9-FPR1 INTERGENIC REGION \*  
 CG5146 2e-06 RU17\_DROME U1 SMALL NUCLEAR RIBONUCLEOPROTEIN KD (U1 SNRNP KD) [PRO\_RICH // NLS\_BP] CG5146  
 LD46256 64E-64E ID:105B4  
 + transcription\_factor \* 6e-14 YJF6\_YEAST HYPOTHETICAL 98.9 KD ZINC FINGER PROTEIN IN BTN1-PEP8 INTERGENIC  
 CG12942 REG \* 1e-18 SUHW\_DROME SUPPRESSOR OF HAIRY WING PROTEIN Hw s \* [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN]  
 CG12942 LD46263 47C6-47C6 ID:105B5  
 CG4617 + DNA\_binding \* hypothetical protein(aa) \* 5e-16 HMGBCG protein \* \* [HMG] CG4617 LD46272 6F5-6F5 ID:105B7  
 + actin\_binding \* talin(aa) \* 7e-11 cytoskeleton assembly control protein SLA2 - yeast (Saccharomyces cerevisiae) \* 8e-08  
 CG6831 merlin \* talin [BAND\_41\_1 // Band\_41 // BAND\_41\_3 // PR] CG6831 LD46304 66D6-66D6 dup:1/2 ID:105B9  
 CG5726 + unknown \* CG5726 LD46389 55B9-55B9 ID:105C10  
 CG16753 + unknown \* [NLS\_BP] CG16753 LD46404 63B5-63B5 dup:1/2 ID:105C12  
 + enzyme \* similar to tumor suppressor p33ING1; similar to \* Unknown protein(aa) \* 5e-17 YNJ7\_YEAST HYPOTHETICAL  
 CG9293 37.0 KD PROTEIN IN RAS2-YPT53 INTERGENIC REGI [PHD // NLS\_BP] CG9293 LD46333 34B6-34B6 ID:105C2  
 + Sry-delta transcription\_factor \* DMSRYG1\_25 Sry- dgr; \* serendipity beta protein(aa) \* 2e-13 contains similarity to multiple C2H2-  
 type zince fingers (Pfam: zf-C2H2.hmm, sc \* 2e-22 O [zf-C2H2 // ZINC\_FINGER\_C2H2\_2] CG17958 LD46336 99D5-99D5  
 CG17958 ID:105C3  
 + unknown \* 5e-69 YG4W\_YEAST HYPOTHETICAL 34.9 KD PROTEIN IN SMI1-PHO81 INTERGENIC REGION \* 2e-29  
 L2CC\_DROME L(2)37CC PROTEIN Cc protein - fruit fly (Drosop \* 3 [PROHIBITIN // Band\_7] CG15081 LD46344 55F2-55F2  
 CG15081 ID:105C4  
 + xl6 RNA\_binding \* similar to pre-mRNA splicing factor like protein; cDNA EST comes from this gene; cDNA EST comes from  
 CG10203 this gene; cDNA EST comes from this gene; cDNA [RBD // ZF\_CCHC // rrm // zf-CCHC // NLS] CG10203 LD46359 27C-27C

ID:105C6

CG10473 + unknown \* 4e-41 protein \* 1e-09 putative protein \* coded for by C. elegans cDNA yk93e11.5; coded for by C. elegans cDNA yk103a11.5; \* [NLS\_BP] CG10473 LD46360 37B11-37B12 ID:105C7

CG3941 + transcription\_factor \* zinc finger homeodomain enhancer-binding protein-1(aa) \* BLASTX 1.9E-18 H.sapiens OZF mRNA.(dna) \* transcription factor RREB-1(aa) \* similar to Z[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG3941 LD46363 59E3-59E3 ID:105C9

CG6453 + receptor \* protein kinase C substrate 80K-H(aa) \* similar to Human protein kinase C substrate, 80KD protein, heavy chain, SWISS-PROT Accession Number \* similar [LDLRA\_2 // ER\_TARGET // EF\_HAND] CG6453 LD46533 36C4-36C4 ID:105D11

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

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

CG9890 + unknown \* 2e-42 similar to Zinc finger, C2H2 type; cDNA EST comes from \* 5e-53 inserted at base 5' end of P element Inverse PCR \* [zf-C2H2 // ZINC\_FINGER\_C2H2\_2] CG9890 LD46465 59C3-59C3 ID:105D4

CG9418 + DNA\_binding \* Smarce1-related protein(aa) \* 4e-05 ORF YBR089c-a \* 0.00000000002\* 5e-09 ribosomal transcription factor UBF2 - Chinese hamster [HMG // HMG\_box // PRO\_RICH // NLS\_BP] CG9418 LD46483 57C3-57C3 ID:105D6

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

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

CG11567 + Cpr enzyme \* NADPH-CYTOCHROME P450 REDUCTASE (CPR)(aa) \* DMNCP450R\_2 Cpr \* NADPH--ferrihemoprotein reductase(aa) \* 3e-92 NADPH-cytochrome P450 reductase precursor [oxidored\_fad // FPNCR // FLAVODOXIN // ] CG11567 LD46590 28C7-26C4 dup:4/4 ID:105E4

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

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

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

+ structural\_protein \* 6e-14 CUP7\_DROME PUPAL CUTICLE PROTEIN EDG-78 PRECURSOR ecdyson \* 2e-28  
 CUD4\_LOCFMI ENDOCUTICLE STRUCTURAL GLYCOPROTEIN (ABD-4A) g \* 7e-16 DMEDG78B\_2 [CUTICLE // insect\_cuticle]  
 CG8505 49A3-49A3 ID:105F10  
 + Gdi signal\_transduction \* 1e-135 GDI1\_YEAST SECRETORY PATHWAY GDP DISSOCIATION INHIBITOR G \* GDP  
 dissociation inhibitor - fruit fly (Drosophila melanogaster) \* Guanine nucleo [RABGDIREP // RABGDI // GDI] CG4422 LD46767  
 30B8-30B9 ID:105F11  
 + \* cyclin G1 - human (fragment)(aa) \* cyclin G2(aa) \* cyclin G - rat(aa) \* cyclin G2(aa) CG11525 100D2-100D2 dup:3/3  
 ID:105F12  
 + 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  
 + transcription\_factor \* 7e-06 MLP2\_DROME MUSCLE LIM PROTEIN MLP84B muscle L \* 2e-41 similar to LIM domain  
 containing proteins (5 domains); cDNA EST yk \* 1e-25 TES2\_M[LIM\_DOMAIN\_1 // LIM // LIM\_DOMAIN\_2] CG11914 LD46723  
 73D1-73D3 dup:2/2 ID:105F4  
 + 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  
 + msl-1 transcription\_factor \* MALE-SPECIFIC LETHAL-1 PROTEIN(aa) \* DMMSL1A\_2 msl-1 \* DMMSL1A\_2 msl-1 \* male-  
 specific lethal-1 protein - fruit fly (Drosophila melanogaster) CG10385 LD46729 37A4-37A4 dup:4/4 ID:105F6  
 + Tim10 unknown \* small zinc finger-like protein(aa) \* small zinc finger-like protein(aa) \* small zinc finger-like protein(aa) \* 5e-10  
 CG9878 hypothetical protein YHR004c-a CG9878 LD46744 57F8-57F8 dup:2/2 ID:105F7  
 + 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  
 CG8253 + unknown \* unknown protein(aa) \* 2e-21 R06C7.6 \* 1e-32 unknown protein \* CG8253 LD46868 52D2-52D2 ID:105G11  
 CG3305 + structural\_protein \* CG3305 LD46816 39E2-39E2 ID:105G3  
 + 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 // ] CG6092  
 LD46840 96F12-96F12 ID:105G6  
 + 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  
 CG7663 + structural\_protein CUTICLE PROTEIN AMP1B CUTICLE, insect\_cuticle CG7663 LD46979 ID:105H11  
 + 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  
 CG6838 + unknown \* [ZF\_RING] CG4813 LD46938 96F3-96F3 ID:105H5  
 CG4813 + unknown \* protein(aa) \* 3e-25 probable membrane protein YPL012w - yeast (Saccharomyces cerevisiae) \* 7e-18 putative  
 CG2691 protein (fragment) \* unknown [NLS\_BP] CG2691 LD46946 12A5-12A6 dup:4/4 ID:105H6  
 CG5954 + l(3)mbt transcription\_factor \* tumor-suppressor(aa) \* DMMBT163 l(3)mbt \* tumor-suppressor \* 2e-18 predicted using Genefinder;

cDNA EST yk292d9.5 comes from this gen [NLS\_BP] CG5954 LD46950 97F4-97F4 ID:105H7

CG8320 + CG8320 ID:105H9  
+ 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

CG7983 ID:106A2  
+ cytoskeletal\_structural\_protein \* 1e-62 cell division cycle protein \* 1e-178 SEP2\_DROME SEPTIN septin \* 3e-82 CDC10 \*  
1e-148 SEP2\_HUMAN SEPTIN HOMOLOG The gen [COPPER\_BLUE // GTP\_CDC // NLS\_BP // ATP] CG2916 LD47044 43F7-43F7 dup:1/2 ID:106A3

CG2916 + Actr13E cytoskeletal\_structural\_protein \* DMARP\_2 Actr13E \* 2e-45 ACT\_YEAST ACTIN actin - yeast (Saccharomyces cerevisiae) \* ACTU\_DROME ACTIN-LIKE PROTEIN 13E actin-related protein \* 1e-70 [actin] CG11678 LD47054 13E15-13E16

CG11678 ID:106A4  
+ ribosomal\_protein \* ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG (L10E)(aa) \* coded for by C. elegans cDNA CEESN26F; coded for by C. elegans cDNA CEESI89F; similar to 60S acidi [Ribosomal\_L10] CG1381 LD47064 46E3-46E3

CG1381 ID:106A5  
+ unknown \* CGI-67 protein(aa) \* Similarity to S. Pombe BEM1/BUD5 suppressor; cDNA EST comes from this gene; cDNA EST yk482d4.3 comes from this gene; cDNA EST y [ESTERASE] CG11935 LD47093 96B19-96B19 ID:106A6

CG11935 + 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\_SER ] CG16705 LD47115 97D8-97D8 dup:1/2 ID:106A7

CG16705 + Rpn7 endopeptidase \* Subunit of the regulatory particle of the proteasome; Rpn7p(aa) \* HYPOTHETICAL PROTEIN \* 1e-66  
CG5378 hypothetical protein YPR108w - yeast (Saccharomyces c [PCI\_DOMAIN // PCI] CG5378 LD47143 94B3-94B3 ID:106A8

CG5378 + unknown \* clot.672(dna)\* 7e-07 YEQ8\_YEAST HYPOTHETICAL 58.0 KD PEPTIDASE IN PTP3-ILV1 INTERGENIC  
CG11367 REGION \* 5e-08 similar to the peptidase family M24B \* 3e-12 CG11367 LD47277 79F2-79F2 dup:2/2 ID:106B10

CG11367 + 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

CG8448 + baz ion\_channel \* BLASTX 4.2E-06 Human super cysteine rich protein mRNA, partial cds.(dna) \* Bazooka protein(aa) \* baz \*  
CG5055 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

CG5055 + enzyme \* 3-hydroxyisobutyryl-coenzyme A hydrolase(aa) \* 4e-37 YDAK\_YEAST HYPOTHETICAL 56.3 KD PROTEIN IN  
CG5044 ARO3-KRS1 INTERGENIC REGION \* 5e-89 similar to enoy [ECH] CG5044 LD47223 88F1-88F1 ID:106B5

CG5044 + 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

CG10255 + endopeptidase \* DMSTUBBLE\_1 Sb \* SERINE PROTEINASE STUBBLE (STUBBLE-STUBBLOID PROTEIN)(aa) \* 2e-32  
CG4386 similar to plasminogen and to trypsin-like serine proteases elega [trypsin // CHYMOTRYPSIN // TRYPSIN\_SER ] CG4386 LD47230 58A2-58A2 ID:106B7

CG4386 + enzyme \* VITELLOGENIN II PRECURSOR (YOLK PROTEIN 2)(aa) \* lipoprotein lipase precursor(aa) \* Chain A, Triacylglycerol LipaseCOLIPASE COMPLEX(aa) \* TRIACYLGL [TAGLIPASE // ESTERASE // lipase // LIPA] CG5966 LD47264 5C10-5D1 ID:106B8

CG5966

+ chaperone \* similar to chaperonins cpn60 and TCP-1 (Pfam: cpn60\_TCP1.hmm, score: 416.20 and 102.94)(aa) \*  
 Component of Chaperonin Containing T-complex subunit s [TCP1\_2 // TCP1\_3 // TCOMPLEXTCP1 // CHA] CG8351 LD47396  
 85E9-85E9 ID:106C10  
 CG8351 + 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  
 CG9705 + motor\_protein \* DMMHC95F Mhc95F \* myosin-A(aa) \* 1e-65 MYS2\_YEAST MYOSIN-2 ISOFORM myosin MYO2 - yeast  
 CG10595 (Saccharo \* 2e-68 myosin V [myosin\_head // MYOSINHEAVY // ATP\_GTP\_A] CG10595 LD47348 29D1-29D1 ID:106C4  
 CG10595 + Sema-2a unknown \* semaphorin II precursor - fruit fly (Drosophila melanogaster)(aa) \* semaphorin-like \* semaphorin 2a  
 CG4700 precursor(aa) \* DMDSEM\_2 sema-I CG4700 LD47367 53C4-53C ID:106C6  
 CG4700 + ligand\_binding\_or\_carrier \* Rab2 \* BACR37P7.a(aa) \* 5e-33 YP51\_YEAST GTP-BINDING PROTEIN YPT51/VPS21 GTP-  
 CG3870 binding pr \* 7e-28 rab1 [ras // ATP\_GTP\_A // RASTRNSFRMNG] CG3870 LD47384 59E-59E ID:106C7  
 CG1103 + unknown \* CG1103 LD47387 82A6-82A6 ID:106C8  
 CG1103 + Gbp signal\_transduction \* striatin, calmodulin-binding protein(aa) \* WD-40-family-member \* 3e-16 SFL2 gene product (AA 1-  
 CG5519 669) \* 2e-19 transcription initiation factor IID-as[GPROTEINBRPT // WD40\_REGION // WD\_REPEA] CG5519 LD47390 55C13-  
 CG5519 55C13 ID:106C9  
 CG5519 + enzyme \* 3e-55 probable membrane protein YPR066w - yeast (Saccharomyces cerevisiae) \* 3e-21 ubiquitin activating  
 CG13343 enzyme \* 1e-111 coded for by C. elegans cDNA [UBA\_NAD // ThiF\_family // NAD\_BINDING /] CG13343 LD47462 50C14-50C14  
 CG13343 ID:106D10  
 CG13343 + dah unknown \* dystrobrevin(aa) \* similar to the kDa Torpedo acetylcholine receptor-associated protein; similar to rat  
 CG6157 apodystrophin-3, PIR Accession Number \* dah [ZF\_ZZ // ZZ] CG6157 LD47411 13C1-13C1 ID:106D2  
 CG6157 + unknown \* hypothetical protein(aa) \* HSPC039 protein(aa) \* 2e-11 LAS1\_YEAST LAS1 PROTEIN LAS1 protein - yeast  
 CG6316 (Saccharomyc \* CG6316 LD47413 70E1-70E1 ID:106D3  
 CG6316 + 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  
 CG4643 + DNA\_binding \* [NLS\_BP] CG4037 LD47433 49F8-49F9 ID:106D5  
 CG4037 + RNA\_binding \* SP62\_HUMAN; SAP 62; SF3A66(aa) \* 1e-13 PR11\_YEAST PRE-MRNA SPLICING FACTOR PRP11 PRP11  
 CG10754 protein \* 4e-94 Similarity to Human spliceosome-associated pro [ZF\_MATRIN // PRO\_RICH] CG10754 LD47455 69E2-69E2 dup:2/2  
 CG10754 ID:106D8  
 CG10754 + Gs1 enzyme \* glutamate-ammonia ligase (glutamine synthase)(aa) \* GLUTAMINE SYNTHETASE 2, CYTOPLASMIC  
 CG2718 (GLUTAMATE--AMMONIA LIGASE 2)(aa) \* predicted using Genefind [GLNA\_1 // gln-synt // GLNA\_ATP] CG2718 LD47536 21B-  
 CG2718 21B dup:4/4 ID:106E11  
 CG2718 + transcription\_factor \* 8e-33 cDNA EST yk416a1.3 comes from this gene; cDNA EST yk466h2.3 comes \* 1e-13 hypothetical  
 CG7845 protein \* [NLS\_BP // WD40] CG7845 LD47540 42A5-42A6 dup:2/2 ID:106E12  
 CG7845 + RNA\_binding CG7269 dup:2/2 ID:106E3  
 CG7269 + unknown \* 2e-16 YKJ2\_CAEEL HYPOTHETICAL 36.9 KD PROTEIN C02D5.2 IN CHROMOSOME III \* 1e-05 INIP\_HUMAN  
 CG9796 GAMMA-INTERFERON-INDUCIBLE PROTEIN IP-30 PRECURSOR \* 4e-1 CG9796 LD47508 87E10-87E10 dup:3/3 ID:106E4  
 CG12759 + Dbp45A RNA\_binding \* DMBP45A\_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  
 + 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 LD47515 47B1-47B1 dup:3/3 ID:106E6  
 CG2182 + unknown \* [NLS\_BP] CG2182 LD47517 83B7-83B7 dup:3/3 ID:106E7  
 + chaperone \* FK506-binding protein FKBP51(aa) \* 6e-20 FKBP\_YEAST FK506-BINDING PROTEIN (FKBP) (PEPTIDYL-  
 PROLYL CIS-TRANS ISOMERASE) (P \* 6e-24 FKB2\_DROME KD FK50 [TPR\_REGION // FKBP // FKBP\_PPIASE\_1 // ] CG4535  
 CG4535 LD47530 30E1-30E1 dup:2/2 ID:106E9  
 + cell\_cycle\_regulator \* sorting nexin 9(aa) \* 2e-11 YJD6\_YEAST HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2  
 INTERGENIC REGION \* 5e-74 similar to PhoX homologous domain, pres[PX // BEM\_DOMAIN // SH3DOMAIN // SH3] CG6757  
 CG6757 LD47602 67B13-67B13 ID:106F10  
 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  
 CG4572 LD47549 92B6-92B6 ID:106F2  
 + signal\_transduction \* Ylr222cp(aa) \* WD repeat protein(aa) \* coatomer alpha subunit(aa) \* BLASTX 2.6E-32  
 YLR222C|Protein of unknown function, has beta-transducin (WD-[GPROTEINBRPT // WD40\_REGION // WD\_REPEA] CG1671  
 CG1671 LD47550 46B13-46B14 ID:106F3  
 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 10A6-10A8  
 CG1453 dup:2/2 ID:106F6  
 + transcription\_factor\_binding \* hypothetical protein(aa) \* 2e-05 serine-threonine kinase receptor-associated protein \* 2e-05  
 CG5632 WD-40 repeat protein \* 3e-05 DMEST6P\_15 Est-P [WD40\_REGION // WD40] CG5632 LD47568 68F8-68F8 dup:1/2 ID:106F8  
 + 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 // MPIPHPTASE] CG1395  
 CG1395 LD47579 99A5-99A6 dup:3/3 ID:106F9  
 + motor\_protein \* 2e-11 C15H9.4 gene product \* 8e-43 protein \* protein \* chromosome X open reading frame TEX28  
 CG1021 [ANTIFREEZEI] CG1021 LD47668 84A4-84A4 ID:106G10  
 + ea endopeptidase \* DMEAST\_4 ea \* SERINE PROTEASE EASTER PRECURSOR(aa) \* 5e-20 kallikrein \* 8e-29 airway  
 CG4920 trypsin-like protease a [ANTENNAPEDIA // trypsin // CHYMOTRYPSIN] CG4920 LD47701 90E1-90E1 ID:106G12  
 CG14965 + motor\_protein \* CG14965 LD47616 63B13-63B13 ID:106G2  
 CG14954 + unknown \* CG14954 LD47625 63F4-63F4 ID:106G4  
 + unknown \* cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA  
 CG8399 EST comes from this gene; cDNA EST yk226e12.3 com CG8399 LD47639 52E1-52E3 dup:2/2 ID:106G6



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

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

CG3281 + transcription\_factor \* ovo \* DMSPALTR\_3 salr \* 6e-29 GLAS\_DROME GLASS PROTEIN finger protein glass - fruit fly [zf-C2H2 // ZINC\_FINGER\_C2H2 // HISTONE\_] CG3281 LD47774 87A7-87A7 ID:106H11

CG11484 + transcription\_factor\_binding \* [UBA] CG11484 LD47780 102D1-102D3 ID:106H12

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

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

CG2843 + unknown \* 2e-09 YNY5\_YEAST HYPOTHETICAL 20.4 KD PROTEIN IN RPA49-SUI1 INTERGENIC REGION \* 2e-08 coded for by C. elegans cDNA yk127b8.5; coded for by C. elegans [NLS\_BP] CG2843 LD47748 23A7-23A7 ID:106H9

CG10283 + unknown \* CG10283 LD47881 36F8-36F9 ID:107A11

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

CG2945 + cin unknown \* BACR37P7.g(aa) \* MOLYBDENUM COFACTOR SYNTHESIS PROTEIN CINNAMON(aa) \* DMCOFACTO\_2 cin \* 3e-05 hypothetical protein YMR244c-a - yeast (Saccharomyces [MOCF\_BIOSYNTHESIS\_1 // MOCF\_BIOSYNTHESIS] CG2945 LD47852 1A5-1A5 dup:1/3 ID:107A8

CG8370 + unknown \* Similar to a C.elegans protein encoded in cosmid C27F2 \* RW1 protein(aa) \* 3e-57 coded for by C. elegans cDNA yk86c6.3; coded for by C. elegans cDNA [NLS\_BP] CG8370 LD47858 52E1-52E1 dup:2/2 ID:107A9

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

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

CG4677 + transcription\_factor \* ZINC FINGER PROTEIN GLI1 (GLI-1)(aa) \* PAIR-RULE PROTEIN ODD-PAIRED(aa) \* hGLI2(aa) \* cubitus interruptus dominant protein(aa) [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG4677 LD47926 94D10-94D10 dup:2/3 ID:107B3

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

CG5568 + enzyme \* 1e-19 FAT2\_YEAST PEROXISOMAL-COENZYME A SYNTHETASE probable AMP \* 3e-11 acetyl-CoA synthetase - fruit fly (Drosophila melanogaster) \* 9e-40 similar [AMP-binding] CG5568 LD47944 64F3-64F3 ID:107B6

CG9646 + unknown \* No definition line found(aa) \* protein(aa) \* No definition line found \* [NLS\_BP] CG9646 LD47968 53F4-53F5

ID:107B7

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

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

CG3800 + unknown \* 5e-20 YNZ5\_YEAST HYPOTHETICAL 17.1 KD PROTEIN IN SIP3-MRPL30 INTERGENIC REGION \* 3e-12 RNA helicase \* 2e-25 cellular nucleic acid binding protein cl [ZF\_CCHC // zf-CCHC] CG3800 LD48005 59B6-59B6 ID:107C1

CG1602 + transcription\_factor \* 4e-91 putative zinc finger protein \* 8e-13 similar to Zinc finger, C2H2 type (4 domains); cDNA EST \* 4e-27 MFG2\_MOUSE ZINC FINGER PROTEIN MFG-2 z[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG1602 LD48073 43D3-43D3 ID:107C11

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

CG3108 + peptidase \* [pdb|1AYE] Human Procarboxypeptidase A2(aa) \* CARBOXYPEPTIDASE B(aa) \* 3e-37 YHT2\_YEAST HYPOTHETICAL 49.8 KD PROTEIN IN ACT3-YCK1 INTERGENIC REGION [CARBOXYPEPT\_ZN\_1 // CRBOXYPTASEA // Zn\_] CG3108 LP01044 5B6-5B8 ID:107D1

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

CG8062 + BcDNA:LD28120 transporter \* similar to the monocarboxylate transporter family(aa) \* Yol119cp(aa) \* contains similarity to monocarboxylate transporters(aa) \* MONOCARBOXYLATE TRA CG8062 LP01259 18C2-18C2 dup:3/5 ID:107D11

CG13594 + unknown ANTIFREEZEI CG13594 LP01106 ID:107D2

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

CG9186 + unknown \* Ypr147cp(aa) \* 1e-11 probable membrane protein YPR147c - yeast (Saccharomyces cerevisiae) \* 1e-20 predicted using Genefinder; Similarity to C.elegan [ESTERASE // LIPASE\_SER] CG9186 LP01162 62B4-62B4 dup:2/2 ID:107D5

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

CG3042 + enzyme \* ribulose-1,5-bisphosphate carboxylase/oxygenase N-methyltransferase(aa) \* ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltra CG3042 LP01222 6E3-6E3 ID:107D9

CG18140 + Cht3 enzyme \* chitinase(aa) \* 2e-22 probable membrane protein YDR371w - yeast (Saccharomyces cerevisiae) \* 2e-63

chitinase \* 1e-44 CHIT\_CAEEL PUTATIVE ENDOCHITIN CG18140 LP01426 40D5-40D5 dup:4/4 ID:107E10

CG1252 + Ccp84Ab structural\_protein cuticle cluster 7 CUTICLE, insect\_cuticle CG1252 LP01435 dup:2/2 ID:107E11

CG4664 + CG4664 dup:2/2 ID:107E12

+ LanA cell\_adhesion \* 7e-05 RA50\_YEAST DNA REPAIR PROTEIN RAD50 (153 KD PROTEIN) RAD50 \* LMA\_DROME LAMININ ALPHA CHAIN PRECURSOR laminin chain A \* 1e-114 similar to [RNP\_1 // EGF\_1 // EGFLAMININ // LAMININ] CG10236 LP01316 65A6-65A6 dup:5/5 ID:107E3

CG10236 + tok endopeptidase \* tok \* development protein tolkin - fruit fly (Drosophila melanogaster) \* 1e-145 similar to developmentally important proteins like human BMP-1 [EGF // CUB // ASTACIN // Astacin // EGF] CG6863 LP01328 96A20-96A22 dup:3/3 ID:107E4

CG6863 + enzyme \* cDNA EST comes from this gene; cDNA EST yk282d3.5 comes from this gene(aa) \* 1e-06 CCA1\_YEAST TRNA NUCLEOTIDYLTRANSFERASE PRECURSOR (TRNA ADENYLYLT [MET\_TRANS // SAM\_BIND] CG1239 LP01332 83C1-83C1 dup:2/2 ID:107E5

CG1239 + unknown \* PUTATIVE GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (GAMMA-BUTYROBETAINE HYDROXYLASE) (GAMMA-BBH)(aa) \* gamma- butyrobetaine hydroxylase; gamma- CG10814 LP01339 50A6-50A6 dup:2/2 ID:107E6

CG10814 + structural\_protein \* Peritrophin-A \* cDNA EST comes from this gene; cDNA EST yk369a9.5 comes from this gene; cDNA EST yk438c12.3 comes from this gene; cDNA EST yk438c12 CG7252 LP01340 68E3-68E3 dup:2/2 ID:107E7

CG7252 + unknown \* CG1153 LP01348 83E2-83E2 dup:2/2 ID:107E8

CG1153 + transcription\_factor \* DMRCPA\_X kel \* leucine-zipper-like transcriptional regulator, 1(aa) \* 4e-12 YG52\_YEAST HYPOTHETICAL 100.0 KD PROTEIN IN YHB1-PFK1 INTERGENIC REGION [BTB] CG3711 LP01394 1C5-1C5 dup:2/2 ID:107E9

CG3711 + signal\_transduction \* similar to epidermal growth factor receptor kinase substrate; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST yk246h9.3 come [SH3 // PRO\_RICH] CG8907 LP01469 92C1-92C1 ID:107F1

CG8907 + unknown \* CG9682 LP01629 99E5-99E5 dup:3/4 ID:107F10

CG9682 + receptor \* 4e-06 LDL receptor-like repeat; orfla \* 2e-47 coded for by C. elegans cDNA yk9e10.5; coded for by C. elegans cDNA yk9e10.3; mu \* 3e-07 very low dens [LDLRA\_2 // ldl\_recept\_a // LDLRA\_1] CG8756 LP01646 76C-76C ID:107F11

CG8756 + unknown \* ECDYSONE-INDUCED PROTEIN 74EFA (ETS-RELATED PROTEIN E74A)(aa) \* 1e-62 ecdysone-induced protein E74A - fruit fly (Drosophila pseudoobscura) \* 5e-91 e CG6273 LP01487 74E-74E ID:107F2

CG6273 + enzyme \* steroid sulfotransferase 3(aa) \* 7e-25 tyrosine-ester sulfotransferase \* 2e-24 SUPM\_HUMAN MONOAMINE-SULFATING PHENOL SULFOTRANSFERASE (SULFOTRANSFER [Sulfotransfer] CG5431 LP01553 59F4-59F4 ID:107F4

CG5431 + enzyme \* 1e-107 ecto-5'-nucleotidase \* 1e-105 5' nucleotidase (CD73) 5'-NUCLEOTID \* 1e-132 putative 5'-nucleotidase \* 3e-08 inserted at base 5' end of P elem [PHOSPHO\_ESTER // 5\_nucleotidase // 5\_NU] CG4827 LP01562 54C6-54C6 ID:107F5

CG4827 + RNA\_binding \* RNA binding motif protein 7(aa) \* predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST yk197f9.5 c [RBD // rrm] CG11454 LP01585 21B-21B dup:1/2 ID:107F7

CG11454 + peptidase \* [pdb|1AYE] Human Procarboxypeptidase A2(aa) \* 4e-45 YHT2\_YEAST HYPOTHETICAL 49.8 KD PROTEIN IN ACT3-YCK1 INTERGENIC REGION PRECURSOR \* 0.0000000006\* [CARBOXYPEPT\_ZN\_1 // CARBOXYPEPT\_ZN\_2 //] CG3097 LP01667 5B6-5B6 ID:107G1

CG3097 + transmembrane\_receptor \* 2e-08 /match=(desc: \* 6e-55 predicted using Genefinder \* No definition line found \* predicted using Genefinder CG14205 LP01839 18D7-18D7 ID:107G10

CG14205

+ cell\_adhesion \* DMSCA\_3 sca \* 4e-15 scabrous protein precursor - fruit fly (*Drosophila melanogaster*) \* 2e-05 coded for by  
 CG6788 *C. elegans* cDNA yk9a2.5; coded for by *C. e* [fibrinogen\_C] CG6788 LP01858 16E2-16E2 ID:107G11  
 + Lcp1 structural\_protein \* 9e-53 CLP1\_DROME LARVAL CUTICLE PROTEIN I PRECURSOR cuticle prot \* 1e-35 larval cuticle  
 CG11650 protein 1, LCP1=Lcp1 gene product {Y allele} miranda \* 4e-53 [CUTICLE // insect\_cuticle] CG11650 LP01670 44C1-44C1 ID:107G2  
 + Lnk signal\_transduction \* 3e-08 corkscrew protein 4A \* 5e-61 Pro-rich, PH, SH2 domain-containing signaling mediator \* 9e-63  
 CG17367 hypothetical protein [SH2DOMAIN // SH2 // PH\_DOMAIN] CG17367 LP01675 96F7-96F ID:107G3  
 + EG:34F3.7 enzyme \* DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 1(aa) \* BLASTX 2.9E-25  
 CG12311 PMT4|Mannosyltransferase (dolichyl phosphate-D-mannose:protein O-D-ma CG12311 LP01681 1C2-1C2 ID:107G4  
 + enzyme \* STERYL-SULFATASE PRECURSOR (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE)  
 (ARYLSULFATASE C) (ASC)(aa) \* 5e-14 weakly similar to arylsulfatase B [Sulfatase // SULFATASE\_2] CG5584 LP01735 75A2-  
 CG5584 75A2 ID:107G6  
 + Lcp65Ag1structural\_protein \* Lcp65Ag1 \* 3e-44 cuticle protein LCP65Ag1 cuticle \* 1e-30 cuticle homolog \* CU15\_MANSE  
 CG10530 CUTICLE PROTEIN CP14.6 PRECURSOR (MSCP14.6) cut [CUTICLE // insect\_cuticle] CG10530 LP01749 65A-65A ID:107G7  
 CG16926 + unknown \* CG16926 LP01766 56D10-56D10 ID:107G8  
 + motor\_protein \* 6e-23 ARP5\_YEAST ACTIN-LIKE PROTEIN ARP5 probable nuclear pro \* 2e-12 ACTU\_DROME ACTIN-  
 CG12321 LIKE PROTEIN 13E actin-related protein \* 6e-11 similar to Act CG12321 LP02120 90E6-90E6 ID:107H11  
 + 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-  
 CG8288 13E18 ID:107H3  
 + unknown \* queuine trna-ribosyltransferase(aa) \* 7e-98 TGT\_CAEEL PUTATIVE QUEUINE TRNA-  
 RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLA \* TGT\_BACSU QUEUINE TR CG4947 LP01967 21F1-21F1  
 CG4947 ID:107H4  
 + 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  
 CG8242 ID:107H6  
 + crol transcription\_factor \* crol \* BLASTX 2.3E-25 Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds.(dna) \*  
 CROL GAMMA \* 4e-14 HSN motor neurons m[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG14938 LP02106 33B1-33B1  
 CG14938 dup:2/2 ID:107H9  
 + Cdlc2 motor\_protein \* 8kd dynein light chain(aa) \* Cdlc1 \* dynein light chain 5(aa) \* 1e-21 DYLL1\_YEAST DYNEIN LIGHT CHAIN  
 CG5450 1, CYTOPLASMIC dynein lig [Dynein\_light // DYNEIN\_LIGHT\_1] CG5450 LP02196 22A-22A ID:108A1  
 CG5468 + unknown \* CG5468 LP02501 97C1-97C1 ID:108A10  
 + receptor \* putative mitochondrial inner membrane protein import receptor(aa) \* MITOCHONDRIAL IMPORT INNER  
 CG11779 MEMBRANE TRANSLOCASE SUBUNIT TIM44 PRECURSOR(aa) \* P CG11779 91F4-91F4 dup:1/2 ID:108A11  
 + ligand\_binding\_or\_carrier \* 2e-08 galactose specific C-type lectin \* 3e-10 lectin lambda \* 7e-13 mannose receptor, C type  
 CG9134 MACROPH \* 3e-08 C-type lectin-like protein [lectin\_c // C\_TYPE\_LLECTIN\_1 // C\_TYPE\_L] CG9134 LP02252 61F4-61F4 ID:108A3  
 CG18179 + unknown \* CG18179 LP02275 67B-67B ID:108A4  
 CG13627 + unknown \* CG13627 LP02282 96A20-96A20 ID:108A5

+ ligand\_binding\_or\_carrier \* retinaldehyde-binding protein 1(aa) \* ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TTP)(aa) \* 8e-07 SC14\_YEAST SEC14 CYTOSOLIC FACTOR (PHOSPHATIDYLINOSI [CRETINALDHBP // CRAL\_TRIO] CG5958 LP02316 27F7-27F7 ID:108A6  
 CG5958  
 + unknown \* CG18596 LP02352 96D4-96D4 ID:108A7  
 CG18596  
 + homology to bifunctional endo-1,4-beta-xylanase and RNA binding protein RGGm [Trypanosoma cruzi] GLUTELIN, PRO\_RICH CG10953 LP02439 ID:108A8  
 CG10953  
 + Akap200 signal\_transduction \* [PRO\_RICH // NLS\_BP] CG13388 29C1-29C3 dup:1/2 ID:108A9  
 CG13388  
 + unknown \* CG18317 LP02521 22B1-22F3 ID:108B1  
 CG18317  
 + P5cr enzyme \* 6e-29 PROC\_YEAST PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) \* 1e-157 pyrroline 5-carboxylate reductase \* 3e-52 similar to pyrroline-5- [P5CR] CG6009 LP02537 91E4-91E4 ID:108B2  
 CG6009  
 + unknown \* 2e-06 inserted at base 3' end of P element Inverse PCR \* \* CG1733 LP02557 12A1-12A2 dup:3/5 ID:108B3  
 CG1733  
 + unknown \* CG10200 LP02570 51C5-51C5 ID:108B4  
 CG10200  
 + enzyme \* 4e-06 cytochrome c oxidase subunit VIIa polypeptide (muscle) \* 1e-05 COXK\_BOVIN CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-HEART PRECURSOR (COX VIIA-M) ( CG9603 LP02592 84F13-84F13 ID:108B5  
 CG9603  
 + 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\_LLECTIN\_2] CG15818 LP02603 27F6-27F6 ID:108B6  
 CG15818  
 + actin\_binding \* kelch protein; ring canal component involved in cytoplasmic bridges; 77% Similarity to \* 2e-93 kelch protein, long form - fruit fly (Drosophila mela [BTB // Kelch] CG17754 LP02641 8D6-8D6 dup:2/2 ID:108B7  
 CG17754  
 + endopeptidase serine proteinase (EC 3.4.21.-) 2 precursor - fruit fly CHYMOTRYPSIN,TRYPSIN\_CATAL, TRYPSIN\_SER,] CG10475 ID:108C1  
 CG10475  
 + 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  
 CG8773  
 CG18546  
 + unknown \* CG18546 LP02835 87A6-87A6 ID:108C4  
 + nucleic\_acid\_binding \* 2e-06 Zinc finger-AT hook protein \* 2e-13 protein \* 5e-09 XFIN\_XENLA XFIN PROTEIN Xfin protein (AA - \* 2e-08 DMRNAD19A D19A [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG14438 LP02916 6C12-6C12 dup:2/3 ID:108C7  
 CG14438  
 + unknown \* lbm \* 1e-09 LBM\_DROME LATE BLOOMER PROTEIN late bloomer me \* 1e-11 lbm \* [TM4\_2] CG4471 LP02988 42E2-42E2 ID:108C9  
 CG4471  
 + 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  
 CG4799  
 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\_enz // ALDOLASE\_CLASS\_I // ] CG6058 LP03138 97A6-97A6  
 CG6058

dup:4/4 ID:108D12

CG7924 + unknown \* putative DNA binding protein=son placenta, Peptide Partial, \* \* CG7924 LP03067 74E1-74E1 ID:108D3  
+ lqf unknown \* EH domain binding protein epsin 2(aa) \* mitotic phosphoprotein 90(aa) \* 1e-31 hypothetical protein YDL161w -  
CG8532 yeast (*Saccharomyces cerevisiae*) \* 1e- [ENTH] CG8532 LP03068 66A-66A3 dup:2/2 ID:108D4  
+ protein\_kinase \* DMCDK46\_3 Cdk4/6 \* DMCDK5\_3 Cdk5 \* SNF1A \* DMMAPKIN\_4 rl [LDLRA\_2 //  
CG8250 RECEPTOR\_TYR\_KIN\_II // PROTE] CG8250 LP03070 53C10-53C11 ID:108D5  
+ enzyme \* hypothetical protein - human(aa) \* putative ubiquitin ligase(aa) \* putative ubiquitin transferase(aa) \* hect-domain-  
CG3356 containing protein, containing k [HECT\_DOMAIN // HECT // CYTOCHROME\_C] CG3356 LP03102 60B11-60B11 ID:108D6  
CG7906 + unknown \* CG7906 LP03104 74E1-74E1 ID:108D7  
+ serpin \* ZG-21p protein - rat(aa) \* protease inhibitor (ovalbumin type)(aa) \* 9e-10 Similar to serine protease inhibitor \* 2e-17  
CG1342 PAI2\_MOUSE PLASMINOGEN ACTIV [serpin] CG1342 LP03106 100A3-100A3 ID:108D8  
+ Ptp4E protein\_phosphatase \* DMRPTP4E\_2 Ptp4E \* DMDPTP101\_2 Ptp10D \* protein-tyrosine-phosphatase (EC 3.1.3.48),  
receptor type 4E, splice form A precursor - fruit fly (D[Y\_phosphatase // TYR\_PHOSPHATASE\_PTP //] CG6899 LP03315 4D1-4D1  
CG6899 dup:2/2 ID:108E10  
+ transporter \* 4e-15 hypothetical protein YDR387c - yeast (*Saccharomyces cerevisiae*) (U \* 2e-35 GTRL\_DROME GLUCOSE  
TRANSPORTER-LIKE PROTEIN glucose transpo \* 3e-[SUGRTRNSPORT // SUGAR\_TRANSPORT\_1 // SU] CG7801 LP03341  
CG7801 48B5-48B5 dup:2/2 ID:108E12  
+ protein\_kinase \* SERINE/THREONINE-PROTEIN KINASE UNC-51(aa) \* 5e-35 APG1\_YEAST AUTOPHAGY  
SERINE/THREONINE-PROTEIN KINASE APG1 \* 3e-24 p90 ribosomal S6 kinase \* [PROTEIN\_KINASE\_ST // TYRKINASE //  
CG10967 PROTE] CG10967 LP03175 69E1-69E2 dup:2/2 ID:108E3  
+ unknown \* predicted using Genefinder; similar to GNS1/SUR4 family; cDNA EST comes from this gene(aa) \* CGI-88  
CG5326 protein(aa) \* 9e-15 SUR4\_YEAST SUR4 PROTEIN (SRE CG5326 LP03255 94B5-94B5 dup:2/2 ID:108E4  
CG11470 + \* CG11470 99B5-99B5 dup:4/4 ID:108E6  
+ unknown \* 3e-53 YEF1\_YEAST HYPOTHETICAL 55.9 KD PROTEIN IN GDA1-UTR2 INTERGENIC REGION \* 1e-115  
CG6145 dJ283E3.6.1 (PUTATIVE novel protein similar to many (archae)ba CG6145 LP03268 50B4-50B5 dup:2/2 ID:108E7  
+ 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 CG10605 LP03275 69C9-69C11 dup:2/2 ID:108E8  
+ enzyme \* 1e-152 Naglu \* 1e-153 N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB) \* 1e-113 alpha-N-  
CG13397 acetylglucosaminidase \* alpha-N-acetylglucosaminida CG13397 LP03571 29C1-29C1 ID:108F10  
+ Lsp1gamma larval\_serum\_protein \* hexamerin A; arylphorin-like protein(aa) \* Lsp1 bgr; \* LARVAL SERUM PROTEIN BETA  
CHAIN PRECURSOR(aa) \* 8e-06 AMYH\_YEAST GLUCOAMYLASE S1/S2 PRECU[hemocyanin // HEMOCYANIN\_2 //  
CG6821 HAEMOCYAN] CG6821 LP03463 61A2-61A2 ID:108F5  
+ enzyme \* hydroxysteroid (17-beta) dehydrogenase 4(aa) \* peroxisomal multifunctional beta-oxidation protein; Fox2p(aa) \*  
ESTRADIOL BETA-DEHYDROGENASE (17-BETA [GDHRDH // adh\_short // ADH\_SHORT // THI] CG3415 LP03478 14B11-14B11  
CG3415 dup:2/2 ID:108F6  
CG2967 + BcDNA:GH09358 unknown \* cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this

gene; cDNA EST comes from this gene; cDNA EST comes from thi CG2967 LP03505 9B6-9B7 dup:4/4 ID:108F7

CG5904 + islet mitochondrial antigen CG5904 LP03542 ID:108F8

CG5844 + enzyme \* contains similarity to enoyl-CoA hydratases/isomerases Score=59.1, E=3.3e-16, N=1)(aa) \* 3e-51 Similar to enoyl-coA hydratase \* 2e-15 ECH1\_MOUSE PRO [ECH] CG5844 LP03547 87B15-87B15 ID:108F9

+ brat transcription\_factor \* transcription factor(aa) \* 1e-142 YOG2\_CAEEL HYPOTHETICAL ZINC FINGER PROTEIN ZK112.2 IN CHROMOSOME III \* 2e-38 protein \* 9e-38 RING finger[ZF\_BBOX // NHL // ZINC\_FINGER\_C2H2 // Z] CG10719 LP03649 37C4-37C dup:3/5 ID:108G1

CG10719 + transcription\_factor \* 3e-09 similar to X box DNA binding protein-1; cDNA EST comes \* 2e-09 X box binding protein-1; XBP-1 \* 8e-11 TREB protein \* 5e-12 hepatocarcinogenesis [B\_ZIP // bZIP // NLS\_BP] CG9415 LP03921 57C3-57C3 dup:2/3 ID:108G12

CG9415 \* 8e-11 TREB protein \* 5e-12 hepatocarcinogenesis [B\_ZIP // bZIP // NLS\_BP] CG9415 LP03921 57C3-57C3 dup:2/3 ID:108G12

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

CG4071 + unknown \* Ymr077cp(aa) \* 2e-08 YMW7\_YEAST HYPOTHETICAL 25.6 KD PROTEIN IN ABF2-CHL12 INTERGENIC REGION \* 8e-05 No definition line found \* 5e-59 I(2)rG270 I(2) CG4071 LP03791 58F1-58F1 ID:108G4

CG4071 + translation\_factor \* kDa protein; Fun12p(aa) \* 1e-120 YAD5\_YEAST 112.3 KD PROTEIN IN PYK1-SNC1 INTERGENIC REGION \* 1e-11 waclaw \* 3e-18 similar to initiation factor IF-[ELONGATNFCT // NLS\_BP // GTP\_EFTU // AT] CG10840 LP03795 63D2-63D2 ID:108G5

CG10840 63D2-63D2 ID:108G5

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

CG8182 + enzyme Glycosyl transferase, similar to N-acetylgalactosaminyltransferase GLYC\_TRANS, Glycos\_transf\_2, RICIN\_B\_LEC] CG8182 LP03835 ID:108G9

CG8182 + enzyme \* HemE homolog(aa) \* uroporphyrinogen decarboxylase; Hem12p(aa) \* UROPORPHYRINOGEN DECARBOXYLASE (UPD)(aa) \* UROPORPHYRINOGEN DECARBOXYLASE (URO-D)(a [UROD\_1 // UROD\_2 // URO-D] CG1818 LP03960 45F4-45F4 ID:108H1

CG1818 + transporter \* renal organic cation transporter(aa) \* solute carrier family (organic cation transporter), member 5(aa) \* sodium-dependent carnitine transporter(aa) [sugar\_tr] CG17752 LP04053 94D3-94D3 ID:108H10

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

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

CG6687 + 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[6PFRUCTKINASE // 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 dup:4/5 ID:108H8

CG14766 + unknown CG14766 LP04033 ID:108H9

+ 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  
 + CG16844 55C9-55C9 dup:1/2 ID:109A11  
 CG16844  
 + 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  
 CG2723 LP04438 84E6-84E6 ID:109A3  
 + unknown \* similar to C. elegans CEES08F encoded by GenBank Accession Number \* No definition line found(aa) \* CGI-27  
 CG8031  
 protein(aa) \* CG8031 LP04475 87D9-87D9 ID:109A6  
 + Cyp1 chaperone \* DMCYP1\_2 Cyp1 \* 1e-63 CYPH\_YEAST PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE)  
 (ROTAMASE) (CYCLOPHILIN) \* 2e-93 CYPH\_DROME PEPTIDYL-PROLYL CIS-TRANS[pro\_isomerase // CSA\_PPIASE\_1 // CSA\_PP] CG9916 LP04479 14B15-14B15 dup:1/2 ID:109A7  
 CG9916  
 CG18337  
 + unknown \* CG18337 LP04503 47E1-47E1 ID:109A8  
 + svr peptidase \* carboxypeptidase precursor(aa) \* svr \* 1e-06 YHT2\_YEAST HYPOTHETICAL 49.8 KD PROTEIN IN ACT3-YCK1 INTERGENIC REGION PRECURSOR \* 2e-76 coded for by [CRBOXYPTASEA // NLS\_BP // Zn\_carbOpept] CG4122  
 CG4122  
 LP04580 1B4-1B5 ID:109A9  
 + DnaJ-60 chaperone \* dnaJ-like protein(aa) \* DMDNAJLP\_2 DnaJ-60 \* 3e-08 SCJ1\_YEAST SCJ1 PROTEIN SCJ1 protein - yeast  
 (*Saccharomyce* \* 1e-114 dnaJ-like protein [DnaJ // DNAJ\_2] CG12240 LP04971 60B9-60B9 dup:3/3 ID:109B12  
 CG12240  
 CG10497  
 + CG10497 dup:1/2 ID:109B5  
 CG10497  
 CG12373  
 + CG12373 ID:109B8  
 + enzyme \* lipoamide dehydrogenase(aa) \* 1e-157 DLDH\_YEAST DIHYDROLIPOAMIDE DEHYDROGENASE PRECURSOR  
 dihydr \* 7e-19 GSHR\_DROME GLUTATHIONE REDUCTASE (GR) (GRAS [HGRDTASE // FADPNR // pyr\_redox // PYRI] CG7430  
 CG7430  
 LP04889 75A4-75A4 ID:109B9  
 + chaperone \* DMTIDT4M\_4 I(2)tid \* 1e-22 MDJ1\_YEAST MDJ1 PROTEIN PRECURSOR heat shock protein MDJ1 \* 2e-42  
 Tid56 protein \* 2e-42 YLW5\_CAEEL HYPOTHETICAL 105.9 K[DnaJ\_CXXCXGXG // DNAJ\_1 // DnaJ // DNAJ] CG7387 LP05202  
 CG7387  
 66B13-66B13 dup:1/2 ID:109C10  
 CG7387  
 CG9021  
 + unknown \* Cr-P11 allergen(aa) \* Cr-P11 \* major allergen Per a \* CG9021 LP05310 26A5-26A5 ID:109C12  
 CG9021  
 + unknown \* 3e-97 transmembrane protein \* 3e-07 similar to cuticulin 1; cDNA EST comes from this gene; \* 4e-99  
 CG15013  
 DMDUSKY\_1 dy \* 5E-84 CG15013 LP05062 64B6-64B6 ID:109C3  
 CG15013  
 + 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  
 + m1 unknown \* M1 protein(aa) \* 4e-82 M1 protein \* 3e-05 Similarity to Crayfish proteinase inhibitor cDNA ES \* 5e-05  
 CG8342  
 IOV7\_CHICK OVOINHIBITOR PRECURSOR ovoinhibito CG8342 LP05127 96F10-96F10 ID:109C5  
 CG8342  
 + Myo31DF motor\_protein \* myosin-1A(aa) \* didum \* actin binding actin binding ) map\_position:31D-F \* Myo31DF [myosin\_head // IQ // MYOSINHEAVY // NLS] CG7438 LP05132 31E4-31E5 ID:109C6  
 CG7438  
 + unknown \* NG22(aa) \* 3e-97 coded for by C. elegans cDNA CEESB82F; coded for by C. elegans cDNA CEES93F \* 1e-79  
 CG11880  
 NG22 \* CG11880 LP05177 99A1-99A1 dup:1/4 ID:109C9  
 CG11880



+ protein\_kinase \* 1e-57 KAPB\_YEAST CAMP-DEPENDENT PROTEIN KINASE TYPE (PKA 2) \* 1e-147 protein kinase (EC 2.7.1.37), cGMP-dependent - fruit fly (*Drosophila melanog*) \* [cNMP\_binding // CNMP\_BINDING\_1 // CNMP\_] CG4839 LP05330 31B-31B ID:109D1  
 CG4839  
 + 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  
 + Oscp enzyme \* DMOSCPPRE\_2 Oscp \* ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)(aa) \* coded for b [ATPASEDELTA // OSCP] CG4307 90D1-90D1 dup:2/2 ID:109D2  
 CG4307  
 + Rrp1 DNA\_repair\_protein \* DMRRP1\_2 Rrp1 \* RECOMBINATION REPAIR PROTEIN (DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE)(aa) \* 7e-63 similar to AP endonucleases family 1; cDNA EST [AP\_NUCLEASE\_F1\_3 // AP\_endonucleas1 // ] CG3178 LP05366 23C2-23C2 ID:109D3  
 CG3178  
 + endopeptidase \* COAGULATION FACTOR X PRECURSOR (STUART FACTOR)(aa) \* chymotrypsinogen B1(aa) \* coagulation factor G beta chain precursor - horseshoe crab (*Tachypleu*) [trypsin // CHYMOTRYPSIN // TRYPSIN\_SER ] CG10764 LP05421 54C3-54C3 ID:109D4  
 CG10764  
 + RNA\_binding \* ventral antigen 1(aa) \* astrocytic NOVA-like RNA-binding protein(aa) \* 0.00000003\* 2e-13 similar to RNA binding protein; cDNA EST comes from th [KH-domain // KH\_DOMAIN // ANTIFREEZEI] CG8144 LP05458 85D-85D ID:109D7  
 CG8144  
 + structural\_protein \* 1e-08 cuticular protein \* \* [insect\_cuticle] CG4818 LP05492 72F1-72F1 ID:109D9  
 CG4818  
 + BG:DS00941.14 unknown \* CG7953 LP05733 34D4-34D4 dup:2/2 ID:109E10  
 CG7953  
 + ppl enzyme \* predicted using Genefinder(aa) \* 5e-19 GCSH\_YEAST GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR F \* 3e-28 predicted using Genefinder \* 7e-32 glycine c [LIPOYL] CG7758 LP05579 78C8-78C8 dup:2/2 ID:109E4  
 CG7758  
 + Cyt-c1 electron\_transfer \* CYTOCHROME C(aa) \* 1e-32 pdb|1YCC| Cytochrome C (Isozyme 1) (Reduced) *Saccharomyces cerevisia* \* 2e-58 CYC1\_DROME CYTOCHROME C-1 cytochrome c[CYTCHRMEDIA // cytochrome\_c // CYTOCHR] CG13263 LP05614 36A7-36A7 dup:2/2 ID:109E5  
 CG13263  
 + structural\_protein \* peritrophin-48a precursor(aa) \* peritrophin-44(aa) \* SW-peritrophin-48 precursor(aa) \* CG6933 LP05638 77A-77A dup:3/3 ID:109E6  
 CG6933  
 + actin\_binding \* 5e-06 alternatively spliced form \* 9e-06 alpha-actinin \* protein \* 9e-06 alpha-actinin - rabbit (fragment) muscle alp [CH\_DOMAIN] CG11685 LP05986 85F7-85F7 ID:109F10  
 CG11685  
 + mas endopeptidase \* mas \* masquerade precursor - fruit fly (*Drosophila melanogaster*) \* 5e-30 similar to peptidase family S1 (trypsin family) \* 4e-38 KAL\_MOUSE PLASMA KA [trypsin // CHYMOTRYPSIN // TRYPSIN\_HIS ] CG15002 LP06006 64A12-64A12 ID:109F11  
 CG15002  
 + 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  
 + unknown \* CG9568 LP05845 29F8-29F8 ID:109F2  
 CG9568  
 + Rab3 signal\_transduction \* enzyme RHO small GTPase ) map\_position:47B \* 2e-47 SEC4\_YEAST RAS-RELATED PROTEIN SEC4 GTP-binding protein SE \* 1e-127 RAB3\_DROME RAS-RELATED PROTEI [ras // ATP\_GTP\_A // RASTRNSFRMNG] CG7576 LP05860 47B7-47B7 ID:109F3  
 CG7576  
 + enzyme \* MEMBRANE-BOUND ALKALINE PHOSPHATASE PRECURSOR (M-ALP)(aa) \* DMALKPHOS\_2 Aph-4 \* 8e-26 CG5656

repressible alkaline phosphatase (EC 3.1.3.1) \* 9e-78 alkaline [ALKPHPHTASE // alk\_phosphatase] CG5656 LP05865 78D5-78D5  
 dup:2/2 ID:109F4  
 CG9795 + unknown \* CG9795 LP05867 82A5-82A5 dup:2/2 ID:109F5  
 CG6264 + 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  
 + endopeptidase \* Ser12 \* Ser6 \* mas \* DMSNAKE\_2 snk [trypsin // CHYMOTRYPSIN // TRYPSIN\_CATA] CG9675 LP05929  
 CG9675 15A1-15A1 ID:109F7  
 CG5770 + unknown \* CG5770 LP06072 55B-55B ID:109G1  
 + structural\_protein \* peritrophin 1(aa) \* 3e-08 Gasp precursor \* 1e-07 R02F2.4 gene product \* 2e-13 insect intestinal mucin  
 CG10154 IIM22 CG10154 LP06444 70A8-70A8 ID:109G11  
 + Pkg protein\_kinase \* 3-phosphoglycerate kinase; Pkg1p(aa) \* DMPGKG\_2 Pkg \* PHOSPHOGLYCERATE KINASE(aa) \* 1e-  
 136 PGK\_YEAST PHOSPHOGLYCERATE KINASE 3-phosphoglycerate kina [PGK // PGLYCERATE\_KINASE // PHGLYCKINAS]  
 CG3127 CG3127 23A7-23A7 dup:2/3 ID:109G12  
 CG4449 + unknown \* CG4449 LP06117 97B1-94E9 ID:109G2  
 CG6968 + unknown \* [NLS\_BP] CG6968 LP06178 78D-78D dup:1/3 ID:109G3  
 CG14681 + unknown \* 1e-08 H06A10.1 \* 1E-168\* CG14681 LP06211 86C2-86C2 ID:109G4  
 CG12115 + unknown \* [NLS\_BP] CG12115 LP06283 8D2-8D2 ID:109G5  
 CG14455 + CG14455 LP06288 ID:109G6  
 + enzyme \* 8e-21 probable membrane protein YOR246c - yeast (Saccharomyces cerevisiae) \* 1e-06 3-hydroxyacyl-CoA  
 CG2070 dehydrogenase type II \* 1e-46 predicted using G [GDHRDH // adh\_short] CG2070 LP06328 43E6-43E6 ID:109G7  
 + Ag5r unknown \* antigen 5-related protein(aa) \* Ag5r \* 1e-156 antigen 5-related \* 6e-33 antigen 5-related protein CG9538  
 CG9538 LP06338 12F5-12F5 ID:109G8  
 + 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  
 CG6197 ID:109H11  
 + cell\_adhesion \* 1e-05 CCR4\_YEAST GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL  
 CG7702 EFFECTOR (C \* 4e-14 CHAO\_DROME CHAOPTIN PRECURSOR (PHOTORECEPTOR CELL-SPE [LRR // LEURICHRPT //  
 LRRCT] CG7702 LP06937 91B7-91B7 ID:109H12  
 + structural\_protein \* Abd-5=endocuticular protein migratoria=migratory locusts, abdomen, Peptide, \* Acp65Aa \* 2e-12 cuticle  
 CG7160 protein ACP65A \* Abd-5=endocuticular protein g [CUTICLE // insect\_cuticle] CG7160 LP06660 78F1-78F1 ID:109H3  
 CG5084 + unknown \* CG5084 LP06708 53E4-53E4 ID:109H7  
 + enzyme \* 3e-12 K03C7.1 gene product \* 3e-13 DNA-directed RNA polymerase (EC 2.7.7.6) II large chain - mouse (M12 \*  
 CG8381 2e-09 elastic titin \* 8e-10 proline-rich p [ADH\_SHORT] CG8381 LP06813 50E4-50E5 dup:1/2 ID:109H9  
 + PpN58A protein\_phosphatase \* serine-threonine protein phosphatase(aa) \* PpN58A \* 1e-108 PP12\_YEAST  
 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-2 pho \* 1e-174 serine-threonine prot[PHOSPHO\_ESTER // STPHPHTASE  
 CG3245 // SER\_THR\_] CG3245 SD01703 58B1-58B1 ID:113A9

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

CG8114 + pbl signal\_transduction \* ect2 oncogene(aa) \* 4e-05 regulatory protein CLS4 - yeast (Saccharomyces cerevisiae) \* 3e-08 /match=(desc;; /ma \* 1e-30 similar to transf[GRF\_DBL // BRCT\_DOMAIN // G\_PROTEIN\_REC] CG8114 SD01796 66A18-66A20 dup:2/4 ID:113B7

CG3322 + 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

CG9443 + unknown \* 8e-21 ERP6\_YEAST ERP6 PROTEIN PRECURSOR probable membrane pro \* 9e-39 similar to emp24/gp25L/p24 family \* 8e-72 associated to apparatus \* 2e-51 G25L [EMP24\_GP25L] CG9443 SD01878 85E4-85E5 dup:1/2 ID:113C5

CG1676 + unknown \* \* 5e-87 lclprt\_seq No definition line found \* YB3C\_SCHPO HYPOTHETICAL 60.9 KD PROTEIN C2F12.12C IN CHROMOSOME II \* [NLS\_BP] CG1676 SD01916 19D2-19D2 ID:113C9

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

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

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

CG13323 + unknown CG13323 ID:113D4

CG8576 + 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

CG10672 + 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

CG1884 + unknown \* similar to S. cerevisiae hypothetical 240.3 kd protein in MSH3 3' \* GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1(aa) \* t7i23.15 protein.(a [LECTIN\_LEGUME\_BETA // FGGY\_KINASES\_2 //] CG1884 SD02024 45F3-45F4 dup:5/7 ID:113D9

CG9437 + transcription\_factor \* DMADF1A\_2 Adf1 \* 6e-05 ADF1\_DROME TRANSCRIPTION FACTOR ADF-1 (ADH DISTAL FACTOR 1) \* 2e-67 inserted at base Both 5' and 3' ends of P element Inverse [NLS\_BP] CG9437 SD02118 57C5-57C5 dup:2/2 ID:113E10

CG6057 + 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

CG5032 + aft unknown \* 2e-05 YBR1\_YEAST HYPOTHETICAL 34.7 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION \* Adrift \* 2e-22 contains similarity to Methanococcus jannaschii cell d CG5032 SD02116 54E10-54E10 dup:3/3 ID:113E9

none + none SD02145 ID:113F3

CG8465 + enzyme\_inhibitor \* protein(aa) \* protein(aa) \* protein(aa) \* [ANK\_REP // ank // ANK\_REP\_REGION] CG8465 SD02148 16B5-16B6 dup:2/4 ID:113F4

CG1655 + unknown \* UNKNOWN; PRC1(aa) \* protein regulating cytokinesis 1; PRC1 \* [G\_PROTEIN\_GAMMA] CG1655 SD02150

9F5-9F5 ID:113F5

CG9042 + enzyme CG9042 ID:113F9  
+ 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  
CG17938 SD02215 36A10-36A10 ID:113G1  
+ fog unknown \* fog \* FOLDED GASTRULATION PROTEIN PRECURSOR(aa) \* fog \* folded gastrulation (fog) precursor - fruit fly  
CG9559 (Drosophila melanogaster) CG9559 SD02223 20A4-20A5 ID:113G3  
+ ligand\_binding\_or\_carrier \* ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TTP)(aa) \* retinaldehyde-binding  
protein, CRALBP Peptide, \* retinaldehyde-binding protein 1(aa) \* tocophero [CRETINALDHBP // CRAL\_TRIO] CG10026 SD02235  
CG10026 37E3-37E3 ID:113G7  
CG9653 + brk transcription\_factor \* putative transcription factor(aa) \* CG9653 SD02279 7A4-7A4 dup:3/6 ID:113H5  
+ nod motor\_protein \* DMKINLA\_3 nod \* KINESIN-LIKE PROTEIN NOD(aa) \* 4e-19 Cin8p kinesin-related \* 9e-46 similar to  
Kinesin motor domain; cDNA EST yk256h1.3 comes from t [kinesin // KINESIN\_MOTOR\_DOMAIN1 // KIN] CG1763 SD02282  
CG1763 10C5-10C6 ID:113H6  
+ signal\_transduction \* beta2-chimerin, cerebellar - human(aa) \* beta2-chimerin, cerebellar - rat (fragment)(aa) \* 2e-07  
BEM2\_YEAST GTPASE ACTIVATING PROTEIN BEM2/IP[RHO\_GAP // RhoGAP // DAG\_PE\_BINDING\_DOM] CG3208 SD02309  
CG3208 5A8-5A8 dup:1/3 ID:113H7  
+ Prosalpha1 unknown \* endopeptidase multicatalytic endopeptidase ) cell 26S proteasome ) map\_position:54B3-5 \* 20S  
CG18495 proteasome subunit alpha1(aa) \* endopeptidase multicata CG18495 SD02332 43F-43F dup:2/2 ID:114A1  
+ 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  
CG8732 SD02373 44D4-44D ID:114A6  
+ Khc motor\_protein \* DMKINHCA\_2 Khc \* cos \* KINESIN HEAVY CHAIN(aa) \* recombinant kinesin heavy chain(aa) [kinesin //  
CG7765 KINESIN\_MOTOR\_DOMAIN1 // KIN] CG7765 SD02406 53A-53A dup:1/2 ID:114A9  
+ enzyme \* type II membrane protein(aa) \* Similarity with yeast hypothetical protein (PIR accession number \* brn \* beta-1,3-  
CG8668 N-acetylglucosaminyltransferase(a [ALDOKETO\_REDUCTASE\_3] CG8668 SD02482 28E-28E ID:114B11  
+ transcription\_factor \* CCAAT-box-binding transcription factor(aa) \* 6e-35 probable membrane protein YDR060w - yeast  
CG7839 (Saccharomyces cerevisiae) \* 1e-76 predicted using Gene [NLS\_BP] CG7839 SD02424 70E1-68A3 ID:114B2  
+ enzyme\_inhibitor \* nuclear inhibitor of phosphatase-1(aa) \* similar to forkhead-associated (FHA) domains (Pfam: FHA.hmm,  
CG8980 score: 28.36)(aa) \* NIPP-1, nuclear inhibitor [FHA\_DOMAIN // FHA] CG8980 SD02428 53E10-53E11 ID:114B3  
+ transcription\_factor \* ovo \* zinc-finger-motif-protein \* zinc finger protein, subfamily 1A, (Ikaros)(aa) \* DMSPALTR\_3 salr  
CG11247 [ZINC\_FINGER\_C2H2 // zf-C2H2 // ZINC\_FIN] CG11247 SD02478 78F4-79A ID:114B9  
+ translation\_factor \* EUKARYOTIC TRANSLATION INITIATION FACTOR (EIF-5)(aa) \* 2e-63 IF5\_YEAST EUKARYOTIC  
TRANSLATION INITIATION FACTOR (EIF-5) \* 2e-87 IF5\_CAEEL EUKARYOTIC [EF\_HAND] CG9177 SD02540 14A1-14A1  
CG9177 dup:2/3 ID:114C10  
+ hts actin\_binding \* adducin homolog - fruit fly (Drosophila melanogaster)(aa) \* similar to alpha-adducins(aa) \* DMADDLIKE\_3  
CG9325 hts \* adducin-like(aa) [Aldolase\_II] CG9325 SD02552 56D5-56D6 ID:114C12

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

+ enzyme \* sn-1,2-diacylglycerol cholinephosphotransferase(aa) \* contains similarity to CDP-alcohol phosphotransferases(aa) \* choline/ethanolaminephosphotrans [CDP\_ALCOHOL\_P\_TRANSF // CDP\_ALCOHOL\_P\_T] CG10355 SD02518 37F1-37F1

CG10355 dup:3/5 ID:114C5

CG7434 + RpL22 ribosomal\_protein Ribosomal protein L22 60S subunit ANTIFREEZEI CG7434 SD02522 ID:114C6

+ ligand\_binding\_or\_carrier \* chromatin assembly factor I (150 kDa)(aa) \* chromatin assembly factor I p150 chain - human \* [NLS\_BP] CG12109 SD02526 7F4-7F5 dup:1/2 ID:114C7

CG12109 + unknown \* BLASTX 1.9E-12 Dictyostelium discoideum AAC-rich mRNA (AAC11).(dna) \* 5e-87 inserted at base Both 5' and 3' ends of P element Inverse PCR \* [PRO\_RICH // NLS\_BP] CG7502 SD02606 18B1-18B1 ID:114D5

CG7502 + DNA\_binding \* 2e-33 inserted at base 5' end of P element Inverse PCR \* \* [MYB\_1 // NLS\_BP] CG15610 SD02691 53E-53E5 dup:2/2 ID:114E11

CG15610 + Pros26.4 \* Pros26.4 \* 1e-177 PRS4\_YEAST 26S PROTEASE REGULATORY SUBUNIT HOMOLOG (TAT-BINDING HOMOLOG 5) \* PRS4\_DROME 26S PROTEASE REGULATORY SUBUNIT (P26S4) P [AAA // NLS\_BP // ATP\_GTP\_A] CG5289 95C-95C dup:2/3 ID:114E3

CG5289 + transcription\_factor\_binding \* ESC virilis, Peptide, \* extra sex combs protein - fruit fly (Drosophila melanogaster)(aa) \* BLASTX 7.9E-26 Precis coenia transcription[GPROTEINBRPT // WD40\_REGION // WD40] CG5202 SD02661 33B9-33B9 dup:2/2 ID:114E4

CG5202 + 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 + nbA ion\_channel \* nbA \* DMCA1\_2 Ca- agr;1D \* CCA1\_DROME CALCIUM CHANNEL ALPHA-1 SUBUNIT (CACOPHONY PROTEIN) (NIGHTBLIND A PR \* unc-2 gene product [NACHANNEL // ion\_trans // CACHANNEL // ] CG1522 10F10-11A1 dup:2/2 ID:114F12

CG1522 + unknown \* 4e-15 MTRP\_MOUSE GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP \* 6e-15 MTRP\_HUMAN

CG8575 GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP \* \* CG8575 SD02746 44D8-44D8 dup:1/2 ID:114F2

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

+ 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 + receptor \* dominant autoantigen gp - rat (fragment)(aa) \* ST7 protein(aa) \* 3e-12 NDL\_DROME SERINE PROTEASE NUDEL PRECURSOR nudel protein \* 1e-26 coded for by [LDLRA\_2 // LDLRECEPTOR // ldl\_recept\_a ] CG12139 SD02842 8D12-8E1 dup:2/2 ID:114G4

CG12139

+ Vha16 enzyme \* DMCSUC\_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  
 + 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-bindin]  
 CG3961 SD02971 75E2-75E2 ID:114H10  
 + Rtc1 enzyme \* RNA 3'-terminal phosphate cyclase(aa) \* DMYP3G Rtc1 \* PROBABLE RNA 3'-TERMINAL PHOSPHATE  
 CYCLASE (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE)(aa) \* 4e-4 [RTC // RCT // NLS\_BP] CG11130 SD02972 12B8-12B8  
 ID:114H11  
 + enzyme \* dihydrosphingosine phosphate lyase (also known as sphingosine phosphate lyase); Dpl1p(aa) \* Similar to  
 CG8946 glutamate decarboxylase(aa) \* sphingosine-1-p CG8946 SD02978 53F10-53F10 dup:3/3 ID:114H12  
 + transporter \* fatty acid transport protein 4; FATP4(aa) \* 1e-64 very long-chain fatty acyl-CoA synthetase \* 1e-129 coded for  
 by C. elegans cDNA yk83h3.3; coded f [AMP\_BINDING // AMP-binding // NLS\_BP] CG7400 SD02910 31E5-31E6 dup:4/4  
 ID:114H2  
 + unknown \* 8e-36 YJX2\_YEAST HYPOTHETICAL 67.0 KD PROTEIN IN PRE3-SAG1 INTERGENIC REGION \* 2e-38 cDNA  
 CG13097 EST yk337b8.5 comes from this gene; cDNA EST yk371b10.5 co [NLS\_BP] CG13097 SD02943 29D1-29D1 ID:114H6  
 + protein\_kinase \* 8e-50 SNF1\_YEAST CARBON CATABOLITE DEREPRESSING PROTEIN KINASE p \* 3e-30 p90  
 ribosomal S6 kinase \* 1e-117 similar to serine/threonine kinase; cDNA E [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM]  
 CG8485 SD02969 50E8-50E8 ID:114H9  
 + electron\_transfer \* thioredoxin(aa) \* 8e-20 TRX1\_YEAST THIOREDOXIN I (TR-I) thioredoxin I - yeast (Sacc \* 1e-17  
 THIO\_DROME THIOREDOXIN (DEADHEAD PROTEIN) thioredoxin-I [THIOREDOXIN // THIOREDOXIN\_2 // thioired] CG3864  
 CG3864 30C-30C2 ID:115A11  
 + unknown \* isopentenyl-diphosphate delta isomerase(aa) \* 1e-44 IPPI\_YEAST ISOPENTENYL-DIPHOSPHATE DELTA-  
 CG5919 ISOMERASE (IPP ISOMERASE) \* 3e-33 YMX3\_CAEEL HYPOTHETIC CG5919 SD03046 93D4-93D4 ID:115A12  
 + \* predicted using Genefinder; similar to thrombospondin like; cDNA EST comes from this gene; cDNA EST comes from this  
 CG2131 gene; cDNA EST yk195c9.3 comes [TSP1 // ig // NLS\_BP // tsp\_1 // ATP\_GT] CG2131 39E7-39F1 dup:1/2 ID:115A3  
 CG13868 + unknown \* 0.000000000000008\* \* CG13868 SD03066 56F17-57A dup:4/4 ID:115B4  
 + unknown \* contains a single LIM domain at the N-terminus.; cDNA EST comes from this gene; cDNA EST comes from this  
 CG10439 gene; cDNA EST yk357g9.5 comes from this ge [LIM\_DOMAIN\_1 // LIM\_DOMAIN\_2] CG10439 SD03168 57B1-57B1 ID:115C12  
 + unknown \* coded for by C. elegans cDNA cm04e9; coded for by C. elegans cDNA CESAC59F(aa) \* unknown(aa) \* \*  
 CG18112 CG18112 SD03121 99C5-99C5 ID:115C3  
 + I(2)not transmembrane\_receptor \* DMNOTB\_2 I(2)not \* Not22(aa) \* putative Dol-P-Man dependent alpha(1-3)  
 CG4084 mannosyltransferase involved in the biosynthesis of the lipid-linked oligosac CG4084 SD03142 59F5-59F5 ID:115C6  
 CG15319 + CG15319 SD03263 ID:115D11  
 CG5444 + transcription\_factor CG5444 dup:3/3 ID:115D3  
 + unknown \* 3e-55 hypothetical protein YOL124c - yeast (Saccharomyces cerevisiae) ( \* 3e-51 hypothetcal protein \*  
 CG1074 Y724\_METTH HYPOTHETICAL PROTEIN MTH724 methyl [N6\_MTASE // N12N6MTFRASE] CG1074 SD03208 82C1-82C1

ID:115D7  
+ Cyp12a4 cytochrome\_P450 \* CYTOCHROME P450 CYP12A2(aa) \* 3e-17 lanosterol 14-demethylase cytochrome P450 \* 5e-24 cytochrome P450 cytochrome P4 \* 4e-20 YS45\_CAEEL PUTATIVE CYTO [EP450II // p450 // P450 // MITP450 // C] CG6042  
CG6042 SD03227 91F3-91F4 ID:115D8  
+ cell\_adhesion \* DMDACHSOU\_2 ds \* contains similarity to multiple cadherin-type repeats(aa) \* cadherin 18(aa) \*  
CG6977 DMDEC\_1 shg [CADHERIN // cadherin] CG6977 SD03311 87A-87A dup:5/5 ID:115E6  
+ EG:63B12.12 unknown \* 9e-50 /match=(desc: \* 7e-40 inserted at base Both 5' and 3' ends of P element Inverse PCR \*  
CG14818 CG14818 SD03316 2B14-2B14 dup:2/2 ID:115E7  
+ unknown \* pre-mRNA cleavage factor Im (25kD)(aa) \* putative protein(aa) \* predicted using Genefinder; cDNA EST  
CG3689 yk236h6.3 comes from this gene; cDNA EST yk23 CG3689 SD03330 67B2-67B2 dup:2/2 ID:115E9  
+ signal\_transduction \* 5e-15 VPS9 protein - yeast (Saccharomyces cerevisiae) (Z46 \* 7e-28 cDNA EST yk210c11.3 comes  
CG9139 from this gene; cDNA EST yk210c11.5 co \* 3e-09 Ras inhi CG9139 SD03358 61F5-62B4 dup:3/4 ID:115F1  
+ RNA\_binding \* 2e-05 SUWA\_DROME SUPPRESSOR OF WHITE APRICOT PROTEIN \* 0.0000003\* 4e-10 predicted  
CG6615 protein \* 2e-07 DMSUWA\_6 su(w<up>a</up>) [SURP // PRO\_RICH] CG6615 SD03435 73E4-73E4 dup:2/2 ID:115F12  
+ Aac11 apoptosis\_inhibitor \* apoptosis inhibitor 5(aa) \* Aac11(aa) \* 1e-110 unknown \* 1e-35 unknown protein CG6582  
CG6582 SD03364 36C3-36C3 ID:115F2  
CG18278 + unknown \* CG18278 SD03412 50A9-50A9 ID:115F5  
+ enzyme \* ripening-induced protein(aa) \* 4e-20 putative protein \* Strong similarity to auxin-induced protein from Vigna radiata  
CG17221 and a \* ripening-induced pro [adh\_zinc] CG17221 SD03451 23C5-23C5 ID:115G6  
+ Es2 enzyme \* HYPOTHETICAL 58.3 KD PROTEIN F42H10.7 IN CHROMOSOME III(aa) \* ES2 protein(aa) \* ES2 protein(aa) \*  
CG1474 Es2 CG1474 SD03464 7E7-7E7 ID:115G8  
+ gammaCoptransporter \* coat protein gamma-cop(aa) \* COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)(aa) \* 1e-123 COPG\_YEAST COATOMER GAMMA SUBUNIT (GAMMA-COAT PROT CG1528 SD03531 100D-100D  
CG1528 ID:115H4  
+ unknown \* PBK1 protein(aa) \* 5e-11 predicted using Genefinder; Weak similarity to Mouse CSA-19 protei \* 2e-16 PBK1  
CG13096 protein \* 7e-08 hypothetical protein [NLS\_BP] CG13096 SD03546 29D1-29D1 ID:115H5  
+ esc transcription\_factor \* DMESCOMBS\_4 esc \* 3e-08 YCW2\_YEAST HYPOTHETICAL 57.0 KD TRP-ASP REPEATS  
CG14941 CONTAINING PROTEIN IN CPR4-SSK2 \* extra sex combs protein - fruit fly (Dr[GPROTEINBRPT // RCC1\_2 // WD40\_REGION /]  
CG14941 SD03549 33B1-33B2 ID:115H6  
CG6665 + unknown \* HSPC012(aa) \* \* [NLS\_BP] CG6665 SD03555 53E6-53E6 ID:115H7  
+ Fas3 cell\_adhesion \* FASCICLIN III PRECURSOR (FAS III)(aa) \* DMFCNIII\_4 Fas3 \* 0.00001\* fasciclin III precursor - fruit fly  
CG5803 (Drosophila melanogaster) CG5803 36F6-36F6 ID:115H8  
CG1363 + blow unknown \* 1E-143 blown fuse\* CG1363 SD03683 dup:2/2 ID:116A10.2  
CG8046 + transporter CG8046 SD03610 dup:1/2 ID:116A2  
CG12004 + unknown CG12004 SD03655 ID:116A6  
CG1973 + protein\_kinase \* unknown protein(aa) \* 2e-22 hypothetical protein YOR112w - yeast (Saccharomyces cerevisiae) \* 3e-06

CDK5\_DROME CELL DIVISION PROTEIN KINASE HOMOLOG [PROTEIN\_KINASE\_DOM] CG1973 SD03656 99C2-99C2 ID:116A7

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

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

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

CG10042 + transcription\_factor transcription factor involved in DNA packaging MBD, NLS\_BP, ZINC\_FINGER\_C2H2 CG10042 SD03893 dup:1/2 ID:116D1

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

+ signal\_transduction \* HYPOTHETICAL 94.2 KD PROTEIN C38D4.5 IN CHROMOSOME III(aa) \* 2e-05 /match=(desc:; /ma \* 2e-05 RIP1 \* 3e-12 98K GTPase-activating protein ABR, brain [RHO\_GAP // RhoGAP] CG7122 SD04011 16F7-16F7 dup:4/5 ID:116E6

CG7122 + Xpd DNA\_repair\_protein Xeroderma pigmentosum D nucleotide-excision repair DEAH\_ATP\_HELICASE, XRODRMPGMNTD CG9433 SD04012 dup:3/3 ID:116E7

CG9433 + CRAL\_TRIO ligand\_binding\_or\_carrier CG1902 SD04017 dup:2/2 ID:116E8

CG1902 + CG12706 SD04019 dup:2/4 ID:116E9.2

CG12706 + translation\_factor \* 3e-06 Pdd1p Pdd1p thermoph \* \* [chromo // CHROMO\_2] CG10712 79F5-79F5 dup:3/4 ID:116F1

CG10712 + unknown CG17556 SD04068 dup:2/2 ID:116F7.2

CG17556 + RNA\_binding CG9344 ID:116F8

CG9344 + alpha-Adaptin transporter \* highly similar to alpha-adaptin (rat and mouse)(aa) \* DMALPADPT\_2 agr;-Adaptin \* adaptor-related protein complex AP-2, alpha subunit(aa) \* ALPHA-AD CG4260 SD04083 21C2-21C2 dup:2/3 ID:116F9

CG4260 + CG7649 SD04095 dup:2/3 ID:116G1.2

CG7649 + 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

CG11033 + unknown CG8593 dup:2/2 ID:116H4

CG8593 + transcription\_factor \* 1e-10 YJF6\_YEAST HYPOTHETICAL 98.9 KD ZINC FINGER PROTEIN IN BTN1-PEP8 INTERGENIC REG \* 7e-12 Kr-h \* 1e-05 similar to Zinc finger, C2H2 type[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG13620 96A13-96A14 dup:3/3 ID:116H5.2

CG13620 + expressed in the embryo (head , mesectoderm , mesoderm , mesoderm anlagen CG5530 SD04373 dup:1/2 ID:117B10

CG5530 + It has been mapped cytologically to 36A2--3 PRO\_RICH CG5953 SD04335 dup:1/3 ID:117B7

CG5953 + unknown PHO85 protein PIPLC\_X\_DOMAIN CG2818 SD04355 dup:1/2 ID:117B8

CG2818



+ alpha-Spec actin\_binding \* DMLETHAL\_2 Actn \* DMSPCA\_2 agr;-Spec \* SPECTRIN ALPHA CHAIN(aa) \* 3e-15 USO1\_YEAST  
 INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1 ( [spectrin // SPEC\_REPEAT // EF\_HAND // S] CG1977 SD04436  
 CG1977 62B-62B dup:2/7 ID:117C8  
 CG14971 + unknown Homo sapiens CGI-15 protein CG14971 SD04505 ID:117D9  
 CG9531 + CG9531 SD04586 dup:3/3 ID:117E5  
 + G\_protein\_linked\_receptor \* CL3BC(aa) \* protein(aa) \* 4e-20 similar to G-protein coupled receptor protein; cDNA EST \* 2e-  
 14 EMR1\_MOUSE CELL SURFACE GLYCOPROTEIN[7tm\_2 // RECEPTOR\_PKD // GAL\_LLECTIN // ] CG8639 SD04590 44D2-  
 CG8639 44D2 dup:5/5 ID:117E6  
 + cell\_adhesion \* robo \* similar to IG (immunoglobulin) superfamily (17 domains), Low-density lipoprotein receptor domain  
 class A (3 domains), Laminin EGF-like (Doma[LDLRA\_2 // ig // RNP\_1 // EGF\_1 // EGF ] CG7981 SD04592 3A2-3A3 dup:4/4  
 CG7981 ID:117E7  
 CG17156 + transcription\_factor CG17156 SD04616 dup:2/2 ID:117E9  
 + defense/immunity\_protein \* tag7(aa) \* 2e-20 peptidoglycan recognition protein precursor \* 4e-20 TNF superfamily, member  
 CG4432 (LTB)-like (peptidoglycan recognition \* 2e-19 peptidogl [HTH\_ARAC\_FAMILY\_1] CG4432 SD04722 67A8-67A9 dup:2/2 ID:117F12  
 CG8151 + CG8151 SD04652 ID:117F3  
 CG7623 + transporter CG7623 SD04658 dup:1/2 ID:117F5  
 + protein\_kinase \* protein(aa) \* cdc2-like protein kinase(aa) \* 3e-65 CTK1\_YEAST CTD KINASE ALPHA SUBUNIT (CTD  
 KINASE KD SUBUNIT) (CTDK-I ALPHA SUB \* 6e-69 posi[PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG7597 SD04681  
 CG7597 78E1-78E1 dup:2/3 ID:117F7.2  
 + enzyme \* mitochondrial and cytoplasmic valyl-tRNA synthetase; Vas1p(aa) \* Valyl tRNA Synthetase(aa) \* VALYL-TRNA  
 SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)(aa) [tRNA-synt\_1 // AA\_TRNA\_LIGASE\_I // TRNA] CG4062 SD04748 49F10-  
 CG4062 49F10 dup:2/5 ID:117G8  
 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  
 CG5608 function(dna) \* BLASTX 7.0E-38 YLR386W|Protein o CG5608 SD04925 87C-87C dup:2/2 ID:118A11  
 + unknown \* 1e-28 weak similarity to chromosomal replicator initiator protein DNAA ( \* similar to a C.elegans protein encoded  
 CG11943 in cosmid \* CG11943 SD04935 19A3-19A3 dup:3/7 ID:118A12  
 CG1707 + CG1707 SD04870 dup:2/2 ID:118A2.2  
 CG15618 + CG15618 SD04871 dup:1/4 ID:118A3  
 CG14800 + no blast hits pioneer protein? CG14800 SD04906 dup:1/2 ID:118A8  
 CG17436 + CG17436 ID:118A9  
 + Mcm6 DNA\_replication\_factor Minichromosome maintenance 6, chromatin binding involved in pre-replicative complex formation  
 CG4039 MCM, MCM\_1, MCM\_2 CG4039 SD04977 dup:3/3 ID:118B11  
 + lic protein\_kinase (licorn) stress activated MAP kinase kinase 3 [Drosophila melanogaster] PROTEIN\_KINASE\_DOM,  
 CG12244 PROTEIN\_KINASE\_ST, p] CG12244 SD04985 ID:118B12

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

CG8929 + unknown \* 1e-149 inserted at base Both 5' and 3' ends of P element Inverse PCR \* BLASTX 4.2E-08 Carrot gene for extensin.(dna) \* 2e-61 inserted at base Both 5 [PRO\_RICH // NLS\_BP] CG8929 SD04973 57A-57A dup:2/3 ID:118B9

+ GTP\_binding 108000000 SD05004 ID:118C1

CG2385 + CG2385 SD05054 dup:1/2 ID:118C5

CG1787 + enzyme CG1787 SD05059 ID:118C6

CG1832 + transcription\_factor CG1832 SD05094 dup:2/5 ID:118C8.2

CG4141 + Pi3K92E enzyme 1-phosphatidylinositol 3-kinase PI3K-C2, PI3K-rbd, PI3Ka, PI3-PI4-kinase CG4141 SD05105 ID:118C9

CG2971 + CG2971 ID:118D1

+ 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 and env protein precursor \* hypothetical [rvt // NLS\_BP] CG2485 SD05236 10B1-10B1 dup:4/7 ID:118D11

CG2485 + enzyme CG9366 SD05212 ID:118D6

CG9366 + none SD05284 ID:118E10

none + enzyme CG17148 SD05284 ID:118E10.2

CG17148 + transporter CG12210 SD05285 dup:2/2 ID:118E11

CG12210 + unknown stomatin-like protein Band\_7, STOMATIN CG7635 SD05291 dup:3/3 ID:118E12

CG7635 + 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

CG5841 + S6kII protein\_kinase ribosomal protein S6 kinase PROTEIN-KINASE-ATP, PROTEIN-KINASE-ST, T] CG17596 SD05277 dup:3/3 ID:118E6

CG17596 + CG8060 SD05384 dup:2/2 ID:118F10.2

CG8060 + DNA\_repair\_protein CG7143 SD05329 dup:2/2 ID:118F3

CG7143 + enzyme \* alpha-1,6-fucosyltransferase(aa) \* No definition line found(aa) \* fucosyltransferase (alpha (1,6) fucosyltransferase)(aa) \* 1e-100 No definition lin CG2448 SD05335 10D4-10D4 dup:2/2 ID:118F5

CG2448 + 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

CG7100 + BcDNA:GH13356 enzyme beta galactosyltransferase MITOCH\_CARRIER, XYLOSE\_ISOMERASE\_2 CG8536 SD05469 dup:1/2 ID:118G11

CG8536 + eIF-4E translation\_factor \* Eif4E \* 2e-28 IF4E\_YEAST EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CA \* 1e-121 IF4E\_DROME EUKARYOTIC TRANSLATION INITIATION CG4035 SD05406 67B2-67B2 dup:3/4 ID:118G2.2

CG4035 + transporter \* Ydr205wp(aa) \* 5e-09 Zn/Cd resistance gene \* 1e-06 cDNA EST yk447c2.5 comes from this gene; cDNA EST co \* 1e-06 zinc transporter ZnT-1 - mouse ZnT-1 [KININOGEN] CG6672 86D7-86D7 dup:1/2 ID:118G3

CG6672

CG6339 + motor\_protein CG6339 SD05424 ID:118G5

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

CG7110 + unknown \* [NLS\_BP] CG7110 SD05480 34B7-34B7 dup:2/3 ID:118H1

CG8902 + CG8902 dup:2/4 ID:118H6

CG13384 + transporter putative amino acid transport protein AROMATIC\_AA\_PERMEASE\_2 CG13384 SD05512 dup:2/4 ID:118H7

CG8368 + enzyme CG8368 SD05518 ID:118H9

CG10254 + enzyme CG10254 SD05555 dup:4/4 ID:119A2.2

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 SD05570 dup:1/2 ID:119A4

CG5721 + pioneer protein CG5721 SD05591 ID:119A7

CG8159 + transcription\_factor CG8159 SD05592 ID:119A8

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

CG7161 + CG7161 SD05642 dup:1/2 ID:119B4

CG12238 + transcription\_factor \* requiem, apoptosis response zinc finger gene; neuroD4; ubi-d4(aa) \* All-1 related protein(aa) \* probable transcription factor requiem - mouse(aa) \* [PHD] CG12238 SD05644 18D9-18D10 dup:2/3 ID:119B5

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

CG9717 + transporter similar to sulfate transport protein, sulphate permease Sulfate\_transp CG9717 SD05675 dup:1/2 ID:119C1

CG8877 + CG8877 SD05715 dup:2/2 ID:119C11.2

CG7821 + CG7821 SD05678 ID:119C2

CG11168 + cytoskeletal\_structural\_protein CG11168 SD05685 ID:119C4

+ RNAS\_binding homology with Drosophila dip1 (disco interacting protein) gene, a new member of the Stauf family of RNA  
 binding proteins CG17452 SD05690 ID:119C6  
 + signal\_transduction \* AND-1 protein(aa) \* bgr;Cop \* 6e-29 Met30p \* 3e-28 Slimb [GPROTEINBRPT // GPROTEINB //  
 CG17437 WD40\_REGIO] CG17437 3A8-3A8 dup:3/3 ID:119D12.2  
 + enzyme \* lysine ketoglutarate reductase/saccharopine dehydrogenase(aa) \* similar to saccharopine dehydrogenases(aa) \*  
 CG7144 lysine-ketoglutarate reductase /sacch CG7144 SD05742 28C9-28D dup:2/2 ID:119D4  
 + enzyme CG11874 SD05769 dup:3/3 ID:119D7.2  
 CG12016 + enzyme \* [ATP\_GTP\_A] CG12016 SD05789 63C5-63C5 dup:1/3 ID:119D9  
 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  
 + protein\_kinase similar to serine/threonine kinases PROTEIN\_KINASE\_ATP, PROTEIN\_KINASE\_DOM, ] CG17090 SD05876  
 CG17090 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  
 + motor\_protein \* 4e-05 unknown \* 5e-06 Similarity with drosophila MSP-300 protein (PIR acc. no. \* 2e-10 rho/rac-interacting  
 CG13889 citron kinase [PEROXIDASE\_1] CG13889 SD05919 61D4-61D4 ID:119F1  
 + DNA\_binding \* selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and  
 CG7421 III(aa) \* nucleolar phosphoprotein - African cla [NLS\_BP // HISTONEH5] CG7421 SD05988 79A5-79A5 ID:119F11  
 + unknown \* protein(aa) \* 4e-83 cDNA EST comes from this gene; cDNA EST co \* CG10080 SD05932 57F5-57F5 dup:2/3  
 CG10080 ID:119F2  
 CG5853 + transporter CG5853 SD06390 dup:2/3 ID:119G10.2  
 CG18019 + CG18019 SD06401 dup:2/2 ID:119G12.2  
 CG1553 + CG1553 SD06318 dup:4/5 ID:119G2.2  
 CG3075 + transcription\_factor CG3075 SD06336 dup:2/2 ID:119G4.2  
 CG4427 + transcription\_factor CG4427 SD06353 dup:2/2 ID:119G5.2  
 + unknown \* 3e-83 YOJ1\_CAEEL HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN CHROMOSOME III \* \* CG14939 33B1-  
 CG14939 33B1 dup:2/3 ID:119G8.2  
 + 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-  
 CG8669 39D2 dup:3/3 ID:119H1  
 CG11860 + BG:DS07851.11 unknown \* CG11860 35C4-35C4 dup:2/2 ID:119H7  
 + unknown \* 3e-05 inserted at base Both 5' and 3' ends of P element Inverse PCR \* \* [PRO\_RICH] CG12305 SD06514 52C4-  
 CG12305 52C5 dup:7/8 ID:119H8  
 CG7090 + enzyme CG7090 SD06635 dup:1/2 ID:120A12.2  
 CG11844 + unknown CG11844 SD06613 dup:1/2 ID:120A6.2

CG1691 + RNA\_binding CG1691 SD07045 dup:1/3 ID:120E7.2  
 + unknown \* 2e-83 inserted at base 5' end of P element Inverse PCR \* 1e-124 inserted at base Both 5' and 3' ends of P  
 CG2765 element Inverse PCR \* CG2765 SD07219 60E5-60E5 dup:3/5 ID:120G10.2  
 CG18218 + CG18218 SD07272 dup:1/4 ID:120H6.2  
 CG4510 + CG4510 SD09607 dup:1/2 ID:124A6.2  
 CG3140 + adenylate\_kinase CG3140 SD09634 dup:1/2 ID:124A9.2  
 CG3608 + chaperone CG3608 SD09850 dup:1/2 ID:124C12.2  
 CG15613 + CG15613 SD09786 dup:1/2 ID:124C3.2  
 CG3879 + transporter CG3879 SD10012 dup:1/3 ID:124E12.2  
 + 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  
 CG3878 ID:124F11.2  
 CG3616 + cytochrome\_P450 CG3616 SD10018 dup:1/2 ID:124F2.2  
 CG15009 + CG15009 SD10052 dup:1/2 ID:124F9.2  
 + pnr transcription\_factor \* GATA-BINDING FACTOR-A (TRANSCRIPTION FACTOR GATA-A) (DGATA-A) (PANNIER  
 CG3978 PROTEIN)(aa) \* pnr \* CG3978 89B5-89B6 dup:1/3 ID:124G11.2  
 CG3973 + CG3973 dup:1/2 ID:124H12.2  
 CG6501 + unknown CG6501 SD10213 dup:1/2 ID:124H5.2  
 CG2604 + unknown CG2604 SD10384 dup:1/2 ID:125B2.2  
 CG12846 + unknown CG12846 SD10395 dup:1/2 ID:125B5.2  
 CG5370 + endopeptidase CG5370 SD10530 dup:1/2 ID:125C11.2  
 + 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  
 CG18022 ID:126A10  
 + 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 CG2331 GH01132 46D1-46D1 dup:1/3 ID:30A11  
 + emb transporter \* CRM1\_YEAST CHROMOSOME REGION MAINTENANCE PROTEIN CRM1 \* strong similarity to CRM1  
 chromosome maintenance protein from y \* exportin (CRM1, yeast, ho [LIPOYL // IBN\_NT] CG13387 GH01059 29C1-29C1 dup:1/2  
 CG13387 ID:30A3  
 + Nmdmc NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE CG18466 GH01066 85C5-85C5  
 CG18466 ID:30A5  
 + BcDNA:GH01073 RNA\_binding \* unknown(aa) \* 7e-08 CYP6\_YEAST PEPTIDYL-PROLYL CIS-TRANS ISOMERASE CYP6  
 (PPIASE) (ROTAMASE) \* 7e-06 RNA-binding protein \* 1e-103 Similarity to pepti [RBD // pro\_isomerase // rrm // CSA\_PPIA]  
 CG5808 CG5808 GH01073 96B1-96B1 ID:30A6

+ structural\_protein \* unknown(aa) \* Allele: hi4(aa) \* gene is related to S.cerevisiae NIC96 gene.(aa) \* 7e-24 NI96\_YEAST KD  
 CG7262 NUCLEOPORIN-INTERACTING COMPONENT nucle CG7262 GH01087 88D8-88D8 ID:30A8  
 CG8979 + enzyme\_inhibitor \* 7e-15 proteasome inhibitor hPI31 subunit \* \* CG8979 GH01278 48D7-48D7 ID:30B10  
 + Traf2 signal\_transduction \* TNF-receptor-associated factor melanoga \* 8e-06 YQ57\_CAEEL HYPOTHETICAL 24.9 KD  
 CG10961 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  
 + transcription\_factor \* crol \* 1e-32 CROL ALPHA \* 1e-17 final three exons similar to C2H2-type zinc finger \* 1e-31 kruppel-  
 CG12397 type zinc finger protein [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG12397 GH01265 42B3-42B3 ID:30B9  
 + DNA\_binding \* ISWI PROTEIN (IMITATION SWI PROTEIN) (NUCLEOSOME REMODELING FACTOR KD SUBUNIT)  
 CG5899 (NURF-140) (CHRAK KD SUBUNIT)(aa) \* DMISWI\_6 lswi \* 8e-94 YAB9\_YEAST [helicase\_C // SNF2\_N] CG5899 GH01406  
 33A1-33A1 ID:30C10  
 + Mer actin\_binding \* merlin \* 1e-105 coded for by C. elegans cDNA yk167f5.5; coded for by C. elegans cDNA yk130f8.5; \* 1e-  
 CG14228 135 MERL\_MOUSE MERLIN (SCHWANNOMIN) merlin - mo [Band\_41 // BAND41 // ERM // ERMFAMILY] CG14228 GH01330  
 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  
 + Hn enzyme \* DMPAH Hn \* phenylalanine 4-monooxygenase (EC 1.14.16.1) - fruit fly (Drosophila melanogaster)(aa) \*  
 CG7399 phenylalanine 4-monooxygenase (EC 1.14.16.1) - f CG7399 GH01426 66A11-66A12 dup:2/2 ID:30D2  
 + enzyme \* inhibitor of growth 1-like(aa) \* 3e-12 YHP0\_YEAST HYPOTHETICAL 32.1 KD PROTEIN IN GAR1-MSR1  
 CG7379 INTERGENIC REGION \* 5e-11 predicted using Genefinder; si [PHD] CG7379 GH01429 93B1-93B1 dup:1/2 ID:30D4  
 + enzyme \* PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-  
 CG1140 TRANSFERASE)(aa) \* 3-oxoacid CoA transferase precursor; succinyl-Co [COA\_TRANSF\_1 // COA\_TRANSF\_2 // CoA\_tra]  
 CG1140 GH01464 62B11-62B11 ID:30D6  
 + dim-7 unknown \* RanBP7(aa) \* 1e-73 NMD5\_YEAST NONSENSE-MEDIATED MRNA DECAY PROTEIN NMD5 \* 8E-26\*  
 CG7935 RanBP7/importin [IBN\_NT] CG7935 GH01576 66B9-67E3 dup:3/3 ID:30E1  
 + function\_unknown \* similar to NifU protein homolog(aa) \* Iron-sulfur cluster nifU-like protein; lsu1p(aa) \* NifU-like protein(aa)  
 CG9836 \* Y45F10D.4(aa) CG9836 GH01635 85B4-85B4 dup:2/2 ID:30E10

CG13240 + BG:DS09217.1 unknown \* 1e-14 predicted using Genefinder; cDNA EST comes from this g \*\* CG13240 GH01660 35D6-35D6 dup:2/2 ID:30E12

CG4847 + endopeptidase \* 3e-64 cysteine proteinase cysteine \* 2e-56 predicted using Genefinder; similar to cathepsin-like protease; cD \* 1e-59 cathepsin K \* 1e-59 cathepsi[THIOL\_PROTEASE\_CYS // PAPAIN // Peptida] CG4847 GH01592 54C9-54C9 dup:3/4 ID:30E3

CG7783 + motor\_protein \* protein(aa) \* HYPOTHETICAL 123.7 KD PROTEIN C14C4.02 IN CHROMOSOME I(aa) \* 2e-65 hypothetical protein YOL034w - yeast (Saccharomyces cerevisiae) \* 3 [ATP\_GTP\_A2 // ATP\_GTP\_A] CG7783 GH01608 78E2-78E3 dup:2/2 ID:30E4

CG1135 + unknown \* nucleolar protein(aa) \* 1e-108 nucleolar protein \* 1e-109 cell cycle-regulated factor p78 \* 8e-06 Hypothetical protein [FHA\_DOMAIN // FHA] CG1135 GH01794 64A4-64A4 ID:30F12

CG5590 + enzyme \* coded for by C. elegans cDNA yk108f3.3; coded for by C. elegans cDNA yk104h5.3; coded for by C. elegans cDNA yk117a1.3; coded for by C. elegans cDN [GDHRDH // adh\_short] CG5590 GH01709 98A6-98A6 ID:30F4

CG11139 + unknown \* 5e-09 SHP1\_YEAST SHP1 PROTEIN hypothetical protein YBL058w - ye \* 1e-34 p47 \* 2e-33 p47 XY40 \* undulin - human (fragment) undulin CG11139 GH01724 43C4-43C5 dup:3/3 ID:30F6

CG12143 + unknown \* 8e-06 belong to the membrane protein group of Transmembrane Super \* 8e-06 First identified non-mammalian member of the Transmembrane S \* 9e-08 TM4SF CG12143 GH01773 42E-42E ID:30F9

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

CG14528 + endopeptidase \* endothelin converting enzyme-2 - bovine (fragment)(aa) \* endothelin converting enzyme-like 1(aa) \* 7e-30 similar to Zinc-binding metalloprotease; cD [NEPRILYSIN // PRENYLATION // ZINC\_PROTE] CG14528 GH01940 98F-98F ID:30G10

CG8445 + endopeptidase \* HYPOTHETICAL 37.7 KD PROTEIN C08B11.7 IN CHROMOSOME II(aa) \* DMUBICTHG\_3 Uch \* BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)(aa) [UCH // UBCTHYDLASE // ATP\_GTP\_A] CG8445 GH01941 52F7-52F7 ID:30G11

CG4533 + I(2)efl chaperone \* similar to the small heat shock protein (HSP20) family(aa) \* DMHS09\_2 Hsp23 \* DMHSP27G\_3 Hsp27 \* HYPOTHETICAL 12.3 KD PROTEIN C14B9.1 IN CHROMOSOME [HSP20 // ACRYSTALLIN] CG4533 GH01960 59F4-59F4 ID:30G12

CG8329 + endopeptidase \* DMC9D2 \* 8e-57 serine protease SER4 precursor \* 6e-12 predicted using Genefinder; similar to transmembrane receptor (r \* 2e-19 serine protease (BSP) [trypsin // CHYMOTRYPSIN // TRYPSIN\_SER ] CG8329 GH01822 67B-67B ID:30G2

CG3301 + enzyme \* antennal-specific short-chain dehydrogenase/reductase(aa) \* 4e-12 YM71\_YEAST HYPOTHETICAL OXIDOREDUCTASE IN MRPL44-MTF1 INTERGENIC REGION \* 8e-08 Si [GDHRDH // adh\_short] CG3301 GH01837 93D4-93D4 ID:30G3

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

CG3459 + transcription\_factor \* regulatory protein LBP1d - human (fragment)(aa) \* NF2d9 - mouse(aa) \* transcription factor LBP1a - human(aa) \* 4e-19 alpha-globin transcription fact CG3459 GH01967 46E6-46E8 ID:30H1

CG2789 + receptor \* 5e-14 cDNA EST comes from this gene; cDNA EST co \* 3e-35 peripheral-type benzodiazepine receptor

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

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 Temperatures ?(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

CG12860 + unknown \* [NLS\_BP] CG12860 GH02210 51B11-51B11 ID:31A8

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

CG3397 + ion\_channel \* 2e-20 YMT1\_YEAST HYPOTHETICAL 38.2 KD PROTEIN IN SUB1-ARGR1 INTERGENIC REGION \* 8e-44 similar to phosphotransferase enzyme II and to members of the [ALDKETRDTASE] CG3397 GH02366 87A8-87A8 dup:2/2 ID:31B6

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 // UBCTHYDRLASE] CG4265 GH02396 23D1-23D1 dup:1/2 ID:31B8

CG9886 + enzyme \* glycerate kinase, putative(aa) \* HYPOTHETICAL 40.0 KD PROTEIN C13B9.2 IN CHROMOSOME III(aa) \* 2e-40 440aa long hypothetical protein \* TUD4\_AGRVI PU CG9886 GH02560 23F1-23F1 ID:31C10

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

CG18104 + arginaseenzyme \* putative \* 1e-11 ARG1\_YEAST ARGINASE (EC 3.5.3.1) - yeast (Saccharo \* 1e-107 /motif=(desc;; /ma \* 1e-08 similar to CG18104 GH02581 1B5-1B5 ID:31C12

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

CG5173 + Argk \* Argk \* ARGININE KINASE (AK)(aa) \* 1e-131 KAG1\_CAEEL PROBABLE ARGININE KINASE F46H5.3 (AK) similar t \* 7e-76 KCRM\_MOUSE CREATINE KINASE, M CHAIN (M-C [GUANIDO\_KINASE // ATP-gua\_Ptrans] CG5173 68E1-68E1 dup:1/3 ID:31C7

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

CG11201 + enzyme \* hypothetical protein(aa) \* TUBULIN--TYROSINE LIGASE (TTL)(aa) \* Ybr094wp(aa) \* 2e-10 ORF2 [NLS\_BP]



CG11201 GH02545 27A1-27A1 ID:31C9

CG9759 + unknown \* CG9759 GH02603 87F-87F ID:31D2

CG13853 + unknown \* CG13853 GH02671 96E1-96E1 ID:31D6

+ 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

CG9090 + unknown \* 1e-25 kraken \* 3e-13 dJ222E13.1 (N-terminal part of novel protein with some similarit \* 7e-05 TPES\_PSEPU  
 TROPINESTERASE (ATROPINESTERASE) (ATROPINE [ESTERASE // abhydrolase] CG5707 GH02816 62D2-62D2 dup:2/2  
 ID:31E3

CG5707 + BG:DS00797.1 unknown \* unknown protein(aa) \* 1e-113 EMP70 protein precursor - yeast (Saccharomyces cerevisiae) \*

CG7364 Similarity to Yeast endosomal P24A protein (SW:EM70\_YEAST CG7364 GH02822 34D1-34D1 dup:2/2 ID:31E4

+ BcDNA:GH02833 RNA\_binding \* DMDBP45A\_18 Dbp45A \* pit \* 3e-64 DBP7\_YEAST ATP-DEPENDENT RNA HELICASE DBP7  
 probable purin \* 1e-58 helicase pitchoune [helicase\_C // HELICASE // DEAD // NLS\_B] CG8611 GH02833 16A1-16A2 dup:3/3  
 ID:31E5

CG8611 + 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

CG6758 + 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

CG3200 + 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

CG1102 + unknown \* BLASTX 8.6E-13 Macaca mulatta mucin (MUC2) mRNA, partial cds.(dna) \*\* CG11073 GH02992 58C1-58C2  
 ID:31F8

CG11073 + BcDNA:GH03163 unknown \* \*\* CG1408 GH03163 100B-100B dup:1/2 ID:31G10

CG1408 + Sema-1b unknown \* similar to semaphorin-I \* 4e-93 cDNA EST comes from this gene; cDNA EST \* 2e-81 semaphorin VIb \* 1e-67  
 UNKNOWN semaphorin F homolog [RECEPTOR\_CYTOKINES\_1 // Sema // ATP\_GTP] CG6446 GH03186 54E1-54E2 dup:1/2  
 ID:31G11

CG6446 + TflIA-S transcription\_factor \* 4e-16 TOA2\_YEAST TRANSCRIPTION INITIATION FACTOR IIA SMALL CHAIN (TFIIA 13.5 KD  
 SUBUNI \* 5e-56 T2AG\_DROME TRANSCRIPTION INITIATION FACTOR IIA GAMMA CG5163 GH03194 95C9-95C9 ID:31G12

CG5163 + unknown \* GLUTAMATE--CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE)  
 (GAMMA-ECS) (GCS LIGHT CHAIN)(aa) \* glutamate-cysteine ligase regu CG4919 GH03051 94C3-94C3 ID:31G2

CG4919 + karyopherin-alpha1 ligand\_binding\_or\_carrier \* karyopherin- agr;1 \* karyopherin alpha 1(aa) \* 1e-129 IMA1\_YEAST IMPORTIN  
 ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (SERINE-RICH RNA[ARM\_REPEAT // Armadillo\_seg // NLS\_BP] CG8548  
 GH03057 76D2-76D3 ID:31G3

CG8548 + BcDNA:GH03108 chaperone \* similar to DnaJ, prokaryotic heat shock protein, Zinc finger, C2H2 type; cDNA EST yk290e12.5

CG2790

comes from this gene; cDNA EST yk290e12.3 comes from th [ZF\_MATRIN // ZINC\_FINGER\_C2H2 // DNAJ\_1] CG2790 GH03108 60E5-60E5 ID:31G7

CG12127 + BcDNA:GH02974 unknown \* 2e-35 YJ05\_CAEEL HYPOTHETICAL 85.1 KD NUCLEASE C41D11.5 simila \* YKK3\_CAEEL HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III >g \* CG12127 8D6-8D6 dup:1/2 ID:31G9

CG7974 + contains similarity to hepatocellular carcinoma-associated antigen 59 NLS\_BP CG7974 GH03217 ID:31H1

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

+ 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

CG1799 + Cnx99A chaperone \* DMALNEX\_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 CG11958 GH03249 99A7-99A7 dup:1/3 ID:31H2

+ 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

CG6287

CG12167 + unknown \* [PRO\_RICH // ATP\_GTP\_A] CG12167 GH03350 83B1-83B1 ID:31H6

+ enzyme \* DMCSUDC\_5 Vha16 \* VACUOLAR ATP SYNTHASE KD PROTEOLIPID SUBUNIT (DUCTIN)(aa) \* ATP synthase subunit(aa) \* proteolipid protein of the proton ATPase; P [VACATPASE // ATP-synt\_C] CG7007 GH03514 90B1-90B1 ID:32A10

CG7007 + 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

CG16941 + BcDNA:GH03502 unknown \* unknown(aa) \* 3e-55 YII3\_YEAST HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1

CG5629 INTERGENIC REGION \* 1e-75 inserted at base Both 5' and 3' ends of P element CG5629 GH03502 91F4-91F4 dup:1/2 ID:32A8

+ structural\_protein \* 2e-05 CUP7\_DROME PUPAL CUTICLE PROTEIN EDG-78 PRECURSOR ecdyson \* 8e-06

CG12045 CU26\_ARADI ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 12.6 (ACP 12.6) \* 2e-07 DM [CUTICLE // insect\_cuticle] CG12045 GH03728 100B-100B ID:32B12

CG12045

CG4784 + structural\_protein \* 2e-05 DMEDG84A\_3 Edg84A \* \* [CUTICLE // insect\_cuticle] CG4784 GH03623 72F1-72F1 ID:32B4

+ Vha26 enzyme \* Vha26 \* ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD(aa) \* VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) (V-ATPASE KD SUBUN CG1088 GH03683 83B4-83B4 ID:32B5

CG1088 + 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

CG5915 + 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

CG3799 + transcription\_factor\_binding \* ankyrin-like with transmembrane domains 1(aa) \* C. elegans ankyrin-related unc-44 \* similar to ankyrin repeats; cDNA EST comes f[ANK\_REP // ank // ANK\_REP\_REGION // CAT] CG10409 GH03924 84E1-84E1 dup:2/4 ID:32C10

CG10409

+ unknown \* HYPOTHETICAL PROTEIN \* 8e-06 development protein \* HYPOTHETICAL PROTEIN \* 8e-06 development  
 CG1116 protein CG1116 82F10-82F10 dup:1/4 ID:32C11  
 CG7738 + CG7738 dup:2/2 ID:32C2  
 CG18178 + unknown \* CG18178 GH03795 67C-67C ID:32C3  
 + transcription\_factor \* pleiomorphic adenoma gene-like 2; PLAG-like 2(aa) \* DMZFH1\_2 zfh1 \* 1e-06 ZFH1\_DROME ZINC-FINGER PROTEIN (ZINC-FINGER HOMEODOMAIN PROTEIN [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG12744 GH03826  
 CG12744 46C1-46C1 dup:1/2 ID:32C5  
 + 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  
 CG8139 85D16-85D16 ID:32C7  
 CG4184 + BcDNA:GH03922 unknown \* CG4184 GH03922 21C3-21C dup:1/3 ID:32C9  
 CG10658 + Os9 unknown \* Os9 \* \* CG10658 GH03980 38B1-38B1 ID:32D2  
 + translation\_factor \* Eif4E \* 1e-23 IF4E\_YEAST EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E)  
 CG8023 (MRNA CA \* 2e-56 IF4E\_DROME EUKARYOTIC TRANSLATION INITIATION [IF4E] CG8023 GH04024 66C-66C ID:32D6  
 + Sptr enzyme \* sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)(aa) \* ORF 7(aa) \* similar to glucose 1-dehydrogenase(aa) \* sepiapterin reductase; [GDHRDH // adh\_short] CG12117 GH04031 7E7-7E7 ID:32D8  
 CG12117 + unknown \* 7e-06 pdb|1BIH|A Chain A, Crystal Structure Of The Insect Immune Protein Hemolin: A New Domain \*  
 CG5597 HEMO\_HYACE HEMOLIN PRECURSOR (P4 PROTEIN) (HEMOCYT [ig] CG5597 GH04238 60A8-60A8 dup:2/2 ID:32E10  
 + BcDNA:GH04245 motor\_protein \* contains TPR domain-like repeats(aa) \* UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE KD SUBUNIT (O-GLCNAC TRANSFERASE [TPR\_REGION // TPR\_REPEAT // TPR // NLS\_] CG10392 GH04245 41A1-41A2 dup:3/4 ID:32E11  
 CG10392 + Trip1 translation\_factor \* 3e-80 IF34\_YEAST EUKARYOTIC TRANSLATION INITIATION FACTOR DELTA SUBUNIT (EIF-3 DELTA \* IF34\_DROME EUKARYOTIC TRANSLATION INITIATION FACTOR DEL[GPROTEINBRPT // WD40\_REGION // WD\_REPEAT] CG8882 GH04085 25B-25B dup:2/2 ID:32E2  
 CG8882 + serpin \* serine protease inhibitor(aa) \* OVALBUMIN (PLAKALBUMIN) (ALLERGEN GAL D 2) (GAL D II)(aa) \* LEUKOCYTE  
 CG9456 ELASTASE INHIBITOR (LEI) (LEUCOCYTE NEUTRAL P [serpin] CG9456 GH04125 42C8-42C8 dup:2/2 ID:32E4  
 + metabolism \* 1e-47 PNPH\_YEAST PROBABLE PURINE NUCLEOSIDE PHOSPHORYLASE (INOSINE PHOSPHORYLASE) (PN \* 3e-51 similar to purine nucleoside phosphorylases \* 4e-73 pu [Mtap\_PNP] CG16758 GH04159 62E6-62E6 dup:5/5 ID:32E5  
 CG16758 + ion\_channel \* 6e-15 similar to PDZ domain (Also known as DHR or GLGF).; cDNA EST EMBL: \* 3e-17 protein co-factor \* 1e-18 E3KARP Na+/H+ exchanger regulatory facto [PDZ // NLS\_BP] CG10939 GH04176 54B18-54C1 dup:2/2 ID:32E6  
 CG10939 + 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  
 CG17259 CG4468 + unknown \* CG4468 GH04205 92B9-92B9 dup:2/2 ID:32E8  
 CG4468 + enzyme \* alpha esterase(aa) \* C. elegans esterase CM06B1 \* similar to esterase(aa) \* DMEST6P\_15 Est-P  
 CG5397 [CYTOCHROME\_B5 // ESTERASE // COesterase] CG5397 GH04232 21F2-21F2 dup:2/2 ID:32E9

+ enzyme \* i-beta-1,3-N-acetylglucosaminyltransferase(aa) \* 1e-10 K09C8.4 \* 8e-16 acetylglucosaminyltransferase-like protein  
 CG3253 \* 5e-24 i-beta-1,3-N-acetylglucosa CG3253 GH04269 60B6-60B6 ID:32F1  
 CG5080 + CG5080 ID:32F10  
 + apoptosis\_inhibitor \* 2e-81 SINA\_DROME DEVELOPMENTAL PROTEIN SEVEN IN ABSENTIA devel \* 8e-67 seven-in-absentia protein homologue-1 \* 2e-73 siah-1A protein - mouse siah-1A [ZF\_RING] CG13030 GH04279 73D1-73D1 ID:32F2  
 CG13030 + 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  
 CG5711  
 CG6186 + CG6186 dup:2/2 ID:32G1  
 + unknown \* 1e-26 VP28\_YEAST VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS28 \* 3e-40 putative protein  
 CG12770 \* 3e-76 inserted at base Both 5' and 3' ends of P elemen CG12770 GH04443 44A4-44A4 ID:32G10  
 + actin\_binding \* dystrophin(aa) \* DMDYDTRO dystrophin \* 1e-126 DYS-1 protein \* cytoskeletal protein CG7240 92A7-92A11 dup:1/2 ID:32G3  
 CG7240 + 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  
 CG7727  
 + enzyme \* aminomethyltransferase (glycine cleavage system protein T)(aa) \* 2e-68 glycine cleavage T protein \* 7e-91 partial CDS, \* 1e-97 GCST\_HUMAN AMINOMETHY CG6415 GH04419 32A2-32A2 dup:1/2 ID:32G8  
 CG6415  
 CG6405 + unknown \* CG6405 GH04442 33D5-33D5 ID:32G9  
 + n-syb transporter \* 2e-21 synaptobrevin isoform B - fruit fly (Drosophila melanogaster) (L142 \* 2e-21 SNB-1; synaptobrevin SNB-1; sy \* 6e-24 SYB2\_MOUSE SYNAPTOBREV1[SYNAPTOBREVN // SYNAPTOBREVIN // synapt] CG17248 GH04664 62A10-62A10 dup:2/2 ID:32H12  
 CG17248  
 + 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  
 CG4070 + 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  
 CG8206 + transcription\_factor \* DMC95B7 \* D19B \* ovo \* DMSRYG1\_25 Sry- dgr; [G\_PROTEIN\_RECEPTOR // zf-C2H2 // ZINC\_F] CG10366 GH04589 37F2-37F2 ID:32H8  
 CG10366  
 + Motor-protein motor\_protein \* 1e-152 motor protein \* 2e-40 coded for by C. elegans cDNA yk119d2.3; coded for by C. elegans cDNA yk86f8.3; c \* 6e-50 motor protein \* 1e-154 DMMOTPR [WD\_REPEATS] CG6455 GH04666 93F14-93F14 ID:33A1  
 CG6455 + BcDNA:GH04753 enzyme \* glutathione transferase (EC 2.5.1.18) D26 - fruit fly (Drosophila melanogaster)(aa) \* glutathione transferase (EC 2.5.1.18) D21 - fruit fly (Drosoph [GST] CG16936 GH04753 60D14-60D14 dup:2/2 ID:33A11  
 CG16936 + transporter \* 4e-41 similar to matrin F/G containing C4-type zinc-fingers \* 4e-79 PGT\_HUMAN PROSTAGLANDIN TRANSPORTER (PGT) prostaglandin tr \* 2e-76 PGT\_RAT PROST CG3811 GH04717 30B10-30B10 ID:33A7  
 CG3811  
 + enzyme \* weakly similar to furin-like proteases; 35% Similarity to \* weakly similar to furin-like proteases in 3' exon(aa) \* 2e-17 weakly similar to furin-I [Acetyltransf // NLS\_BP] CG8481 GH04732 85E8-85E8 ID:33A9  
 CG8481  
 CG14997 + unknown \* 1e-87 cDNA EST yk500f6.3 comes from this gene; cDNA EST come \* 1e-119 unknown \* 1e-88 hypothetical

protein \* CGI-44 protein [FADPNR] CG14997 GH04863 64E2-64B4 ID:33B10  
 + signal\_transduction \* 9e-12 hypothetical protein \* unknown \* phosphatidylinositol-4-phosphate 5-kinase isolog \* CG10233  
 CG10233 GH04877 83A1-83A1 ID:33B12  
 + alphaCopsignal\_transduction \* agr;Cop \* coatomer alpha subunit(aa) \* alpha-COP (Z466 \* 5e-67 Similarity to Human Coatomer  
 beta' subunit (SW:COPP\_HUMAN); cDNA E [GPROTEINBRPT // WD40\_REGION // WD\_REPEA] CG7961 GH04856 62A10-  
 CG7961 62A10 dup:2/3 ID:33B8  
 + unknown \* HSPC015(aa) \* 8e-45 hypothetical protein YOR173w - yeast (Saccharomyces cerevisiae) ( \* hypothetical protein  
 CG2091 YLR270w - yeast (Saccharomyces cerevisiae) CG2091 GH04919 83C-83C ID:33C2  
 + Lim1 transcription\_factor \* HOMEBOX PROTEIN LIM-1(aa) \* Lim3 \* 7e-20 LIM homeodomain transcription factor \* 9e-30  
 homeotic protein lin-11 - Caenorhabditis elegans (fragment) [HOMEBOX\_1 // homeobox // HTHREPRESSR /] CG11354  
 CG11354 GH04929 8A4-8B1 ID:33C4  
 CG18616 + CG18616 GH04932 ID:33C5  
 + Mipp1 protein\_phosphatase \* multiple inositol polyphosphate phosphatase 1; MIPP1(aa) \* Mipp1 \* 1e-22 multiple inositol  
 CG4123 polyphosphate phosphatase \* 2e-23 multiple inositol polyp [acid\_phosphat] CG4123 GH04949 77A1-77A1 dup:4/7 ID:33C7  
 + BcDNA:GH04978 protein\_kinase \* 2e-39 YAK1\_YEAST PROTEIN KINASE YAK1 protein kinase YAK1 (EC 2. \* 3e-43  
 serin/threonin-kinase \* 1e-126 similar to serine/threonine kinase; cDNA EST[PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM]  
 CG7028 CG7028 GH04978 61A6-61A6 ID:33D1  
 CG4250 + unknown \* [EGF\_2] CG4250 GH05106 58F3-58F3 dup:2/2 ID:33D11  
 + chaperone \* KD HEAT SHOCK PROTEIN, MITOCHONDRIAL (HSP10) (10 KD CHAPERONIN)(aa) \* 1e-17 CH10\_YEAST  
 KD HEAT SHOCK PROTEIN, MITOCHONDRIAL (HSP10) (10 KD CHAPERONI [LUM\_BINDING // CHAPERONIN10 // cpn10]  
 CG11267 CG11267 GH05109 69F2-69F2 ID:33D12  
 + 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  
 CG3564 GH04989 4C4-4C4 ID:33D2  
 + enzyme \* phosphatidylserine-specific phospholipase A1 deltaC(aa) \* PS-PLA1(aa) \* DMYOLK\_4 Yp1 \* VITELLOGENIN I  
 CG4979 PRECURSOR (YOLK PROTEIN 1)(aa) [TAGLIPASE // ESTERASE // lipase] CG4979 GH05003 89B7-89B7 dup:2/2 ID:33D4  
 + CoVa enzyme \* 2e-14 COX6\_YEAST CYTOCHROME C OXIDASE POLYPEPTIDE VI PRECURSOR cy \* 6e-81 cytochrome c  
 CG14724 oxidase subunit Va preprotein melanogaste \* 6e-27 predicted u CG14724 GH05011 86F10-86F11 ID:33D5  
 + DNA\_repair\_protein \* REV1 protein(aa) \* 2e-56 REV1\_YEAST DNA REPAIR PROTEIN REV1 REV1 protein - yeast \* 2e-78  
 similar to DNA repair protein (REV1); cDNA EST co[UMUC\_DOMAIN // IMS // BRCT\_DOMAIN // BR] CG12189 GH05320 61C8-  
 CG12189 61C8 dup:2/2 ID:33E10  
 + endopeptidase \* DMSER2\_7 Ser99Db \* 2e-45 serine proteinase (EC 3.4.21.-) precursor - fruit fly (Drosophila melanogast \*  
 9e-24 similar to peptidase family S1 (tr[trypsin // CHYMOTRYPSIN // TRYPSIN\_SER] CG10472 GH05321 65A2-65A2 dup:2/2  
 CG10472 ID:33E11  
 + unknown \* hypothetical PSU1-like protein(aa) \* similar to Bacterial mutT protein; cDNA EST yk352h11.5 comes from this  
 CG6169 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

+ enzyme \* HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN F01F1.6(aa) \* antiquitin=26g turgor protein  
 homolog {C-terminal} intestinal mucosa, Peptide Partial [aldehyd // ALDEHYDE\_DEHYDR\_GLU] CG9629 GH05218 76A3-76A3  
 dup:2/2 ID:33E7  
 CG9629  
 + unknown \* CG3273 GH05256 42B3-42B3 dup:2/2 ID:33E8  
 + electron\_transfer \* 3e-17 cytochrome b5 \* 1e-18 Similarity to Human cytochrome b5 (SW:CYB5\_HUMAN); cDNA EST  
 EMBL:D \* 5e-18 CYB5\_MOUSE CYTOCHROME B5 \* 7e-22 cytochrome b [CYTOCHROME\_B5 // CYTOCHROME\_B5\_2 // NLS\_] CG3566  
 CG3566 GH05526 5E1-5E1 ID:33F10  
 + 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  
 CG17246 56D4-56D4 dup:3/3 ID:33F2  
 + EG:22E5.3 enzyme \* RNA 3'-terminal phosphate cyclase(aa) \* 1e-10 RTC1\_YEAST RNA 3'-TERMINAL PHOSPHATE CYCLASE  
 (RNA-3'-PHOSPHATE CYCLASE) (RNA CY \* /match=(desc; /ma \* [RCT] CG4061 GH05410 2C7-2C7 ID:33F4  
 CG4061  
 + Mlc1 \* DMMYLALK\_2 Mlc1 \* indirect flight muscle isoform; putative(aa) \* 1e-07 YGK6\_YEAST HYPOTHETICAL CALCIUM-  
 BINDING PROTEIN IN TAF60-G4P1 INTERGENIC REGI [THIOL\_PROTEASE\_HIS // EF\_HAND\_2] CG5596 98A6-98A6 dup:2/4  
 CG5596 ID:33F5  
 CG10151  
 + unknown \* [GRAM\_POS\_ANCHORING // ATP\_GTP\_A] CG10151 GH05433 51C2-51C2 ID:33F6  
 + enzyme\_inhibitor \* COMPLEMENT C3 PRECURSOR (CONTAINS: C3A ANAPHYLATOXIN)(aa) \* alpha-2-  
 macroglobulin(aa) \* alpha-2-macroglobulin(aa) \* 1e-121 similar to Alpha-2-macrog [A2M // ALPHA\_2\_MACROGLOBULIN] CG7068  
 CG7068 GH05679 28C-28C ID:33G11  
 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  
 + unknown \* 9E-24\* 4e-21 0.9-kb RNA transcript \* 6e-21 DMRNAPER\_2 anon-3B1.2 \* per circadian controlled protein  
 precursor - fruit fly (Drosophila mela CG11853 GH05615 96C4-96C4 ID:33G6  
 CG11853  
 + unknown \* CG3364 GH05668 42D5-42D6 ID:33G9  
 CG3364  
 + unknown \* CG18238 GH05783 84F-84F ID:33H10  
 CG18238  
 + qkr58E-1RNA\_binding \* how \* qkr58E-1 \* QKR58E-1(aa) \* 5e-10 hypothetical protein YLR116w - yeast (Saccharomyces  
 cerevisiae) ( [KH-domain // KH\_DOMAIN] CG3613 GH05812 58D8-58D8 ID:33H11  
 CG3613  
 + 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  
 CG9313  
 + enzyme \* 5e-32 GAA1\_YEAST GAA1 PROTEIN membrane protein END2 - yeast (Sa \* 4e-26 No definition line found \* 3e-67  
 CG3033 UNKNOWN hGAA1 \* CG3033 GH05723 5C2-5C3 ID:33H2  
 + unknown \* 1E-178\* 1e-105 inserted at base Both 5' and 3' ends of P element Inverse PCR \* CG6770 GH05738 33B12-  
 CG6770 33B12 ID:33H4  
 + l(2)gl tumor\_suppressor (lethal (2) giant larvae) L2GL\_DROME LETHAL(2) GIANT LARVAE PROTEIN (P127 LETHAL2GIANT,  
 NLS\_BP, RCC1\_2, WD\_REPEATS] CG2671 GH05740 dup:2/2 ID:33H6  
 CG2671  
 + BcDNA:GH05741 enzyme \* agr;-Est10 \* 8e-48 alpha esterase \* 6e-46 ACE1\_CAEEL ACETYLCHOLINESTERASE  
 CG4757

PRECURSOR (ACHE) acetyl \* 3e-54 ACES\_MOUSE ACETYLCHOLINESTERASE PRECURSOR [CARBOXYLESTERASE\_B\_1  
 // ESTERASE // COe] CG4757 GH05741 86D4-86D5 ID:33H7  
 + 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  
 CG10139 + unknown \* CG10139 GH05836 51B9-51B9 ID:34A1  
 + 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  
 CG7050 dup:1/4 ID:34A10  
 + 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-  
 CG3529 67B4 ID:34A11  
 + unknown \* 1e-21 BIM1\_YEAST BIM1 PROTEIN hypothetical protein YER016w - y \* 6E-40\* 2e-74 coded for by C. elegans  
 cDNA cm17d4; Similar to epoxide hydrolase. \* 8 [EPOXHYDRLASE // abhydrolase] CG15101 GH05945 55F4-55F4 dup:1/3  
 CG15101 ID:34A12  
 + transporter \* solute carrier family (organic anion transporter), member 7(aa) \* BLASTX 4.2E-24 Rattus organic cation  
 CG9317 transporter OCT1A mRNA, complete cds.(dna) \* [sugar\_tr] CG9317 GH05908 38E3-38E3 dup:1/2 ID:34A5  
 CG15900 + unknown \* CG15900 GH05918 41E4-41E4 ID:34A6  
 + unknown \* SEC14 (S. cerevisiae)-like(aa) \* HYPOTHETICAL 84.0 KD PROTEIN T23G5.2 IN CHROMOSOME III(aa) \* 4e-21  
 CG9528 pdb|1AUA| Phosphatidylinositol Transfer Protein [CRAL\_TRIO] CG9528 GH05975 26D3-26D4 ID:34B2  
 + cytoskeletal\_structural\_protein \* 7e-12 YIL2\_YEAST HYPOTHETICAL 123.6 KD PROTEIN IN POR2-COX5B INTERGENIC  
 REGION \* 3e-11 ankyrin ankyrin m \* 1e-10 contains similarity to[ANK\_REP // ank // ANK\_REP\_REGION] CG5822 GH05978 25C1-  
 CG5822 25C1 dup:3/4 ID:34B3  
 + VhaSFD transporter \* kDa vacuolar H(+)-ATPase subunit(aa) \* coded for by C. elegans cDNA yk89e9.5; coded for by C. elegans  
 CG17332 cDNA cm7g5; coded for by C. elegans cDNA cm14 CG17332 GH05981 36A7-36A7 ID:34B4  
 + endopeptidase \* human factor XII(aa) \* 7e-31 masquerade precursor - fruit fly (Drosophila melanogaster) \* 2e-05 similar to  
 Trypsin \* 5e-25 MCT6\_MOUSE MAST CELL PRO [trypsin // CHYMOTRYPSIN // TRYPSIN\_CATA] CG6639 GH06092 36C2-36C2  
 CG6639 ID:34C3  
 + 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  
 CG7908 99D3-99D3 ID:34D2  
 + angel enzyme \* DMANGEL\_3 angel \* GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL  
 EFFECTOR (CARBON CATABOLITE REPRESSOR PROTEIN 4)(aa) \* NOCTURNIN (RHYTHM CG12273 GH06351 59F4-59F4  
 CG12273 dup:2/2 ID:34E2  
 + 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

+ acyl-CoA\_dehydrogenase \* fadE19(aa) \* PROBABLE GLUTARYL-COA DEHYDROGENASE PRECURSOR (GCD)(aa) \* acyl-Coenzyme A dehydrogenase, short/branched chain precursor(aa) \* acyl-CoA [Acyl-CoA\_dh] CG9547 GH06693 26D7-26D7 ID:34G1  
 CG9547  
 + 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  
 CG5538 + unknown \* [NLS\_BP] CG5538 87C-87C dup:1/3 ID:34G11  
 + enzyme \* 3e-40 4-nitrophenylphosphatase (EC 3.1.3.41) - yeast (Saccharomyces cerevisiae) \* 6e-26 by content; 1-meth \* 4e-52 contains similarity to 4-nitrophe CG5567 GH06744 75A4-75A4 ID:34G7  
 CG5567  
 CG1163 + RpABC14 CG1163 GH06755 ID:34G8  
 + unknown \* 6e-10 microfilarial chitinase \* microfilarial chitinase \* CHIT\_BRUMA ENDOCHITINASE PRECURSOR (MF1 ANTIGEN) chitinas \* CG14125 68E3-68E3 dup:2/2 ID:34H10  
 CG14125  
 CG3752 + enzyme CG3752 dup:1/2 ID:34H5  
 CG12279 + chaperone HEAT SHOCK PROTEIN 67B2 RHODANESE, RHODANESE\_2 CG12279 dup:2/2 ID:34H6  
 + enzyme \* transcriptional adaptor (ADA2, yeast homolog)-3 like (PCAF histone acetylase complex)(aa) \* 4e-32 ADA3-like protein \* CG7098 16F7-16F7 dup:3/3 ID:34H7  
 CG7098  
 + mfas signal\_transduction \* midline fasciclin precursor \* 3e-31 p68(beta ig-h3) beta-ig-h3 gene musc \* 1e-29 transforming growth factor, beta-induced, 68kD TRANSFORM \* 3e-29 RG [BIGH3\_DOMAIN] CG3359 87A8-87A dup:3/3 ID:34H9  
 CG3359  
 CG10652 + CG10652 ID:35A1  
 + unknown \* 2e-22 YJJ7\_YEAST HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION \* 4e-40 No definition line found \* 2e-68 inserted at base Both 5' and CG6746 GH07085 33B9-33B9 ID:35A11  
 CG6746  
 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  
 CG5059 + unknown \* CG5059 GH07036 77C4-77C4 ID:35A4  
 CG4918 + CG4918 dup:1/2 ID:35A5  
 + 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 91F6-91F7 dup:1/2 ID:35A7  
 CG5555  
 CG9921 + unknown \* 6e-05 HSPC010 \* 1e-05 putative protein \* CG9921 GH07174 14B15-14B15 ID:35B4  
 + electron\_transfer \* 7e-19 C561\_CAEEL PUTATIVE CYTOCHROME B561 (CYTOCHROME B-561) hy \* 1e-20 cytochrome B561 \* 2e-20 HCYTO B561 \* 9e-24 cytochrome B561 CG8776 GH07176 49B8-49B8 dup:1/3 ID:35B5  
 CG8776  
 + ribosomal\_protein \* Similar to 40S ribosomal protein S29; coded for by C. elegans cDNA cm10c2; coded for by C. elegans cDNA yk61d8.5; coded for by C. elegans cDNA yk10 [RIBOSOMAL\_S14 // Ribosomal\_S14] CG8495 GH07263 86D1-86D1 dup:1/2 ID:35C1  
 CG8495  
 CG13850 + unknown \* CG13850 GH07286 96E1-96E1 ID:35C4  
 CG4152 + I(2)35DfRNA\_binding \* MTR4\_YEAST ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4) \*



YH27\_CAEEL PUTATIVE HELICASE W08D2.7 IN CHROMOSOME IV \* 1e-153 hypoth [HELICASE // DEAD // ATP\_GTP\_A]  
CG4152 GH07290 35D6-35D6 ID:35C5  
+ Rab-RP1 enzyme \* rab-related protein 3(aa) \* Rab-RP3 \* 4e-28 YPT7\_YEAST GTP-BINDING PROTEIN YPT7 GTP-binding protein Y \* 2e-25 strong similarity to the YPT1 sub-fami [ras // NLS\_BP // PROTEIN\_KINASE\_ATP // ] CG8024 GH07310 45B3-45B4 ID:35C8

CG8024  
CG18444 + alphaTryunknown \* CG18444 GH07737 47F1-47F1 dup:2/2 ID:35E12

CG1017 + structural\_protein \* MICROFIBRILLAR-ASSOCIATED PROTEIN (ASSOCIATED MICROFIBRIL PROTEIN) (AMF)(aa) \* predicted using Genefinder; similar to MICROFIBRILLAR-ASSOCIATED PRO CG1017 GH07619 62B10-62B11 dup:2/2 ID:35E3  
+ BcDNA:GH07643 endopeptidase \* unknown(aa) \* 1e-59 similar to Zinc-binding metalloprotease; cDNA EST come \* 1e-132 NEP\_MOUSE NEPRILYSIN (NEUTRAL ENDOPEPTIDASE) (NEP) (ENKE[NEPRILYSIN // ZINC\_PROTEASE // Peptidas] CG9761 GH07643 82D6-82D7 dup:2/2 ID:35E5

CG9761  
CG13480 + unknown \* CG13480 GH07663 70E4-70E4 dup:2/2 ID:35E7  
+ cell\_adhesion \* DMSLIT\_2 sli \* DMNOTCH3\_2 N \* 2e-05 NOTC\_DROME NEUROGENIC LOCUS NOTCH PROTEIN PRECURSOR growth \* 7e-07 GLP1\_CAEEL GLP-1 PROTEIN PRECURSOR glp1 prote [EGF\_2] CG9572 GH07746 19C1-19C1 ID:35F1

CG9572  
CG8855 + BG:DS00180.12 cell\_adhesion \* 7e-18 C901 protein \* 2e-23 similar to EGF-like domain; cDNA EST yk299a12.3 comes from this \* 7e-18 Ten-m2 \* 1e-14 acetyl LDL receptor; SREC=scavenge [EGF\_1 // EGF\_2] CG8855 GH07762 34E1-34E1 ID:35F2  
+ BcDNA:GH07921 RNA\_binding \* homeobox-containing protein Wariai(aa) \* 3e-05 PEP\_DROME ZINC FINGER PROTEIN ON ECDYSONE PUFFS PEP prote \* 3e-05 Pep protein - fruit fly (Dr[ZINC\_FINGER\_C2H2 // NLS\_BP // CYTOCHROM] CG8108 GH07921 67C3-67C3 dup:1/4 ID:35G10

CG8108  
CG14789 + EG:BACN32G11.6 unknown \* BACN32G11.c \* 1e-53 protein \* BACN32G11.l \* BACN32G11.m [AA\_TRNA\_LIGASE\_I] CG14789 GH07929 2B1-2B1 ID:35G12

CG14789  
CG8701 + unknown \* CG8701 GH07855 44B9-44B9 ID:35G4  
+ transcription\_factor \* skeletal muscle LIM protein(aa) \* DRAL gene product(aa) \* skeletal muscle LIM-protein 1(aa) \* testin(aa) [LIM] CG11916 GH07858 73D4-73D4 ID:35G5

CG11916  
CG6059 + motor\_protein \* very strong similarity to C. elegans myosin heavy chain B \* 6e-09 MYS1\_YEAST MYOSIN-1 ISOFORM (TYPE II MYOSIN) myosin heavy \* 1e-12 nonmuscle myosin [PEROXIDASE\_3] CG6059 GH07888 97E8-97E8 dup:1/2 ID:35G7  
+ 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 99C5-99C5 ID:35H1

CG7829  
CG7199 + Hr78 transcription\_factor \* DMSVP1\_2 svp \* Hr78 \* nuclear receptor XR78E/F(aa) \* HR78\_DROME NUCLEAR HORMONE RECEPTOR HR78 (DHR78) (NUCLEAR RECEPTOR XR78E/F) [STROIDFINGER // hormone\_rec // zf-C4 //] CG7199 GH08073 78D7-78D7 ID:35H10

CG7199  
CG12091 + unknown \* similar to Protein phosphatase 2C (2 domains); cDNA EST yk279g8.5 comes from this gene(aa) \* HYPOTHETICAL 41.2 KD PROTEIN IN ERG7-NMD2 INTERGENIC R CG12091 GH07996 62A6-62A6 ID:35H5

CG12091  
CG3223 + unknown \* [UBA // PHOSPHOPANTETHEINE] CG3223 GH08043 84E6-84E6 dup:1/2 ID:35H7

CG3223  
CG3308 + unknown \* No definition line found(aa) \* 8e-31 IPPI\_YEAST ISOPENTENYL-DIPHOSPHATE DELTA-ISOMERASE (IPP

ISOMERASE) \* 4e-44 isopentenyl-diphosphate delta isome [UPF0006] CG3308 GH08045 93D4-93D4 ID:35H8

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

CG9712 + motor\_protein \* signaling molecule(aa) \* contains similarity to Mus musculus tumor susceptibility protein TSG101 \* tumor susceptibility protein TSG101(aa) \* 4e-11 [TPR\_REPEAT] CG9712 GH09529 73C4-73C4 ID:37B1

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

CG12582 + unknown \* 4e-24 MANB\_CAEEL PROBABLE BETA-MANNOSIDASE PRECURSOR (MANNANASE) (MANNASE) \* 2e-39 mannosidase, beta A, lysosomal BETA-MANNOSIDASE PRECURSOR \* 1e-40 CG12582 GH09594 82A-82A ID:37B4

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

CG8298 + glycerol\_kinase \* 3e-59 GLPK\_YEAST GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE) (GLYCEROKINASE) ( \* 6e-86 similar to glycerol kinase \* 1e-107 GLPK\_MOUSE GLYCER [FGGY\_KINASES\_2 // FGGY] CG8298 GH09939 48D8-48D8 ID:37D12

CG8439 + Cct5 chaperone \* 1e-179 chaperonin TCP1 epsilon - yeast (*Saccharomyces cerevisiae*) \* 7e-63 TCPA\_DROME T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) \* [TCP1\_1 // TCP1\_3 // TCOMPLEXTCP1 // CHA] CG8439 GH10122 48F1-48F1 ID:37F2

CG5784 + cytoskeletal\_structural\_protein \* 2e-21 contains similarity to leucine-rich repeats, strongest similarity is to rat leuc \* 6e-37 acidic nuclear phosphoprotein pp32 \* 3e-37 PHA1\_HUMAN [LRR] CG5784 GH10170 54F6-55A1 ID:37F6

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

CG17309 + protein\_kinase \* DMDFR2\_2 btl \* 3e-43 ABL\_DROME TYROSINE-PROTEIN KINASE DASH/ABL protein-tyrosine \* 7e-41 Tyrosine-protein kinase ABL-1; cDNA EST comes from th[PROTEIN\_KINASE\_TYR // TYRKINASE // PROT] CG17309 GH10267 86E18-86E19 dup:1/2 ID:37G1

CG12152 + BcDNA:GH10333 unknown \* 2e-91 hypothetical protein \* \* [ALDOKETO\_REDUCTASE\_3] CG12152 GH10333 7B8-7B8 ID:37G11

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

CG4104 + BcDNA:GH08860 \* 9e-86 cif1 \* 1e-37 predicted using Genefinder; similar to trehalose phosphate synthase \* 4e-86 TPS1\_KLULA ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (U [TrehaloseP\_syn] CG4104 24F1-24F1 dup:1/3 ID:37G7

CG3620 + norpA enzyme \* contains similarity to phosphatidylinositol-specific phospholipase C, X domains (Pfam: PI-PLC-X.hmm, score: 200.23)(aa) \* phospholipase C beta-4(aa) \* CG3620 GH10316 4B6-4B6 dup:2/2 ID:37G8

CG5374 + T-cp1 chaperone \* DMTCP1\_2 T-cp1 \* T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA)(aa) \* 1e-178 T complex protein (put.); putative \* similar to T-complex [TCP1\_1 // TCP1\_2 // TCP1\_3 // TCOMPLEXT] CG5374 GH10347 94B4-94B4 ID:37H1

CG1469 + Fer2LCH ligand\_binding\_or\_carrier FERRITIN PRECURSOR CG1469 ID:37H10

CG10536 + ubiquitin-protein\_ligase ubiquitin-conjugating enzyme E2B (RAD6 homolog) UBIQUITIN\_CONJUGAT\_2 CG10536 GH10432 ID:37H11

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

CG11228 + protein\_kinase \* Pak \* DMAURG\_2 aur \* MST1(aa) \* SERINE/THREONINE-PROTEIN KINASE PLO1(aa) [TYRKINASE // PROTEIN\_KINASE\_DOM // pkin] CG11228 GH10354 56D10-56D10 ID:37H3

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

CG9056 + unknown \* 1e-07 cDNA clone for has a 574-bp insertion at positio \* BLASTX 8.8E-06 SRP40|Suppressor of mutant AC40 subunit of RNA polyme \* [PRO\_RICH // NLS\_BP] CG9056 GH10459 13F7-13F8 dup:1/2 ID:38A3

CG7757 + structural\_protein \* U4/U6-associated RNA splicing factor(aa) \* 9e-24 hypothetical protein YDR473c - yeast (Saccharomyces cerevisiae) (U \* 1e-101 cDNA EST comes from thi [NLS\_BP] CG7757 GH10477 76D7-76D7 ID:38A4

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

CG6054 + Su(fu) unknown \* DMSF\_2 Su(fu) \* Su(fu) protein(aa) \* gene suppressor of fused protein - fruit fly (Drosophila melanogaster) \* 6e-80 Su(fu) protein CG6054 GH10488 87C8-87C8 ID:38A6

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

CG18284 + unknown \* CG18284 GH10507 31F5-31F5 ID:38A9

CG10159 + BEAF-32 DNA\_binding \* boundary element-associated factor, 32k - fruit fly (Drosophila melanogaster)(aa) \* 1e-146 DMBEAF32A\_2 BEAF-32 \* boundary element associated factor [NLS\_BP] CG10159 GH10592 51C3-51C3 ID:38B2

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

CG9889 + unknown \* royal jelly protein RJP57-2 - honeybee(aa) \* DMYELLOW\_7 y \* 9e-32 YELL\_DROME YELLOW PROTEIN yellow protein - fruit fly (Dros \* 2e-34 milk protein ma CG9889 GH10609 59D9-59D9 ID:38B4

CG10863 + BcDNA:GH10614 enzyme \* 2e-49 GCY\_YEAST GCY PROTEIN GCY1 protein - yeast (Saccharomyces \* 3e-58 Similarity to Human aldose reductase (SW:ALDR\_HUMAN) \* 1e-77 ALDR\_MOUSE ALDO [ALDKETRDASE // ALDOKETO\_REDUCTASE\_1 //] CG10863 GH10614 64A1-64A1 ID:38B5

CG3074 + endopeptidase similar to cysteine protease Peptidase\_C1, THIOL\_PROTEASE\_HIS CG3074 GH10620 dup:1/3 ID:38B6  
+ Cyp6a17 cytochrome\_P450 \* CYP6A2(aa) \* 4e-43 YRV2\_CAEEL PUTATIVE CYTOCHROME P450 T10B9.2 IN CHROMOSOME II \* 2e-68 cytochrome P450IIIA \* 4e-67 cytochrome P450, subfamily IIIA [EP450II // p450 // P450 // MITP450 // C]

CG10241 CG10241 GH10635 51D2-51D2 ID:38B8

CG1623 + unknown \* CG1623 GH10642 46B12-46B13 ID:38B9  
+ unknown \* 1e-45 YABC\_ECOLI HYPOTHETICAL 34.9 KD PROTEIN IN FRUR-FTSL INTERGENIC REGION (ORFB) >g \*

CG14683 1E-170\* hypothetical protein \* hypothetical protein CG14683 GH10770 86C2-86C2 ID:38C10  
+ ligand\_binding\_or\_carrier \* 1e-31 peptidyl-di-peptidase 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

CG9047 + BcDNA:GH10777 protein\_kinase \* 2e-13 KB9S\_YEAST PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR274W \* 7e-69 tyrosine kinase \* 8e-73 YWR1\_CAEEL PUTATIVE TYROSINE-PROTEIN KI[UBA // PROTEIN\_KINASE\_TYR // TYRKINASE ]

CG14992 CG14992 GH10777 64A8-64A9 dup:2/5 ID:38C12  
+ 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

CG7146

CG9133 + unknown \* CG9133 GH10732 61F4-61F4 dup:1/3 ID:38C6  
+ unknown \* No definition line found(aa) \* putative protein(aa) \* 5e-71 putative protein \* hypothetical protein CG6910

CG6910 GH10741 68F7-68F7 dup:1/2 ID:38C7  
+ Su(H) DNA\_binding \* DMSUHA\_2 Su(H) \* RBJK\_DROME J KAPPA-RECOMBINATION SIGNAL BINDING PROTEIN (RBP-J KAPPA) (SUPPRESSO \* 1e-134 DNA-binding protein LAG-1 lag-1 ge \* RB [LIPOCALIN] CG3497 GH10914 35C1-35C1 dup:2/2 ID:38D10

CG3497

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

CG5045

CG2145 + endopeptidase \* 5e-32 Similarity to human placental protein \* 2e-42 glucocorticoid-sensitive T cell-specific protein - mouse \* 5e-41 placental protein (serine protease) CG2145 GH10845 10A1-10A1 dup:2/2 ID:38D4  
+ 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

CG7361

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

CG6567

CG7486 + Dredd endopeptidase \* DREDD isoform delta \* 2e-16 interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans \* 1e-18 caspase-8 caspase-8 \* 5e-18 caspas[CASPASE\_P10 // ICE\_p10 // CASPASE\_P20 /] CG7486 GH10971 1B10-1B10 dup:2/2 ID:38E5

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

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

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

+ tumor\_suppressor \* 3e-09 /match=(desc;; /ma \* 3e-16 predicted using Genefinder; Similarity to Human leukocyte surface \* 4e-26 CD82\_MOUSE CD82 ANTIGEN (INDUCIBLE MEMBRA [transmembrane4 // TMFOUR // TM4\_2] CG4999 GH11168 66E3-66E3 ID:38F10

CG4999 + receptor \* glutaminy cyclase(aa) \* 3e-32 YFI8\_YEAST HYPOTHETICAL 41.0 KD PROTEIN IN UGS1-FAB1 INTERGENIC REGION \* 3e-62 similar to guanylate cyclase; cDNA EST CG10487 GH11174 64F4-64F4 ID:38F11

CG10487 + 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

CG2910 + BcDNA:GH11112 unknown \* CG1927 GH11112 62B11-62B11 ID:38F4

CG1927 + transcription\_factor \* zinc finger protein(aa) \* patched related protein translocated in renal cancer(aa) \* protein(aa) \* required to degrade misfolded ER lumenal and i[zf-C3HC4 // PRO\_RICH // ZF\_RING] CG1937 GH11117 100E3-100E3 dup:1/2 ID:38F5

CG1937 + unknown \* similar to GABA and glycine receptors(aa) \* 6e-75 similar to GABA and glycine receptors \* [TPR\_REPEAT] CG4525 GH11140 89A6-89A6 ID:38F8

CG4525 + TFIIEalpha transcription\_factor \* 6e-23 T2EA\_YEAST TRANSCRIPTION INITIATION FACTOR IIE, ALPHA SUBUNIT (TFIIE-ALPHA) (TRA \* TFIIE large subunit \* 7e-35 cDNA EST yk210d12.5 comes from CG10415 GH11150 68C13-68C13 ID:38F9

CG10415 + Rab-RP4 enzyme \* Rab4 \* rab-related protein 4(aa) \* 2e-29 SEC4\_YEAST RAS-RELATED PROTEIN SEC4 GTP-binding protein SE \* 1e-32 strong similarity to the YPT1 sub-family [SIGMA54\_INTERACT\_1 // SAR1GTPBP // ras] CG3129 GH11193 5A12-5A12 ID:38G1

CG3129 + 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

CG13830 + BcDNA:GH11322 cell\_adhesion \* Pxn \* 6e-20 roundabout \* 2e-15 hemicentin precursor \* 1e-10 rig-1 protein [ig // fn3] CG16857 GH11322 24E4-24E4 dup:2/5 ID:38G12

CG16857 + unknown \* [NLS\_BP] CG10599 GH11223 37B3-37B3 ID:38G3

CG10599 + unknown \* 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase(aa) \* 5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) trans [ATP\_GTP\_A] CG11089 GH11240 96B4-96B5 ID:38G4

CG11089 + Nmd3 unknown \* 1e-115 NMD3\_YEAST NONSENSE-MEDIATED MRNA DECAY PROTEIN Nmd3p \* 1e-125 Similarity to Yeast nonsense-mediated mRNA decay protein (SW:NMD3\_Y \* 1e-143 CG [CYTOCHROME\_C] CG3460 GH11261 2E1-2E1 ID:38G5

CG3460 + flp signal\_transduction \* 2e-35 IRS1\_MOUSE INSULIN RECEPTOR SUBSTRATE-1 insulin receptor sub \* 9e-35 IRS1\_HUMAN INSULIN RECEPTOR SUBSTRATE-1 (IRS-1) insulin \* 2e-35 IRS1\_RAT [INSULINRSI // PH\_DOMAIN] CG5686 GH11263 31C1-31C3 ID:38G6

CG5686 + Acp36DE signal\_transduction \* 36DE accessory gland protein(aa) \* 1e-156 accessory gland protein Acp36DE \* 1e-124 Acp36DE

CG7157

\* CG7157 GH11288 36F6-36F6 ID:38G8  
 + unknown \* unknown(aa) \* 4e-12 putative Bop-like zinc finger protein \* 1e-19 DMC103B4 [IPNS\_1 // CYTOCHROME\_C]  
 CG8503 CG8503 GH11294 50E8-50E8 ID:38G9  
 + Ugt35b enzyme \* antennal-enriched UDP-glycosyltransferase melanogas \* 3e-31 similar to UDP-glucuronosyltransferase \* 5e-62  
 CG6649 UDB5\_MOUSE UDP-GLUCURONOSYLTRANSFERASE 2B [UDPGT] CG6649 GH11333 86D5-86D5 ID:38H1  
 + BcDNA:GH11415 unknown \* 1e-104 mab-21 \* 1e-139 CAGR1 cell fate specificati \* 1e-140 XMAB21 \* cDNA EST yk376f11.5  
 CG4766 comes from this gene; cDNA EST yk282h5.5 comes CG4766 GH11415 5D1-5D1 ID:38H10  
 + endopeptidase \* encodes a-cell barrier activity on alpha factor; Bar1p(aa) \* similar to eukaryotic aspartyl proteases(aa) \*  
 CG13095 BLASTX 1.4E-29 PEP4|Protease A (PrA) (y [asp // ASP\_PROTEASE // PEPSIN] CG13095 GH11417 29D1-29D1 ID:38H11  
 CG3624 + cell\_adhesion \* [ig] CG3624 GH11432 58D7-58D7 dup:2/2 ID:38H12  
 + Rpn5 endopeptidase \* proteasome (prosome, macropain) 26S subunit, non-ATPase, 12(aa) \* 5e-42 hypothetical protein  
 CG1100 YDL147w - yeast (Saccharomyces cerevisiae) \* 2e-81 No d [PCI\_DOMAIN // PCI // NLS\_BP] CG1100 GH11341 83C-83C ID:38H3  
 + enzyme \* HYPOTHETICAL 37.1 KD PROTEIN ZK892.4 IN CHROMOSOME III(aa) \* 3e-53 similar to L-carnitine  
 CG9319 dehydratase; cDNA EST yk206h7.5 comes from \* 9e-87 alpha-m CG9319 GH11368 38E4-38E4 ID:38H4  
 + enzyme \* peroxinectin - signal crayfish(aa) \* ovoperoxidase(aa) \* peroxidase(aa) \* coded for by C. elegans cDNA yk30f1.3;  
 CG8913 coded for by C. elegans cDNA yk40 [ANPEROXIDASE // PEROXIDASE\_3] CG8913 GH11385 92C1-92C1 ID:38H5  
 + NaCP60E ion\_channel \* DMSODCHA\_6 para \* DMCA1\_2 Ca- agr;1D \* sodium channel protein - fruit fly (Drosophila  
 melanogaster) (fragments) \* 4e-76 similar to dihydropyridine- [NACHANNEL // ion\_trans // CATION\_CHANNE] CG9071 GH11402  
 CG9071 60E4-60E5 dup:2/2 ID:38H6  
 + RNA\_binding \* pre-mRNA splicing factor(aa) \* contains similarity to G-beta repeats(aa) \* 1e-76 Cdc40p \* 3e-15  
 T2D4\_DROME TRANSCRIPTION INITIATION FACTOR TFIID KD [GPROTEINBRPT // WD40\_REGION // WD\_REPEA] CG6015  
 CG6015 GH11406 94A1-94A1 ID:38H8  
 CG17567 + unknown \* 1E-78\*\* CG17567 GH11551 37C-37C ID:39A10  
 + RNA\_binding \* polyadenylate binding protein II - human(aa) \* myelin gene expression factor 2(aa) \* DMB52\_2 B52 \* Gbp1p  
 CG9373 protein - Chlamydomonas reinhardtii(aa) [RBD // rm] CG9373 GH11495 86C1-86C1 dup:1/2 ID:39A4  
 + vkg cell\_adhesion \* DMINTGRNB\_2 Cg25C \* vkg \* collagen type IV alpha \* 7e-25 Similar to cuticular collagen; F58F6.2  
 CG16858 [COLLAGEN\_REP // Collagen // C4] CG16858 GH11516 25C1-25C1 ID:39A7  
 CG12907 + unknown \* 1E-145\* \* [PRO\_RICH // NLS\_BP] CG12907 GH11521 47A-47A ID:39A8  
 + \* 1e-29 cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes \* 3e-12 conserved hypothetical secreted  
 CG13865 protein pylori \* putative pylori \* c CG13865 cyto\_unknown dup:3/3 ID:39B1  
 + Pcaf enzyme \* Pcaf SPTR(aa) \* BLASTX 2.0E-35 GCN5|Component of the nucleosomal histone acetyltransferase (Spt-Ada-  
 CG4107 Gcn5-Acetyltransferase or SAGA) complex(dna) \* B [NLS\_BP] CG4107 GH11602 69C3-69C3 dup:2/2 ID:39B3  
 + 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  
 CG7149 ID:39B5  
 + signal\_transduction \* 3e-48 cdc4, incomplete, len: 579, CAI, 0.15, CC4\_YEAST CELL DIVISI \* 2e-61 Slimb \* 5e-32  
 CG15010 YKY4\_CAEEL HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CO[GPROTEINBRPT // F-box // WD\_REPEATS // ] CG15010

GH11648 64B4-64B4 dup:2/3 ID:39B6

CG3825 + unknown \* CG3825 GH11727 60A14-60A14 dup:1/3 ID:39C1

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

CG17027 + transporter \* 40-kDa V-ATPase subunit(aa) \* 3e-85 VATX\_YEAST VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (V-ATPASE \* 1e-172 Ac39/physophilin \* 1e- CG2934 GH11776 4A1-4A1 ID:39C4

CG2934 + enzyme \* FLAVONOL 3-SULFOTRANSFERASE (F3-ST)(aa) \* steroid sulfotransferase 3(aa) \* sulfotransferase family 2B, member 1(aa) \* sulfotransferase, estrogen-pre [Sulfotransfer] CG5428 GH11818 59F4-59F4 ID:39C6

CG5428 + 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

CG12162 + unknown \* inserted at base Both 5' and 3' ends of P element Inverse PCR \*\* CG13928 GH11843 62A-62A ID:39C8

CG13928 + transporter \* 2e-50 Na(+)-dependent inorganic phosphate cotransporter mela \* 7e-54 YLD2\_CAEEL HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III \* 2e-45 NPT1 [sugar\_tr] CG15095 GH11849 55F1-55F1 ID:39C9

CG15095 + unknown \* CG9284 GH11908 58A2-58A2 ID:39D1

CG9284 + transporter \* Contains similarity to equilibrative nucleoside transporter from Homo sapiens. ESTs and come from this gene.(aa) \* NBMPR-insensitive nucleoside tr [DERENTRNSPRT] CG11045 GH12067 26E2-26E2 ID:39D11

CG11045 + Rpt5 endopeptidase \* contains similarity to the AAA family of ATPases (Pfam; AAA, score; 259.07); most similar to human probable 26S protease subunit TBP-1 \* putative [AAA // MITOCH\_CARRIER // ATP\_GTP\_A] CG10370 GH12068 95B7-95B7 ID:39D12

CG10370 + unknown \* HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III(aa) \* IMPLANTATION-ASSOCIATED PROTEIN(aa) \* N33 PROTEIN(aa) \* 9e-99 kDa encoded by N33 [THIOREDOXIN\_2] CG7830 29A4-29A4 dup:2/2 ID:39D4

CG7830 + 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

CG11796 + BcDNA:GH11973 unknown \* 2e-05 CD94 C-type lectin receptor musculus \* 4e-05 regenerating islet-derived alpha (pancreatic stone protein, pancreatic thread protein) \* 7e-05 PA2 [lectin\_c // C\_TYPE\_LLECTIN\_2 // NLS\_BP] CG6014 GH11973 78D4-78D4 dup:3/3 ID:39D7

CG6014 + unknown \* 2e-12 HNK-1 sulfotransferase HNK-1 sulfotransferase \* 2e-12 HNK-1 sulfotransferase \* [PRO\_RICH] CG14024 GH11985 25D4-25D5 ID:39D8

CG14024 + unknown \* CG1146 GH12037 62E6-62E6 ID:39D9

CG1146 + BcDNA:GH12174 DNA\_binding \* 1e-05 eyelid \* 6e-45 YP83\_CAEEL HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II \* 5e-06 FMO5\_MOUSE DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FO [ARID] CG3274 GH12174 42B2-42B3 dup:4/4 ID:39E10

CG3274 + Pfk enzyme \* DMPFK\_5 Pfk \* DMPFK\_5 Pfk \* 1e-151 phosphofructokinase, beta subunit \* K6PF\_DROME 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) [PFK // PHFRCTKINASE] CG4001 GH12192 46E4-46E4 dup:4/5 ID:39E11

CG4001

+ enzyme \* 1e-30 YHX6\_YEAST HYPOTHETICAL 42.4 KD PROTEIN IN ENO2-STB5 INTERGENIC REGION \* 9e-53 similar to flavin-containing monooxygenases \* 2e-29 FMO3\_MOUSE [ADXRDTASE // FADPNR // FMO-like // PNDR] CG3174 GH12207 42B3-42B3 dup:2/2 ID:39E12  
 CG3174  
 + unknown \* 2e-10 YEA3\_YEAST HYPOTHETICAL 14.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION \* 7e-28  
 CG6302  
 prefoldin subunit \* 2e-68 I(3)j9B4 I(3)j9B4 inserted at base Bo CG6302 GH12095 70E1-70E1 dup:2/2 ID:39E2  
 + bw transporter \* BROWN PROTEIN(aa) \* DMBROWN\_1 bw \* brown protein(aa) \* BROWN PROTEIN(aa) [ATP\_GTP\_A2 // ABC\_tran // DA\_BOX] CG17632 GH12107 59E-59E3 dup:2/2 ID:39E3  
 CG17632  
 + EG:115C2.11 unknown \* 2e-37 hypothetical protein YOL133w - yeast (Saccharomyces cerevisiae) \* 9e-60 /match=(desc: \* 8e-50 Similarity to yeast hypothetical protein PIR acc [ZF\_RING] CG16982 GH12110 1B10-1B10 dup:2/2 ID:39E4  
 CG16982  
 CG9119 + unknown \* 2e-25 No definition line found \* \* CG9119 61F3-61F3 dup:5/5 ID:39E5  
 CG17420 + CG17420 dup:2/2 ID:39E6  
 + BcDNA:GH12144 unknown \* Contains similarity to Pfam domain: (TPR), Score=38.0, E-value=6.9e-08, N=6(aa) \* weakly similar to E. nidulans bimA gene product \* \* [TPR\_REGION // TPR\_REPEAT] CG4341 GH12144 21D4-21E dup:3/3 ID:39E7  
 CG4341  
 CG4929 + CG4929 dup:2/2 ID:39E8  
 CG10841 + unknown \* CG10841 GH12158 87F6-87F6 dup:2/2 ID:39E9  
 + 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 ID:39F1  
 CG3937  
 + ligand\_binding\_or\_carrier \* ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TTP)(aa) \* 4e-08 YKJ1\_YEAST 36.1 KD PROTEIN IN BUD2-MIF2 INTERGENIC REGION \* 5e-10 62D9.a \* 2e-25 cellular [CRETINALDHBP // CRAL\_TRIO] CG5973 GH12376 27F7-28A1 ID:39F12  
 CG5973  
 + enzyme \* Ynr027wp(aa) \* 8e-44 YEC9\_YEAST HYPOTHETICAL 35.6 KD PROTEIN IN MCM3-VMA3 INTERGENIC REGION \* 2e-57 PDXK\_CAEEL PUTATIVE PYRIDOXINE KINASE (PYRIDOXAL [pfkB] CG4446 GH12231 67B1-67B1 ID:39F3  
 CG4446  
 + Phm enzyme \* Phm \* 4e-65 peptidylglycine alpha-hydroxylating monooxygenase \* 8e-05 similar to peptidyl-glycine alpha-amidating monooxygenases elega \* 5e-09 AMD\_M [PAMONOXGNASE // Cu2\_monooxygen // CU2\_M] CG3832 GH12243 60A14-60A14 ID:39F4  
 CG3832  
 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 GH12350 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 20B1-20B1 dup:1/2 ID:39G1  
 CG12466  
 + peptidase \* PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III(aa) \* Chain A, Bovine Lens Leucine Aminopeptidase Complexed With L-Leucine Phosphonic Acid(aa) \* [Peptidase\_M17] CG4750 GH12543 53C-53C ID:39G10  
 CG4750  
 + 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 // ENOYL\_COA\_HYDRATASE] CG4389 GH12558 30B12-30B12 ID:39G12  
CG4389 + signal\_transduction \* 1e-115 disc growth factor \* 2e-14 CHIT\_CAEEL PUTATIVE ENDOCHITINASE coded for by C. elegans  
CG5154 \* 7e-26 BRP39 protein - mouse BRP39 protein m \* 5e-30 Ch [Glyco\_hydro\_18] CG5154 GH12410 55C9-55C9 ID:39G4  
CG4829 + enzyme \* DMC23E12 \* gamma-glutamyltransferase (EC 2.3.2.2) precursor - rat(aa) \* gamma-glutamyl transpeptidase (EC 2.3.2.2)(aa) \* gamma-glutamyl transpeptida [G\_glu\_transpept] CG4829 GH12430 15A8-15A8 dup:1/2 ID:39G5  
CG10691 + l(2)37Ccunknown \* HYPOTHETICAL 31.8 KD PROTEIN IN CHROMOSOME II(aa) \* DMCCR\_5 l(2)37Cc \* mitochondrial protein, prohibitin homolog; similar to S. cerevisiae Phb2p; Ph [PROHIBITIN // Band\_7] CG10691 GH12454 37C1-37C1 ID:39G6  
CG5575 + ken transcription\_factor \* ken \* ken(aa) \* 8e-09 AZF1\_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin \* 9e-10 zinc finger protein PAG-3 [BTB // zf-C2H2 // ZINC\_FINGER\_C2H2 // Z] CG5575 GH12495 60A6-60A7 ID:39G8  
CG3318 + Dat ligand\_binding\_or\_carrier \* DMNAT1\_2 Aanat1 \* N-acetyltransferase(aa) \* aralkylamine N-acetyltransferase (EC 2.3.1.87) - fruit fly (Drosophila melano \* CG3318 GH12636 60B9-60B9 ID:39H12  
CG4475 + Idgf2 enzyme \* IDGF2 \* 5e-09 probable membrane protein YDR371w - yeast (Saccharomyces cerevisiae) \* disc growth factor \* 3e-24 CHIT\_CAEEL PUTATIVE ENDOCHITINASE co [2SGLOBULIN // Glyco\_hydro\_18] CG4475 GH12581 36A1-36A1 ID:39H4  
CG4461 + chaperone \* embryonal lethal (2)13-1 (el(2)13-1) - fruit fly (Drosophila melanogaster)(aa) \* 4e-16 HS27\_DROME HEAT SHOCK PROTEIN heat shock protein - f \* 9e-10 [HSP20] CG4461 GH12586 67B1-67B1 ID:39H6  
CG1889 + cell\_adhesion \* DMSCA\_3 sca \* 2e-21 sca protein \* 1e-09 coded for by C. elegans cDNA yk9a2.5; coded for by C. elegans cDNA yk9a2.3; simi \* 5e-30 ficolin-A [fibrinogen\_C] CG1889 GH12692 9A3-9A3 ID:40A10  
CG3116 + metabolism \* 4e-05 epithin \* 7e-06 gp330 precursor \* 4e-05 complement C3b/C4b inactivator (EC 3.4.21.-) precursor - 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  
CG9668 + Rh4 G\_protein\_linked\_receptor \* opsin(aa) \* Rh4 \* OPS4\_DROME OPSIN RH4 (INNER R7 PHOTORECEPTOR CELLS OPSIN) \* 2e-15 YXX5\_CAEEL PUTATIVE NEUROPEPTIDE Y RECEPTOR (NPY-R) simila [GPCRRHODOPSN // OPSIN // OPSINRH3RH4] CG9668 GH12673 73C5-73D1 ID:40A5  
CG12131 + translation\_factor \* UNKNOWN(aa) \* 7e-86 inserted at base Both 5' and 3' ends of P element Inverse PCR \* eukaryotic translation initiation factor eIF3, p35 subunit \* CG12131 GH12681 46C10-46C11 ID:40A7  
CG8402 + 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 // STPHPHTA] CG8402 GH12714 85E6-85E6 ID:40B1  
CG6166 + unknown \* ABC transporter, ATP-binding protein, putative(aa) \* 2e-18 conserved protein \* daunorubicin resistance membrane protein (drrB) \* CG6166 GH12746 97A9-97A9 dup:1/2 ID:40B5  
CG3991 + TppII peptidase \* tripeptidyl peptidase II; dTPP II; subtilisin-like serine protease \* 1e-135 YQS6\_CAEEL HYPOTHETICAL SUBTILASE-TYPE PROTEINASE F21H12.6 IN CHROMOSOME [Peptidase\_S8 // SUBTILASE\_SER // SUBTIL] CG3991 GH12811 49F7-49F7 ID:40B7  
CG8775 + peptidase \* 1e-112 APE2\_YEAST AMINOPEPTIDASE II (YSCII) aminopeptidase yscII \* 1e-110 Similarity to Human

aminopeptidase N (SW:AMPN\_HUMAN); cDNA EST EMB \* 1e-16 [ALADIPTASE // Peptidase\_M1 // ZINC\_PROT] CG8775  
 GH12821 87E6-87E6 dup:2/2 ID:40B8  
 + structural\_protein \* nuclear pore protein; Nsp1p(aa) \* nucleoporin p62(aa) \* similar to nucleoporins(aa) \* NUCLEAR PORE  
 CG6251 GLYCOPROTEIN P62 (NUCLEOPORIN P62)(aa) CG6251 GH12838 53B1-53B1 ID:40B9  
 + signal\_transduction \* centaurin beta 1A(aa) \* BLASTX 1.6E-48 Human mRNA for gene, partial cds.(dna) \* HYPOTHETICAL  
 CG6742 PROTEIN \* centaurin beta2(aa) [ANK\_REP // ArfGap // GLYCOSYL\_HYDROL\_F5] CG6742 GH12888 94E-94E dup:1/2 ID:40C1  
 + unknown \* 9e-07 PAC2\_YEAST PAC2 PROTEIN PAC2 protein - yeast (Saccharomy \* 3e-46 No definition line found \* 1e-23  
 CG12214 tubulin-specific chaperone e cofactor E \* CG12214 GH13040 46F1-46F1 dup:1/2 ID:40C10  
 + transporter \* similar to ADP/ATP translocase(aa) \* 2e-17 probable membrane protein YPL134c - yeast (Saccharomyces  
 cerevisiae) \* 1e-32 colt \* 1e-58 similar to mito [mito\_carr // MITOCARRIER // MITOCH\_CARR] CG4995 GH13054 31D8-31D8  
 CG4995 ID:40C11  
 CG5506 + unknown \* CG5506 GH13083 75A6-75A6 ID:40C12  
 + unknown \* Similar to Plasmodium falciparum glutamic acid-rich protein precursor \* cDNA EST comes from this gene; cDNA  
 CG10955 EST comes from this gene; cDNA EST come [PRO\_RICH] CG10955 GH12904 58D6-58D6 dup:1/3 ID:40C2  
 + unknown \* protein(aa) \* lml1p(aa) \* 9e-46 YJ9G\_YEAST HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6  
 CG12090 INTERGENIC REGION \* 4e-75 Proline rich domain; cDNA EST comes CG12090 GH12915 62A5-62A6 dup:3/3 ID:40C3  
 + protein\_kinase \* v-akt murine thymoma viral oncogene homolog 2(aa) \* protein kinase C(aa) \* PROTEIN KINASE C, THETA  
 TYPE (NPKC-THETA)(aa) \* PROTEIN KINASE C-LIKE (P[PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG2049 GH12918  
 CG2049 45C-45C dup:2/2 ID:40C5  
 + metabolism \* DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) GLUTAMATE 5-KINASE (GAMMA-  
 GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMA [GLU5KINASE // PROA // aldedh  
 CG7470 // GLUTAMA] CG7470 GH12945 79B3-79B3 dup:1/5 ID:40C6  
 CG6306 + unknown \* CG6306 GH12946 17B1-17B1 ID:40C7  
 + transporter \* VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) (V-ATPASE KD ACCESSORY  
 PROTEIN)(aa) \* 1e-58 VATD\_YEAST VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPAS CG8186 GH12958 52A10-52A10  
 CG8186 ID:40C8  
 + peptidase \* Chain A, Bovine Lens Leucine Aminopeptidase Complexed With L-Leucine Phosphonic Acid(aa) \* 6e-20  
 YOJ6\_CAEEL PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROM [LAMNOPPTDASE // Peptidase\_M17] CG6372 GH13022  
 CG6372 68C1-68C1 dup:2/2 ID:40C9  
 + E2f2 transcription\_factor \* E2f2 \* 1e-174 E2F-like transcription factor (E2F2) \* 7e-14 predicted using Genefinder; cDNA EST  
 CG1071 comes from this \* 3e-18 E2F5\_MOUSE TRANSCRIPTION FAC CG1071 GH13089 39B3-39B3 ID:40D1  
 + unknown \* cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST yk410c1.3 comes from this gene;  
 CG12113 cDNA EST yk410c1.5 comes from this gene; cDNA [ATP\_GTP\_A] CG12113 GH13214 7F1-7F3 ID:40D10  
 CG6575 + Gliolectin unknown \* Gliolectin \* gliolectin(aa) \* 1e-99 Gliolectin \* CG6575 GH13232 93F-93F ID:40D12  
 + ligand\_binding\_or\_carrier \* mannose receptor, C type 1(aa) \* 1e-05 similar to Lectin C-type domain short and long forms (2  
 domains) \* 9e-06 lectin lambda \* 6e-0[lectin\_c // C\_TYPE\_LLECTIN\_1 // C\_TYPE\_L] CG8343 GH13116 42A10-42A10 dup:2/2  
 CG8343 ID:40D2

+ 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) \* HYPOTHETICAL 64.2 KD PROTEIN R08D7.3 IN CHROMOSOME II CG10161 GH13209 97D8-97D8 dup:3/4 ID:40D9  
 CG10161  
 + transcription\_factor \* HYPOTHETICAL 43.4 KD PROTEIN C6F12.11C IN CHROMOSOME I(aa) \* transcription factor IIIC63(aa) \* 1e-05 TFC1\_YEAST TRANSCRIPTION FACTOR TAU KD SUBUNIT CG10563 GH13253 37C1-37C1 dup:2/2 ID:40E1  
 CG10563  
 + transcription\_factor \* zf30C \* DMSPALTR\_3 salr \* 5e-05 YEW0\_YEAST PUTATIVE 50.3 KD ZINC FINGER PROTEIN IN PAK1-RPS26B INTERGENIC REGIO \* 9e-06 spalt-related [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG2199 GH13336 61F7-61F7 dup:2/2 ID:40E10  
 CG2199  
 + ribosomal\_protein \* ribosomal protein L10a(aa) \* 60S RIBOSOMAL PROTEIN L10A (CSA-19)(aa) \* 60S RIBOSOMAL PROTEIN L10A(aa) \* 2e-06 predicted using Genefinder; Weak simil [Ribosomal\_L1] CG7283 GH13356 68D3-68D3 dup:3/3 ID:40E11  
 CG7283  
 + 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  
 CG7874  
 + 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  
 CG4581  
 + Mipp2 protein\_phosphatase \* Mipp2 \* multiple inositol polyphosphate phosphatase 2; MIPP2 \* 1e-27 multiple inositol polyphosphate phosphatase \* 1e-25 multiple inositol polyphosp [CYTOCHROME\_B\_QO] CG4317 GH13296 5D2-5D2 dup:4/4 ID:40E4  
 CG4317  
 + Pgym78 enzyme \* phosphoglyceromutase - fruit fly (Drosophila melanogaster)(aa) \* DMPGLY\_4 Pgym78 \* 7e-48 pdb|4PGM|A Chain A, Saccharomyces Cerevisiae Phosphoglycer [PGAM // PG\_MUTASE] CG1721 GH13304 99A1-99A1 dup:2/2 ID:40E5  
 CG1721  
 + enzyme \* phosphoglucomutase(aa) \* 1e-152 PGM2\_YEAST PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE 2) (PGM 2) \* coded for by C. elegans cDNA cm17h1; coded for by [PGM\_PMM // PGMPMM // ATP\_GTP\_A] CG5165 GH13311 72D7-72D7 dup:2/2 ID:40E6  
 CG5165  
 + 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  
 CG9451  
 + actin\_binding \* 2e-12 putative actin-binding protein UNC-115 \* 2e-11 protein \* 2e-05 talin homologue \* 5e-05 qua CG9489 GH13330 85E5-85E5 dup:3/3 ID:40E9  
 CG9489  
 + transporter \* 5e-75 Na(+)-dependent inorganic phosphate cotransporter mela \* 7e-67 YLD2\_CAEEL HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III \* 4e-46 NPT1 [NLS\_BP] CG3036 GH13494 26D1-26D1 dup:3/4 ID:40F10  
 CG3036  
 + unknown \* /match=(desc;; /match=(desc:(aa) \* 1e-36 /match=(desc;; /ma \* \* CG10513 GH13495 96C7-96C7 ID:40F11  
 CG10513

+ RNA\_binding \* LET 858(aa) \* conserved hypothetical protein(aa) \* BLASTX 7.4E-44 Caenorhabditis elegans Nucampholin  
 CG12750 (let-858) mRNA, complete cds.(dna) \* BLASTX 3 [NLS\_BP] CG12750 GH13383 36F7-36F7 dup:3/3 ID:40F2  
 CG5903 + unknown \* 6e-06 K02F3.10 gene product \* \* CG5903 GH13386 89B9-89B9 ID:40F3  
 + enzyme \* MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME) (ME) (NADP-DEPENDENT  
 MALIC ENZYME) (NADP-ME)(aa) \* malic enzyme(aa) \* 4e-86 MAOX\_YEAST [MALOXRDTASE // malic // ATP\_GTP\_A] CG5889  
 CG5889 GH13437 97E11-97F ID:40F4  
 + Fpps enzyme \* 8e-80 FPPS\_YEAST FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL  
 DI \* farnesyl pyrophosphate synthase melanogas \* 2e-37 predicted [polyprenyl\_synt // POLYPRENYL\_SYNTHET\_1] CG12389  
 CG12389 GH13450 47E5-47E6 dup:2/2 ID:40F5  
 + OstStt3 enzyme \* STT3\_YEAST OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT STT3 \* STT3\_CAEL  
 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG \* STT3\_MOUSE OLIGOSACCHARYL  
 CG7748 [ATPASE\_ALPHA\_BETA] CG7748 GH13452 98F6-98F6 ID:40F6  
 CG7021 + Ela unknown \* [COLLAGEN\_REP] CG7021 GH13458 96B4-96B4 ID:40F7  
 + DNA\_repair\_protein \* 2e-29 CHL1\_YEAST CHL1 PROTEIN CHL1 protein - yeast (Saccharomyce \* 1e-31 /match=(desc;  
 CG4078 /ma \* 1e-112 similar to DEAH-type helicase; cDNA EST comes f [PHOSPHOPANTETHEINE] CG4078 GH13485 5B3-5B3 ID:40F8  
 + Pgd enzyme \* 6-phosphogluconate dehydrogenase(aa) \* DMPGD\_1 Pgd \* 1e-177 6PG1\_YEAST 6-PHOSPHOGLUCONATE  
 DEHYDROGENASE, DECARBOXYLATING \* 6PGD\_DROME 6-PHOSPHOGLU [6PGD // 6PGDHDRGNASE] CG3724 GH13486  
 CG3724 2D6-2D6 ID:40F9  
 + chaperone \* t-complex polypeptide 20(aa) \* 1e-142 TCPZ\_YEAST T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-  
 ZETA) (CCT-ZETA) \* 7e-46 CCT-gamma protein \* 1e-178 TCPZ\_ [TCP1\_1 // TCP1\_2 // TCP1\_3 // TCOMPLEXT] CG8231  
 CG8231 GH13725 13E17-13E17 ID:40G12  
 + Pgi enzyme \* glucosephosphate isomerase(aa) \* DMPGIAAAA\_11 \* glucose-6-phosphate isomerase(aa) \* G6PI\_YEAST  
 GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (PHOSPHOGLUCOSE [PGI // P\_GLUCOSE\_ISOMERASE\_1 // P\_GLUCO]  
 CG8251 CG8251 GH13575 44F9-44F9 ID:40G4  
 + RNA\_binding \* 3e-16 RNA-binding protein cabeza - fruit fly (Drosophila melanogaster) ( \* 4e-14 EWS\_MOUSE RNA-  
 BINDING PROTEIN EWS RNA-binding protein E \* 2e-15 TLS [RBD // zf-RanBP // rrm // ZF\_RANBP] CG14718 GH13594 86F1-  
 CG14718 86F1 ID:40G5  
 + ligand\_binding\_or\_carrier \* TRANSFERRIN PRECURSOR(aa) \* transferrin precursor(aa) \* transferrin precursor(aa) \*  
 CG3666 transferrin precursor(aa) [PROTEIN\_SPLICING] CG3666 GH13735 52F10-52F10 ID:40H1  
 + 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 CG3041 GH13824 88A4-88A4 ID:40H11  
 + glutathione\_transferase \* predicted using Genefinder; similar to Glutathione S-transferases.(aa) \* 2e-11 YKJ3\_CAEL  
 CG6662 HYPOTHETICAL 42.8 KD PROTEIN C02D5.3 IN CHROMOSOME III \* 7 [GST] CG6662 66D5-66D5 dup:2/2 ID:40H2  
 + bun transcription\_factor \* shortsighted class 2(aa) \* DMSHSA\_5 bun \* shortsighted class \* 2e-07 protein [TSC22] CG5461  
 CG5461 GH13775 33E-33E6 ID:40H5  
 CG2046 + unknown \* CG2046 GH13924 83C-83C ID:41A10

+ 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  
 CG10590  
 + 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  
 CG8721  
 + 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  
 CG10060  
 + protein\_kinase \* serine/threonine protein kinase; Cdc7p(aa) \* protein kinase Cdc7(aa) \* DMSTPK Pk61C \* HsCdc7(aa) [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG5790 GH13884 36F-36F ID:41A7  
 CG5790  
 + enzyme \* *C. elegans* glyceraldehyde 3-phosphate dehydrogenase \* GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE II (GAPDH II)(aa) \* GLYCERALDEHYDE 3-PHOSPHATE DEHYDR [G3PDHDRGNASE // gpdh // GAPDH] CG9010 GH13901 53E6-53E6 ID:41A8  
 CG9010  
 CG7251 + unknown \* [NLS\_BP] CG7251 GH13914 27D1-27D1 ID:41A9  
 CG1112 + alpha-Est7 enzyme \* alpha esterase(aa) \* alpha esterase(aa) \* alpha esterase(aa) \* alpha esterase(aa) [CARBOXYLESTERASE\_B\_1 // ESTERASE // COe] CG1112 GH13950 84D5-84D5 dup:3/3 ID:41B1  
 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  
 CG7131 + unknown \* CG7131 GH14048 90F7-90F7 ID:41B9  
 CG9775 + unknown \* [NLS\_BP] CG9775 GH14260 82D2-82D2 dup:1/2 ID:41C10  
 CG2176 + unknown \* CG2176 GH14263 99E2-99E2 ID:41C11  
 CG3662 + structural\_protein \* E25 protein(aa) \* integral membrane protein 2(aa) \* 2e-07 putative integral membrane pro \* 1e-08 dJ696H22.1 (mouse E25 like protein) [NLS\_BP] CG3662 GH14111 21D2-21D2 ID:41C3  
 CG2155 + v enzyme \* DMVERM\_2 v \* VERM\_DROME TRYPTOPHAN 2,3-DIOXYGENASE (TRYPTOPHAN PYRROLASE) (VERMILION PROTEIN) \* 1e-102 T23O\_CAEEL PUTATIVE TRYPTOPHAN 2,3-DIOXYGENA CG2155 GH14143 9F13-10A1 ID:41C4  
 CG4899 + Pdh enzyme \* Pdh \* 1e-08 FOX2\_YEAST PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL \* 1e-146 pigment cell dehydrogenase reductase \* 2e-10 pr [GDHRDH // UBA\_NAD // adh\_short // ADH\_S] CG4899 GH14170 72F1-72F1 ID:41C6  
 none + none GH14214 ID:41C7  
 CG3671 + Mvl unknown \* MALVOLIO PROTEIN(aa) \* Mvl \* 7e-42 SMF1\_YEAST TRANSPORTER PROTEIN SMF1/ESP1 vacuolar trans \* 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  
 CG9131 + unknown \* Ylr193cp(aa) \* bromodeoxyuridine-sensitive transcript protein - chicken(aa) \* hypothetical protein(aa) \* CGI-107

protein(aa) CG9131 GH14384 26B2-26B3 ID:41D12

CG11919 + endopeptidase \* VESICULAR-FUSION PROTEIN NSF1 (N-ETHYLMALIMIDE-SENSITIVE FUSION PROTEIN 1) (NEM-SENSITIVE FUSION PROTEIN 1) (COMATOSE PROTEIN)(aa) \* 8e-67 CC48\_YEA [AAA // ATP\_GTP\_A] CG11919 GH14288 47C6-47C6 dup:2/2 ID:41D2

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

CG7567 + unknown \* CG7567 GH14364 99B5-99B5 ID:41D8

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

CG5523 + defense/immunity\_protein \* UNKNOWN(aa) \* 3e-07 peptidoglycan recognition protein precursor \* TNF superfamily, member (LTB)-like (peptidoglycan recognition \* hypothetical prote CG5523 GH14535 66A5-66A5 dup:2/2 ID:41E10

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

+ signal\_transduction \* 2e-17 activin beta precursor \* 3e-14 CET-1 \* 2e-22 IHBA\_MOUSE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN) \* 5e-23 inhibin, beta A[TGF-beta // TGF\_BETA // TGF\_BETA\_2 // Z] CG16987 GH14433 23B2-23B2 dup:2/2 ID:41E2

CG16987

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

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

CG7834 + electron\_transfer \* 3e-39 ETFB\_YEAST PROBABLE ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF) \* 7e-61 contains similarity to electron transfer flavoprotein beta [ETF\_beta] CG7834 GH14462 99C4-99C4 dup:2/2 ID:41E7

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

CG3315 + electron\_transfer \* 9e-06 PDI\_YEAST PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) / DOLICHYL-DIPHOSPHOOLIGOS \* 2e-08 PDI\_DROME PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) [THIOREDOXIN // THIOREDOXIN\_2 // thiored] CG3315 GH14562 4F2-4F2 ID:41F1

CG5164 + enzyme \* DMGST\_3 GstD1 \* 2e-10 probable membrane protein YLL060c - yeast (Saccharomyces cerevisiae) \* 3e-37 GTT1\_DROME GLUTATHIONE S-TRANSFERASE 1-1 (CLASS-T [GST] CG5164 GH14654 55C9-55C9 ID:41F10

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

+ structural\_protein \* 3e-05 MAGE tumor antigen D1 \* 5e-13 FMRA\_ANTEL ANTHO-RFAMIDE NEUROPEPTIDE PRECURSOR Antho-RFa \* LWamide neuropeptide precursor protein \* 33K hydroxy CG11395 GH14572 54A2-54A2 dup:2/2 ID:41F2

CG11395

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

CG5258 + ribosomal\_protein \* similar to Ribosomal protein L7Ae; cDNA EST comes from this gene(aa) \* 2e-18 NHP2\_YEAST HIGH

MOBILITY GROUP-LIKE NUCLEAR PROTEIN hi \* 2e-27 similar [Ribosomal\_L7Ae // L7ARS6FAMILY // NUCLE] CG5258  
 GH14757 70F6-70F6 ID:41G10  
 + enzyme \* NADH-ubiquinone oxidoreductase B22 subunit homolog(aa) \* 6e-22 similar to NADH-ubiquinone oxidoreductase  
 CG9306 B22 (B. taurus, SP:NI2M \* 1e-26 NI2M\_BOVIN CG9306 GH14794 34B6-34B6 ID:41G11  
 + EG:86E4.2 enzyme \* 6e-67 YH04\_YEAST HYPOTHETICAL 91.2 KD PROTEIN IN RPS7A-SCH9 INTERGENIC REGION \*  
 /match=(desc;; /ma \* 1e-157 similar to mannosyl-oligosaccharide alph [GLYHDLASE47] CG3810 GH14693 2B15-2B16 dup:1/2  
 CG3810 ID:41G2  
 + motor\_protein \* Cdic \* cytoplasmic dynein intermediate chain isoform DIC2c(aa) \* DYNEIN INTERMEDIATE CHAIN 3,  
 CG10859 CILIARY(aa) \* 3e-07 cytoplasmic dynein intermediate ch [NLS\_BP] CG10859 GH14707 34B7-34B7 ID:41G3  
 + unknown \* TRANSMEMBRANE PROTEIN PFT27(aa) \* probable membrane protein; Ybr187wp(aa) \* 5e-34 YB37\_YEAST  
 CG4196 HYPOTHETICAL 30.3 KD PROTEIN IN MBA1-RPS13 INTERGENIC R [UPF0016] CG4196 GH14710 88E7-88E7 ID:41G4  
 + enzyme \* 1e-103 IDH2\_YEAST ISOCITRATE DEHYDROGENASE MITOCHONDRIAL SUBUNIT PRECURSOR (IS \* 1e-139  
 CG12233 IDHA\_CAEEL PROBABLE ISOCITRATE DEHYDROGENASE (NAD), MITOCHON [IDH\_IMDH // isodh] CG12233 GH14729 18D3-  
 18D3 ID:41G6  
 + endopeptidase \* DMSER2\_7 Ser99Db \* 1e-57 serine proteinase (EC 3.4.21.-) precursor - fruit fly (Drosophila melanogast \*  
 CG3088 1e-15 KAL\_MOUSE PLASMA KALLIKREIN PRECURSOR [trypsin // CHYMOTRYPSIN // TRYPSIN\_CATA] CG3088 GH14734  
 67B9-67B9 ID:41G7  
 + eff enzyme \* DMUBCD1\_2 eff \* Ubiquitin conjugating enzyme(aa) \* similar to ubiquitin conjugating enzymes(aa) \* ubiquitin  
 CG7425 conjugating enzyme(aa) [UBIQUITIN\_CONJUGAT // UQ\_con // UBIQUIT] CG7425 GH14739 88D2-88D2 ID:41G8  
 + HmgZ DNA\_binding \* 2e-07 cerevisiae mitochondrial protein gene, complete gene produc \* 5e-42 HMGZ\_DROME HIGH  
 CG17921 MOBILITY GROUP PROTEIN Z (HMG-Z) high mob \* 2e-11 SSRP\_CAE [HMG // HMG\_box // NLS\_BP] CG17921 GH14749 57F8-  
 57F9 ID:41G9  
 + unknown \* 3e-06 LBM\_DROME LATE BLOOMER PROTEIN late bloomer me \* 4e-08 lbm \* \* [transmembrane4 // TMFOUR  
 CG12840 // TM4\_2] CG12840 GH14950 42E2-42E2 ID:41H10  
 + enzyme \* Yjr105wp(aa) \* Similarity to Human adenosine kinase cDNA EST comes from this gene; cDNA EST comes from  
 CG11255 this gene; cDNA EST comes from this gene; cD [PFKB\_KINASES\_2 // ADENOKINASE // pfkB] CG11255 GH14845 69F2-69F2  
 ID:41H4  
 + Cyp6g1 cytochrome\_P450 \* CYP6-like microsomal cytochrome P450 \* 1e-33 YRV5\_CAEEL PUTATIVE CYTOCHROME P450  
 CG8453 T10B9.5 IN CHROMOSOME II \* 1e-59 cytochrome P450 3A11 - mouse c[EP450II // p450 // P450 // MITP450 // C] 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 \*  
 CG9008 3e-35 putative protein \* AAPC\_PENCL POSSIBLE APOSPORY-ASSOCIATED PR CG9008 GH14910 34D1-34D1 ID:41H8  
 + metabolism \* similar to glutamate synthase; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST  
 CG9674 comes from this gene; cDNA EST comes from thi [ADXRDTASE // FADPNR // PNDRDTASEII] CG9674 GH14941 73C-73C2  
 dup:4/5 ID:41H9  
 + \* ribosomal protein L24(aa) \* Ribosomal protein L24B (rp29) (YL21) (L30B); Rpl24bp(aa) \* 60S RIBOSOMAL PROTEIN L24  
 CG9282 (L30)(aa) \* Similar to 60S ribosoma [Ribosomal\_L24e // NLS\_BP] CG9282 34B6-34B6 dup:1/5 ID:42A12

CG8136 + unknown \* CG8136 GH14973 85B2-85B2 dup:1/2 ID:42A2

CG11999 + 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

+ 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 + EG:63B12.8 unknown \* 1e-50 PEP8\_YEAST VACUOLAR PROTEIN SORTING/TARGETING PROTEIN PEP8 \* /match=(desc;; /ma \* 1e-111 YLNO\_CAEEL HYPOTHETICAL 37.4 KD PROTEIN T20D3.7 IN CH [NLS\_BP] CG14804 GH15034 2B13-2B13 ID:42A6

CG14804 + 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 + unknown \* [NLS\_BP] CG2149 GH15120 44B9-44B9 dup:1/2 ID:42B2

CG2149 + unknown \* 2e-81 YN28\_YEAST HYPOTHETICAL 41.2 KD PROTEIN IN PLC1-SEC21 INTERGENIC REGION \* 4e-94 C26E6.3 gene product \* 1e-124 protein involved in sexual devel CG14213 GH15157 18D10-18D10 ID:42B4

CG14213 + cell\_cycle\_regulator \* 6e-16 YG13\_YEAST CULLIN B hypothetical protein YGR003w - yeas \* 2e-71 LI19\_DROME LIN-19 HOMOLOG PROTEIN lin19 protein \* 1e-173 CUL5\_CAEEL CUL-5 P[CULLIN\_2 // NLS\_BP // ANTIFREEZEI // Cu] CG1401 GH15159 98F10-98F10 ID:42B5

CG1401 + enzyme \* coded for by C. elegans cDNA yk16b2.3; coded for by C. elegans cDNA yk16b2.5; Similar to amidase.(aa) \* PUTATIVE AMIDASE AMIA2(aa) \* 3364, putative [CRYSTALLIN\_BETAGAMMA // Amidase] CG7910 GH15201 84E10-84E10 ID:42B9

CG7910 + unknown \* CG18522 GH15266 88F-88F8 dup:1/2 ID:42C1

CG18522 + transcription\_factor \* HYPOTHETICAL 46.7 KD PROTEIN C50C3.8 IN CHROMOSOME III(aa) \* hypothetical protein(aa) \* intracisternal A particle-promoted polypeptide(aa) \* 2e-08 [BTB] CG11275 GH15267 58C5-58C5 ID:42C2

CG11275 + unknown \* [EF\_HAND // NLS\_BP] CG2127 GH15271 44B9-44B9 ID:42C3

CG2127 + scf ligand\_binding\_or\_carrier \* scf \* 1e-110 supercoiling factor \* 1e-72 coded for by C. elegans cDNA yk67a3.5; coded for by C. elegans cDNA yk90a3.5; co \* 7e-90 calumenin [EF\_HAND // EF\_HAND\_2] CG9148 GH15277 62B4-62B4 ID:42C4

CG9148 + signal\_transduction \* predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST comes from this gene; cDNA EST comes from thi [ArfGap // ZF\_GCS // REVINTRACTNG] CG8243 GH15285 44F9-44F9 ID:42C5

CG8243 + ligand\_binding\_or\_carrier \* DMC30B8 \* ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TTP)(aa) \* alpha tocopherol transfer protein(aa) \* 62D9.a(aa) [CRETINALDHBP // CRAL\_TRIO] CG2663 GH15295 83A6-83A6 ID:42C7

CG2663 + signal\_transduction \* serine/threonine kinase with Dbp- 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 + Mst85C unknown \* CG11993 LD21554 85C6-85C6 ID:43A6

CG11993



+ transcription\_factor\_binding \* 6e-06 DIP2\_YEAST DOM34 INTERACTING PROTEIN DIP2 protein - y \* 2e-06 similar to beta transducin proteins containing TRP-ASP domains el \* 6e-11 ap[WD40\_REGION // WD\_REPEATS // WD40] CG14722 LD21659 86F6-86F6 ID:43A8  
 CG14722  
 + motor\_protein \* 1e-34 3-hydroxyisobutyrate dehydrogenase \* 1e-10 inserted at base Both 5' and 3' ends of P element  
 CG4747 Inverse PCR \* YKWC\_BACSU HYPOTHETICAL 30.7 KD PR CG4747 LD22344 30F5-30F5 ID:43B10  
 CG3510 + CycB cell\_cycle\_regulator G2/MITOTIC-SPECIFIC CYCLIN B CYCLINS, cyclin CG3510 dup:2/4 ID:43B3  
 + DNA\_binding \* SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1(aa) \* BAF57(aa) \* 1e-08 HMG1-related DNA-binding [HMG // HMG\_box // PRO\_RICH] CG7055 LD22182 8C17-8D1 ID:43B5  
 CG7055  
 CG17252 + BCL7-like CG17252 LD22180 dup:2/2 ID:43B6  
 CG8954 + unknown \* [NLS\_BP] CG8954 LD22235 34D6-34D6 dup:2/2 ID:43B8  
 + BcDNA:LD21293 enzyme \* unknown(aa) \* 1e-27 unknown \* [ATP\_GTP\_A2 // ATP\_GTP\_A] CG7139 LD22250 79C2-79C3 ID:43B9  
 CG7139  
 + not endopeptidase \* PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN[UCH\_2\_1 // UCH\_2\_3 // UCH-1 // NLS\_BP /] CG4166 LD22730 75D1-75D1 dup:1/2 ID:43C10  
 CG4166  
 + noi RNA\_binding \* noi \* noisette(aa) \* 1e-30 PR09\_YEAST PRE-MRNA SPLICING FACTOR PRP9 PRP9 protein - ye \* noisette [ZF\_MATRIN] CG2925 LD22754 83B4-83B4 ID:43C11  
 CG2925  
 + Mcm2 DNA\_replication\_factor \* BLASTX 4.1E-84 Homo sapiens mRNA for DNA replication licensing factor (huMCM2), complete cds.(dna) \* BLASTX 4.1E-84 Homo sapiens mRNA for DNA replic [MCM // MCM\_1 // MCM\_2] CG7538 LD22409 84F-84F dup:1/2 ID:43C3  
 CG7538  
 + enzyme \* 1e-34 GLO2\_YEAST HYDROXYACYLGLUTATHIONE HYDROLASE ISOZYME (GLYOXALASE II) (GLX II) \* 8e-60 similar to Metallo-beta-lactamase superfamily el \* 3e-85 [lactamase\_B] CG4365 77E-77E dup:1/3 ID:43C6  
 CG4365  
 CG7752 + transcription\_factor CG7752 ID:43C7  
 + signal\_transduction \* DM60AP \* 1e-11 60A\_DROME 60A PROTEIN PRECURSOR TGF-beta-related protein \* 2e-09 protein homolog \* 1e-14 BMP2\_MOUSE BONE MORPHOGENETIC PROTEIN PRECUR [TGF-beta // TGF\_BETA // TGF\_BETA\_2]  
 CG1901 CG1901 102D1-102D1 dup:2/2 ID:43C8  
 + Mpcp transporter \* 2e-71 YEO3\_YEAST PUTATIVE MITOCHONDRIAL CARRIER YER053C hypoth \* phosphate transporter precursor melanogas \* 1e-132 MPCP\_CAEEL MITOCHONDRIAL PHOSPHA [mito\_carr // RCC1\_2 // MITOCH\_CARRIER] CG4994 LD23031 70E-70E dup:3/4 ID:43D12  
 CG4994  
 + unknown \* myelodysplasia/myeloid leukemia factor 1(aa) \* Y17G7B.17(aa) \* 6e-27 myeloid leukemia factor myelodysplasia/myel \* t(3;5)(q25.1;p34) fusion gene CG8295 LD22883 52D11-52D11 dup:2/2 ID:43D3  
 CG8295  
 + transcription\_factor \* 6e-09 predicted using Genefinder; cDNA EST comes from this g \* 4e-05 hepatoma-derived growth factor \* 2e-20 BS69 protein - human binds directly to a [PWWP // NLS\_BP] CG8569 LD22977 49A10-49A10 dup:2/2 ID:43D7  
 CG8569  
 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

CG3004 + signal\_transduction G-protein beta-subunit 6 GPROTEINBRPT, RCC1\_2, WD40, WD40\_REGION,] CG3004 LD23129  
dup:3/3 ID:43E6

CG7611 + 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

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

CG6538 + TfiIFbeta transcription\_factor \* TfiIF bgr; \* TRANSCRIPTION INITIATION FACTOR IIF, BETA SUBUNIT (TFIIF-BETA)(aa) \* 6e-  
05 T2FB\_YEAST TRANSCRIPTION INITIATION FACTOR IIF, BETA SUBUNIT CG6538 LD23340 86C4-86C4 dup:1/2 ID:43F2

CG7614 + Mat1 transcription\_factor CDK7/cyclin H assembly factor NLS\_BP, ZF\_RING, ZINC\_FINGER\_C3HC4, zf-C] CG7614 LD23429  
ID:43F4

CG17903 + Cyt-c2 electron\_transfer \* DMCYCDC4\_4 Cyt-c2 \* 9e-36 pdb|2YCC| Cytochrome c (Isozyme 1) (Oxidized) (Mutant With Cys  
Replaced By Thr) (C102T \* 1e-59 CYC2\_DROME CYTOCHROME C-2 c [CYTCHRMEDIA // cytochrome\_c] CG17903 LD23501  
36A7-36A7 ID:43F5

CG7581 + 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 LD23540 99B-99B ID:43F6

CG6254 + transcription\_factor \* zinc-finger protein - African clawed frog(aa) \* 1e-15 YJF6\_YEAST HYPOTHETICAL 98.9 KD ZINC  
FINGER PROTEIN IN BTN1-PEP8 INTERGENIC REG \* 6[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG6254 LD23879 85F13-  
85F13 dup:1/2 ID:43F9

CG5231 + cell\_cycle\_regulator \* lipoic acid synthase; Lip5p(aa) \* LIPOIC ACID SYNTHETASE PRECURSOR(LIP-SYN)(aa) \* similar to  
lipoic acid synthase; cDNA EST yk283b6.3 comes from th CG5231 LD24887 77C1-77C1 ID:43G10

CG8153 + mus210 DNA\_repair\_protein \* DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS HOMOLOG (XERODERMA  
PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN HOMOLOG) (XPCDM)(aa) \* DMXPCCF\_2 Xpcc \* 4e- [MYB\_1 //  
NLS\_BP] CG8153 51F4-51F5 dup:1/3 ID:43G11

CG7846 + 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

CG4258 + dbe unknown \* DMDRIBBLE dbe \* 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

CG4735 + chaperone \* FK506-binding protein 6(aa) \* FK506-binding protein - Arabidopsis thaliana(aa) \* FKBP (FK506 binding protein)  
13; peptidylprolyl cis-trans isomerase [FKBP // FKBP\_PPIASE\_3 // TPR\_REPEAT] CG4735 LD24746 60A4-60A4 ID:43G6

CG4029 + Dom transcription\_factor \* DOMINA protein (WHN-homologue)(aa) \* 1e-12 FKH2\_YEAST FORK HEAD PROTEIN HOMOLOG  
FKH2 protein - y \* 4e-16 SLP1\_DROME FORK HEAD DOMAIN TRANSCRIPTION F [Fork\_head // FORKHEAD] CG4029 LD24749  
86A2-86A3 ID:43G7

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

CG7600 + NLS\_BP, PLANT\_GLOBIN CG7600 LD25031 dup:1/2 ID:43H1

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

+ Srp54k ligand\_binding\_or\_carrier \* 1e-119 SR54\_YEAST SIGNAL RECOGNITION PARTICLE KD PROTEIN HOMOLOG (SRP54) \* similar to signal recognition particle protein (SRP54); cDNA EST E \* SR5 [SRP54 // ATP\_GTP\_A] CG4659 LD25385 64C12-64C12 dup:1/3 ID:43H11  
 CG4659  
 + enzyme possible protein methyltransferase N12N6MTFRASE, N6\_MTASE, SAM\_BIND CG9666 LD25448 dup:1/3 ID:43H12  
 CG9666  
 + protein\_phosphatase \* DPP2C1(aa) \* protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform(aa) \* 3e-44 P2C2\_YEAST PROTEIN PHOSPHATASE 2C HOMOLOG (PP2C-2) [PP2C\_1 // PP2C // PP2C\_2] CG1906 LD25115 99B6-99B6 ID:43H5  
 CG1906  
 CG9967 LD25280 dup:1/2 ID:43H7  
 + ATPsyn-beta \* DMATPSYNB ATPsyn- bgr; \* 1e-173 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor - yeast (Sacch \* ATPB\_DROME ATP SYNTHASE BETA CHAIN [ATP-synt\_ab // ATP-synt\_ab\_C // ATPASE\_] CG11154 102F6-102F6 dup:3/4 ID:43H8  
 CG11154  
 + \* ORF; Method: conceptual translation supplied by author.(aa) \* similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST comes from [rrm] CG14641 82A-82A dup:2/4 ID:44A11  
 CG14641  
 + transcription\_factor homology to uncharacterized human zinc finger proteins ZINC\_FINGER\_C2H2, ZINC\_FINGER\_C2H2\_2, zf] CG8301 LD25464 dup:1/4 ID:44A2  
 CG8301  
 + motor\_protein \* 1e-155 inserted at base 5' end of P element Inverse PCR \* \* [bZIP] CG3183 LD25484 42B3-42B3 dup:1/2 ID:44A3  
 CG3183  
 + 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  
 + unknown \* 4e-21 YS48\_CAEEL HYPOTHETICAL 66.5 KD PROTEIN ZK177.8 IN CHROMOSOME II (U \* 2e-20 MG11\_MOUSE INTERFERON-GAMMA INDUCIBLE PROTEIN MG11 unkn \* 4e-20 hy CG9670 LD25913 76A5-76A6 dup:3/3 ID:44B11  
 CG9670  
 + huckebein transcription\_factor specific RNA polymerase II transcription factor ZINC\_FINGER\_C2H2, ZINC\_FINGER\_C2H2\_2, zf] CG9768 LD25709 dup:2/3 ID:44B3  
 CG9768  
 + unknown \* Putative homolog of subunit of bovine prefoldin, a chaperone comprised of six subunits; Gim5p(aa) \* c-myc binding protein MM-1(aa) \* 4e-21 YMJ4\_YEAS CG7048 LD25740 94B4-94B4 ID:44B4  
 CG7048  
 + Similar sequences have been identified in Caenorhabditis elegans , Homo sapiens and Schizosaccharomyces pombe CG5383 LD25827 dup:2/2 ID:44B7  
 CG5383  
 + endopeptidase serine proteinase [Anopheles gambiae] CHYMOTRYPSIN, TRYPSIN\_CATAL, TRYPSIN\_HIS] CG11836 LD25830 dup:2/2 ID:44B8  
 CG11836  
 + peroxidase MITOCHONDRIAL THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE AhpC-TSA CG5826 LD25877 dup:2/3 ID:44B9  
 CG5826  
 + RNA\_binding \* son3 protein - human (fragment)(aa) \* SON DNA binding protein(aa) \* Pad-1(aa) \* similar to RNA binding proteins(aa) [RBD // rrm // NLS\_BP] CG16788 LD26185 85D25-85D25 ID:44C10  
 CG16788  
 CG11329  
 + unknown \* 1e-16 inserted at base 5' end of P element Inverse PCR \* \* CG11329 LD26217 26F6-26F6 ID:44C11

+ chaperone \* SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like(aa) \* 2e-24 NPL1\_YEAST NPL1  
 PROTEIN (SEC63 PROTEIN) heat shock prote \* 6e-05 [DNAJ\_1 // DnaJ // DNAJPROTEIN // DNAJ\_2] CG8583 LD25939 65F4-  
 CG8583 65F4 ID:44C3  
 + PEK protein\_kinase \* 8e-30 protein kinase GCN2 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) \* 2e-24 eIF-2alpha kinase \*  
 2e-55 similar to serine/threonine kinase (2 do [Bacterial\_PQQ // PROTEIN\_KINASE\_ST // P] CG2087 LD25978 83A8-83A8  
 CG2087 ID:44C5  
 + unknown \* 9e-61 inserted at base Both 5' and 3' ends of P element Inverse PCR \* \* [SAM\_DOMAIN] CG8572 LD26045  
 CG8572 65F5-65F5 dup:2/2 ID:44C6  
 + BcDNA:LD26050 motor\_protein \* 1e-05 strong similarity to the SNF2/RAD54 family of helicases; partial CDS \* 1e-104 inserted at  
 CG12340 base Both 5' and 3' ends of P element Inverse PCR \* [fn3] CG12340 LD26128 47C-47C dup:2/4 ID:44C9  
 CG13322 + unknown CG13322 LD26432 dup:2/3 ID:44D11  
 + motor\_protein \* PLECTIN(aa) \* plectin 1, intermediate filament binding protein, 500kD(aa) \* 4e-07 integrin homolog - yeast  
 (Saccharomyces cerevisiae) \* 9e-05 myo[GRAM\_POS\_ANCHORING // PRO\_RICH // NLS\_B] CG11098 LD26265 26F3-26F3  
 CG11098 dup:4/9 ID:44D2  
 + aret RNA\_binding \* aret \* 8e-06 polyadenylate-binding protein \* 1e-148 testis-specific RNP-type RNA binding protein \* 2e-29  
 CG6319 elav-type ribonucleoprotein coded [RBD // HUDSXL RNA // rrm] CG6319 33D-33D4 dup:3/3 ID:44D5  
 + signal\_transduction \* Polyadenylation Factor I subunit; Pfs2p(aa) \* 3e-17 alpha-COP (Z466 \* 3e-18 lissencephaly-1 \* 3e-15  
 CG1109 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  
 + Sr-CII cell\_adhesion Scavenger receptor class C, type II MAM, MAM\_2, SOMATOMEDIN\_B, Somatomedin\_B] CG8856  
 CG8856 LD26673 dup:3/3 ID:44E10  
 + cdc2 protein\_kinase \* CDK5 kinase(aa) \* DMCDC2\_2 cdc2 \* 1e-101 CC28\_YEAST CELL DIVISION CONTROL PROTEIN  
 protein kinase \* 1e-174 CC2\_DROME CELL DIVISION CONTROL PROT[PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM]  
 CG5363 CG5363 LD26702 31D11-31D11 dup:3/3 ID:44E11  
 CG11504 + CG11504 LD26477 dup:3/3 ID:44E2  
 CG2994 + CG2994 LD26546 dup:4/4 ID:44E6  
 + 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  
 CG6860 ID:44E7  
 CG16928 + CG16928 dup:3/3 ID:44E9  
 + endopeptidase \* Saccharolysin (oligopeptidase yscD); Prd1p(aa) \* NEUROLYSIN PRECURSOR (NEUROTENSIN  
 ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOP [Peptidase\_M3] CG11771 LD26931  
 CG11771 98F1-98F1 dup:4/5 ID:44F10  
 CG4785 + CG4785 LD26982 dup:2/2 ID:44F11  
 + protein\_phosphatase \* 4e-56 P2C2\_YEAST PROTEIN PHOSPHATASE 2C HOMOLOG (PP2C-2) hyp \* 9e-20 unknown \*  
 CG17746 1e-108 P2C2\_CAEEL PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (PP2C) \* 4 [PP2C // PP2C\_1 // PP2C\_2] CG17746

64A3-64A3 dup:4/4 ID:44F12

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

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

CG5222 + unknown unknown protein CIT987SK\_2A8\_1 [Homo sapiens] CG5222 LD26912 dup:1/2 ID:44F9  
+ signal\_transduction homology to actin interacting protein 1 and WD repeat-containing protein 1 GPROTEINBRPT, WD40,  
CG10724 WD40\_REGION CG10724 LD27045 dup:2/3 ID:44G2

CG4303 + Bap60 Brahma associated protein 60kD NLS\_BP, PRO\_RICH CG4303 LD27052 dup:1/2 ID:44G4  
+ Faf unknown \* Fly Fas-associated factor (FFAF)(aa) \* Faf \* 1e-12 probable membrane protein YDL091c - yeast  
CG10372 (Saccharomyces cerevisiae) \* 7e-10 similar to mouse FAF [UX\_DOMAIN] CG10372 LD27106 37A4-37A4 dup:1/2 ID:44G7  
+ transcription\_factor \* 9e-06 Z33A\_HUMAN ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (HA09 \* 8e-05  
zinc finger protein XFDL \* 3e-05 DMDROSOPH\_4 wdn \* zinc finger;[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG11906  
CG11906 LD27134 56C7-56C8 ID:44G9  
+ Klp67A motor\_protein kinesin family protein 3B ATP\_GTP\_A, KINESINHEAVY, KINESIN\_MOTOR\_D] CG10923 LD27326  
CG10923 dup:2/2 ID:44H12

CG6564 + unknown CG6564 LD27203 ID:44H2  
+ transcription\_factor \* 2e-10 CROL GAMMA \* 5e-16 predicted using Genefinder; similar to Zinc finger, C2H2 type (5 d \* 1e-11  
CG3847 zinc finger protein - mouse zinc finger protein [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG3847 LD27244 5E5-5E5 ID:44H4  
+ chaperone \* DMNINAA\_7 ninaA \* DMCYP1\_2 Cyp1 \* 5e-23 CYPC\_YEAST PEPTIDYL-PROLYL CIS-TRANS ISOMERASE  
C PRECURSOR (PPIASE) (ROTAMASE) ( \* 1e-20 CYPH\_DROME PEPTIDYL [pro\_isomerase // CSA\_PPIASE\_2 // WD40\_R]  
CG3511 CG3511 LD27277 60D5-60D5 dup:1/2 ID:44H8  
+ enb signal\_transduction \* map\_position:56B5 \* clot.396(dna)\* 1e-124 Abl substrate ena (enabled) - fruit fly (Drosophila  
melanogaster) \* 6e-39 neural variant mena+ protein [WH1 // PRO\_RICH // RANBP1\_WASP] CG15112 LD27343 56B5-56B5  
CG15112 dup:3/5 ID:45A1  
+ transcription\_factor similar to crol protein ZINC\_FINGER\_C2H2, ZINC\_FINGER\_C2H2\_2, z] CG2678 LD27553 dup:1/2  
CG2678 ID:45A10

CG18608 + unknown \* CG18608 LD27570 56A-56A dup:1/2 ID:45A11  
+ BcDNA:LD22910 endopeptidase \* reserved(aa) \* 1e-12 UBP9\_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE  
(UBIQUITIN THIOLESTERASE 9) ( \* 1e-08 UBPX\_CAEEL PROBABLE UBIQUITIN CARBOXYL[UCH\_2\_2 // UCH\_2\_3 //  
CG15817 PRO\_RICH // UCH-2] CG15817 99A5-99A5 dup:2/2 ID:45A6  
+ unknown \* Ygr090wp(aa) \* hypothetical protein(aa) \* 4e-17 YG2L\_YEAST HYPOTHETICAL 140.5 KD PROTEIN IN CTT1-  
CG12785 PRP31 INTERGENIC REGION CG12785 LD27528 89B17-89B17 dup:2/2 ID:45A9  
+ Ac3 enzyme adenyl cyclase isoform DAC3 [Drosophila melanogaster] GUANYLATE\_CYCLASES,  
CG1506 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-  
CG9446 76 CORO\_YEAST CORONIN-LIKE PROTEIN hypothe [WD40\_REGION // ARGINASE\_2 // WD\_REPEATS] CG9446 42C8-42C8

dup:3/3 ID:45B2

CG8632 + embryonic lung protein [Homo sapiens] CG8632 LD27783 dup:1/2 ID:45B7  
+ unknown \* Ser/Arg-related nuclear matrix protein (plenty of prolines 101-like)(aa) \* 7e-33 cDNA EST comes from this gene;  
CG11274 cDNA EST co \* 2e-43 plenty-of-prolin [RIBOSOMAL\_S12 // NLS\_BP] CG11274 LD28048 69F2-69F2 dup:1/2 ID:45C10  
CG11970 + BcDNA:LD23876 similar to nuclear factor related to kappa B binding protein CG11970 LD28082 dup:2/4 ID:45C12  
+ RNA\_binding \* similar to RNA recognition motif. (aka RRM, RBD, or RNP domain) (2 domains); cDNA EST yk211a9.5 comes  
CG4806 from this gene; cDNA EST yk266e11.5 comes from [RNP\_1 // RBD // rrm // NLS\_BP] CG4806 LD27920 60D10-60D10 ID:45C2  
CG5126 + unknown \* CG5126 LD27921 21F1-21F1 dup:1/2 ID:45C3  
+ lio protein\_kinase \* LIO\_DROME LINOTTE PROTEIN linotte protein mela \* lio \* \* [NLS\_BP] CG10739 LD27947 37C-37C  
CG10739 dup:2/2 ID:45C4  
CG9506 + protein\_phosphatase \* CG9506 LD27991 28D1-28D1 dup:1/2 ID:45C6  
CG7825 + Rad17 DNA\_repair\_protein DNA repair protein ATP\_GTP\_A, ATP\_GTP\_A2, RFC CG7825 LD27993 ID:45C7  
CG10018 + DNA\_repair\_protein homology to mouse and human SNM1 protein NLS\_BP CG10018 LD28027 dup:1/2 ID:45C8  
CG4609 + fax failed axon connections protein CG4609 LD28084 dup:2/2 ID:45D1  
+ unknown \* 1e-106 probable membrane protein YPL217c - yeast (Saccharomyces cerevisiae) \* 2e-11 No definition line found  
CG7728 \* 1E-152\* 1e-100 conserved hypothetical [NLS\_BP // ATP\_GTP\_A] CG7728 LD28182 73E3-73E4 dup:3/3 ID:45D11  
CG5003 + unknown \* [FBOX\_DOMAIN] CG5003 LD28210 98B2-98B2 ID:45D12  
CG6994 + cytoskeletal\_structural\_protein CG6994 LD28101 dup:2/2 ID:45D5  
+ 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 CG14650 LD28109 82C1-82C1 dup:3/3 ID:45D6  
CG9213 + enzyme CG9213 LD28117 dup:2/2 ID:45D7  
+ unknown \* 5e-24 hypothetical protein YDL087c - yeast (Saccharomyces cerevisiae) \* 4e-34 YP68\_CAEEL HYPOTHETICAL  
CG7564 37.0 KD PROTEIN IN CHROMOSOME II (U2 \* 2e-23 p [NLS\_BP] CG7564 LD28402 74D1-74D1 dup:4/4 ID:45E12  
+ enzyme \* nudix (nucleoside diphosphate linked moiety X)-type motif 3(aa) \* 7e-40 diphosphoinositol polyphosphate  
CG6391 phosphohydrolase (A \* [MUTT // mutT] CG6391 LD28241 67F4-67F4 dup:3/4 ID:45E3  
+ Weak homology to SNF2 family (CHD1 subfamily) chromodomain protein [Arabidopsis thaliana] CHROMO\_2 CG9933  
CG9933 LD28372 dup:5/5 ID:45E9  
CG14749 + CG14749 dup:3/3 ID:45F10  
+ Gdh enzyme \* 7e-28 glutamate dehydrogenase dehyd \* glutamate dehydrogenase (NAD(P)+) \* 1e-180 Similarity to Drosophila  
Glutamate dehydrogenase cDNA \* DHE3\_MOUSE [GLFV\_DEHYDROGENASE // GLFDHDRGNASE // G] CG5320 95C-95C13  
CG5320 dup:2/2 ID:45F11  
+ 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  
CG8783 + unknown Conserved gene telomeric to alpha globin cluster [Homo sapiens] CG8783 LD28428 dup:2/3 ID:45F2

+ EG:66A1.2 transcription\_factor\_binding \* map\_position:4C6 \* map\_position:4C6 \* map\_position:4C6 \* by match; 1-mat  
 CG12179 LD28429 4C6-4C7 ID:45F3  
 CG14657 + unknown CG14657 LD28447 ID:45F4  
 CG4300 + unknown spermine synthase SAM\_BIND CG4300 LD28457 ID:45F5  
 + 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  
 dup:3/4 ID:45F9  
 CG2947  
 CG12000 + CG12000 ID:45G11  
 + ribosomal\_protein \* 1e-48 RL7A\_YEAST 60S RIBOSOMAL PROTEIN YL17-A ribosomal protein \* 4e-66 ribosomal protein  
 L17 60S RIBOSOM \* 1e-65 RL17\_RAT 60S RIBOSOMAL PROTEIN L17 [Ribosomal\_L22 // RIBOSOMAL\_L22] CG3203 6C10-  
 CG3203 6C10 dup:1/5 ID:45G12  
 + unknown \* Cys-rich protein(aa) \* FIM protein(aa) \* zinc finger protein 261(aa) \* BLASTX 3.6E-13 Dictyostelium discoideum  
 CG5965 sp96 gene for spore coat protein SP9 CG5965 97F4-97F4 dup:2/3 ID:45G2  
 + sgg protein\_kinase \* DMSGG46\_2 sgg \* 5e-98 MDS1\_YEAST SERINE/THREONINE-PROTEIN KINASE MDS1/RIM11 pr \*  
 zeste-white 3-A - fruit fly (Drosophila melanogaster) \* 1e-141 pred [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG2621  
 CG2621 3B2-3B3 dup:1/2 ID:45G9  
 + unknown \* phosphatidylinositol glycan, class B(aa) \* 2e-29 YGO2\_YEAST HYPOTHETICAL 72.6 KD PROTEIN IN MRF1-  
 CG12006 SEC27 INTERGENIC REGION \* 5e-08 coded for by C. ele CG12006 64C4-64C4 dup:2/2 ID:45H10  
 CG11207 + unknown CG11207 dup:2/2 ID:45H2  
 CG2890 + CG2890 dup:2/3 ID:45H3  
 CG10640 + CG10640 dup:4/4 ID:45H8  
 + smg \* cloned by ability to arrest the cell cycle when expressed in the fission yeast Schizosaccharomyces pombe(aa) \* 1e-124  
 CG5263 cloned by ability to arrest th CG5263 66F1-66F1 dup:1/5 ID:46A10  
 CG8309 + CG8309 dup:2/3 ID:46A12  
 CG16944 + sesB transporter ADP/ATP translocase ADPTRNSLCASE, MITOCARRIER CG16944 ID:46A4  
 + ncd motor\_protein \* DMCLARET\_4 ncd \* 3e-75 KAR3\_YEAST KINESIN-LIKE PROTEIN KAR3 (NUCLEAR FUSION  
 PROTEIN) \* NCD\_DROME CLARET SEGREGATIONAL PROTEIN \* 4e-61 YNZ2\_CAEEL PU [kinesin //  
 CG7831 KINESIN\_MOTOR\_DOMAIN1 // KIN] CG7831 99C5-99C5 ID:46A9  
 + protein\_kinase \* DMTKABL3\_2 Abl \* TAK1 (TGF-beta-activated kinase)(aa) \* TGF-beta activated kinase 1b(aa) \* TGF-beta  
 CG1388 activated kinase 1c(aa) [PROTEIN\_KINASE\_ST // EGF\_1 // TYRKINASE] CG1388 19E1-19E1 dup:1/4 ID:46B1  
 + 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  
 CG6605 + motor\_protein CG6605 ID:46B12  
 CG6343 + ND42 enzyme \* NADH-ubiquinone oxidoreductase kDa subunit(aa) \* DMNUBO42K ND42 \* NADH-UBIQUINONE

OXIDOREDUCTASE KD SUBUNIT PRECURSOR (COMPLEX I-42KD) (CI-42KD)(aa [ATP\_GTP\_A] CG6343 93F14-94A1 ID:46B3

CG9805 + translation\_factor eukaryotic translation initiation factor 3 subunit NLS\_BP, PCI\_DOMAIN CG9805 ID:46B4

CG7414 + CG7414 79A4-79A4 dup:2/2 ID:46B6

CG10990 + unknown \* MA3(aa) \* 3e-70 apoptosis protein MA-3 - mouse apoptosis-i \* 1e-69 nuclear protein H731 - human nuclear antigen H731 \* nuclear antigen H731-like pr [RCC1\_2 // NLS\_BP] CG10990 12B8-12B8 ID:46B7

CG4916 + RNA\_binding CG4916 dup:2/2 ID:46C4

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

CG9057 + unknown \* 1e-07 ADPR\_MOUSE ADIPOSE DIFFERENTIATION-RELATED PROTEIN (ADPR) \* \* [ATP\_GTP\_A] 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

CG1101 + CG1101 dup:4/5 ID:46D7

CG10928 + CG10928 LD29844 dup:3/3 ID:46E11

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

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

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

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

CG14459 + none none CG14459 LD29969 ID:46F11

CG8730 + drosha RNA binding ribonuclease III DSRBD, PRO\_RICH, RIBONUCLEASE\_III, RNASE] CG8730 LD29995 dup:2/3 ID:46F12

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

CG10082 + unknown \* PiUS(aa) \* 6e-18 KCS1 protein - yeast (Saccharomyces cerevisiae) (Z49 \* 7e-27 cDNA EST comes from this gene \* 2e-43 Similar to S.cerevisiae protein CG10082 LD29913 57F6-57F6 dup:2/2 ID:46F6

CG1225 + RhoGEF3 signal\_transduction RHO guanyl-nucleotide exchange factor ATP\_GTP\_A, GRF\_DBL, RhoGEF, SH3 CG1225 LD29915 dup:1/2 ID:46F8

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

CG6224 + dbo actin\_binding CG6224 LD29988 dup:1/3 ID:46G1

CG7288 + endopeptidase \* hypothetical protein unip - mouse(aa) \* Sad1p(aa) \* putative protein(aa) \* Contains similarity to Pfam domain: (UCH-1), Score=13.8, E-value=0.14, N= [UCH\_2\_3 // UCH-2] CG7288 LD30129 17E4-17E4 dup:1/3 ID:46G10

CG10065 + enzyme \* 1e-29 GTT1\_DROME GLUTATHIONE S-TRANSFERASE 1-1 (CLASS-THETA) glu \* 6e-12 GTT1\_MOUSE GLUTATHIONE S-TRANSFERASE THETA (CLASS-THETA) \* 3e-11 glutathion [GST] CG10065 LD30165 84C-84C dup:1/3



ID:46G12  
+ Dp1 DNA\_binding \* 2e-44 SCP160 \* 4e-09 KH-domain putative RNA binding protein \* 951003: Homology with human lipoprotein-binding protein (PIR Acc. \* high density lipop [KH-domain // KH\_DOMAIN // NLS\_BP] CG5170 LD29992 55C10-55C11 dup:1/5 ID:46G2

CG5170  
CG3309 + unknown \* 3e-62 No definition line found \* No definition line found \* CG3309 LD30005 4F2-4F2 dup:1/2 ID:46G3

CG17681 + unknown \* CG17681 LD30009 36E-36E ID:46G4  
+ transmembrane\_receptor \* nucleoporin Nup84(aa) \* 6e-46 nucleoporin 88kD 88kDa nuclear \* 3e-47 nucleoporin Nup84 \*

CG6819 CG6819 LD30108 87C7-87C7 ID:46G7  
+ transcription\_factor\_binding \* 4e-71 YER2\_YEAST HYPOTHETICAL 62.3 KD PROTEIN IN PTP3-ILV1 INTERGENIC REGION \* 9e-94 Similarity to Yeast hypothetical protein YER2 (SW:YER2\_YEAS[WD40\_REGION // WD\_REPEATS // WD40]

CG2260 CG2260 LD30339 7D11-7D11 ID:46H10  
+ Transcription factor IIA L transcription\_factor general RNA polymerase II transcription factor, PHOSPHOPANTETHEINE CG5930

CG5930 LD30231 dup:2/2 ID:46H2

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

CG1647 + glass transcription\_factor photoreceptor determination ZINC\_FINGER\_C2H2 CG1647 LD30287 dup:2/2 ID:46H5

CG14005 + unknown \* CG14005 LD30293 26A2-26A2 dup:2/3 ID:46H6  
+ motor\_protein \* 4e-28 KIP1\_YEAST KINESIN-LIKE PROTEIN KIP1 kinesin-related prot \* 6e-33 PAV-KLP protein \* 4e-33 Similar to kinesin-like protein; coded for by C. ele [kinesin // KINESIN\_MOTOR\_DOMAIN2 // KIN] CG12298 LD30305 54E7-54E7

CG12298 ID:46H7  
+ chaperone It encodes a chaperone involved in proteolysis and peptidolysis which is a component of the mitochondrion

CG4164 DNAJPROTEIN, DNAJ\_1, DNAJ\_2, DnaJ CG4164 LD30318 ID:46H8

CG1677 + CG1677 LD30482 ID:47A10

CG2682 + transcription\_factor CG2682 ID:47A11

CG12306 + protein\_kinase CG12306 ID:47A2

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

CG17947 + snRNP70KRNA\_binding \* U1 SMALL NUCLEAR RIBONUCLEOPROTEIN KD (U1 SNRNP KD) (SNRNP70)(aa) \* DMRNP70K\_6 snRNP27D \* ribonucleoprotein antigen(aa) \* small nuclear ribonucleopr [RNP\_1 // RBD // rrm // NLS\_BP] CG8749 LD30455 27C7-27C7 dup:1/2 ID:47A8

CG8749 + transcription\_factor \* b34l8.1 (Kruppel related Zinc Finger protein 184)(aa) \* 2e-15 AZF1\_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin \* 8e-24 SUHW\_DROME SUPPRESSO[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG9797

CG9797 LD30467 85B2-85B2 ID:47A9  
+ 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

CG12202 LD30511 18C8-18D1 dup:3/6 ID:47B1

+ transcription\_factor \* general transcription factor IIH, polypeptide (52kD subunit)(aa) \* TFIIH subunit Tfb2; has homology to  
 CG7764 CAK and human IIH subunits; Tfb2p(aa) \* 9e-71 CG7764 LD30622 71D3-71D4 ID:47B11  
 CG9231 + \* 2e-14 pIL2 hypothetical protein - rat (fragment) growth and trans \* \* CG9231 76B9-76B9 dup:2/2 ID:47B12  
 CG6502 + E(z) transcription\_factor \* enhancer of zeste (Drosophila) homolog 2(aa) \* enhancer of zeste homolog (Drosophila)(aa) \*  
 DM180\_2 E(z) \* ENHANCER OF ZESTE PROTEIN(aa) [SET\_DOMAIN // SET // NLS\_BP] CG6502 LD30505 67E4-67E4 ID:47B2  
 + transcription\_factor \* similar to PHD-finger. (2 domains), SET domain; cDNA EST yk453a7.5 comes from this gene; cDNA  
 CG5591 EST yk453a7.3 comes from this gene; cDNA EST yk273c7.3 [PHD] CG5591 LD30514 60A9-60A9 dup:2/2 ID:47B3  
 CG3508 + unknown \* HMBA-inducible(aa) \* 3e-11 HIS1 protein \* [NLS\_BP] CG3508 LD30520 88C11-88C11 ID:47B4  
 + chaperone \* 1e-09 SCJ1\_YEAST SCJ1 PROTEIN SCJ1 protein - yeast (Saccharomyce \* 4e-11 csp29 cysteine string protein  
 CG7133 \* 6e-12 similar to DnaJ, prokaryotic heat sho [DnaJ // DNAJPROTEIN // DNAJ\_2] CG7133 LD30543 79C3-79C3 ID:47B6  
 + fzy cell\_cycle\_regulator \* fzy \* 2e-76 YGA3\_YEAST HYPOTHETICAL 62.8 KD TRP-ASP REPEATS CONTAINING PROTEIN  
 IN PMC1-TFG2 \* Method: conceptual translation supplied by au[WD40\_REGION // FIZZY\_DOMAIN // WD\_REPEA] CG4274  
 CG4274 LD30572 35F8-35F8 dup:1/2 ID:47B7  
 CG18683 + unknown \* CG18683 LD30576 99C6-99C6 ID:47B8  
 + SNF4Agamma protein\_kinase \* SNF4A ggr; \* protein kinase protein serine/threonine kinase ) map\_position:93C \* 8e-29  
 SNF4\_YEAST NUCLEAR PROTEIN SNF4 (REGULATORY PROTEIN CAT3) \* 1 [CBS // SNF4\_REP // NLS\_BP] CG17299  
 CG17299 LD30628 93C4-95F5 dup:1/11 ID:47C1  
 + chaperone \* transport complex protein (90 kDa)(aa) \* 6e-59 putative S transport complex 90kD subunit brain-specific isoform  
 CG6549 \* CG6549 LD30785 36C3-36C4 ID:47C10  
 + transporter \* 8e-72 contains similarity to xanthine/uracil permeases family elegans \* 1e-136 yolk sac permease-like molecule \*  
 CG6293 1e-136 sodium-dependent vitamin C tr [xan\_ur\_permease // XANTH\_URACIL\_PERMASE] CG6293 LD30822 86A2-86A2 ID:47C11  
 + FK506-bp1 ligand\_binding\_or\_carrier \* DMFKBP39\_2 FK506-bp1 \* KD FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-  
 PROLYL CIS-TRANS ISOMERASE) (PPIASE)(aa) \* 7e-24 hypothetical protein YLR4[FKBP // FKBP\_PPIASE\_2 //  
 CG6226 FKBP\_PPIASE\_3] CG6226 LD30817 90E1-90E1 ID:47C12  
 CG6962 + CG6962 ID:47C2  
 + unknown \* predicted using Genefinder; cDNA EST comes from this gene; cDNA EST yk278a11.3 comes from this gene;  
 CG4968 cDNA EST yk278a11.5 comes from this gene; cDNA CG4968 LD30683 31D6-31D6 ID:47C3  
 + msl-3 tumor\_suppressor \* MALE-SPECIFIC LETHAL-3 PROTEIN(aa) \* DMMSL3\_2 msl-3 \* 7e-08 hypothetical protein \*  
 CG8631 DMMSL3\_2 msl-3 CG8631 LD30726 65E5-65E5 dup:1/2 ID:47C5  
 + unknown \* 2e-34 hypothetical protein YPR131c - yeast (Saccharomyces cerevisiae) ( \* 8e-20 contains similarity to N-terminal  
 CG14222 acetyltransferase complex subunit [Acetyltransf] CG14222 LD30731 18D9-18D9 dup:1/2 ID:47C6  
 + unknown \* 4e-09 predicted using Genefinder; similar to emp24/gp25L/p24 family; cDN \* 1e-08 putative T1/ST2 receptor  
 CG10733 binding protein precursor \* 2e-07 putative [EMP24\_GP25L] CG10733 LD30746 65A3-65A3 ID:47C7  
 CG11490 + unknown CG11490 dup:1/3 ID:47C9  
 + unknown \* xenotropic and polytropic murine leukemia virus receptor X3(aa) \* polytropic murine leukemia virus receptor  
 CG7536 SYG1(aa) \* predicted using Genefinder; CG7536 LD30826 16F7-16F7 ID:47D1

+ transcription\_factor \* with similarity to Homo sapiens TAFII55 encoded by Genbank Accession Number and C. elegans  
 CG2670 unknown protein encoded by Genbank Accession Number \* an CG2670 LD30980 84E1-84E1 ID:47D11  
 + transcription\_factor \* putative ring zinc finger protein NY-REN-43 antigen(aa) \* putative protein(aa) \* hypothetical protein,  
 CG11982 similar to PRAJA1 \* DMGOLTHA\_3 gol [zf-C3HC4 // ZF\_RING] CG11982 LD30985 85C4-85C4 dup:3/3 ID:47D12  
 + unknown \* 3e-05 No definition line found \* 1e-32 topoisomerase I-binding RS protein \* 8e-11 ring finger protein \* tumor  
 CG15104 protein p53-binding protein p53 bindin [zf-C3HC4 // ZINC\_FINGER\_C3HC4 // NLS\_BP] CG15104 56A-56A dup:3/3 ID:47D3  
 + Mcm3 DNA\_replication\_factor \* Mcm3 \* DNA replication factor MCM3(aa) \* 1e-168 MCM3\_YEAST MINICHROMOSOME  
 CG4206 MAINTENANCE PROTEIN minichrom \* MCM3 [MCM // MCM\_1 // MCM\_2] CG4206 LD30950 4F2-4F2 ID:47D8  
 + transporter \* DMC103B4 \* 8e-09 YNM5\_YEAST HYPOTHETICAL 73.8 KD PROTEIN IN SPC98-TOM70 INTERGENIC  
 CG3409 REGION \* 3e-37 /match=(desc;; /ma \* 2e-24 similar to the monocarb CG3409 LD30953 42C6-42C1 ID:47D9  
 + protein\_phosphatase \* 4e-25 PVH1\_YEAST PROTEIN-TYROSINE PHOSPHATASE YVH1 (PTPASE YVH1) \* 8e-13  
 CG14211 puckered protein \* 1e-14 predicted using Genefinder; similar to D[PTS\_HPR\_SER // DSPc // TYR\_PHOSPHATASE\_] CG14211  
 LD31102 18D9-18D9 dup:2/2 ID:47E10  
 CG7730 + unknown \* CG7730 LD31138 73E4-73E4 dup:2/2 ID:47E12  
 CG6506 + unknown \* CG6506 LD31003 16D6-16D6 dup:3/3 ID:47E2  
 + cell\_adhesion THYROGLOBULIN PRECURSOR 4\_DISULFIDE\_CORE, ATP\_GTP\_A, EGF\_1, THYR] CG5639 LD31017  
 CG5639 dup:2/2 ID:47E4  
 + tos DNA\_repair\_protein \* DMTOSCAP1\_2 tos \* Tosca(aa) \* 7e-47 EXO1\_YEAST EXONUCLEASE I (EXO I) (DHS1 PROTEIN)  
 CG10387 DHS1 pr \* Tosca [53EXO\_N\_DOMAIN // 53EXO\_I\_DOMAIN // XPG] CG10387 LD31018 37A4-37A4 dup:2/2 ID:47E5  
 + chaperone \* 7e-25 PA10\_YEAST PAC10 PROTEIN PAC10 protein - yeast (Sacchar \* 7e-27 YFM9\_CAEEL  
 CG6719 HYPOTHETICAL 20.9 KD PROTEIN T06G6.9 IN CHROMOSOME I \* 2e-43 VBP1\_H CG6719 LD31046 86E4-86E4 dup:4/4  
 ID:47E7  
 + chaperone \* 1e-10 XDJ1 protein - yeast (Saccharomyces cerevisiae) Xdj1p: H \* 2e-08 DNJ1\_DROME DNAJ PROTEIN  
 HOMOLOG (DROJ1) droj1 \* 6e-56 predicted using Genefin [DNAJ\_1 // DnaJ // DNAJ\_2 // NLS\_BP] CG7872 LD31069 13E3-13E3  
 CG7872 dup:2/2 ID:47E9  
 + 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-  
 CG4943 54D3 dup:2/3 ID:47F12  
 + unknown \* 7e-05 YHOB\_DROME TRANSPOSABLE ELEMENT HOBO KD HYPOTHETICAL PROTEIN \* 9e-05 transposase  
 CG17153 \* 7e-05 ORF1 \* Hermes transposase CG17153 LD31163 68F3-68F3 ID:47F2  
 + Cbp80 RNA\_binding \* cap-binding protein - human(aa) \* nuclear cap binding protein, 80kD(aa) \* 4e-17 GCR3\_YEAST GCR3  
 CG7035 PROTEIN (STO1 PROTEIN) (SUT1 PROTEIN) \* by match; 1- [NLS\_BP] CG7035 LD31211 4C7-4C7 ID:47F4  
 + ligand\_binding\_or\_carrier \* 3e-51 ARF1\_YEAST ADP-RIBOSYLATION FACTOR ADP-ribosylation fac \* 3e-49  
 ARF1\_DROME ADP-RIBOSYLATION FACTOR ADP-ribosylation fac \* 1e-52 ARFL\_CA[arf // SAR1GTPBP // RASTRNSFRMNG]  
 CG7197 CG7197 LD31204 66C5-66C5 dup:2/5 ID:47F5  
 CG8440 + signal\_transduction CG8440 ID:47F8  
 CG5100 + unknown \* [PRO\_RICH // NLS\_BP] CG5100 LD31243 77C4-77C4 dup:1/4 ID:47G1

+ RNA\_binding \* 13878, ribosomal protein S14 (not transcribed)(aa) \* 9e-84 PR43\_YEAST PRE-MRNA SPLICING FACTOR  
 RNA HELICASE PRP43 (HELICASE JA1) \* 8E-32 \* 5e-90 YQZN [HELICASE // NLS\_BP // Ribosomal\_S14 // ] CG12211 LD31543  
 CG12211 18C8-18C8 ID:47G11  
 + motor\_protein \* coded for by C. elegans cDNA yk38d7.3; coded for by C. elegans cDNA cm06h5; coded for by C. elegans  
 cDNA yk38d7.5(aa) \* Yml093wp(aa) \* 5e-33 YMJ3\_Y [NLS\_BP] CG12301 LD31322 71D4-71D4 dup:1/2 ID:47G3  
 CG12301  
 + motor\_protein \* CG8149 LD31448 86C1-86C1 ID:47G6  
 CG8149  
 + cell\_adhesion \* tip associating protein(aa) \* tip associating protein(aa) \* tip associating protein(aa) CG4118 LD31449 77A1-  
 CG4118 73A7 dup:1/2 ID:47G7  
 + enzyme \* 2e-05 DMANKY\_5 Ank \* \* [ANK\_REP // ank // ANK\_REP\_REGION // NLS] CG10632 LD31582 69C4-69C6  
 CG10632 ID:47H1  
 CG18592 + \* CG18592 25C3-25C3 dup:1/2 ID:47H11  
 + \* contains weak similarity to HIV P17 matrix protein \* 7e-13 RL1\_SERMA 50S RIBOSOMAL PROTEIN L1 ribosomal protein  
 CG7494 L1 - S \* RL1\_HAEDU 50S RIBOSOMAL P [Ribosomal\_L1] CG7494 84F9-84F9 dup:2/2 ID:47H12  
 CG1530 + unknown CG1530 ID:47H2  
 + transcription\_factor \* DMMLP84B\_2 Mlp84B \* ajuba; jub(aa) \* BLASTX 7.1E-07 Human LIM protein (LPP) mRNA, partial  
 CG11063 cds.(dna) \* 8e-06 LRG1 [LIM\_DOMAIN\_1 // LIM // LIM\_DOMAIN\_2 // ] CG11063 LD31670 12B9-12B9 ID:47H4  
 + unknown \* 2e-10 predicted using Genefinder \* 9e-11 CLCP \* 3e-24 chloride intracellular channel CLIC2 sapiens \* 1e-22  
 CG10997 chloride channel 64K chain - bovine CG10997 LD31682 12B9-12B9 dup:2/2 ID:47H6  
 + enzyme \* PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR (LYSYL HYDROXYLASE)  
 (LH)(aa) \* PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR ( [GLYC\_TRANS //  
 CG6199 HTH\_LYSR\_FAMILY] CG6199 LD31687 68A8-68A8 dup:3/4 ID:47H7  
 + unknown \* hypothetical protein(aa) \* 4e-06 VPS9\_YEAST VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN  
 VPS9 \* 3e-31 C05D9.6 gene product \* 1e-14 Rab5 GDP/GTP exch [RAS\_GTPASE\_ACTIV\_2 // PTS\_HPR\_HIS // NL] CG1657  
 CG1657 LD31729 10B8-10B8 dup:2/2 ID:47H8  
 + translation\_factor \* translation repressor NAT1(aa) \* eukaryotic protein synthesis initiation factor(aa) \* 2e-19 IF41\_YEAST  
 CG3845 EUKARYOTIC INITIATION FACTOR 4F SUBUNIT P150 CG3845 LD32057 49E1-49E1 dup:1/2 ID:48A10  
 + transcription\_factor \* 1e-11 AZF1\_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin \* 4e-20 CROL BETA \*  
 2e-08 similar to Zinc finger, C2H2 type (4 domains); cDNA EST \*[ZF\_MATRIN // zf-C2H2 // ZINC\_FINGER\_C2H] CG17806  
 CG17806 LD32088 93B1-93B1 ID:48A11  
 CG5995 + unknown \* CG5995 LD31910 97F3-97F4 dup:1/2 ID:48A2  
 + enzyme \* /match=(desc;; /match=(desc:(aa) \* similar to Arabidopsis thaliana male sterility protein \* DMC103B4 \* acyl CoA  
 CG8306 reductase(aa) [HELIX\_LOOP\_HELIX // NLS\_BP] CG8306 LD31990 53C7-53C8 dup:1/3 ID:48A5  
 CG10364 + msb1l unknown \* CG10364 LD32040 37F2-37F2 ID:48A8  
 + enzyme \* cystathionine beta-synthetase; CBS(aa) \* BLASTX 8.7E-06 CYS4|Cystathionine beta-synthase (beta-CTSase),  
 CG1753 converts serine and homocysteine to cystathi [CBS // SNF4\_REP // S\_T\_dehydratase // C] CG1753 LD32051 19E6-19E6 ID:48A9  
 + ligand\_binding\_or\_carrier \* 2e-13 62D9.a \* 2e-25 retinaldehyde-binding protein C \* 2e-15 DMC30B8 \* /match=(desc;; /ma  
 CG10657 [CRETINALDHBP // CRAL\_TRIO] CG10657 LD32330 69C2-69C2 dup:2/2 ID:48B10

+ 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  
 CG1487 LD32202 100F5-100F5 ID:48B3  
 + 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  
 CG5203 + weak homology to extensin-like protein [Lycopersicon esculentum], proline-rich protein PRP2 precursor [Lupinus luteus]  
 CG15486 LD32537 ID:48C11  
 + unknown \* 3e-26 YKJ5\_YEAST 32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION \* 3e-47 similar to S. cerevisiae YJU2 protein \* 5e-67 unknown \* 1e-35 hypothetical p CG8435 LD32459 52F5-52F5 ID:48C4  
 CG8435 + ksr protein\_kinase \* KSR(aa) \* KSR(aa) \* ksr \* 6e-19 hypothetical protein YPL141c - yeast (Saccharomyces cerevisiae) ([PROTEIN\_KINASE\_TYR // DAG\_PE\_BINDING\_DO] CG2899 83B1-83B1 dup:2/2 ID:48C6  
 CG2899 + mub RNA\_binding \* DMMUB\_6 mub \* PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP)(aa) \* nucleic acid binding protein(aa) \* 4e-13 YB83\_YEAST HYPOTHETI [KH-domain // KH\_DOMAIN] CG7437 LD32520 79B1-79B1 ID:48C7  
 CG7437 + RnrS enzyme \* 1e-113 RIR2\_YEAST RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE R \* 1e-107 RIR2\_DROME PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTA [RIBORED\_SMALL] CG8975 LD32770 48D8-48D8 ID:48D10  
 CG8975 + enzyme \* similar to Transketolase; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene [E1\_dehydrog // NLS\_BP] CG8199 LD32808 85D25-85D25 dup:2/2 ID:48D12  
 CG8199 + transcription\_factor \* 5e-87 inserted at base 5' end of P element Inverse PCR \* \* [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG8961 LD32631 53F5-53F5 ID:48D3  
 CG8961 + signal\_transduction \* protein(aa) \* BLASTX 4.9E-08 Mus musculus TDAG51 (TDAG51) mRNA, complete cds.(dna) \* BLASTX 7.3E-13 Rattus PSD-95/SAP90-related gene (chapsyn isoform) [GUANYLATE\_KINASE\_2 // PDZ // NLS\_BP] CG6509 LD32687 33A2-33A2 ID:48D7  
 CG6509 + RNA\_binding \* 4e-80 DBP2\_YEAST P68-LIKE PROTEIN RNA helicase DBP2 - yeast (Sac \* 1e-68 RM62\_DROME PUTATIVE ATP-DEPENDENT RNA HELICASE P62 RNA he \* 1e-154 similar [helicase\_C // HELICASE // DEAD // DEAD\_] CG6418 LD32732 67F4-67F4 dup:2/2 ID:48D8  
 CG6418 + motor\_protein \* ARX(aa) \* 1e-58 UBA2\_YEAST UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN \* 2e-28 ubiquitin activating enzyme \* 1e-67 similar [UBA\_NAD // ThiF\_family // NAD\_BINDING /] CG7528 LD33023 67E3-67E3 dup:5/5 ID:48E10  
 CG7528 + unknown \* 1e-142 inserted at base Both 5' and 3' ends of P element Inverse PCR \* \* CG15893 LD32923 5E4-5E4 dup:2/2 ID:48E5  
 CG15893 + nop5 unknown \* nucleolar protein NOP5/NOP58(aa) \* 1e-100 NOP5\_YEAST NUCLEOLAR PROTEIN NOP5 hypothetical protein \* 1e-119 contains similarity to S. cerevisiae Prp31 [NLS\_BP] CG10206 LD32943 27C-27C dup:2/2 ID:48E7  
 CG10206 + BG:DS09218.3 chaperone \* 8e-19 ERP5\_CAEEL PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR \* 4e-21 protein disulfide isomerase-related protein \* 9e-21 ERP5\_RAT PROBABLE PRO CG4455 LD33101 35F10-35F10 dup:2/3 ID:48F10  
 CG4455

CG18551 + unknown \* CG18551 LD33058 88E1-88E1 ID:48F3  
+ elav RNA\_binding \* DMELAVK\_2 elav \* 1e-16 polyadenylate-binding protein \* ELAV\_DROME ELAV PROTEIN (EMBRYONIC LETHAL ABNORMAL VISUAL PROTEIN) \* 1e-58 Similar to the hu [RNP\_1 // RBD // HUDSXL RNA // rrm] CG4262 LD33076 1B5-1B5 ID:48F5

CG4262 + rtGEF signal\_transduction \* 5e-60 rho type GEF \* 6e-62 rtGEF \* rtGEF \* rho type GEF(aa) [GRF\_DBL // RhoGEF // SH3DOMAIN // SH3 /] CG10043 LD33092 38C7-38C8 dup:2/2 ID:48F9

CG10043 + unknown \* Yjr072cp(aa) \* ATP(GTP)-binding protein(aa) \* HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III(aa) \* putative protein(aa) [ATP\_GTP\_A] CG3704 LD33276 1D1-1D1 ID:48G10

CG3704 + 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

CG10938 + unknown \* protein(aa) \* 3e-09 PC11\_YEAST PCF11 PROTEIN hypothetical protein YDR228c - \* 3e-21 YRR2\_CAEEL HYPOTHETICAL 91.1 KD PROTEIN R144.2 IN CHROMOSOME III [PRENYLATION // PRO\_RICH // NLS\_BP // CY] CG10228 LD33132 51D2-51D2 ID:48G2

CG10228 + motor\_protein \* kda paraneoplastic cerebellar degeneration-associated antigen Peptide, \* MYOSIN HEAVY CHAIN D (MHC D)(aa) \* CLIP-190 \* 7e-05 microtubule binding pro [NLS\_BP] CG1962 38E-38E dup:3/5 ID:48G3

CG1962 + unknown \* protein(aa) \* SSXT PROTEIN (SYNOVIAL SARCOMA, TRANSLOCATED TO X CHROMOSOME) (SYT PROTEIN)(aa) \* synovial sarcoma, translocated to X chromosome(aa) \* [PRO\_RICH] CG10555 LD33241 7E2-7E3 dup:2/2 ID:48G6

CG10555 + 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

CG3350 + 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

CG8000 + DNA\_binding \* protein(aa) \* 3e-65 YEZ9\_YEAST PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION > \* 2e-26 Similarity to Human XE169 protein (SW:X CG15835 LD33386 43F5-43F5 ID:48H3

CG15835 + chromatin\_binding \* pheromone response pathway suppressor; Srm1p(aa) \* similar to RCC1 proteins(aa) \* regulator of chromosome condensation(aa) \* retinitis pigmentosa [RCC1 // RCC1\_2 // RCCNDNSATION] CG9135 LD33431 26B3-26B3 dup:1/2 ID:48H4

CG9135 + BG:DS01068.4 unknown \* 1e-05 mtDBP protein \* AAs \* \* CG18124 LD33443 35A1-35A1 ID:48H5

CG18124 + Lac cell\_adhesion \* DMLACH\_2 Lac \* LACH\_DROME LACHESIN PRECURSOR lachesin melanoga \* 2e-16 predicted protein contains a large number of Ig superfamily repeat \* 5e-20 c [ig] CG12369 LD33460 49A7-49A7 ID:48H6

CG12369 + 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

CG1454 + 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

+ unknown \* 5-oxo-1,2,5-tricarboxylic-3-penten acid decarboxylase/isomer(aa) \* 3e-26 YNQ8\_YEAST HYPOTHETICAL 28.8  
 CG5793 KD PROTEIN IN PSD1-SKO1 INTERGENIC REGION \* 9e CG5793 LD33646 95F1-95F1 ID:49A1  
 + enzyme \* 1e-10 FMS1\_YEAST FMS1 PROTEIN FMS1 protein - yeast (Saccharom \* 6e-11 Cs protein \* 8e-33 No definition  
 CG7737 line found \* 2e-13 protein [ADXRDTASE // AMINEOXDASEF // NAD\_BINDIN] CG7737 LD33764 47D6-47D7 dup:1/2 ID:49A10  
 + transcription\_factor \* transcription factor 17(aa) \* zinc finger protein(aa) \* RENAL TRANSCRIPTION FACTOR KID-1  
 CG7357 (TRANSCRIPTION FACTOR 17)(aa) \* crol [zf-C2H2 // ZINC\_FINGER\_C2H2\_2] CG7357 LD33778 93B1-93B1 ID:49A11  
 CG15736 + transcription\_factor \* CG15736 LD33780 11A4-11A4 ID:49A12  
 + 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  
 CG12276 ID:49A3  
 + unknown \* similar to the postsynaptic membrane 43K protein from Xenopus \* LGN protein(aa) \* 4e-13 C10A gene product \*  
 CG5692 2e-29 hypothetical protein [TPR\_REGION // TPR\_REPEAT // NLS\_BP] CG5692 LD33695 98A3-98A3 ID:49A6  
 + RNA\_binding \* DMRM62RH\_2 Rm62 \* RNA helicase(aa) \* mitochondrial DEAD box protein(aa) \* VASA PROTEIN(aa)  
 CG7878 [helicase\_C // KH-domain // KH\_DOMAIN //] CG7878 LD33749 84F1-84F1 ID:49A7  
 + Caf1 signal\_transduction \* Caf1 \* Rack1 \* CHROMATIN ASSEMBLY FACTOR P55 SUBUNIT (CAF-1 P55 SUBUNIT) (DCAF-  
 CG4236 1)(aa) \* 2e-73 HAT2\_YEAST HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT hy [GPROTEINBRPT // WD40\_REGION //  
 WD\_REPEA] CG4236 LD33761 88E8-88E8 ID:49A9  
 + unknown \* 1e-27 cDNA EST yk476a1.5 comes from this gene \* 4e-28 Unknown \* cDNA EST comes from this gene; cDNA  
 CG3887 EST yk256g7.5 come \* F28H7.4 CG3887 LD33828 25C1-25C1 ID:49B2  
 + RNA\_binding \* 3e-05 NSR1\_YEAST NUCLEAR LOCALIZATION SEQUENCE BINDING PROTEIN (P67) \* 7e-06 protease \*  
 CG10837 3e-05 Similarity to Bovine Poly-A binding protein II cDNA \* [RNP\_1 // RBD // rrm] CG10837 LD33831 cyto\_unknown ID:49B3  
 + enzyme \* 2e-60 COXX\_YEAST CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR \* 5e-94 heme A:  
 farnesyltransferase \* 4e-46 putative heme A:farnesyltransfera [COX10\_ctaB\_cyoE // COX10\_CTAB\_CYOE] CG5037 LD33876  
 CG5037 31D9-31D9 dup:3/3 ID:49B6  
 + unknown \* 6e-97 N2,N2-dimethylguanosine tRNA methyltransferase c \* 1e-105 similar to N2,N2-dimethylguanosine tRNA  
 CG6388 methyltransferase; cDNA ES \* 1E-125\* 1e-111 [SAM\_BIND] CG6388 LD33880 33D5-33E ID:49B7  
 + I(3)03670 unknown \* DMC507\_2 anon-I \* 5e-93 head-elevated expression in 0.9 kb \* 8e-92 inserted at base Unknown 5' end of P  
 CG1715 element Plasmid rescue \* CG1715 LD33960 100B-100B ID:49B8  
 CG1913 + CG1913 dup:6/7 ID:49B9  
 + unknown \* 3e-47 YKT6\_YEAST HYPOTHETICAL 22.7 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION \* 7e-53  
 CG1515 YMP8\_CAEEL HYPOTHETICAL 82.6 KD PROTEIN IN CHROMOSOME III \* 1e- [SYNAPTOBREVN // synaptobrevin] CG1515  
 LD34211 7C8-7C8 ID:49C12  
 + unknown \* Ydl060wp(aa) \* No definition line found(aa) \* 8e-91 hypothetical protein YDL060w - yeast (Saccharomyces  
 CG7338 cerevisiae) \* 0.0000000006 [NLS\_BP] CG7338 LD34093 78D-78D dup:2/4 ID:49C5  
 + unknown \* RRM3/PIF1 helicase homolog(aa) \* PIF1(aa) \* putative helicase(aa) \* DNA helicase homolog(aa) [NLS\_BP //  
 CG3238 ATP\_GTP\_A] CG3238 LD34105 25A3-25A3 ID:49C6  
 CG3024 + EG:84H4.1 chaperone \* by content; by match; 2-match\_description=TORSINA.; 2-match\_species=HOMO SAP...(aa) \* 7e-55

similarity to 35.1KD hypothetical yeast protein (Swiss [CLPPROTEASEA] CG3024 LD34179 4C7-4C7 ID:49C9  
 + transporter \* MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM20 HOMOLOG (MITOCHONDRIAL KD OUTER  
 MEMBRANE PROTEIN) (OUTER MITOCHONDRIAL MEMBRANE RECEPTOR TOM20)(aa) \* 2e [NLS\_BP] CG7654 LD34461  
 CG7654 76E2-76E2 ID:49D10  
 CG7869 + motor\_protein \* [SNF2\_N // NLS\_BP] CG7869 LD34474 70E1-70E1 ID:49D11  
 + peptidase \* PROBABLE CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)(aa) \* leucine  
 aminopeptidase(aa) \* PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III( [LAMNOPPTDASE // RCC1\_2 //  
 CG7340 Peptidase\_M17] CG7340 LD34492 87D7-88E1 ID:49D12  
 + pelo unknown \* pelo \* 9e-61 DOM34 protein - yeast (Saccharomyces cerevisiae) (X77 \* PELO\_DROME PELOTA PROTEIN  
 CG3959 pelota \* 1e-120 YNU6\_CAEEL HYPOTHETICAL 42.9 KD PROT CG3959 LD34262 30C6-30C7 ID:49D2  
 + peptidase \* 1e-62 S2P \* 2e-62 S2P \* SP2 metalloprotease \* S2P metalloprotease [ZINC\_PROTEASE // SREBPS2PTASE]  
 CG8988 CG8988 LD34294 48C-48C ID:49D4  
 + 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  
 CG4050 dup:3/4 ID:49D5  
 + CH1-2 endopeptidase \* COP9 complex homolog subunit 1-2 DCH1-2(aa) \* 3e-14 YE28\_CAEEL HYPOTHETICAL 47.6 KD  
 PROTEIN F49C12.8 IN CHROMOSOME IV \* 1e-157 GPS1\_HUMAN G PROTEIN [PCI\_DOMAIN // PCI] CG3889 LD34304 75E2-  
 CG3889 75E2 dup:1/2 ID:49D6  
 + motor\_protein \* 7e-09 by content; 1-meth \* 2e-07 homeotic most like HMPB\_DROME: homeotic proboscipedia protein \* 9e-  
 CG8677 07 Williams-Beuren syndrome deletion transcript [PHD // NLS\_BP // ATP\_GTP\_A] CG8677 LD34730 39C1-39C1 dup:5/5 ID:49E10  
 + electron\_transfer \* 1e-11 C05E11.1 gene product \* 2e-07 hypothetical protein \* 3e-45 inserted at base Both 5' and 3' ends of  
 CG8735 P element Inverse PCR \* [CYTOCHROME\_C] CG8735 LD34731 44D-44D2 dup:3/3 ID:49E11  
 + 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  
 CG12130 ID:49E12  
 + enzyme \* nuclear protein methyltransferase (mono- and asymmetrically dimethylating enzyme); Hmt1p(aa) \* protein N-  
 CG6563 methyltransferase 3(aa) \* protein N-methy [SAM\_BIND] CG6563 LD34544 88E8-88E8 dup:2/2 ID:49E3  
 CG12011 + unknown \* CG12011 LD34635 62A12-62A12 dup:2/2 ID:49E7  
 + unknown \* predicted using Genefinder(aa) \* cDNA EST yk301g10.3 comes from this gene; cDNA EST yk301g10.5 comes  
 CG6236 from this gene(aa) \* cDNA EST yk321f3.5 comes CG6236 LD34692 90E1-90E1 dup:3/3 ID:49E8  
 + TfiIS transcription\_factor \* 2e-20 DST1 DNA strand transferase alpha \* 1e-124 TFS2\_DROME TRANSCRIPTION ELONGATION  
 CG3710 FACTOR S-II (RNA POLYMERASE II ELONGATION FA \* 3e-42 TFS2\_CAEEL [TFIIS] CG3710 LD34766 35C1-35C1 ID:49F1  
 + DNA\_binding \* zinc finger protein (RING finger, C3HC4 type)(aa) \* 4e-34 YL23\_YEAST HYPOTHETICAL 29.7 KD PROTEIN  
 IN REC102-SFH1 INTERGENIC REGION \* 5e-65 similar t [ZF\_CCCH // zf-C3HC4 // ZINC\_FINGER\_C3HC] CG4973 LD35003  
 CG4973 92C4-92C4 ID:49F12  
 + DNA\_binding \* DNA helicase(aa) \* HYPOTHETICAL 175.7 KD PROTEIN C05C10.2 IN CHROMOSOME II(aa) \* DNA  
 CG6967 helicase A; Hcs1p(aa) \* hypothetical helicase(aa) [ATP\_GTP\_A] CG6967 LD34829 53F5-53F6 ID:49F6



+ unknown \* P38IP(aa) \* Lola-like protein(aa) \* GAGA-581 Adf-2 isoform(aa) \* 0.000002 [NLS\_BP] CG17689 LD34837 70B2-70B2 ID:49F7  
 CG17689  
 + unknown \* [NLS\_BP] CG9754 LD34845 57D4-57D4 ID:49F8  
 CG9754  
 + Dox-A2 endopeptidase \* component of the regulatory module of the 26S proteasome, homologous to human p58 subunit; Rpn3p(aa) \* proteasome (prosome, macropain) 26S subunit, [PCI\_DOMAIN // PCI // TPR\_REPEAT] CG10484 LD34970 37B12-37B12 dup:3/3 ID:49F9  
 CG10484  
 + 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  
 + unknown \* 1e-146 inserted at base Unknown 5' end of P element Plasmid rescue \* \* [ZINC\_FINGER\_C2H2 // ZINC\_FINGER\_C2H2\_2 ] CG5580 LD35038 55C4-55C4 ID:49G3  
 CG5580  
 + DNA\_binding \* 1e-125 hypothetical protein YDR334w - yeast (Saccharomyces cerevisiae) ( \* 1e-67 iswi protein - fruit fly (Drosophila melanogaster) ISWI p \* 2e-67 p [helicase\_C // DNA\_LIGASE\_A1 // MYB\_3 //] CG9696 LD35056 57D5-57D8 dup:3/4 ID:49G4  
 CG9696  
 + 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  
 + unknown \* 3e-80 YKL6\_CAEEL HYPOTHETICAL 103.8 KD PROTEIN C03C10.6 IN CHROMOSOME III \* E03A3.6 \* E03A3.7 \* [AA\_TRNA\_LIGASE\_II\_2 // PRO\_RICH // CYTO] CG5237 GH01039 91F10-91F11 ID:54A4  
 CG5237  
 + enzyme\_inhibitor \* 7B2(aa) \* cDNA EST comes from this gene(aa) \* 2e-22 cDNA EST comes from this gene \* CG1168 GH01053 83A5-83A5 ID:54A6  
 CG1168  
 + enzyme \* 5e-19 VIT1\_DROME VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1) vitell \* 6e-23 pancreatic lipase related protein \* 3e-25 pancreatic lipase-related protei [TAGLIPASE // ESTERASE // lipase] CG17292 GH01208 29B3-29B3 ID:54B11  
 CG17292  
 + enzyme \* 2e-18 pdb|1GKY| Guanylate Kinase (E.C.2.7.4.8) Complex With Guanosine Monophosphate \* 2e-70 Camguk \* 2e-67 LIN2\_CAEEL LIN-2 PROTEIN LIN-2A \* 5e-97 D [Guanylate\_kin // GUANYLATE\_KINASE\_1 // ] CG13219 GH01140 47D7-47D7 ID:54B3  
 CG13219  
 + unknown \* CG11400 GH01142 54A-54A ID:54B4  
 CG11400  
 + ion\_channel \* Glu-RIIB \* glutamate receptor precursor - human (fragment)(aa) \* 9e-14 glutamate receptor DGluRIIB \* 4e-17 ionotropic glutamate receptor - Caenorhab [lig\_chan // ATP\_GTP\_A] CG17274 GH01149 93A1-93A1 ID:54B6  
 CG17274  
 + unknown \* [NLS\_BP] CG17926 GH01154 66D6-66D7 ID:54B7  
 CG17926  
 + unknown \* cDNA EST yk481g5.5 comes from this gene(aa) \* \* CG10671 GH01192 64C12-64C12 ID:54B9  
 CG10671  
 + enzyme \* 7e-52 acyl-coenzyme A oxidase \* 1e-120 similar to ACYL-COENZYME A OXIDASE, PEROXISOMAL (EC 1.3.3.6)  
 CG9707

(PALM \* 1e-125 peroxisomal acyl-CoA oxidase \* 1e CG9707 GH01226 57D11-57D11 dup:1/3 ID:54C1  
 + unknown \* MALE STERILITY PROTEIN 2(aa) \* DMC103B4 \* male sterility 2-like protein(aa) \* /match=(desc;;  
 CG10096 /match=(desc:(aa) CG10096 GH01346 87B13-87B14 ID:54C10  
 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 // SYNAPTOTAGMN // C2 // C2] CG3139 GH01240 23B1-  
 CG3139 23B2 dup:1/4 ID:54C2  
 + Dph5 enzyme \* similar to dipthine synthase(aa) \* 7e-73 DPH5\_YEAST DIPHTHINE SYNTHASE (DIPHTAMIDE  
 BIOSYNTHESIS METHYLTRANSFERASE) \* 1e-84 CGI-30 protein \* 3e-74 [TP\_methylase] CG5275 GH01248 94B8-94B9  
 CG5275 ID:54C3  
 CG5107 + unknown \* CG5107 GH01257 99B4-99B4 ID:54C4  
 + BcDNA:GH07485 enzyme \* 3e-55 CAO\_YEAST ACYL-COENZYME A OXIDASE (ACYL-COA OXIDASE) ac \* 1e-130 Similarity to  
 CG5009 Rat Acyl-CoA oxidase I (SW:CAO1\_RAT); cDNA EST EMBL: \* 1e-145 p CG5009 GH01266 54E8-54E8 dup:1/2 ID:54C6  
 + enzyme \* similar to pig tubulin-tyrosine ligase.(aa) \* 1e-41 similar to tubulin tyrosine ligase; cDNA EST comes fro \* 2e-55  
 CG16716 protein \* 8e-16 TTL\_BOVIN TUBULIN [NLS\_BP] CG16716 GH01307 56D15-56E1 ID:54C7  
 + neurotransmitter\_transporter \* 3e-06 cocaine-sensitive serotonin transporter \* 8e-11 NTGL\_MOUSE SODIUM- AND  
 CHLORIDE-DEPENDENT GLYCINE TRANSPORTER (GLYT-1) \* 1e-10 NTGL\_HUMAN SODI [NA\_NEUROTRAN\_SYMP\_3]  
 CG13796 CG13796 GH01326 28C2-28C2 dup:1/3 ID:54C9  
 + odd transcription\_factor \* DMODDS\_1 odd \* transcription factor specific RNA polymerase II transcription factor ) cell nucleus )  
 map\_position:24A1-3 \* Sob protein(aa) \* 5e-19[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG3851 GH01449 25B1-25B1  
 CG3851 ID:54D10  
 + structural\_protein \* Peritrophin-A \* cDNA EST comes from this gene; cDNA EST yk369a9.5 comes from this gene; cDNA  
 CG11142 EST yk438c12.3 comes from this gene; cDNA EST yk438c12 CG11142 GH01453 26A-26A ID:54D11  
 + Diacyl glycerol kinase enzyme EDgk gene product is expressed predominantly in the embryonic CNS and adult nervous system  
 CG1535 and muscle DAGK, DAGKa, DAGKc, NLS\_BP CG1535 GH01459 dup:2/2 ID:54D12  
 CG7058 + unknown \* CG7058 GH01369 17E1-17E1 ID:54D2  
 + 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  
 CG12071 GH01388 100B-100B ID:54D4  
 + RecQ5 DNA\_repair\_protein \* Recq helicase 5(aa) \* Recq helicase 5(aa) \* 3e-73 SGS1\_YEAST HELICASE SGS1 (HELICASE  
 CG4879 TPS1) DNA helicase TP \* 1e-06 RM62\_DROME PUTATIVE ATP-DEPENDENT [helicase\_C // HELICASE // DEAD] CG4879  
 GH01404 70E6-70E7 ID:54D5  
 CG5532 + unknown \* CG5532 GH01442 59F7-59F7 ID:54D9  
 CG1545 + unknown \* CG1545 GH01560 10A-10A dup:2/2 ID:54E10  
 + cell\_adhesion \* DMARTAN\_7 trn \* 5e-08 tartan protein \* 6e-16 5T4 oncofetal trophoblast glycoprotein \* 6e-18 oncofetal  
 CG6959 trophoblast glycoprotein 5T4 precursor - human [LRR // LRRCT] CG6959 GH01562 86F11-86F11 dup:2/2 ID:54E11

+ transporter \* 4e-71 similar to the NUPC family of transporters \* 1e-82 purine-selective Na<sup>+</sup> nucleoside cotransporter \* 2e-82  
 CG8083 solute carrier family (sodium-coupled CG8083 GH01486 45A10-45A10 dup:3/3 ID:54E3  
 + 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  
 CG6483 ID:54E6  
 + defense/immunity\_protein \* cuticular molt protein precursor(aa) \* 2e-29 peptidoglycan recognition protein precursor \* 2e-31  
 CG8995 TNF superfamily, member (LTB)-like (peptidoglycan r CG8995 GH01554 13F1-13F1 dup:2/2 ID:54E9  
 CG10680 + \* CG10680 38B1-38B1 dup:2/3 ID:54F11  
 + protein\_kinase \* protein kinase(aa) \* PUTATIVE SERINE/THREONINE-PROTEIN KINASE C01C4.3 IN CHROMOSOME  
 CG4945 X(aa) \* 5e-17 SNF1\_YEAST CARBON CATABOLITE DEREPRESSING PROTE[PROTEIN\_KINASE\_ST //  
 PROTEIN\_KINASE\_DOM] CG4945 GH01572 53C7-53C7 dup:3/4 ID:54F3  
 + enzyme \* long-chain-fatty-acid--CoA ligase (fadD-8)(aa) \* similar to 4-coumarate-coA ligase; cDNA EST yk455e10.3 comes  
 CG4563 from this gene; cDNA EST yk455e10.5 c [AMP-binding] CG4563 GH01595 60D2-60D2 ID:54F5  
 + enzyme \* 2e-07 CN1C\_RAT CALCIUM/CALMODULIN-DEPENDENT 3',5'-CYCLIC NUCLEOTIDE PHOSPHODIESTERASE  
 CG14942 \* \* [kazar // KAZAL] CG14942 GH01602 33B2-33B2 dup:2/2 ID:54F6  
 CG18212 + unknown \* [NLS\_BP] CG18212 GH01770 90C-90C ID:54G11  
 + unknown \* PROTEIN 22A3(aa) \* 8e-46 YL22\_YEAST HYPOTHETICAL 28.3 KD PROTEIN IN PPR1-SNF7 INTERGENIC  
 REGION \* 4e-56 YOM4\_CAEEL HYPOTHETICAL 29.1 KD PROTEIN W06E [UPF0023] CG8549 GH01786 66D10-66D10  
 CG8549 ID:54G12  
 + karyopherin-alpha3 ligand\_binding\_or\_carrier \* coded for by *C. elegans* cDNA yk173a10.5; coded for by *C. elegans* cDNA  
 CG9423 yk96a12.5; coded for by *C. elegans* cDNA cm06h1; coded for by *C. elegans* cDNA CG9423 GH01702 86C3-85D27 ID:54G5  
 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  
 CG3290 GH01891 58C7-58C7 ID:54H10  
 CG3955 + unknown \* CG3955 GH01933 49F5-49F5 ID:54H12  
 + 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  
 HES1\_MOUSE TRANSCRIPTION FACTOR HES-1 (HAIRY[HLH // HELIX\_LOOP\_HELIX // HELIX\_LOOP\_H] CG14548 GH01842  
 CG14548 96F10-96F10 ID:54H5  
 CG15217 + transmembrane\_receptor \* CG15217 GH01875 40C2-40C2 ID:54H7  
 CG8605 + unknown \* 3e-08 pi034 \* \* CG8605 GH01880 65F2-65F2 ID:54H8  
 CG8401 + unknown \* CG8401 GH01937 52E3-52E4 ID:55A1  
 CG5778 + CG5778 GH02030 ID:55A10

+ 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  
 CG5588 + Mtl enzyme CG5588 GH01976 ID:55A4  
 CG18214 + unknown \* guanine nucleotide exchange factor UNC-73A(aa) \* \* CG18214 GH01987 61E2-61E2 dup:1/2 ID:55A5  
 + \* MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM-SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1)(aa) \* 2e-41 hypothetical p [inositol\_P // INOSPHPTASE // IMP\_1 // ] CG9391 78C7-78C7  
 CG9391 dup:2/2 ID:55B1  
 CG11293 + unknown \* CG11293 GH02327 59F4-59F4 ID:55B11  
 CG2657 + ion\_channel glutamate receptor, delta-2 subunit-like SBP\_GLUR CG2657 GH02344 ID:55B12  
 CG11317 + transcription\_factor \* [ZINC\_FINGER\_C2H2 // ZINC\_FINGER\_C2H2\_2] CG11317 GH02265 100B5-100B5 ID:55B5  
 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  
 + cell\_adhesion \* orphan G protein-coupled receptor FEX(aa) \* BLASTX 7.5E-06 *Santalum album* proline rich protein mRNA, complete cds.(dna) \* 9e-05 protein \* 5e-05 kek1 [LRR // LEURICHRPT // NLS\_BP // LRRCT] CG3413 GH02310 58D2-58D3  
 CG3413 ID:55B8  
 CG4716 + unknown \* CG4716 GH02313 50A1-50A1 dup:2/3 ID:55B9  
 + enzyme \* DMPGMII\_3 agr;-Man-II \* alpha-mannosidase(aa) \* alpha-mannosidase (EC 3.2.1.24) precursor - human(aa) \*  
 CG9466 LYOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANN [Glyco\_hydro\_38] CG9466 GH02475 29F1-29F1 ID:55C11  
 + enzyme \* 1e-47 CACP\_YEAST CARNITINE O-ACETYLTRANSFERASE PRECURSOR (CARNITINE ACETYLASE) \* 4e-37  
 CG12428 choline acetyltransferase \* 3e-66 similar to Carnitate acyltr [Carn\_acyltransf] CG12428 GH02484 98A8-98A9 dup:1/4 ID:55C12  
 + 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 GH02457  
 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  
 + unknown \* 4e-11 YMH6\_CAEEL HYPOTHETICAL 19.1 KD PROTEIN F58A4.6 IN CHROMOSOME III \* \* CG12123  
 CG12123 GH02722 7E6-7E6 ID:55D12  
 CG2578 + cell\_adhesion \* 1e-180 odd Oz product \* 8e-31 similar to tenascin \* 1e-107 Ten-m4 \* 1e-101 (mouse DOC4 LIKE protein)

|         |  |
|---------|--|
|         | [NLS_BP] CG2578 GH02628 11B1-11B1 ID:55D3  |
| CG7366  | + unknown * CG7366 GH02649 67E7-67E7 ID:55D4   |
|         | + unknown * 2e-22 YKQ5_YEAST HYPOTHETICAL 105.7 KD PROTEIN IN TPK3-PIR1 INTERGENIC REGION * 6e-36                                |
| CG6790  | Mcd4p homolog * 1e-18 hypothetical protein * unknown protein CG6790 GH02677 86E15-86E15 ID:55D6                                  |
|         | + Dgp-1 translation_factor * 1e-07 EF1A_YEAST ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) translat * 8e-05                            |
|         | EF11_DROME ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (50 KD FEMALE-SPECIFIC PR [NLS_BP // GTP_EFTU //                               |
| CG5729  | ATP_GTP_A] CG5729 GH02692 55B9-55B9 dup:2/4 ID:55D7  |
|         | + Chi DNA_binding * neural src interacting protein, long form; NSIP long form(aa) * Nuclear LIM interactor(aa) * short form of   |
| CG3924  | CHIP(aa) * CHIP(aa) [NLS_BP] CG3924 GH02919 60B1-60B1 dup:3/4 ID:55E11   |
| CG1537  | + unknown * CG1537 GH02938 10A-10A dup:2/2 ID:55E12  |
|         | + unknown * No definition line found(aa) * 3e-46 No definition line found * 1e-140 protein * [CLATHRIN_REPEAT // ZF_RING]        |
| CG10144 | CG10144 GH02853 65B2-65B2 dup:2/2 ID:55E3  |
|         | + unknown * molybdenum cofactor biosynthesis protein E isolog(aa) * molybdenum cofactor synthesis 2(aa) * 8e-28 similar to       |
| CG10238 | molybdenum cofactor biosynthesis pro CG10238 GH02855 96B20-96B20 dup:2/2 ID:55E4   |
|         | + enzyme * Sar oxidase(aa) * * 7e-63 cDNA EST comes from this gene; cDNA EST co * 2e-41 unknown protein CG3270                   |
| CG3270  | GH02863 42C6-42C6 dup:2/2 ID:55E5  |
|         | + transporter * 8e-16 GPI-anchored protein - mouse (fragment) hum * 2e-16 P137_HUMAN GPI-ANCHORED PROTEIN P137                   |
| CG4144  | GPI-anchored prote * 2e-17 gram negative binding prot CG4144 GH02872 75D2-75D2 dup:3/3 ID:55E6                                   |
| CG4714  | + unknown * 6e-05 centromere protein E CENTROMERIC * 6e-05 CENP-E protein * CG4714 GH03085 50A1-50A1 ID:55F11                    |
|         | + 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  |
|         | + actin_binding * filamin(aa) * 1e-103 similar to endothelial actin-binding protein repeats; cDNA EST EMB * 7e-11 actin binding  |
| CG11605 | protein ABP-280 * 3e-90 gamma filamin [Filamin // FILAMIN_REPEAT] CG11605 GH03013 58F7-58F7 dup:1/3 ID:55F5                      |
| CG16772 | + unknown * CG16772 GH03035 38B1-38B1 ID:55F6  |
| CG9005  | + cell_adhesion * 0.000000000000000003 * * CG9005 GH03037 48B1-48B2 dup:2/5 ID:55F7  |
|         | + serpin * THYROXINE-BINDING GLOBULIN PRECURSOR (T4-BINDING GLOBULIN)(aa) * alpha-1-antichymotrypsin                             |
| CG9334  | precursor(aa) * 8e-42 Similar to serine protease inhibito [serpin] CG9334 GH03095 38E9-38E9 ID:55G1                              |
|         | + unknown * 2e-17 FMR2 protein * 1e-17 X mental retardation X ment * lymphoid nuclear protein related to AF4 * [HMGI_Y //        |
| CG8817  | NLS_BP] CG8817 GH03237 23C1-23C1 dup:1/2 ID:55G11  |
|         | + tim transcription_factor * TIM_DROME TIMELESS PROTEIN TIM * 3e-16 timeless * 3e-16 UNKNOWN timeless homolog *                  |
| CG3234  | TIM CG3234 GH03106 23F3-23F5 ID:55G2   |
|         | + Eip63F-1ligand_binding_or_carrier * Eip63F-1 * 2e-74 E631_DROME CALCIUM-BINDING PROTEIN E63-1 calcium-binding pr *             |
| CG15855 | 3e-17 similar to EF-hand calcium binding proteins; most similar to ca CG15855 GH03109 63F7-63F7 ID:55G4                          |
|         | + wrapper cell_adhesion * wrapper protein(aa) * 9e-17 predicted protein contains a large number of Ig superfamily repeat * 2e-16 |
| CG10382 | NCA1 MOUSE NEURAL CELL ADHESION MOLECULE, LAR [iq] CG10382 GH03113 58D6-58D6 ID:55G5   |

+ 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  
 CG4008  
 + 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  
 CG3390  
 + transcription\_factor \* LTG19 - human(aa) \* BLASTX 1.2E-10 Caenorhabditis elegans cosmid ZK354.(dna) \* 1e-11 YNK7\_YEAST HYPOTHETICAL 26.0 KD PROTEIN IN CYB5-LEU4 INTERGENIC [NLS\_BP] CG4913 GH03493 90E1-90E1 dup:1/2 ID:55H10  
 CG4913  
 CG8620 + unknown \* CG8620 GH03505 65E6-65E6 ID:55H11  
 CG12106 + unknown \* 1e-05 bup=5'of bmi-1 proviral insertion locus Peptide, s \* \* CG12106 GH03263 8D2-8D2 ID:55H2  
 + 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  
 CG8128  
 CG5914 + unknown \* 1E-179\* \* CG5914 GH03315 5D2-5D2 ID:55H6  
 CG4782 + unknown \* CG4782 GH03334 86D6-86D6 ID:55H7  
 + 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  
 CG10212  
 CG14617 + unknown \* 0.00000002\* 0.00000002\* CG14617 GH03511 19F6-20A1 ID:56A1  
 CG6272 + transcription\_factor C/EBP CCAAT/enhancer-binding protein B\_ZIP, NLS\_BP CG6272 GH03576 ID:56A6  
 + 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  
 CG5140  
 CG1844 + unknown \* 1E-172\* \* CG1844 GH03581 10F4-10F4 ID:56A8  
 CG9803 + unknown \* [PRO\_RICH] CG9803 GH03629 59D6-59D6 ID:56B1  
 + ion\_channel \* calcium-activated potassium channel rSK3(aa) \* 2e-52 Weak similarity to potassium channel proteins; cDNA EST \* 3e-41 intermediate conductance potass [CHANNEL\_PORE\_K] CG10706 GH03729 4F5-4F7 ID:56B10  
 CG10706  
 CG3124 + unknown \* CG3124 GH03736 59D4-59D4 ID:56B12  
 + unknown \* ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9)(aa) \* CG5172 ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (N CG5172 GH03633 15E5-15E5 ID:56B2  
 CG5172  
 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  
 + Cyt-b5 electron\_transfer \* CYBR\_DROME PROTEIN TU-36B (CYTOCHROME B5-RELATED PROTEIN) \* 9e-66 CYBR\_DROVI CYTOCHROME B5 RELATED PROTEIN cytochrome b5 \* DMTU36B\_4 Cyt-b5 \* delta [CYTOCHROME\_B5\_2 // heme\_1] CG13279 GH03691 36A9-36A9 ID:56B5  
 CG13279  
 CG18358 + unknown \* CG18358 GH03717 15A3-15A3 ID:56B7  
 CG9861 + DNA\_binding \* [NLS\_BP] CG9861 GH03827 59D6-59D6 ID:56C11

CG2767 + enzyme aldose reductase ALDOKETO\_REDUCTASE\_1, ALDOKETO\_REDUCTASE] CG2767 ID:56C2

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

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

CG15608 + unknown \* 2e-06 CGI-62 protein \* \* [NLS\_BP] CG15608 GH03957 53F6-53F7 dup:1/3 ID:56D12

+ Pkg21D protein\_kinase \* Pkg21D \* 1e-64 cAMP-dependent protein kinase subunit (put.); putative \* protein kinase (EC 2.7.1.37), cGMP-dependent - fruit fly (Drosophila melanog [PROTEIN\_KINASE\_ST // CGMPKINASE // cNMP] CG3324 GH03852 21E1-21E1 ID:56D3

CG3324 + 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

CG3481 + chromatin\_binding HUMAN HETEROCHROMATIN PROTEIN 1 HOMOLOG GAMMA (HP1 BETA) CHROMODOMAIN, CHROMO\_1, CHROMO\_2, Chromo] CG7041 GH03916 ID:56D7

CG7041 + Klc motor\_protein KINESIN LIGHT CHAIN (KLC) ATP\_GTP\_A, KINESINLIGHT,KINESIN\_LIGHT, T] CG5433 ID:56D9

CG5433 + unknown \* CG18210 GH04075 13C5-13C5 dup:2/2 ID:56E10

CG18210 + Bc larval\_serum\_protein \* pro-phenol oxidase A1 \* pro-phenol oxidase subunit 1; proPO-p1 \* DMORA\_2 Bc \* prophenoloxidase [TYROSINASE\_2 // hemocyanin // HEMOCYANIN] CG5779 GH04080 55A1-55A1 dup:2/2 ID:56E11

CG5779 + unknown \* 1e-35 hypothetical protein YDR531w - yeast (Saccharomyces cerevisiae) (U \* 3e-27 No definition line found \* 5e-42 putative protein \* coded for by C. CG5725 GH04001 77B6-77B6 dup:3/3 ID:56E4

CG5725 + unknown \* dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)(aa) \* androgen-regulated protein FAR-17 - golden hamst CG3625 GH04039 21B5-21B5 dup:2/2 ID:56E6

CG3625 + peptidase \* 5e-10 carboxypeptidase s \* 3e-90 Similarity to Human aminoacylase-1 (SW:ACY1\_HUMAN) \* 1e-109 aminoacylase AMINOACYLASE-1 (N-A \* 1e-103 ACY1\_PIG AMIN [ARGE\_DAPE\_CPG2\_1 // ARGE\_DAPE\_CPG2\_2] CG6465 GH04054 86C2-86C2 dup:2/2 ID:56E8

CG6465 + unknown \* antigen 5-related 2(aa) \* antigen 5-related protein(aa) \* Ag5r2 \* 7e-12 predicted using Genefinder; Similarity to Human testis-specific pr [SCP // GATASE\_TYPE\_II] CG9400 GH04057 12E2-12E2 dup:2/2 ID:56E9

CG9400 + unknown \* CG17977 GH04104 44A3-44A3 ID:56F1

CG17977 + 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 // ALKPHPHTASE // ] CG1809 GH04113 45F3-45F3 ID:56F2

CG1809 + structural\_protein \* Similarity to Yeast YIP1 protein cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from t CG3652 GH04132 24F1-24F1 dup:2/3 ID:56F4

CG3652 + transcription\_factor \* 7e-10 AZF1\_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin \* 2e-37 transcription factor YY1 homolog \* 1e-14 contains similarity to C2H2-type z[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG3445 67B4-67B4 dup:3/4 ID:56G10

CG3445

+ unknown \* secretory carrier membrane protein 2(aa) \* 1e-43 partial CDS \* 4e-54 SCA3\_MOUSE SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN \* 7e-64 SCA1\_HUMAN SEC [PHOSPHOPANTETHEINE] CG9195 GH04264 13D1-13D1 dup:2/2 ID:56G2  
 CG9195  
 + \* DMC132E8 \* similar to thioredoxin(aa) \* thioredoxin - Chloroflexus aurantiacus(aa) \* 4e-15 TRX1\_YEAST THIOREDOXIN I (TR-I) thioredoxin I - yeast (Sa [THIOREDOXIN // THIOREDOXIN\_2 // thioired] CG8993 62E-62E ID:56G3  
 CG8993  
 CG6541 + Mst33A unknown \* [NLS\_BP] CG6541 GH04277 33A3-33A3 ID:56G4  
 + CycJ cell\_cycle\_regulator \* CycJ \* 4e-11 CG22\_YEAST G2/MITOTIC-SPECIFIC CYCLIN cyclin B2 - yeast \* cyclin J \* 3e-05  
 CG10308 Similar to cyclin [cyclin // HELIX\_LOOP\_HELIX // NLS\_BP] CG10308 GH04281 63D2-63D2 ID:56G5  
 + enzyme \* 4e-08 probable membrane protein YDR284c - yeast (Saccharomyces cerevisiae) \* 2e-40 wunen \* 1e-20  
 CG11425 YSX3\_CAEEL HYPOTHETICAL 39.0 KD PROTEIN T28D9.3 IN [PA\_PHOSPHATASE] CG11425 GH04282 79E4-79E4 ID:56G6  
 + cell\_adhesion \* protein(aa) \* DMCONNECTN\_1 Con \* 4e-18 adenylate cyclase \* 1e-25 CAPRICIOUS [LRR // LEURICHRPT // LRRCT] CG7896 GH04292 99D3-99D3 dup:1/2 ID:56G8  
 CG7896  
 + I(3)82Fdunknown \* L82A(aa) \* map\_position:82F5-6 \* [NLS\_BP // ATP\_GTP\_A] CG10199 GH04293 83A2-83A3 dup:2/3 ID:56G9  
 CG10199  
 CG3918 + NLS\_BP, ZF\_CCHC CG3918 ID:56H5  
 + unknown \* 1e-102 predicted using Genefinder; Weak similarity to elongation factors; \* 1e-90 putative G-protein \* 3e-90 GTP binding protein putative G-protein [GTP\_EFTU // ATP\_GTP\_A] CG2017 GH04432 83C4-83C4 dup:3/3 ID:56H9  
 CG2017  
 + RNA\_binding \* DOUBLE STRANDED RNA BINDING PROTEIN A (XLRBPA)(aa) \* TAR (HIV) RNA-binding protein 2(aa) \* TAR (HIV) RNA binding protein 2(aa) \* 1e-05 contains simi [dsrm // DSRBD] CG6866 GH04468 34B6-34B6 dup:1/2 ID:57A1  
 CG6866  
 CG18609 + unknown \* CG18609 GH04567 55E10-55E10 ID:57A10  
 CG18609  
 CG5348 + Sodium/calcium exchanger protein Na+/Ca2+,K+-exchanging protein homolog Na\_Ca\_Ex CG5348 GH04570 ID:57A12  
 CG5348  
 + ligand\_binding\_or\_carrier \* 3e-07 similar to agrin and follistatin; egf-like repeats \* 2e-08 FSA\_MOUSE FOLLISTATIN PRECURSOR (FS) (ACTIVIN-BINDING PROTEIN) \* 9e-08 follistatin [kazal] CG12955 GH04473 51E9-51E9 ID:57A2  
 CG12955  
 + transporter \* 3e-23 YNK1\_YEAST HYPOTHETICAL 80.0 KD PROTEIN IN POL1-RAS2 INTERGENIC REGION \* 4e-58 cDNA EST comes from this gene; cDNA EST \* 7e-21 putative amino [AROMATIC\_AA\_PERMEASE\_2] CG8785 GH04538 49B7-49B7 ID:57A5  
 CG8785  
 + enzyme \* putative nicotinate phosphoribosyltransferase(aa) \* 1e-169 putative nicotinate phosphoribosyltransferase \* hypothetical protein \* similar to nicotin CG3714 25E1-25E1 dup:2/3 ID:57A8  
 CG3714  
 CG10342 + npf signal\_transduction \* neuropeptide F(aa) \* \* CG10342 GH04563 89D5-89D5 ID:57A9  
 CG10342  
 + RNA\_binding \* Putative RNA helicase(aa) \* BRR2\_YEAST PRE-MRNA SPLICING HELICASE BRR2 hypothetical \* 1e-23 mus308 \* similar to Helicases conserved C-terminal doma [EF\_HAND // HELICASE // DEAD // ATP\_GTP\_] CG5931 GH04577 72C1-72C1 dup:1/2 ID:57B1  
 CG5931  
 + enzyme \* DMALKPHOS\_2 Aph-4 \* 7e-27 PPB\_YEAST REPRESSIBLE ALKALINE PHOSPHATASE PRECURSOR al \* 2e-86 alkaline phosphatase \* 1e-100 PPBT\_MOUSE ALKALINE PHOSPHAT [ALKPHPTASE // alk\_phosphatase] CG5150 GH04680 64E-64E ID:57B10  
 CG5150  
 CG4524 + unknown \* CG4524 GH04692 14F5-14F5 ID:57B12  
 CG4524



CG4962 + unknown \* CG4962 GH04593 72E2-72E2 ID:57B2  
+ cell\_adhesion \* Kallmann syndrome KAL product - quail(aa) \* 3e-18 similar to WAP-type (Whey Acidic Protein) 'four-disulfide core', F \* 4e-29 Kallmann syndrome prote [wap // 4\_DISULFIDE\_CORE // 4DISULPHCORE] CG6173 GH04611 95E1-95E1 ID:57B4

CG6173 + transporter \* similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST comes from this gene(aa) \* 6e-50 MRS3\_YEAST MITOCHONDRIAL RNA SPLICING PROTEIN MRS [mito\_carr // MITOCARRIER // MITOCH\_CARR] CG4963 GH04641 98B2-98B2 dup:2/2 ID:57B5

CG4963 + unknown \* tubby homolog(aa) \* tub protein, testis - mouse(aa) \* 3e-80 YQQ4\_CAEEL HYPOTHETICAL 46.2 KD PROTEIN F10B5.4 IN CHROMOSOME III \* 5e-97 tub homolog [TUB\_1 // Tub // TUB\_2] CG9398 GH04653 57C2-57C2 ID:57B6

CG9398 + RNA\_binding \* 2e-05 coded for by C. elegans cDNA yk102b7.3; coded for by C. elegans cDNA yk124e5.3; \* 6e-05 ROG\_MOUSE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (H [RBD // rrm // NLS\_BP] CG6995 GH04738 96B1-96B2 dup:3/5 ID:57C1

CG6995 + Optix unknown \* transcription factor RNA polymerase II transcription factor ) cell nucleus ) \* \* CG18455 GH04859 44A2-44A2 ID:57C11

CG18455 + unknown \* 2e-23 predicted using Genefinder; cDNA EST yk414f4.5 comes from this g \* 9e-27 HSPC007 \* CG5497 GH04861 55E4-55E4 ID:57C12

CG5497 + dib cytochrome\_P450 \* 2e-17 cytochrome P-450 - fruit fly (Drosophila melanogaster) (fragment) \* 1e-10 YS45\_CAEEL PUTATIVE CYTOCHROME P450 ZK177.5 IN CHROMOSOME II \* 3e-30 [EP450II // p450 // P450 // MITP450 // C] CG12028 GH04745 64A5-64A5 ID:57C3

CG12028 CG7515 + CG7515 GH04814 ID:57C5

CG7515 + enzyme \* ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (PROTEIN 9) (SUBUNIT C)(aa) \* 5e-12 ATP synthase (EC 3.6.1.-) c chain - Caenorhabditis elegans \* 3e- [ATPASE\_C // ATPASEC // ATP-synt\_C] CG1746 GH04827 100B9-100B9 ID:57C6

CG1746 + enzyme \* 4e-16 LIPB\_YEAST PROBABLE LIPOATE-PROTEIN LIGASE B PRECURSOR (LIPOATE BIOSYNTHESIS PR \* 6e-09 lipoate-protein ligase B \* 8e-36 LIPB\_ARATH PUTATIVE L [LIPB] CG9804 GH04831 82C1-82C1 ID:57C7

CG9804 CG4294 + motor\_protein \* [PPASE // PRO\_RICH // NLS\_BP] CG4294 GH04951 58F1-58F1 dup:3/4 ID:57D11

CG4294 CG18004 + unknown \* CG18004 GH04870 47C6-47C6 dup:2/2 ID:57D2

CG18004 + enzyme \* Similar to acyl-coenzyme A oxidase; coded for by C. elegans cDNA yk133e10.5(aa) \* ACYL-COENZYME A OXIDASE PXP-2 (ACYL-COA OXIDASE)(aa) \* ACYL-COENZY CG17544 GH04872 37E1-37E1 dup:3/3 ID:57D3

CG17544 + endopeptidase \* COAGULATION FACTOR XII PRECURSOR (HAGEMAN FACTOR) (HAF)(aa) \* Chain A, Coagulation Factor Xa-Trypsin Chimera Inhibited With D-Phe-Pro-Arg-Chlorometh [trypsin // TRYPSIN\_CATAL] CG6069 GH04903 97A4-97A5 ID:57D5

CG6069 + unknown \* hypothetical protein - Chinese hamster (fragment)(aa) \* DHFR-coamplified protein \* hypothetical protein - Chinese hamster (fragment)(aa) \* 4e-44 ins [ACTININ\_1] CG7231 GH04938 30C1-30C1 dup:2/3 ID:57D8

CG7231 CG9686 + unknown \* CG9686 GH05060 9A2-9A2 dup:2/2 ID:57E11

CG9686 + CaMKI protein\_kinase \* CaMKI \* calcium/calmodulin dependent protein kinase I(aa) \* 1e-28 KCC1\_YEAST CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE I \* 5e-17 Contains si[PROTEIN\_KINASE\_ST // TYRKINASE // PROTE]

CG1495

CG1495 GH04968 102B7-102B7 dup:7/7 ID:57E2

CG5071 + chaperone \* DMCYP1\_2 Cyp1 \* 1e-10 CYPH\_YEAST PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) \* 1e-14 CYPH\_DROME PEPTIDYL-PROLYL CIS-TRANS [pro\_isomerase // CSA\_PPIASE\_2 // ZF\_BBO] CG5071 GH04969 96E6-96E6 dup:2/2 ID:57E3

CG17646 + transporter \* WHITE PROTEIN HOMOLOG(aa) \* 4e-43 ORF YOL075c \* 7e-39 SCRT\_DROME SCARLET PROTEIN scarlet protein mel \* 4e-37 Similarity to Drosophila white protein[ATP\_GTP\_A2 // ABC\_TRANSPORTER // ABC\_tr] CG17646 GH05015 22F3-22F3 dup:3/3 ID:57E6

CG4571 + 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

CG15867 + unknown CG15867 GH05072 ID:57F2

CG9162 + unknown \* CG9162 GH05093 26B3-26B4 ID:57F4

CG13607 + unknown \* CG13607 GH05104 95D10-95D10 ID:57F5

CG9896 + unknown \* [NLS\_BP] CG9896 GH05301 59C1-59C1 ID:57G12

CG11344 + unknown \* CG11344 GH05223 21E2-21E2 ID:57G3

CG6016 + enzyme \* predicted using Genefinder; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST yk199c3.5 comes from this gene; cDNA EST yk199c3 [CDP\_ALCOHOL\_P\_TRANSF // CDP\_ALCOHOL\_P\_T] CG6016 GH05229 50B1-50B1 dup:1/2 ID:57G4

none + none GH05253 ID:57G7

CG13280 + transcription\_factor\_binding \* oxidoreductase(aa) \* 3e-20 YULF\_BACSU HYPOTHETICAL 36.5 KD PROTEIN IN GBSA-TLPB INTERGENIC REGION \* YMO1\_RHIME HYPOTHETICAL 36.4 KD PROTEIN IN MOC [GFO\_IDH\_MocA] CG13280 GH05468 36A9-36A10 dup:2/2 ID:57H11

CG3312 + CG3312 ID:57H12

CG5073 + CG5073 ID:57H3

CG14008 + 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, KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP- \* 1e-06 DYNA\_HUMAN CG9808 GH05455 85B3-85B4 dup:3/4 ID:57H9

CG5783 + unknown \* 3e-07 hypothetical protein \* \* CG5783 GH05617 36E6-36E6 ID:58A12

CG10248 + Cyp6a8 cytochrome\_P450 \* DMCYP6A2A\_5 Cyp6a2 \* cytochrome p450 monooxygenase \* 3e-37 predicted using Genefinder; similar to cytochrome P450 \* 5e-49 cytochrome P450 3A11 - mou [EP450II // p450 // P450 // MITP450 // C] CG10248 GH05558 51D2-51D2 ID:58A6

CG11477 + unknown \* CG11477 GH05565 12E2-12E2 ID:58A7

CG4402 + enzyme \* lysyl oxidase-like 2(aa) \* 8e-09 Similarity to Human M130 antigen cDNA EST \* 1e-103 lysyl oxidase-related protein \* 5e-99 lysyl oxidase homolog [SCAVENGER\_RECEPTOR // Lysyl\_oxidase // ] CG4402 GH05569 58A2-58A2 ID:58A8

CG12749 + Hrb87F RNA\_binding \* Rbm(aa) \* similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST yk474h4.3 comes from this gene; cDNA EST yk505c10.3 comes from [RNP\_1 // RBD // rrm] CG12749 GH05625 87F7-87F7 ID:58B2

CG7507 + Dhc64C motor\_protein \* DMCYTHA\_2 Dhc64C \* DYHC\_YEAST DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) dynein he \* DYHC\_DROME DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) dynein h \* DYHC\_CA [CRYSTALLIN\_BETAGAMMA // THIOL\_PROTEASE\_] CG7507 64C-64C dup:2/3 ID:58B4

CG1980 + don juanunknown It encodes a product which is expressed in the adult (testis ) NLS\_BP CG1980 GH05702 ID:58B6

CG9337 + 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

CG9689 + unknown \* CG9689 GH05731 9A2-9A2 ID:58B9

CG9085 + \* 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

CG9218 + 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 + CG7296 GH05801 ID:58C6

CG2830 + chaperone \* DMHSP60\_2 Hsp60 \* CHAPERONIN HOMOLOG HSP60 PRECURSOR (HEAT SHOCK PROTEIN 60) (HSP-60)(aa) \* MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYT [CHAPERONINS\_CPN60 // TCOMPLEXTCP1 // CH] CG2830 GH05807 21D1-21D1 ID:58C8

CG7413 + Rbf cell\_cycle\_regulator \* DMRBFPRTN\_2 Rbf \* EST comes from the 3' UTR m \* 3e-24 similar to retinoblastoma proteins \* 1e-84 RBL1\_MOUSE RETINOBLASTOMA-LIKE PROTEIN (107 KD RETI CG7413 GH05946 1C2-1C2 ID:58D10

CG10373 + unknown \* gene product(aa) \* 6e-19 gene product \* 2e-23 JWA protein \* JM4 CG10373 GH05842 37A4-37A4 ID:58D2

CG7163 + 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

CG3920 + unknown \* CG3920 GH05923 24C-24C dup:1/2 ID:58D7

CG2077 + enzyme \* by content; by match; 2-match\_description=4-NITROPHENYLPHOSPHATASE.; 2-match...(aa) \* similar to N-acetyl-glucosamine catabolism(aa) \* Similar to CG2077 GH05933 63B3-63B3 ID:58D8

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

CG9577 + enzyme \* 659aa long hypothetical 3-hydroxybutyryl-CoA dehydratase(aa) \* PhaB(aa) \* 9e-10 YDAK\_YEAST HYPOTHETICAL 56.3 KD PROTEIN IN ARO3-KRS1 INTERGENIC REGI [ECH] CG9577 GH06131 19C1-19C1 dup:2/2 ID:58E12

CG6656 + enzyme \* acid phosphatase (EC 3.1.3.2) Acph-1 precursor, lysosomal - fruit fly (Drosophila melanogaster)(aa) \* acid phosphatase-1(aa) \* PUTATIVE ACID PHOSPH [acid\_phosphat] CG6656 GH06011 93F-93F dup:3/3 ID:58E4

CG12612 + CG12612 GH06062 dup:2/2 ID:58E6

CG12529 + Zw enzyme \* 1e-129 glucose-6-phosphate dehydrogenase (ZWF1) (EC 1.1.1.49) \* glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - fruit fly (Drosophila mela \* 1e- [G6PD // G6PDHGRNASE // G6P\_DEHYDROGENA] CG12529 GH06084 18D12-18D12 dup:3/3 ID:58E7

CG9510 + enzyme \* lyase(aa) \* lyase(aa) \* lyase (EC 4.3.2.1)(aa) \* [DCRYSTALLIN // FUMRATELYASE // FUMARATE] CG9510

GH06087 29F6-29F6 dup:2/2 ID:58E8

CG8619 + cell\_adhesion \* sdk \* DMNRGAA\_3 Nrg \* fra \* 8e-23 LAR\_DROME PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (PROTEIN-TYROSINE-PHOSPHAT [ig // FNTYPEIII // fn3] CG8619 GH06134 65E7-65E7 dup:2/2 ID:58F1

CG11221 + protein\_kinase \* Mlc-k \* Lk6 \* DMRSK\_2 S6kl \* DMDAKT1\_2 Akt1 [PROTEIN\_KINASE\_ST // TYRKINASE // PROTE] CG11221 GH06138 27A2-27A2 ID:58F2

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

CG10277 + unknown \* ring finger protein 13(aa) \* RING zinc finger protein(aa) \* 2e-09 GOL1\_DROME GOLIATH PROTEIN (G1 PROTEIN) regulatory protei \* 6e-24 similar to Zinc [GRAM\_POS\_ANCHORING // zf-C3HC4 // CYTOC] CG10277 GH06194 84A4-84A4 dup:2/2 ID:58F6

CG18494 + unknown \* [PFKB\_KINASES\_1] CG18494 GH06208 32A1-32A1 ID:58F8

CG10631 + transcription\_factor \* 6e-06 TF3A\_YEAST TRANSCRIPTION FACTOR IIIA (TFIIIA) transcriptio \* 2e-11 zinc finger motif protein \* 5e-09 similar to Zinc finger, C2H2 typ[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG10631 GH06278 38A2-38A dup:1/3 ID:58G1

CG3380 + transporter \* organic anion transporter-K2(aa) \* solute carrier family (prostaglandin transporter), member 2(aa) \* SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (O CG3380 GH06385 58D1-58D1 dup:1/2 ID:58G11

CG14786 + 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.l CG14786 GH06301 2B1-2B1 ID:58G4

CG6643 + 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

CG10550 + \* 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

CG5571 + \* [G\_PROTEIN\_RECEPTOR] CG5571 77B6-77B6 dup:1/2 ID:58H1

CG3748 + unknown \* CG3748 GH06504 30B-30B ID:58H11

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

CG4377 + unknown \* CG4377 GH06474 58A3-58A3 ID:58H6

CG7062 + Rab-RP3 signal\_transduction \* Rab1 \* Rab-RP3 \* 3e-47 coding sequence YP2 gene \* 1e-121 rab-related protein [ras // ATP\_GTP\_A // RASTRNSFRMNG] CG7062 GH06528 66C5-66C5 ID:59A1

CG8592 + stil unknown \* 1e-171 STAND STILL (Y \* 1e-173 stil \* \* [NLS\_BP] CG8592 GH06596 49B2-49B2 ID:59A10

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

CG10204 + CG10204 102B4-102B5 ID:59A6

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

CG2727 + emp transmembrane\_receptor \* DMEMP\_3 emp \* epithelial membrane protein - fruit fly (*Drosophila melanogaster*)(aa) \* 2e-40 predicted using Genefinder; similar to CD36 family; cDNA [CD36] CG2727 GH06663 60E7-60E8 ID:59B5

CG14904 + Scp2 ligand\_binding\_or\_carrier \* 6e-95 calcium-binding protein Cex C \* 1e-15 YSO6\_CAEEL HYPOTHETICAL CALCIUM-BINDING PROTEIN F56D1.6 IN CHROMOSOME II \* 2e-33 calexcitin \* 7[EF\_HAND // EF\_HAND\_2 // ATP\_GTP\_A] CG14904 GH06666 92A1-89D4 dup:2/4 ID:59B6

CG4347 + enzyme \* UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) (UGPASE)(aa) \* similar to UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRA CG4347 GH06691 67A9-67B1 dup:1/3 ID:59B7

CG7557 + unknown \* [ATP\_GTP\_A] CG7557 GH07076 68C3-68C3 ID:59C11

CG2246 + enzyme \* 41-kDa phosphoribosylpyrophosphate synthetase-associated protein(aa) \* 3e-48 KPR1\_YEAST RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (PHOSPHORIBOSYL PYROPHOSP [Pribosyltran] CG2246 GH07082 100A-100A2 dup:2/4 ID:59C12

CG3762 + \* 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

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

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

CG2469 + transmembrane\_receptor \* BLASTX 4.3E-09 *Mus musculus* putative myelin regulatory factor mRNA, partial cds.(dna) \* TPR-containing, SH2-binding phosphoprotein(aa) \*[TPR\_REGION // TPR\_REPEAT // TPR // NLS\_] CG2469 GH07228 62B4-62B4 dup:4/5 ID:59D12

CG4323 + transporter \* 9e-43 hypothetical protein YLR348c - yeast (*Saccharomyces cerevisiae*) (U \* 1e-74 Oxoglutarate/malate carrier protein - *Caenorhabditis elegans* \* 8e-2 [mito\_carr // MITOCARRIER // MITOCH\_CARR] CG4323 GH07093 92E7-92E7 ID:59D2

CG17035 + unknown \* [PA2\_HIS] CG17035 GH07145 72C1-72C1 ID:59D4

CG10116 + \* TRIACYLGLYCEROL LIPASE (LIPASE, PANCREATIC)(aa) \* 2e-16 VIT1\_DROME VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1) vitell \* 2e-19 LIPL\_MOUSE LIPOPROTEIN L [lipase] CG10116 73D5-73D5 dup:2/2 ID:59D6

CG18512 + CG18512 GH07187 ID:59D7

CG4682 + unknown \* CG4682 GH07323 94D10-94D10 dup:2/2 ID:59E10

CG3588 + EG:100G7.6 structural\_protein \* map\_position:3C5 \* \* \* [PRO\_RICH] CG3588 GH07242 3C4-3C4 dup:2/2 ID:59E3

CG2926 + transcription\_factor \* putative PHD-type zinc finger(aa) \* *Atu*(aa) \* myeloid/lymphoid or mixed-lineage leukemia 2(aa) \* ATP-dependent chromatin assembly factor la[zf-C3HC4 // ZINC\_FINGER\_C3HC4 // PHD //] CG2926 GH07267 83B4-83B4 dup:4/4 ID:59E6

CG4357 + transporter \* solute carrier family (sodium/chloride transporters), member 3(aa) \* BUMETANIDE-SENSITIVE SODIUM-(POTASSIUM)-CHLORIDE COTRANSPORTER (NA-K-CL SYMPORT [AMINO\_ACID\_PERMEASE\_2] CG4357 GH07280 69B-69B2 dup:7/8 ID:59E7

CG8577 + 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

+ 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  
 CG15151 GH07373 36E-36E ID:59F3  
 + Karybeta3 ligand\_binding\_or\_carrier \* karyopherin (importin) beta 3(aa) \* 1e-118 IMB3\_YEAST IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT) (PROTEIN SECRET \* IMB3\_HUMAN IMPORTIN BE [HEAT\_REPEAT] CG1059 GH07384  
 CG1059 82D2-82D2 dup:3/4 ID:59F4  
 + enzyme \* similar to Gila monster phospholipase A2; similar to \* PHOSPHOLIPASE A2 ISOZYMES PA2/PA4  
 CG3009 (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE)(aa) \* 2e-21 PA2\_APIME [PA2\_HIS] CG3009 GH07387 4C7-4C7 ID:59F5  
 + ana unknown \* ana \* neuroblast proliferation inhibitor ana - Drosophila(aa) \* ana \* neuroblast proliferation inhibitor=ana eye  
 CG8084 disc, Peptide, [WW\_DOMAIN\_1] CG8084 GH07389 45A9-45A10 ID:59F6  
 + peptidase \* alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)(aa) \* 8e-98 AAP1\_YEAST ALANINE/ARGININE [ALADIPTASE // Peptidase\_M1 // HEMOPEXIN] CG11955 GH07390 99A5-99A5 dup:2/3 ID:59F7  
 CG11955  
 CG10912 + unknown \* CG10912 GH07575 55B2-55B2 ID:59G12  
 + 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  
 CG14689 + unknown CG14689 GH07528 ID:59G5  
 none + none GH07529 ID:59G6  
 + BG:DS00180.8 cell\_adhesion \* DMTENA\_3 Ten-a \* DMC901PRT C901 \* DMDELTA\_4 DI \* 3e-20 C901 protein [EGF\_2]  
 CG16882 CG16882 GH07717 34E1-34E1 dup:3/4 ID:59H10  
 + enzyme \* DMADHA1\_9 Adh \* DMSCU scu \* 7e-17 SP19\_YEAST SPORULATION PROTEIN SPS19 (SPORULATION-SPECIFIC PROTEIN SPX19) \* 4e-05 3-hydroxyacyl-CoA dehydrogenase [CPSASE\_2 // adh\_short\_C2 // GDHRDH // a] CG2907  
 CG2907 GH07691 83B6-83B6 ID:59H8  
 + endopeptidase \* kuz \* a disintegrin and metalloprotease domain (ADAM) 10(aa) \* 1e-109 kuzbanian \* 1e-102 ADAM similar to [DISINTEGRINS\_2 // ADAM\_MEPRO // ZINC\_PR] CG1964 GH07695 99C1-99C1 ID:59H9  
 CG1964  
 CG8678 + CG8678 dup:1/2 ID:60A10  
 + motor\_protein \* dynein light chain-A(aa) \* DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A)(aa) \* 1e-38 cDNA EST comes from th [ATP\_GTP\_A] CG1938 GH07739 10A10-10A10 dup:2/3 ID:60A3  
 CG1938  
 CG3092 + unknown \* CG3092 GH07743 59D-59D dup:1/2 ID:60A5  
 CG7859 + unknown \* [NLS\_BP] CG7859 GH07769 93D9-93D9 dup:1/2 ID:60A6  
 + unknown \* cDNA EST yk429e10.5 comes from this gene; cDNA EST yk431d3.5 comes \* gene e1 protein - mouse \* is a human counterpart of mouse e1 gene. \* 7e-20 hypo CG14967 GH07785 63C1-64A3 dup:1/3 ID:60A7  
 CG14967  
 CG11877 + unknown \* protein(aa) \*\* CG11877 GH07807 99A1-99A1 dup:2/3 ID:60A8

+ TM4SF unknown \* TM4SF \* 1e-156 belong to the membrane protein group of Transmembrane Super \* 9e-07 CD53\_MOUSE  
 LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROT [TMFOUR // TM4\_2] CG11303 GH07902 60A7-60A7  
 CG11303 dup:2/3 ID:60B10  
 + enzyme \* 9e-10 contains similarity to enoyl-CoA hydratases/isomerases Score=59 \* 2e-38 D3D2\_MOUSE 3,2-TRANS-  
 CG4592 ENOYL-COA ISOMERASE, MITOCHONDRIAL PRECURSOR (DOD [ECH] CG4592 GH07905 33A1-33A1 dup:1/2 ID:60B11  
 CG16887 + BG:DS00941.11 unknown \* AAs(aa) \* AAs(aa) \* CG16887 GH07914 34D4-34D4 dup:2/3 ID:60B12  
 CG17124 + unknown \* CG17124 GH07856 32A4-32A4 dup:1/2 ID:60B6  
 CG6332 + unknown \* [NLS\_BP] CG6332 GH07879 93F14-93F14 dup:1/2 ID:60B8  
 CG8568 + unknown \* 4e-05 C09D4.2 gene product \* \* [NLS\_BP] CG8568 GH07892 16A4-16A5 dup:1/2 ID:60B9  
 + Rbp9 RNA\_binding \* 3e-14 PUB1\_YEAST NUCLEAR AND CYTOPLASMIC POLYADENYLATED RNA-BINDING PROTEIN  
 PUB1 (ARS \* 1e-175 RNA-binding protein \* 5e-70 Similar to the human para [RNP\_1 // RBD // HUDSXL RNA // rrm] CG3151  
 CG3151 GH07919 23C1-23C2 dup:1/2 ID:60C1  
 + endopeptidase \* coded for by C. elegans cDNA CEESC71F; similar to the S25B family of peptidases(aa) \* PROTEASOME  
 COMPONENT C7-I (MACROPAIN SUBUNIT C7-I) (MULTI[PROTEASOME\_B // PROTEASOME\_PROTEASE // ] CG17302  
 CG17302 GH07971 23A3-23A3 dup:1/3 ID:60C10  
 CG11018 + unknown \* [DNA\_LIGASE\_A1] CG11018 GH07940 56E2-56E2 dup:1/2 ID:60C2  
 + Rpl7 ribosomal\_protein RL7\_DROME 60S RIBOSOMAL PROTEIN L7 CG4897 Ribosomal\_L30, THIOL\_PROTEASE\_HIS  
 CG4897 ID:60C3  
 CG9338 + unknown \* CG9338 GH07967 38F1-38F1 dup:1/2 ID:60C9  
 + Cpn ligand\_binding\_or\_carrier \* 1e-128 CPN\_DROME CALPHOTIN calcium-binding protein calphotin - f \* 1e-129 calphotin -  
 CG4795 Drosophila calphotin \* 1e-131 binding or carrier, G \* DMCLPTN\_6 CG4795 GH08002 87B4-87B4 dup:1/2 ID:60D1  
 + transporter \* 8e-07 predicted using Genefinder; cDNA EST yk416g4.5 comes from this g \* 2e-05 hypothetical protein - rabbit  
 CG4526 ORF might exte \* CG4526 GH08173 73A3-73A4 dup:3/6 ID:60D10  
 + 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  
 CG9377 GH08193 34B6-34B6 dup:1/2 ID:60D12  
 + unknown \* 7e-30 weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase \* 1e-58 CGI-16 protein \* 6e-27  
 CG1774 hypothetical protein \* contains weak simil CG1774 GH08048 100D2-100D2 dup:2/3 ID:60D2  
 CG11808 + unknown \* [NLS\_BP] CG11808 GH08125 51E9-51E9 dup:1/2 ID:60D4  
 + BG:DS02780.1 cell\_adhesion \* Toll protein(aa) \* 9e-05 cell-surface molecule connectin - fruit fly (Drosophila melanogaster) \* 2e-  
 CG5888 06 predicted using Genefinder; Similarity to Dr [LRR] CG5888 GH08155 35F12-36A1 dup:1/2 ID:60D6  
 + cell\_adhesion \* DMLACH\_2 Lac \* 1e-09 LACH\_DROME LACHESIN PRECURSOR lachesin melanoga \* 5e-06 hemicentin  
 CG5308 precursor \* 4e-05 elastic titin [ig] CG5308 GH08163 86E9-86E10 dup:2/3 ID:60D7  
 + unknown \* hypothetical protein(aa) \* DMRNAPER\_2 anon-3B1.2 \* 2e-08 0.9-kb RNA transcript \* 7e-10 DMRNAPER\_2  
 CG7096 anon-3B1.2 CG7096 GH08336 93B5-93B5 dup:3/3 ID:60E10  
 CG14183 + endopeptidase \* 3e-11 TBP6\_YEAST PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG 6) \* 3e-08

MEI1\_CAEEL MEIOTIC SPINDLE FORMATION PROTEIN MEI-1 mei-1 \* 0.000 CG14183 GH08353 76E3-76E4 dup:3/3 ID:60E12

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

CG18380 + unknown \* CG18380 GH08307 47A-47A dup:2/2 ID:60E5

CG1742 + Mgstl enzyme (Microsomal glutathione S-transferase-like) microsomal glutathione S-transferase-like protein [Drosophila  
melanogaster] >g MAPEG CG1742 GH08455 dup:1/2 ID:60F10

CG6255 + enzyme \* SUCCINYL-COA SYNTHETASE ALPHA CHAIN (SCS-ALPHA)(aa) \* DMSUCCOAA Scs agr; \* 9e-77  
SUCA\_YEAST PROBABLE SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN [SUCCINYL\_COA\_LIG\_2 // ligase-CoA //  
SUC] CG6255 GH08383 92A6-92A6 dup:2/4 ID:60F3

CG8327 + enzyme \* spermidine synthase(aa) \* SPERMIDINE SYNTHASE (PUTRESCINE AMINOPROPYLTRANSFERASE)  
(SPDSY)(aa) \* 1e-77 SPEE\_YEAST SPERMIDINE SYNTHASE (PUTRESCINE AMI [SAM\_BIND // ATP\_GTP\_A] CG8327  
GH08387 85E2-85E2 dup:2/3 ID:60F4

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

CG7669 + unknown \* [NLS\_BP] CG7669 GH08407 91A-91A dup:1/2 ID:60F7

CG4678 + peptidase \* carboxypeptidase D(aa) \* CARBOXYPEPTIDASE PRECURSOR(aa) \* \* CpepE [CARBOXYPEPT\_ZN\_1 //  
CARBOXYPEPT\_ZN\_2 //] CG4678 GH08425 15A2-15A3 dup:2/3 ID:60F8

CG11656 + unknown \* CG11656 GH08448 87D9-87D9 dup:1/2 ID:60F9

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

CG3138 + cytoskeletal\_structural\_protein \* Similarity to some phosphatases and kinases; cDNA EST comes from this gene(aa) \* 2e-87  
Similarity to some phosphatases and kinases; cDNA ES[PX // RA\_DOMAIN // BEM\_DOMAIN] CG3138 GH08671 5B2-5B2 dup:1/2  
ID:60G12

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

none + none GH08762 ID:60H10

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

CG14830 + \* 1E-102\* \* CG14830 65E10-65E10 dup:2/3 ID:60H4



+ ligand\_binding\_or\_carrier \* DMC30B8 \* retinaldehyde-binding protein 1(aa) \* tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with vitamin E deficiency)(aa) \* 62D[CRETINALDHBP // CRAL\_TRIO] CG10237 GH08711 37E3-37E3 dup:2/3 ID:60H5  
 CG10237  
 + bgcn unknown \* EUKARYOTIC TRANSLATION INITIATION FACTOR (EIF-6)(aa) \* map\_position:60A2+ \* EUKARYOTIC TRANSLATION INITIATION FACTOR (EIF-6)(aa) \* integrin beta bin CG17611 GH08760 60A4-60A4 dup:1/2 ID:60H9  
 CG17611  
 + 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  
 CG3966  
 + 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  
 CG9246  
 CG9445 + unknown \* CG9445 42C7-42C7 dup:3/3 ID:61B11  
 CG13432 + unknown CG13432 GH08941 dup:1/2 ID:61B12  
 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  
 CG11334 + translation\_factor \* hypothetical translation initiation factor(aa) \* HYPOTHETICAL 40.9 KD PROTEIN C01G10.9 IN CHROMOSOME V(aa) \* 3e-66 YP18\_YEAST HYPOTHETICAL 45.0 KD P [IF-2B] CG11334 GH08894 100C-100C dup:1/2 ID:61B5  
 CG12024 + signal\_transduction \* 5e-25 BAW protein \* \* [NLS\_BP] CG12024 GH08896 62E3-62E3 dup:1/2 ID:61B6  
 CG5406 + sif signal\_transduction (still life) Guanine-nucleotide dissociation stimulators CDC24 family signatur GRF\_DBL, NLS\_BP, PDZ, PH\_DOMAIN, PRO\_RIC] CG5406 GH08923 dup:1/2 ID:61B8  
 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 // PAPAIN // Peptida] CG8947 70C9-70C9 dup:1/2 ID:61C5  
 CG18404 + unknown \* CG18404 GH09039 99E5-99E5 dup:1/2 ID:61C7  
 CG7841 + unknown \* CG7841 GH09068 71C4-71C4 dup:1/2 ID:61D1  
 CG18452 + scro transcription\_factor (scarecrow) homeobox protein Nkx2-1 homeobox CG18452 GH09166 dup:2/3 ID:61D10  
 CG6304 + unknown \* [NLS\_BP] CG6304 GH09088 36A14-36A14 dup:2/3 ID:61D2  
 CG3987 + unknown \* CG3987 GH09123 88E4-88E5 dup:2/3 ID:61D3  
 CG13604 + 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

CG8508 + unknown \* CG8508 GH09161 87E2-87E2 dup:1/2 ID:61D9  
+ endopeptidase \* TRYPSIN DELTA PRECURSOR(aa) \* Ser12 \* Ser6 \* Dvtry-1 trypsin precursor(aa) [trypsin //  
CG4653 CHYMOTRYPSIN // TRYPSIN\_HIS ] CG4653 GH09333 15A1-15A1 ID:61F1  
+ unknown \* coded for by C. elegans cDNA cm16h1; coded for by C. elegans cDNA yk13a7.5; coded for by C. elegans cDNA  
CG8919 yk13a7.3; similar to S. cerevisiae SAC3 pro [RBD] CG8919 GH09410 15E1-15E1 dup:2/3 ID:61F10  
+ endopeptidase \* prolyl endopeptidase(aa) \* 3e-06 PPCE\_PIG PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING  
ENZYME) (PE) \* prolyl oligopeptidase (EC 3.4.21.26) - human [PROLIGOPTASE // Peptidase\_S9 // ESTERAS] CG2528 GH09342  
CG2528 40A6-40A6 dup:2/2 ID:61F2  
none + none GH09355 ID:61F3  
+ Eip71CD enzyme \* 6e-11 PMSR\_YEAST PUTATIVE PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O)  
CG7266 REDUC \* 1e-123 put. Eip (aa 1-255) \* 2e-29 similar to drosophila e CG7266 GH09363 71C4-71C4 dup:2/3 ID:61F4  
CG10508 + unknown \* [WW\_DOMAIN\_2] CG10508 GH09378 78C4-78C4 dup:3/6 ID:61F6  
+ enzyme \* DMCATHPO\_2 Cat \* CATALASE(aa) \* 1e-110 CATA\_YEAST CATALASE A catalase (EC 1.11.1.6), peroxisomal -  
\* 1e-158 catalase (EC 1.11.1.6) - Caenorhabditis [CATALASE // catalase // CATALASE\_1] CG9314 GH09387 29E4-29E4 dup:1/2  
CG9314 ID:61F8  
CG4302 + CG4302 CG11051 GH09393 ID:61F9  
CG4891 + BG:DS04095.1 unknown \* CG4891 GH09478 35F1-35F1 dup:1/2 ID:61G1  
+ nAcRalpha-96Ab ion\_channel \* DMARD1\_2 nAcR bgr;-64B \* DMNARAS nAcR bgr;-96A \* DMDA2\_2 nAcR agr;-96Ab \*  
ACH2\_DROME ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-LIKE CHAIN PRECU[NICOTINICR // neur\_chan //  
CG6844 NEUROTR\_ION\_] CG6844 GH09582 96A2-96A2 dup:1/3 ID:61G11  
CG8403 + SP2353 cell\_adhesion agrin-like ATP\_GTP\_A, EGF, EGF\_1, EGF\_2, LAM\_G\_DOMA] CG8403 GH09608 dup:1/3 ID:61G12  
+ 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 //  
CG6593 STPHPHTASE // SER\_THR\_] CG6593 GH09488 96A5-96A5 ID:61G3  
+ enzyme \* sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)(aa) \* SPHINGOMYELIN  
PHOSPHODIESTERASE PRECURSOR (ACID SPHINGOMYELINASE)(aa [PHOSPHO\_ESTER // SAP\_B] CG3376 GH09489  
CG3376 60C1-60C2 dup:2/5 ID:61G4  
+ signal\_transduction \* agrin(aa) \* 8e-33 similar to agrin and follistatin; egf-like repeats \* 4e-13 FSA\_MOUSE FOLLISTATIN  
CG7159 PRECURSOR (FS) (ACTIVIN-BINDING PROTEIN) \* 4e-13 [kazal] CG7159 GH09510 66C12-66C12 ID:61G5  
+ enzyme \* 7e-62 SYWM\_YEAST TRYPTOPHANYL-TRNA SYNTHETASE, MITOCHONDRIAL (TRYPTOPHAN--TRNA  
LIGASE) \* 1e-60 SYWM\_CAEEL PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE, MIT [TRNASYNTHTRP // tRNA-synt\_1b //  
CG7441 AA\_TRNA] CG7441 GH09538 75A4-75A4 dup:1/3 ID:61G8  
+ cell\_adhesion \* 6e-05 similar to the protein kinase domain of myosin light chain kinases \* 6e-05 myosin light chain kinase  
CG5699 isoform \* 5e-05 KMLS\_CHICK MYOSIN LIGHT C CG5699 GH09541 62C3-62C3 dup:2/3 ID:61G9  
CG2204 + G-alpha47A signal\_transduction GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT (CLASS-I) >gil]

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

+ unknown \* 2e-13 YJT6\_YEAST HYPOTHETICAL 36.2 KD PROTEIN IN UBP12-CDC6 INTERGENIC REGION \* 8e-18 YLF4\_CAEEL HYPOTHETICAL 34.1 KD PROTEIN C40H1.4 IN CHROMOSOME CG9798 GH09808 82C1-82C2 dup:3/4 ID:61H12

CG9798 + enzyme \* similar to pig tubulin-tyrosine ligase.(aa) \* 4e-06 YBU4\_YEAST HYPOTHETICAL 86.4 KD PROTEIN IN PHO5-VPS15 INTERGENIC REGION \* 1e-76 similar to tubul CG16833 GH09663 32C5-34A5 dup:1/3 ID:61H3

CG16833 + transcription\_factor \* 3e-05 HUNB\_TRICA HUNCHBACK PROTEIN hunchback \* 2e-06 DMHBG\_10 hb \* Hunchback protein

CG9932 \* [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG9932 GH09733 34A-34A dup:1/2 ID:61H6

CG17809 + alpha-Man-I enzyme mannosyl-oligosaccharide 1,2-alpha-mannosidase GLYHDLASE47 CG17809 GH09743 dup:1/2 ID:61H7

CG9312 + unknown \* [NLS\_BP] CG9312 GH09754 87F13-87F13 dup:1/2 ID:61H8

+ 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 + TBPH RNA\_binding \* map\_position:60A5-6 \* TAR-binding protein(aa) \* TBPH \* 2e-16 NAB4\_YEAST NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4 [RNP\_1 // RBD // rrm // NLS\_BP] CG10327 GH09868 60A5-60A6 dup:1/2 ID:62A7

CG10327 + unknown \* [NLS\_BP] CG11074 GH09884 42F2-42F2 ID:62A8

CG11074 + \* 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 + CG1822 dup:2/2 ID:62B10

CG1822 + 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 (Saccharomyces cerevisiae) \* 4e-73 FUCO\_CAE [Alpha\_L\_fucos // GLHYDLASE29] CG6128 GH09976 68C4-68C5 ID:62B4

CG6128 + unknown \* [PRO\_RICH // NLS\_BP] CG2467 GH09980 10F7-10F8 dup:2/2 ID:62B5

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

CG6247 + metabolism \* NADH-UBIQUINONE OXIDOREDUCTASE SGDH SUBUNIT PRECURSOR (COMPLEX I-SGDH) (CI-SGDH)(aa) \* NADH dehydrogenase (ubiquinone) beta subcomplex, (16kD, SGDH) CG9762 GH10129 68F5-68F5 ID:62C1

CG9762

+ unknown \* DMRHO\_2 ve \* RHOMBOID PROTEIN (VEINLET PROTEIN)(aa) \* 5e-32 similar to transmembrane of D.  
 CG1697 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  
 CG10521 12F1-12F3 dup:1/2 ID:62C5  
 + transmembrane\_receptor \* 2e-09 /match=(desc: \* 2e-52 YP84\_CAEEL HYPOTHETICAL 90.9 KD PROTEIN C08B11.4 IN  
 CG3106 CHROMOSOME II \* predicted using Genefinder \* cDNA EST comes from thi CG3106 GH10201 8F2-8F2 ID:62C6  
 + unknown \* similar to several putative T1/ST2receptor binding protein precursors(aa) \* 3e-14 EM24\_YEAST ENDOSOMAL  
 CG9308 P24B PROTEIN PRECURSOR (24 KD ENDOMEMBRANE P [EMP24\_GP25L] CG9308 GH10235 58B9-58B9 ID:62C9  
 + chaperone \* 5e-06 YB05\_YEAST HYPOTHETICAL 44.1 KD PROTEIN IN RPB5-CDC28 INTERGENIC REGION \* 1e-10  
 CG6980 Hsp70/Hsp90 organizing protein homolog \* 1e-08 coded for by C. [TPR\_REGION] CG6980 GH10293 98E1-98E1 ID:62D2  
 + enzyme \* 5e-18 4-nitrophenylphosphatase (EC 3.1.3.41) - yeast (Saccharomyces cerevisiae) \* 1e-10 by content; 1-meth \*  
 CG5577 1e-24 YMQ1\_CAEEL HYPOTHETICAL 88.1 KD P CG5577 GH10306 75A4-75A4 ID:62D3  
 CG9164 + enzyme \* protein(aa) \* \* CG9164 GH10344 13C5-13C5 ID:62D5  
 CG6130 + unknown \* CG6130 GH10346 90E4-90E4 ID:62D6  
 + 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 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)  
 CG17238 (isoform 1) \* c431H6.1.3 (PUTATIVE novel prot CG17238 GH10365 87E1-87E1 dup:2/2 ID:62D8  
 CG18069 + CaMKII protein\_kinase proline rich calmodulin-dependent protein kinase PROTEIN\_KINASE\_DOM, pkinase CG18069 ID:62D9  
 + cell\_adhesion \* 9e-05 tenascin-like protein precursor - fruit fly (Drosophila melanogaster) \* 2e-47 C09F9.2 \* 5e-06 Ten-m2 \*  
 CG12781 2e-05 predicted using hexExon; MAL3P2.1 [EGF\_1 // EGF\_2 // NLS\_BP] CG12781 GH10539 59B4-59B4 dup:4/4 ID:62E10  
 + motor\_protein \* 2e-05 cellular myosin heavy chain \* 8e-07 myosin heavy chain, neuronal - rat \* 1e-05 Klp68D \* myosin heavy  
 CG4681 chain IIb CG4681 GH10544 60D6-60D6 dup:2/2 ID:62E11  
 + unknown \* 2e-05 No definition line found \* 4e-16 type II membrane protein \* 1E-175\* [SAP\_B // ER\_TARGET] CG12918  
 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  
 CG13917 dup:3/3 ID:62E3  
 + ligand\_binding\_or\_carrier \* 1e-22 YBE9\_YEAST HYPOTHETICAL 16.1 KD PROTEIN IN SEC17-QCR1 INTERGENIC  
 CG15309 REGION \* 8e-21 putative zinc-binding protein melanogaste \* 1e-18 No definitio CG15309 GH10478 9B6-9B6 dup:2/2 ID:62E4  
 CG11191 + unknown \* CG11191 GH10486 43F9-43F9 dup:2/2 ID:62E6  
 + tafazzin unknown \* 2e-17 hypothetical protein YPR140w - yeast (Saccharomyces cerevisiae) ( \* 4e-39 ZK809.2 \* 1e-59 tafazzin  
 CG8766 TAFAZZIN \* 2e-40 Similar to tafazzins prote [GLYCEROL\_ACYLTRANS // TAFAZZIN] CG8766 GH10529 49C1-49C1 dup:2/2  
 ID:62E9  
 CG16979 + unknown \* 3e-61 F38A5.1 gene product \* 1e-40 putative protein \* CG16979 GH10640 71D3-71D3 ID:62F11

CG10433 + \* [PRENYLATION] CG10433 57F3-57F3 dup:4/5 ID:62F12

CG13848 + 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

+ enzyme \* DMHISSEAC\_3 Rpd3 \* histone deacetylase mHDA1(aa) \* histone deacetylase HDA2(aa) \* histone deacetylase, shares sequence similarity with Rpd3p, Hos1p [LECTIN\_LEGUME\_BETA // Hist\_deacetyl] CG1770 GH10588 11E1-11E3 dup:1/3 ID:62F3

CG1770

CG2267 + transcription\_factor \* CG2267 100A2-100A2 dup:2/2 ID:62F6

+ signal\_transduction \* protein(aa) \* 1e-31 Sec7p \* 2e-76 similar to S. cerevisiae protein transport protein SEC7 \* 1e-38

CG10577 cytohesin [SEC7 // Sec7 // NLS\_BP] CG10577 GH10594 78B1-78B1 dup:1/2 ID:62F7

+ DNA\_binding \* 2e-05 ROX1\_YEAST ROX1 REPRESSOR (HYPOXIC FUNCTION REPRESSOR) (HEME-DEPENDENT REPRESSIO \* 7e-14 bobby sox \* 4e-30 similar to HMG box transcription fa [LIPOCALIN // HMG // HMG\_box // PRO\_RICH] CG5067 GH10633 95A4-92D9 ID:62F8

CG5067

+ 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\_2 //] CG9151 GH10637 13C1-13C4 ID:62F9

CG9151

+ unknown \* 1e-36 predicted using Genefinder; Similarity to Human leukocyte surface \* 7e-22 CD63\_MOUSE CD63 ANTIGEN CD63/ME491 antigen homolog - mou \* 3e-44 tet [transmembrane4 // TMFOUR // TM4\_2] CG10742 GH10778 3A9-3A9 dup:1/2 ID:62G10

CG10742

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

CG3544

+ enzyme \* similar to chitin synthases(aa) \* 9e-13 CHS3\_YEAST CHITIN SYNTHASE (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 3) \* 8e-06 hyaluronan synthase \* 8e- CG2666 GH10726 83A5-83A5 ID:62G3

CG2666

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

CG4462

none + none GH10751 ID:62G7

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

CG10374

+ 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

CG11280

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

CG7029 + motor\_protein \* CG7029 GH10817 94C8-94D dup:2/5 ID:62H3

+ enzyme \* similar to plant chloroplast and prokaryotic carbonic anhydrases(aa) \* 2e-63 similar to plant chloroplast and prokaryotic carbonic anhydrases \* 2e-1 [Pro\_CA] CG11967 GH10821 85C3-85C3 ID:62H4

CG11967

+ ninaC motor\_protein \* DMNINAC\_2 ninaC \* ligand binding or carrier calmodulin binding ) protein kinase protein serine/threonine kinase ) cell non-muscle myosin ) map\_posit [myosin\_head // PROTEIN\_KINASE\_TYR // IQ] CG5125 GH10824 27F5-27F6 ID:62H5

CG5125

+ 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  
 CG8362 + transporter \* 3e-29 ITR2\_YEAST MYO-INOSITOL TRANSPORTER myo-inositol transp \* 1e-24 glucose transporter 1; CeGT1 \* 9e-22 Contains similarity to Pfam domain: (suga [SUGRTRANSPORT // SUGAR\_TRANSPORT\_1 // SU] CG1213 GH10929 83C4-83C4 dup:1/3 ID:63A7  
 CG1213  
 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 66E6-66E6 ID:63B10  
 CG5288  
 + enzyme \* similarity to enoyl CoA hydratase. Amino terminus shows similarity to acyl-CoA binding domains; cDNA EST comes from this gene; cDNA EST comes from [ECH // NLS\_BP] CG13890 GH11143 61D4-61D4 ID:63B12  
 CG13890 + transcription\_factor \* 9e-06 TBP-like factor \* 9e-06 TATA box binding protein-related factor \* CG9879 GH11020 23A3-23A3 ID:63B2  
 CG9879  
 + enzyme \* 1e-09 URE2\_YEAST URE2 PROTEIN glutathione transferase homolog U \* 4e-78 glutathione transferase (EC 2.5.1.18) D1 - fruit fly (Drosophila melanogaste [GST] CG10091 GH11034 87B12-87B12 ID:63B3  
 CG10091 + endopeptidase \* serine protease 18D(aa) \* 1e-34 SNAK\_DROME SERINE PROTEASE SNAKE PRECURSOR serine proteina \* 1e-15 kallikrein \* 1e-22 coagulation factor XI [trypsin // CHYMOTRYPSIN // TRYPSIN\_SER] CG11841 GH11046 98F9-98F10 dup:2/2 ID:63B4  
 CG11841 + unknown \* 6e-05 transducer \* 6e-05 chemotactic transducer \* [VWA\_DOMAIN] CG16868 GH11109 56F16-56F16 dup:1/2 ID:63B9  
 CG16868  
 + enzyme \* Ac76E \* 5e-56 adenyl cyclase 76E \* 2e-45 Similar to guanylate cyclase \* 2e-54 adenyl cyclase type I [GUANYLATE\_CYCLASES // guanylate\_cyc // ] CG5712 GH11267 62D3-62D4 ID:63C10  
 CG5712 + unknown \* 2e-15 YHC1\_YEAST HYPOTHETICAL 53.1 KD PROTEIN IN SPO11-OPI1 INTERGENIC REGION \* 1e-44 similar to gamma-butyrobetaine,2-oxoglutarate dioxygenase; cDN CG14630 GH11273 1E1-1E1 ID:63C11  
 CG14630 + Rack1 signal\_transduction \* Rack1 \* GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (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  
 CG7111 + enzyme \* gamma-aminobutyric acid transaminase(aa) \* PROBABLE 4-AMINOBUTYRATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (GAMMA-AMINO-N-BUTYRATE TRANSAMINASE) CG7433 GH11161 76E2-76E2 dup:1/4 ID:63C3  
 CG7433  
 + EG:100G10.4 enzyme \* by content; by match; 2-match\_description=4-NITROPHENYLPHOSPHATASE.; 2-match...(aa) \* BLASTX 8.9E-14 PHO13[4-Nitrophenylphosphatase(dna) \* 1e-20 4- CG2680 GH11163 3B5-3B5 ID:63C4  
 CG2680  
 CG12727 + unknown \* CG12727 GH11189 11F7-11F7 ID:63C5  
 + unknown \* 1e-37 Contains similarity to Pfam domain: (zf-C3HC4), Score=13.0 \* 9e-33 nicotinic acetylcholine receptor-associated 46K protein - mouse (J03 \* 5e-3 [TPR\_REPEAT // ZF\_RING] CG1909 GH11191 102C5-102C5 dup:1/3 ID:63C6  
 CG1909 + PebIII ligand\_binding\_or\_carrier \* PebIII \* 2e-48 ejaculatory bulb specific protein III \* 2e-31 chemosensory protein CSP-sg1 \* olfactory protein CG11390 GH11257 60B1-60B1 ID:63C9  
 CG11390

+ 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  
 CG4370 POTASSIUM CHANNEL (GIRK3) (POTASSIUM CHANNEL, INWARDL [CHANNEL\_PORE\_K // IRK] CG4370 GH11459 97D1-97D1 ID:63D11  
 + porin ion\_channel \* DMMITPORN\_2 porin \* 1e-24 porin - yeast (Saccharomyces cerevisiae) outer mitochondri \* 1e-162 voltage  
 CG6647 dependent anion-selective channel \* 2e-55 code [Euk\_porin // EUKARYTPORIN // EUKARYOTIC] CG6647 GH11331 32B3-32B4  
 dup:2/3 ID:63D2  
 + unknown \* 1e-16 ERS1\_YEAST TRANSMEMBRANE PROTEIN ERS1 (ERD SUPPRESSOR) ER \* 6e-39 similarity to the  
 CG17119 transmembranous domains of yeast ERS1 protein; c \* 5e-76 c [TONB\_DEPENDENT\_REC\_1] CG17119 GH11342 94D12-94D12  
 ID:63D3  
 CG18418 + unknown \* CG18418 GH11346 65A10-65A10 ID:63D4  
 + jim transcription\_factor \* stripe a/b protein - fruit fly (Drosophila melanogaster)(aa) \* zinc finger protein/embryonic muscle  
 development-related transcriptional re[ZINC\_FINGER\_C2H2 // zf-C2H2 // ZINC\_FIN] CG11352 GH11419 79F3-79F3 dup:3/3  
 CG11352 ID:63D8  
 + Dynein heavy chain at 93AB motor\_protein DYNEIN BETA CHAIN, CILIARY ATP\_GTP\_A, MITOCH\_CARRIER, NLS\_BP,  
 CG3723 THIOL] CG3723 GH11420 ID:63D9  
 + EG:25E8.1 chaperone \* Similarity to HSP70's.; cDNA EST CEESD26F comes from this gene; cDNA EST CEMSB16F comes from  
 this gene; cDNA EST CEMSB16FB comes from this gene; cDN [HEATSHOCK70 // HSP70 // HSP70\_3] CG2918 GH11566 2F1-2F2  
 CG2918 dup:2/2 ID:63E12  
 CG6441 + unknown \* CG6441 GH11511 28A1-28A1 dup:2/2 ID:63E3  
 CG12638 + CG12638 GH11525 dup:2/2 ID:63E7  
 + unknown \* cold inducible glycoprotein 30(aa) \* 5e-15 SUR4 \* 8e-53 YYS3\_CAEEL HYPOTHETICAL 51.5 KD PROTEIN IN  
 CG3971 CHROMOSOME IV (U \* 2e-49 membrane glycoprotein CI CG3971 GH11554 73B1-77B1 dup:2/2 ID:63E9  
 + 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 // efhand // EF\_HAND\_2] CG6702 GH11671 53E7-53E10 ID:63F12  
 + cytoskeletal\_structural\_protein \* DMTUBA1\_2 agr;Tub84B \* 1e-117 TBA1\_YEAST TUBULIN ALPHA-1 CHAIN tubulin alpha-  
 CG7794 1 chain \* 1e-132 TBA1\_DROME TUBULIN ALPHA-1 CHAIN tubulin alpha-1 chain [tubulin] CG7794 GH11574 90D2-90D2 ID:63F2  
 CG3306 + unknown \* CG3306 GH11578 67B9-67B9 ID:63F3  
 + receptor \* 5e-05 LIRP\_LOCFI LIRP PRECURSOR (LOCUSTA INSULIN-RELATED PEPTIDE) \* \* [INSULIN // Insulin //  
 CG8167 NLS\_BP] CG8167 GH11579 67C-67C ID:63F4  
 CG1324 + unknown \* [ATP\_GTP\_A] CG1324 GH11587 19E3-19E3 ID:63F6  
 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 L34(aa) \* 1e-47 RL34\_AEDAL 60S RIBOSOMAL PROTEIN L34 (L3 NLS\_BP, RIBOSOMAL\_L34E CG9354 ID:63F9  
 CG9354 + grh transcription\_factor \* DMELF1\_2 grh \* transcription factor NTF1 - fruit fly (Drosophila melanogaster) (fragment) \* 1e-22  
 CG5058 alpha-globin transcription factor CP2 - mouse \* 9e [NLS\_BP] CG5058 GH11672 54F1-54F4 ID:63G1  
 + RNA\_binding \* putative RNA-binding protein(aa) \* Wbscr1(aa) \* 7e-05 NSR1\_YEAST NUCLEAR LOCALIZATION SEQUENCE BINDING PROTEIN (P67) \* 2e-13 RNA recognition motif-t [RNP\_1 // RBD // rrm // NLS\_BP] CG1340 GH11731 100A-100A dup:2/2 ID:63G10  
 CG1340 + motor\_protein \* 3e-08 hook1 protein \* p230 peripheral membrane pr \* autoantigen, subfamily a, > \* CG14039 GH11749  
 CG14039 25C3-25C3 dup:1/4 ID:63G11  
 + Sin3A transcription\_factor \* 3e-58 SIN3\_YEAST PAIRED AMPHIPATHIC HELIX PROTEIN regulatory \* transcription factor \* 2e-31 cDNA EST comes from this gene; cDNA EST co \* 1e-135 co-r [ATPASE\_ALPHA\_BETA // NLS\_BP] CG8815 GH11769 49B2-49B3 dup:1/2 ID:63G12  
 CG8815 + endopeptidase \* similar to the M13 or zinc metalloprotease family of peptidases(aa) \* endothelin converting enzyme 1(aa) \* endothelin converting enzyme-2 - bovine [ZINC\_PROTEASE // Peptidase\_M13] CG9505 GH11680 28D1-28D1 ID:63G3  
 CG9505 + unknown \* CG14355 GH11706 88A12-88B1 ID:63G5  
 CG14355 + unknown \* 1e-10 immune induced protein \* 0.000000000002\* 1E-141\* CG18107 GH11719 55C9-55C9 ID:63G6  
 CG18107 + unknown \* CG11404 GH11730 79E-79E ID:63G9  
 CG11404 + Nacalphaunknown \* 4e-13 EGD2\_YEAST EGD2 PROTEIN EGD2 protein - yeast (Saccharomyc \* 5e-73 alpha NAC \* 1e-34 alpha NAC/1.9.2. protein alpha-NAC, non-musc \* 1e-34 Nasce CG8759 GH11940 49C2-49C2 dup:2/2 ID:63H12  
 CG8759 + unknown \* 1e-06 ectodermal (ect) - fruit fly (Drosophila melanogaster) (strain Oregon-R) \* \* [NLS\_BP] CG6611 GH11838  
 CG6611 67D2-67D2 ID:63H3  
 + enzyme \* DNA-DIRECTED RNA POLYMERASE II KD POLYPEPTIDE (RNA POLYMERASE II SUBUNIT 5)(aa) \* polymerase (RNA) II (DNA directed) polypeptide G(aa) \* 7e-33 RPB7\_ [S1] CG6572 GH11867 88E8-88E8 ID:63H5  
 CG6572 none + none GH11889 ID:63H7  
 none + BcDNA:GH07066 enzyme \* 8e-47 PLSB\_CAEEL PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT) \* 6e-77 PLSB\_MOUSE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (G [GLYCEROL\_ACYLTRANS] CG5508 GH11892 98B2-98B2 dup:2/2 ID:63H8  
 CG5508 + zfh2 transcription\_factor \* ZINC-FINGER PROTEIN (ZINC-FINGER HOMEODOMAIN PROTEIN 2)(aa) \* DMZFH2\_2 zfh2 \* 7e-40 Contains similarity to Pfam domain: (zf-C2H2), Score=[HOMEODOMAIN\_1 // homeobox // ZF\_MATRIN // ] CG1449 GH11902  
 CG1449 102C1-102C3 dup:2/2 ID:63H9  
 CG10286 + unknown \* CG10286 GH12023 83E6-83E6 dup:1/2 ID:64A12  
 + 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



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

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

CG4261 + Hel89B DNA\_binding \* TBP-associated factor 172(aa) \* Hel89B \* 89B helicase(aa) \* MOT1\_YEAST PROBABLE HELICASE MOT1 MOT1 protein - yeast (S [helicase\_C // SNF2\_N] CG4261 GH12153 89B3-89B3 dup:1/2 ID:64C3

CG3541 + unknown \* 6e-05 transmembrane protein \* 2e-12 Similarity to C.elegans cuticulin (SW:CUT1\_CAEEL) \* 7e-07 DMDUSKY\_1 dy \* similar to cuticlin CG3541 GH12163 60D7-60D8 dup:1/2 ID:64C4

CG1007 + 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

CG6367 + 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

CG5291 + cell\_adhesion CG5291 GH12331 dup:2/3 ID:64D5

CG15560 + unknown \* 8e-42 YMS5\_CAEEL HYPOTHETICAL 159.2 KD PROTEIN K03H1.5 IN CHROMOSOME III \* 8e-17 alpha tectorin \* 2e-16 tectorin alpha alpha-tectorin \* 1e-15 alpha CG15560 GH12365 100B8-100B8 ID:64D8

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

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

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

CG1794 + \* membane-type metalloproteinase precursor(aa) \* MATRIX METALLOPROTEINASE-14 PRECURSOR (MMP-14) (MEMBRANE-TYPE MATRIX METALLOPROTEINASE 1) (MT-MMP 1) [Peptidase\_M10 // hemopexin // ZINC\_PROT] CG1794 45F6-46A1 dup:4/5 ID:64E7

CG7651 + transporter \* protein(aa) \* DMATPA\_2 Atp agr; \* SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA CHAIN (SODIUM PUMP) (NA+/K+ ATPASE)(aa) \* BLASTX 3.4E-17 Rat alternativ [NAKATPASE // HATPASE // CATATPASE // E1] CG7651 GH12627 79F3-79F3 ID:64F10

CG2903 + signal\_transduction \* 5e-23 VP27\_YEAST VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27 \* 3e-10 /match=(desc;; /ma \* 9e-65 coded for by C. elegans cDNA yk21d11.3; coded [FYVE\_DOMAIN // FYVE // HRS\_DOMAIN] CG2903 GH12653 23A6-23A7 ID:64F12

CG9122 + enzyme \* DMPAH Hn \* 1e-114 phenylalanine hydroxylase \* 1e-117 tryptophan hydroxylase \* 1e-149 TR5H\_MOUSE TRYPTOPHAN 5-MONOOXYGENASE (TRYPTOPHAN 5-HYDROXYLASE [FYWHYDRXLASE // biopterin\_H // BIOPTERIN] CG9122 GH12537 61F3-61F3 ID:64F2

CG6282 + unknown \* hypothetical protein \* 1E-162\* hypothetical protein \* hypothetical protein, 5' partial [S5A\_REDUCTASE] CG6282 GH12549 68C1-68C1 dup:3/4 ID:64F4

CG11146 + signal\_transduction Shb=Src homology 2 protein ANTIFREEZE1, SH2 CG11146 ID:64F5

+ nucleic\_acid\_binding \* 2e-11 coded for by C. elegans cDNA yk98h8.3; coded for by C. elegans cDNA yk98h8.5 \* \*  
 CG14682 CG14682 GH12580 86C2-86C2 ID:64F6  
 CG14821 + unknown \* [PRO\_RICH] CG14821 GH12583 65D5-65D5 ID:64F7  
 + signal\_transduction \* Ras-binding protein SUR-8(aa) \* 4e-25 adenylate cyclase \* 9e-32 gene flightless-I protein - fruit fly  
 CG5407 (Drosophila melanogaster) ( \* 1e-152 Ras-bindi [LRR // LEURICHRPT] CG5407 GH12617 90A6-92E12 ID:64F8  
 + transporter \* cellutagmin I sytVI - rat(aa) \* DMPKC53E\_2 inaC \* DMSYT\_2 syt \* 4e-40 SY65\_DROME SYNAPTOTAGMIN  
 CG3020 (P65) synaptotagmin - fruit fly ( [SYNAPTOTAGMN // C2 // C2\_DOMAIN\_2 // PR] CG3020 GH12656 71A3-71A4 ID:64G1  
 CG3982 + unknown \* CG3982 GH12755 67B3-67B3 dup:2/2 ID:64G10  
 + enzyme \* 2e-61 wunen \* 1e-24 YSX3\_CAEEL HYPOTHETICAL 39.0 KD PROTEIN T28D9.3 IN CHROMOSOME II (U2 \* 6e-  
 CG11426 35 Phosphatidic acid phosphatase \* 5e-36 phosphatidic [PA\_PHOSPHATASE] CG11426 GH12758 79E4-79E4 ID:64G11  
 + RNA\_binding \* BLASTX 2.0E-34 Arabidopsis thaliana Col-O putative RNA helicase A mRNA, complete cds.(dna) \*  
 DMMLE\_2 mle \* 1e-79 hypothetical protein YLR419w - yeas [PROTEIN\_SPLICING // G\_PROTEIN\_RECEPTOR ] CG9323  
 CG9323 GH12763 38E5-38E5 ID:64G12  
 + unknown \* 3e-08 probable membrane protein YLR251w - yeast (Saccharomyces cerevisiae) \* 1e-08 /match=(desc: \* 3e-15  
 CG10854 PMP2\_MOUSE KD PEROXISOMAL MEMBRANE PROTEIN CG10854 GH12661 64C4-64C4 ID:64G2  
 + enzyme \* diacylglycerol kinase(aa) \* 2e-30 diacylglycerol kinase (EC 2.7.1.107) - fruit fly (Drosophila melanogaster) \* 1e-57  
 CG5875 alpha diacylglycerol kinase; a [DAG\_PE\_BINDING\_DOMAIN // RA // C1 // DA] CG5875 GH12677 95D1-97F1 dup:2/5 ID:64G5  
 CG10806 + transporter \* protein:Na+/H+ antiporter(aa) \* cdu2(aa) \* cdu2 cd \* CG10806 GH12682 27C-27C ID:64G6  
 + Snap transporter \* Snap \* soluble NSF attachment protein(aa) \* 3e-40 transport vesicle fusion protein SEC17 - yeast  
 CG6625 (Saccharomyces cerevisiae) \* 1e-73 coded for by C. [NSFATTACHMNT] CG6625 GH12751 77B3-77B3 dup:1/2 ID:64G9  
 + unknown \* androgen-induced prostate proliferative shutoff associated protein(aa) \* protein(aa) \* 1e-28 unknown \* 6e-40  
 CG17509 cDNA EST comes from this gene elegan CG17509 GH12788 48E2-48E2 dup:3/3 ID:64H3  
 + endopeptidase \* DMEAST\_4 ea \* serine proteinase(aa) \* 1e-09 easter \* 5e-07 anticoagulant protein C [trypsin //  
 CG17837 TRYPSIN\_CATAL] CG17837 GH12831 92F5-92F5 dup:2/2 ID:64H6  
 + protein\_phosphatase \* DMPP1A1\_2 Pp1 agr;-96A \* serine-threonine protein phosphatase(aa) \* type 1-related protein  
 phosphatase(aa) \* 1e-110 PP12\_YEAST SERINE/THREONINE PR[PHOSPHO\_ESTER // STPHPHTASE // SER\_THR\_] CG10138  
 CG10138 GH12873 58B9-58B9 ID:65A1  
 CG13918 + unknown \* CG13918 GH13002 62A-62A ID:65A12  
 CG7634 + unknown \* [TPR\_REPEAT] CG7634 GH12875 78E2-78E2 dup:2/2 ID:65A2  
 + protein\_kinase \* 5e-06 DRK\_DROME PROTEIN E(SEV)2B (SH2-SH3 ADAPTOR PROTEIN DRK) \* 1e-05 SEM5\_CAEEL  
 CG8179 SEX MUSCLE ABNORMAL PROTEIN sem-5 protein - \* 9e-12 stac \* 6e-13 s [SH3] CG8179 GH12942 52A2-52A4 dup:1/2 ID:65A6  
 + 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  
 CG6734 ID:65A8  
 + structural\_protein \* 9e-09 cuticle protein LCP65Ac cuticle p \* 2e-11 CUD4\_LOCM1 ENDOCUTICLE STRUCTURAL  
 GLYCOPROTEIN (ABD-4A) g \* 1e-10 Lcp65Ac \* cuticle homolog [CUTICLE // insect\_cuticle] CG8511 GH12964 49A3-49A3  
 CG8511 ID:65A9

|         |  |
|---------|--|
| CG1970  | + enzyme * NADH-UBIQUINONE OXIDOREDUCTASE KD SUBUNIT PRECURSOR (COMPLEX I-49KD) (CI-49KD)(aa) * BLASTX 2.1E-17 Bovine mRNA fragment for kDa subunit of mitochon [COMPLEX1_49K // complex1_49Kd] CG1970 GH13128 102C5-102C5 dup:2/3 ID:65B10                |
| CG11509 | + unknown * CG11509 GH13132 2B6-2B6 ID:65B11   |
| CG7549  | + unknown * [HTH_LACI_FAMILY] CG7549 GH13023 84F-84F ID:65B2   |
| CG6114  | + protein_kinase * serine/threonine kinase(aa) * predicted using Genefinder; Similarity to Arabidopsis serine/threonine protein kinase (PIR Acc. No. cDNA EST comes f [PROTEIN_KINASE_ST // TYRKINASE // PROTE] CG6114 GH13047 72A5-72B1 ID:65B6           |
| CG5253  | + DNA_binding * putative chromatin structure regulator(aa) * HYPOTHETICAL PROTEIN IN REGION E(aa) * TEX PROTEIN(aa) * similar to hypothetical proteins(aa) [NLS_BP] CG5253 GH13080 94B10-94B11 ID:65B8   |
| CG6123  | + unknown * [NLS_BP] CG6123 GH13094 17A7-17A7 ID:65B9  |
| CG18065 | + unknown * CG18065 GH13245 57A8-57A8 ID:65C11   |
| CG7229  | + transcription_factor * Pcaf SPTR(aa) * CREB-BINDING PROTEIN(aa) * HAT A1(aa) * 5.9 kb fsh membrane protein(aa) [BROMODOMAIN_2 // BROMODOMAIN_1 // bromo] CG7229 GH13144 56C-56C ID:65C2  |
| CG3121  | + unknown * FLAGELLAR RADIAL SPOKE PROTEIN 4(aa) * radial spokehead(aa) * 9e-13 predicted using Genefinder; similar to Sugar transporter; cDNA EST * 5e-55 radia [ER_TARGET] CG3121 GH13165 60A16-60A16 dup:1/2 ID:65C3                                    |
| CG2209  | + unknown * CG2209 GH13175 11D3-11D3 ID:65C5   |
| CG5741  | + unknown * No definition line found(aa) * 4e-06 probable membrane protein YPR091c - yeast (Saccharomyces cerevisiae) * 6e-43 No definition line found * 3e-05 h CG5741 GH13177 66E4-66E4 ID:65C6  |
| CG3483  | + enzyme * 5e-49 IDH1_YEAST ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT PRECURSOR (IS * 6e-57 IDHA_CAEEL PROBABLE ISOCITRATE DEHYDROGENASE (NAD), MIT [isodh] CG3483 GH13226 60D2-60D2 ID:65C9   |
| CG9364  | + enzyme * 2e-20 alpha-alpha-trehalase * 1e-102 similar to family glycosyl hydrolases; most similar to trehalase * 1e-124 TREA_HUMAN TREHALASE PRECURSOR (ALPHA [Trehalase // TREHALASE_1 // GLHYDRLASE3] CG9364 GH13461 57B20-57C dup:4/4 ID:65D10        |
| CG14889 | + structural_protein * [COLLAGEN_REP // Collagen] CG14889 GH13492 92A1-92A1 dup:1/2 ID:65D11   |
| CG17010 | + * ribokinase(aa) * ribokinase RbsK(aa) * DMC115C2 * 1e-71 /match=(desc;; /ma [pfkB // PRO_RICH // RIBOKINASE] CG17010 33D3-33D3 dup:2/2 ID:65D12   |
| CG1891  | + 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/threoni[PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG1891 GH13369 43E18-43E18 dup:2/2 ID:65D2 |
| CG13784 | + unknown * CG13784 GH13387 27E4-27E5 ID:65D3  |
| CG6903  | + unknown * CG6903 GH13389 4D1-4D1 ID:65D4   |
| CG8613  | + unknown * conserved protein(aa) * 1e-133 YP65_CAEEL HYPOTHETICAL 81.5 KD PROTEIN IN CHROMOSOME II (U2 * 1e-125 YYAL_BACSU HYPOTHETICAL 78.8 KD PROTEIN IN TET [CARBOXYPEPT_ZN_2] CG8613 GH13403 50F6-50F6 ID:65D5  |
| CG11763 | + enzyme * 4e-09 YGX7_YEAST HYPOTHETICAL 108.2 KD PROTEIN IN SAP4-OST5 INTERGENIC REGION * 3e-06   |

DEAD-box protein \* 8e-43 predicted using Genefinder; similar t [SPRY\_DOMAIN // PHOSPHOPANTETHEINE // SP] CG11763 GH13409 47A7-47A7 dup:3/3 ID:65D6

CG4087 + RpP2 ribosomal\_protein \* DMRP21C\_2 RpP2 \* 60S ACIDIC RIBOSOMAL PROTEIN P1 (RP21C) (ACIDIC RIBOSOMAL PROTEIN RPA2)(aa) \* 5e-14 acidic ribosomal protein P1.e.A, cytosolic - ye [60s\_ribosomal // RIBOSOMALP2] CG4087 GH13422 21C2-21C2 dup:3/3 ID:65D7

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

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

CG8529 + 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

CG4668 + cell\_adhesion \* bt \* 3e-17 projectin \* 6e-18 twitchin - Caenorhabditis elegans twitchin \* 1e-14 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma pr[FNTYPEIII // RIBOSOMAL\_S2\_1 // PRO\_RICH] CG4668 GH13550 36A6-36A6 dup:3/3 ID:65E2

CG7342 + transporter \* HYPOTHETICAL 48.6 KD PROTEIN IN CHROMOSOME II(aa) \* DMORCT2\_2 Orct \* solute carrier family (organic cation transporter), member 1(aa) \* 1e-42 putati [sugar\_tr] CG7342 GH13557 92A11-94D3 dup:2/2 ID:65E3

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

CG6117 + Pka-C3 protein\_kinase \* PROTEIN KINASE DC2(aa) \* DMDC2\_2 Pka-C3 \* 5e-88 cAMP-dependent protein kinase subunit (put.); putative \* 2e-99 KAPC\_CAEEL CAMP-DEPENDENT PROTEIN KIN CG6117 GH13608 72B1-72B2 dup:3/3 ID:65E5

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

CG2062 + Cyp4e1 cytochrome\_P450 \* cytochrome P450, Cyp4e2 - fruit fly (Drosophila melanogaster) (U5 \* 6e-79 predicted using Genefinder; similar to cytochrome P450 \* 3e-50 CYP4B1 [EP450II // p450 // P450 // MITP450 // C] CG2062 GH13635 44C1-44C2 dup:2/2 ID:65E8

CG5594 + transporter \* furosemide-sensitive K-Cl cotransporter(aa) \* BLASTX 7.2E-55 Rattus furosemide-sensitive K-Cl cotransporter (KCC2) mRNA, complete cds.(dna) \* 6e-49 [AMINO\_ACID\_PERMEASE\_2 // KCLTRNSPORT] CG5594 GH13642 60A9-60A10 dup:4/5 ID:65E9

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

CG14995 + 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

CG1441 + 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

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

CG6230 + 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

CG5198 + unknown \* SMC2orf(aa) \* CD2 antigen (cytoplasmic tail)-binding protein 2(aa) \* 1e-08 YHV6\_YEAST HYPOTHETICAL 40.4 KD PROTEIN IN SPO16-REC104 INTERGENIC REGIO CG5198 GH13760 33D1-33D1 ID:65F7

CG3690 + 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

CG11210 + unknown \* 4e-14 probable membrane protein YOL084w - yeast (Saccharomyces cerevisiae) \* 1e-103 protein \* 6e-17 hypothetical protein \* 3e-54 inserted at base Bo CG11210 GH13794 44A4-44A4 ID:65F9

CG2025 + endopeptidase \* INSULIN-DEGRADING ENZYME (INSULYSIN) (INSULINASE) (INSULIN PROTEASE)(aa) \* DMD1DE\_2 Ide \* 2e-63 STE23 protein - yeast (Saccharomyces cerevisiae) Ste [Peptidase\_M16 // INSULINASE] CG2025 GH13968 10F2-10F2 ID:65G10

CG8683 + 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

CG6676 + cell\_adhesion \* coded for by C. elegans cDNA yk9a2.5; coded for by C. elegans cDNA yk9a2.3; similar to fibrinogen-like protein A precursor(aa) \* 3(aa) \* FIBRINOGEN [FIBRIN\_AG\_C\_DOMAIN // fibrinogen\_C] CG6676 GH13859 58C2-58C2 ID:65G3

CG9331 + 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

CG3168 + transporter \* transmembrane transporter - electric ray (Discopyge ommata)(aa) \* 1e-09 HXT3\_YEAST LOW-AFFINITY GLUCOSE TRANSPORTER HXT3 hexose t \* 2e-14 putative o [SUGAR\_TRANSPORT\_1 // SUGAR\_TRANSPORT\_2] CG3168 GH13883 6C9-6C10 ID:65G5

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

CG9438 + 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

CG15390 + unknown \* CG15390 GH14074 22E-22E ID:65H11

CG5845 + peptidase \* AMINOPEPTIDASE N (MICROSOMAL AMINOPEPTIDASE) (MEMBRANE GLYCOPROTEIN H11)(aa) \* aminopeptidase N homolog(aa) \* 5e-88 aminopeptidase yscII \* 5e-97 Sim [ALADIPTASE // Peptidase\_M1] CG5845 GH14075 93F6-93F6 dup:2/2 ID:65H12

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

CG3372 + unknown \* CG3372 GH14065 60C1-60C1 ID:65H8

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

CG3184 + chaperone \* hypothetical protein(aa) \* 3e-22 YB96\_YEAST HYPOTHETICAL 43.3 KD PROTEIN IN ALG7-ENP1 INTERGENIC REGION \* WD-40 repeat protein \* [WD40\_REGION // WD40] CG3184 GH14157 6C7-6C7 ID:66A12

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

+ DNA\_binding \* component of CCR4 transcriptional complex; Caf17p(aa) \* putative protein(aa) \* Similarity to S.pombe  
 CG8043 hypothetical protein C21E11.07 (SW:YAL7\_SCHPO CG8043 GH14121 85B-85B ID:66A7  
 + 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  
 CG1009 dup:1/2 ID:66B1  
 CG4416 + transcription\_factor ZINC\_FINGER\_C2H2, ZINC\_FINGER\_C2H2\_2, zf] CG4416 GH14307 dup:2/3 ID:66B10  
 CG9264 + transporter \* CG9264 GH14216 39A6-39A7 ID:66B5  
 + Gs2 enzyme \* GLUTAMINE SYNTHETASE 2, CYTOPLASMIC (GLUTAMATE--AMMONIA LIGASE 2)(aa) \* GLUTAMINE  
 SYNTHETASE (GLUTAMATE--AMMONIA LIGASE)(aa) \* glutamine synthetase [GLNA\_1 // gln-synt // GLNA\_ATP] CG1743  
 CG1743 GH14412 10B13-10B14 dup:1/2 ID:66C10  
 none - noe gene + noe none - noe gene GH14418 ID:66C11  
 + Sox14 DNA\_binding \* DMDSOX14 Sox14 \* putative(aa) \* POP-1 PROTEIN(aa) \* SOX-2(aa) [HMG // HMG\_box // NLS\_BP]  
 CG3090 CG3090 GH14320 60A14-60A14 dup:1/3 ID:66C2  
 + unknown \* 2e-05 CU19\_LOCM1 CUTICLE PROTEIN (LM-19) (LM-ACP 19) Lm-ACP1 \* \* [GRAM\_POS\_ANCHORING //  
 CG9665 insect\_cuticle] CG9665 GH14349 73D-73D6 ID:66C3  
 + jar motor\_protein \* DMMHC95F Mhc95F \* 1e-116 MYS4\_YEAST MYOSIN-4 ISOFORM myosin MYO4 - yeast (Saccharo \*  
 MYS9\_DROME MYOSIN HEAVY CHAIN 95F (95F MHC) myosin heavy \* sim [myosin\_head // IQ // MYOSINHEAVY // NLS]  
 CG5695 CG5695 GH14351 95F-95F ID:66C4  
 CG10097 + Brassica napus 'male sterility protein 2' EMBL:X99922 CG10097 ID:66C5  
 + actin\_binding \* DMRCPA\_X kel \* protein(aa) \* [BTB // KELCHREPEAT // Kelch] CG3571 GH14381 87A-87A dup:2/2  
 CG3571 ID:66C6  
 CG11871 + unknown \* CG11871 GH14385 86A1-86A1 ID:66C8  
 + unknown \* predicted trithorax protein(aa) \* INTEGRAL MEMBRANE PROTEIN DGCR2/IDD PRECURSOR (SEIZURE-  
 CG4285 RELATED MEMBRANE-BOUND ADHESION PROTEIN)(aa) \* BLASTX 7.0E [RCC1\_2] CG4285 GH14388 90D1-90D1 ID:66C9  
 + ligand\_binding\_or\_carrier \* 5e-13 DKA1\_YEAST DKA1 PROTEIN (NSP1 PROTEIN) (TFS1 PROTEIN) DKA \* 3e-44  
 OBA5\_DROME PUTATIVE ODORANT-BINDING PROTEIN A5 PRECURSOR (ANTENNAL PROTEIN 5 [PBP] CG17919 GH14494  
 CG17919 83E-83E ID:66D10  
 CG9813 + unknown \* [ATPASE\_ALPHA\_BETA] CG9813 GH14502 87E8-87E9 dup:1/2 ID:66D11  
 + receptor \* LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (LDL RECEPTOR 1)(aa) \* low density lipoprotein  
 receptor-related protein 7(aa) \* LDL receptor member LR3(a [LDLRA\_2 // LDLRECEPTOR // EGF // EGF\_2 ] CG8909 GH14506  
 CG8909 13F10-13F12 ID:66D12  
 + ion\_channel \* 7e-59 DrosGluCl \* 1e-48 Contains similarity to Pfam domain: (neur\_chan), Score=39 \* 7e-67 glycine receptor  
 CG14723 subunit alpha \* 8e-68 glycine receptor al [neur\_chan // NEUROTR\_ION\_CHANNEL // NRI] CG14723 GH14445 86F9-86F9 ID:66D2  
 none + none GH14469 ID:66D6  
 + translation\_factor \* HYPOTHETICAL 64.2 KD PROTEIN R08D7.3 IN CHROMOSOME III(aa) \* UNKNOWN(aa) \* eIF3  
 CG4810 p66(aa) \* 9e-98 putative elongation initiation factor subunit CG4810 GH14470 87B5-87B5 ID:66D7

+ enzyme\_activator \* 2e-40 inserted at base Both 5' and 3' ends of P element Inverse PCR \* \* [EF\_HAND\_2] CG3565  
 CG3565 GH14476 60D8-60D8 ID:66D8  
 CG8332 + CG8332 dup:3/5 ID:66D9  
 + transporter \* DMORCT2\_2 Orct \* organic cation transporter(aa) \* Similarity to Rat organic cation transporter cDNA EST  
 CG7084 comes from this gene; cDNA EST comes from [sugar\_tr] CG7084 GH14589 94A11-96D1 dup:2/2 ID:66E11  
 + Con cell\_adhesion \* DMCONNECTN\_1 Con \* 1e-180 cell-surface molecule connectin - fruit fly (Drosophila melanogaster) \* 3e-  
 CG7503 15 coded for by C. elegans cDNA yk132e5.5; coded [LRR // LRRCT] CG7503 GH14524 64C6-64C7 dup:2/2 ID:66E2  
 + enzyme \* GCSP\_YEAST GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXY \*  
 CG3999 similar to glycine dehydrogenase \* GCSP\_HUMAN GLYCINE DEHYDROGEN CG3999 GH14537 85F16-85F16 dup:2/2 ID:66E3  
 CG9321 + unknown \* [ATP\_GTP\_A] CG9321 GH14542 29E4-29E4 dup:3/3 ID:66E4  
 + unknown \* 2e-24 cDNA EST CEMSE83F comes from this gene; cDNA EST comes \* \* CG16791 GH14545 93D6-93D6  
 CG16791 dup:3/3 ID:66E5  
 + endopeptidase \* phosphate regulator(aa) \* endothelin converting enzyme, ECE=putative zinc-binding metalloprotease aortic  
 CG6265 endothelial cells, Peptide, \* Similarity t CG6265 GH14576 97E2-97E3 dup:2/2 ID:66E8  
 CG9469 + unknown \* [PRO\_RICH // NLS\_BP // ATP\_GTP\_A] CG9469 GH14660 42E1-42E1 dup:2/3 ID:66F10  
 + A(225) unknown \* bt \* MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (MLCK)  
 CG18255 (CONTAINS: TELOKIN)(aa) \* CG18255 GH14667 52D14-52D15 dup:3/3 ID:66F11  
 + Rpn6 endopeptidase \* 26S proteasome subunit p44.5(aa) \* BLASTX 3.9E-25 YDL097C|Protein of unknown function(dna) \* 2e-  
 CG10149 90 hypothetical protein YDL097c - yeast (Saccharomyc [PCI\_DOMAIN // PCI] CG10149 GH14689 51C2-51C2 ID:66F12  
 + endopeptidase \* similar to the M13 or zinc metalloprotease family of peptidases(aa) \* endothelin converting enzyme 1(aa) \*  
 endothelin converting enzyme-2 - bovine [CNMP\_BINDING\_2 // NEPRILYSIN // PRENYLA] CG9507 GH14621 28D1-28D1  
 CG9507 ID:66F3  
 CG1394 + unknown \* CG1394 GH14622 10A11-10A11 ID:66F4  
 + transporter \* UDP-galactose transporter related(aa) \* 4e-18 probable membrane protein YPL244c - yeast (Saccharomyces  
 CG5802 cerevisiae) \* 2e-16 No definition line found CG5802 95F1-95F1 dup:2/3 ID:66F5  
 + cell\_adhesion \* 4e-06 UNC-89 \* 6e-05 VGR2\_MOUSE VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR  
 CG7607 PRECURSOR (VEGFR-2) (PR \* 1e-05 protein tyrosine phosphatase, receptor t [ig] CG7607 GH14648 68A8-68A8 ID:66F6  
 + signal\_transduction \* cAMP-dependent Rap1 guanine-nucleotide exchange factor(aa) \* HYPOTHETICAL 139.4 KD  
 PROTEIN T20G5.5 IN CHROMOSOME III(aa) \* 2e-07 KAPR\_YEAST [cNMP\_binding // RasGEF // DEP\_DOMAIN //] CG3427  
 CG3427 GH14655 42C4-42D1 dup:2/3 ID:66F8  
 CG12699 + unknown \* CG12699 GH14656 54B7-54B7 ID:66F9  
 + enzyme \* 2e-15 FOX2\_YEAST PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE)  
 (MULTIFUNCTIONAL \* 4e-14 3-hydroxyacyl-CoA dehydrogenase type II \* 3e-42 strong [GDHRDH // adh\_short] CG3603 GH14791  
 CG3603 3C5-3C5 ID:66G11  
 + enzyme \* Ac76E \* type VIII adenylyl cyclase - human(aa) \* Ac35C \* ADENYLATE CYCLASE, TYPE VIII (ATP  
 PYROPHOSPHATE-LYASE) (CA(2+)/CALMODULIN ACTIVATED ADENYLY [guanylate\_cyc // GUANYLATE\_CYCLASES\_2]  
 CG5983 CG5983 GH14744 36A2-36A2 ID:66G6

+ transporter \* 8e-59 MDL1\_YEAST ATP-DEPENDENT PERMEASE MDL1 MDL1 protein - y \* MDR5\_DROME MULTIDRUG  
 RESISTANCE PROTEIN HOMOLOG (P-GLYCOPROTEIN 65) \* similar to mu [ATP\_GTP\_A2 // ABC\_TRANSPORTER // ABC\_tr]  
 CG10226 GH14758 65A7-65A7 ID:66G7  
 CG11960 + unknown \* [NLS\_BP] CG11960 GH14769 56D8-56D8 dup:1/2 ID:66G8  
 + transcription\_factor \* ZINC-FINGER PROTEIN (ZINC-FINGER HOMEODOMAIN PROTEIN 1)(aa) \* DMDROSOPH\_4 wdn \*  
 transcriptional repressor(aa) \* DMBTDGN\_2 btd [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG8591 GH14774 65F4-65F4  
 CG8591 ID:66G9  
 CG9137 + unknown \* CG9137 GH14903 61F4-61F4 ID:66H10  
 CG18314 + unknown \* CG18314 GH14918 64B9-64B9 dup:1/3 ID:66H11  
 + unknown \* hypothetical protein(aa) \* similar to human 5'-nucleotidase \* Unknown(aa) \* 6e-46 similar to human 5'-  
 CG1814 nucleotidase CG1814 GH14884 45F4-45F4 ID:66H7  
 + boss G\_protein\_linked\_receptor \* DMBRSEVM\_5 boss \* BOSS\_DROME BRIDE OF SEVENLESS PROTEIN PRECURSOR  
 CG8285 (X558 \* 4e-06 CELF35-1 \* 2e-07 Unknown gene product CG8285 GH14887 96F9-96F9 dup:2/2 ID:66H8  
 + \* cDNA EST yk335d8.5 comes from this gene; cDNA EST yk335d8.3 comes from this gene(aa) \* 2e-23 cDNA EST  
 CG4972 yk335d8.5 comes from this gene; cDNA EST yk335 CG4972 31D7-31D8 dup:2/2 ID:67A10  
 + 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  
 CG8212 dup:1/2 ID:67A11  
 CG15512 + unknown \* CG15512 GH14951 99C7-99C7 dup:2/4 ID:67A3  
 + 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 // SUGRTRANSPORT // SUGAR\_TRANS] CG3285 GH15136  
 CG3285 25A1-25A1 ID:67B12  
 + chaperone \* similar to chaperonins cpn60 and TCP-1 (Pfam: cpn60\_TCP1.hmm, score: 416.20 and 102.94)(aa) \*  
 Cytoplasmic chaperonin subunit gamma; Cct3p(aa) \* chap [TCP1\_1 // TCP1\_2 // TCP1\_3 // TCOMPLEX] CG7033 GH15038  
 CG7033 8C13-8C13 dup:2/2 ID:67B3  
 + alpha-Est2 enzyme \* alpha esterase(aa) \* agr;-Est2 \* carboxylesterase MdaE7(aa) \* alpha esterase [CHOLNESTRASE //  
 CG2505 ESTERASE // COesterase] CG2505 GH15053 84D6-85A3 ID:67B5  
 + electron\_transfer \* CYTOCHROME B5 (CYTB5)(aa) \* 3e-17 cytochrome b5 \* 1e-25 Similarity to Human cytochrome b5  
 (SW:CYB5\_HUMAN); cDNA EST EMBL:D \* 2e-30 CYB5\_MOUSE CY[Cytochrome\_B5 // CYTOCHROME\_B5 // CYTOCH] CG2140  
 CG2140 GH15091 43D-43D dup:3/3 ID:67B9  
 CG18369 + unknown \* CG18369 GH15231 50B9-50B9 ID:67C11  
 + endopeptidase \* PROCLOTTING ENZYME PRECURSOR(aa) \* DMEAST\_4 ea \* 6e-67 EAST\_DROME SERINE  
 PROTEASE EASTER PRECURSOR serine protein \* 3e-29 anticoagulant protein C [trypsin // CHYMOTRYPSIN // TRYPSIN\_SER]  
 CG3066 CG3066 GH15156 85B1-85B1 dup:2/5 ID:67C3  
 + endopeptidase \* cathepsin L-like protease precursor(aa) \* cysteine proteinase 1(aa) \* cathepsin H(aa) \* Cp1 [PAPAIN //  
 CG11459 Peptidase\_C1 // THIOL\_PROTEAS] CG11459 GH15170 83E1-83E1 ID:67C4



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

CG7626 + transcription\_factor \* chromatin structural protein homolog Supt5hp(aa) \* suppressor of Ty (S.cerevisiae) homolog(aa) \* 9e-59 SPT5\_YEAST TRANSCRIPTION INITIATION PROTEIN CG7626 GH15359 56D7-56D7 dup:4/5 ID:67D10

CG17769 + And ligand\_binding\_or\_carrier \* similar to calmodulin-like protein.(aa) \* Homo sapiens(aa) \* CALMODULIN(aa) \* Eip63F-1 [efhand // EF\_HAND\_2] CG17769 GH15245 99D1-99D1 ID:67D2

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

+ transcription\_factor \* 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

CG5455 + Scp1 ligand\_binding\_or\_carrier \* calcium-binding protein alpha-a chain - penaeid shrimp (Penaeus sp.)(aa) \* Scp1 \* 5e-94 calcium-binding protein \* 2e-43 SCPB\_PENSP SARCOPLASMIC CALC CG15848 GH15296 cyto\_unknown ID:67D6

CG15848 + th apoptosis\_inhibitor \* DMDIAP1X\_3 th \* APOPTOSIS INHIBITOR (INHIBITOR OF APOPTOSIS 1) (DIAP1) (THREAD PROTEIN)(aa) \* 2e-05 similar to Zinc finger, C3HC4 type (RIN[zf-C3HC4 // BIR // BIR\_REPEAT // BIR\_RE] CG12284 GH15335 72D1-72D1 dup:2/3 ID:67D8

CG12284 + signal\_transduction \* 1e-06 fimbriae-associated protein Fap1 \* \* [NLS\_BP] CG11451 GH15349 77E-77E8 dup:1/2 ID:67D9

CG11451 + pn signal\_transduction \* PRUNE protein(aa) \* DMPRUNEG\_2 pn \* 1e-16 PPX1\_YEAST EXOPOLYPHOSPHATASE (METAPHOSPHATASE) exopolyph \* PRUNE protein CG3461 GH15456 2E1-2E1 dup:2/2 ID:67E10

CG3461 + unknown \* CG18437 GH15426 98A6-98A6 dup:2/2 ID:67E2

CG18437 + enzyme \* 1e-12 FOX2\_YEAST PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL \* 0.000000000000002\* 2e-26 predicted using Genefinder; Similar [GDHRDH // adh\_short // ADH\_SHORT] CG17121 GH15451 94D12-94D12 dup:2/2 ID:67E8

CG17121 + 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

CG14895 + \* [ER\_TARGET] CG8420 85D2-85D3 dup:3/3 ID:67F12

CG8420 + unknown \* [TMFOUR] CG12142 GH15469 42E-42E ID:67F2

CG12142 + CG14178 GH15480 ID:67F6

CG14178 + 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

CG13356 + transcription\_factor \* ash1 \* polybromo protein - chicken(aa) \* DMFSHA\_2 fs(1)h \* similar to HMG (high mobility group) box, Bromodomain (5 domains), Zinc finger, C2H2 [BROMODOMAIN\_2 // BAH // HMG // HMG\_box ] CG11375 98E1-98E1 dup:1/2 ID:67G4

CG11375 + unknown \* CG2225 GH15653 39E5-39E ID:67H2

CG2225 + unknown \* [FLAGELLA\_BB\_ROD] CG7105 GH15664 28D3-28D3 ID:67H3

CG7105 + 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

CG11316

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

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

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

CG8462 + ligand\_binding\_or\_carrier \* antennal binding protein X(aa) \* Pbprp1 \* 3e-06 PBP1\_DROME PHEROMONE-BINDING PROTEIN-RELATED PROTEIN PRECURSOR (PBPRP-1) \* 4e-08 Pbprp1 [PBP\_GOBP] CG8462 GH15777 56E5-56E5 ID:68A5

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

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

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

CG6432 + 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

CG1514 + cytoskeletal\_structural\_protein \* 8e-19 protein \* sorting nexin \* Y254\_HUMAN HYPOTHETICAL PROTEIN KIA \* [BEM\_DOMAIN // GRK] CG1514 GH16154 7C8-7C8 ID:68C11

CG14891 + unknown \* CG14891 GH16156 92A1-92A1 ID:68C12

CG4550 + ninaE \* DMOPSA\_2 ninaE \* OPS1\_DROME OPSIN RH1 (OUTER R1-R6 PHOTORECEPTOR CELLS OPSIN) \* 1e-06 serotonin receptor \* 1e-35 OPSX\_MOUSE VISUAL PIGMENT-LIKE REC [OPSINRH1RH2 // GPCRRHODOPSN // OPSIN //] CG4550 92B8-92B9 dup:1/5 ID:68C2

CG14477 + unknown \* CG14477 54B16-54B17 ID:68C6

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

CG8468 + transporter \* K05B2.5 gene product(aa) \* 1e-13 YKW1\_YEAST HYPOTHETICAL 52.3 KD PROTEIN IN FRE2 5'REGION \*

2e-82 /match=(desc;; /ma \* 1e-40 predicted using Genefin CG8468 GH16148 50E-50E7 dup:2/5 ID:68C9  
+ 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  
CG15279 GH16161 35B7-35B7 ID:68D1  
CG17349 + unknown \* E04F6.2 gene product(aa) \* 1E-130\* CG17349 GH16267 37D6-37D7 ID:68D11  
+ Ace enzyme \* DMACHE\_5 Ace \* cell growth and maintenance acetylcholine catabolism ) cell growth and maintenance carbamate resistance ) cell growth and maintenance [CHOLNESTRASE // ESTERASE // COesterase ] CG17907 GH16177 87E3-87E3 dup:2/2 ID:68D2  
CG17907 + unknown \* 1e-109 weak similarity to Bacillus and Pseudomonas probable glucarate transporters (G \* 2e-06 conserved  
CG1358 hypothetical protein \* 2E-46\* C05G5.1 CG1358 GH16188 43E3-43E4 dup:2/2 ID:68D3  
CG7897 + 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  
CG11188 + \* ZRP protein(aa) \* 4e-10 hypothetical protein YDR299w - yeast (Saccharomyces cerevisiae) (U \* 3e-26 ZRP protein \* 2e-06 inserted at base Both 5' and [NLS\_BP] CG11188 27A1-27A1 dup:2/2 ID:68D6  
CG5600 + unknown \* 5e-08 myosin phosphatase, target subunit (A \* 1e-07 PP1M M21 subunit=protein phosphatase 1M kda regulatory subunit \* myosin phosphatase, target subu CG5600 GH16214 72D3-72D4 dup:2/4 ID:68D7  
CG3365 + drongo signal\_transduction \* drongo \* 9e-25 Drongo \* 4e-12 HIV-1 Rev binding protein NUCLEOPO \* 1E-151 [ArfGap // ZF\_GCS // REVINTRACTNG] CG3365 GH16240 21D2-21E3 dup:2/2 ID:68D8  
CG17999 + 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  
CG9968 + 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  
CG11715 + 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  
CG18111 + unknown \* 4e-10 male-specific protein \*\* CG18111 GH16332 99B-99B dup:2/2 ID:68E4  
CG8507 + motor\_protein \* receptor-associated protein(aa) \* 9e-14 predicted using Genefinder; Similarity to Human alpha-2-macroglobu \* 2e-16 heparin binding protein \* 5e-18 CG8507 GH16343 86D1-86D1 dup:3/3 ID:68E5  
CG7125 + protein\_kinase \* protein kinase C, mu(aa) \* DMPKC98F\_2 Pkc98E \* protein kinase C, mu(aa) \* 6e-42 DUN1\_YEAST DNA DAMAGE RESPONSE PROTEIN KINASE DUN1 protei [DAG\_PE\_BINDING\_DOMAIN // PROTEIN\_KINASE] CG7125 GH16373 90F8-90F9 dup:3/3 ID:68E7  
CG9672 + 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  
CG9772 + \* 3e-30 No definition line found \* 5e-48 SCF complex protein Skp2 \* 1e-42 S-phase kinase-associated protein (p45) cyclin A/CDK2-associate \* YKK7\_CAEE FBOX\_DOMAIN CG9772 ID:68F1  
CG12191 + cell\_adhesion \* 8e-05 adhesion molecule L1.1 \*\* [ig] CG12191 GH16485 61D4-61D4 ID:68F12

CG4767 + BG:DS02252.2 cytoskeletal\_structural\_protein \* 2e-48 tektin \* 2e-34 testicular tektin B1-like protein \* 3e-59 tektin A1 - sea urchin (Strongylocentrotus purpuratus) \* tektin C1 [TEKTIN] CG4767 GH16413 35E-35E ID:68F2

CG8707 + signal\_transduction \* (putative) small GTPase, similar to Gtr1; Gtr2p(aa) \* yeast gtr2 homolog, novel small GTPase subfamily protein(aa) \* homologous to the yeast YGR163 [CRYSTALLIN\_BETAGAMMA // ATP\_GTP\_A] CG8707 GH16429 44B-44B ID:68F3

CG3881 + unknown \* 9e-36 by content; 1-meth \* 1e-43 YS15\_CAEEL HYPOTHETICAL 41.1 KD PROTEIN IN CHROMOSOME II \* 1e-42 Sqv-8-like protein \* 7e-47 UDP-glucuronyltransfera CG3881 GH16433 30C2-30C2 ID:68F5

CG4759 + \* ribosomal protein L27 homolog(aa) \* 7e-26 RL27\_YEAST PROBABLE 60S RIBOSOMAL PROTEIN L27 ribosomal p \* 5e-27 RL27\_CAEEL 60S RIBOSOMAL PROTEIN L27 rib [RIBOSOMAL\_L27E // NLS\_BP] CG4759 96E10-96E10 dup:2/2 ID:68F8

CG2088 + BcDNA:GH02712 motor\_protein \* BLASTX 8.9E-08 YOL155C[Protein with similarity to S. cerevisiae glucan 1,4-alpha-glucosidase(dna) \* BLASTX 2.5E-06 P.falciparum interspersed repeat [PRO\_RICH] CG2088 GH16490 43E5-43E6 dup:1/3 ID:68G1

CG15068 + CG15068 GH16622 ID:68G10

CG9166 + unknown \* 5e-07 YM62\_CAEEL HYPOTHETICAL 23.2 KD PROTEIN K12H4.2 IN CHROMOSOME III \* 5e-09 YBEB\_ECOLI HYPOTHETICAL 11.6 KD PROTEIN IN MRDA-PHPB INTERGENIC REGI CG9166 GH16625 61F8-61F8 ID:68G11

CG4067 + Pug enzyme \* Pug \* C1TM\_YEAST C-1-TETRAHYDROFOLATE SYNTHASE MITOCHONDRIAL PRECURSOR (C1-THF SYNTHAS \* C1-THF synthase homolog \* Contains similarity to Pfam doma [THF\_DHG\_CYH\_2 // THFDHDRGNASE // FTHFS ] CG4067 GH16587 86C2-86C2 dup:2/2 ID:68G5

CG9630 + RNA\_binding \* pit \* 2e-78 SPB4\_YEAST ATP-DEPENDENT RRNA HELICASE SPB4 RNA helicase S \* 2e-69 helicase pitchoune \* 8e-87 YOQ2\_CAEEL PUTATIVE ATP-DEPENDENT RNA HELI [helicase\_C // HELICASE // DEAD // NLS\_B] CG9630 GH16590 84F-84F ID:68G6

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

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

none + none GH16763 ID:68H11

CG10426 + enzyme \* pharbin(aa) \* 7e-35 YNK6\_YEAST HYPOTHETICAL 133.3 KD PROTEIN IN CYB5-LEU4 INTERGENIC REGION \* 2e-31 /match=(desc;; /ma \* 4e-17 similar to Inositol p [IPPC // PRENYLATION] CG10426 GH16681 69A3-69A3 ID:68H4

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

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

CG11064 + RfaBp unknown \* retinoid- and fatty acid-binding glycoprotein \* 1e-15 C. elegans vitellogenin precursor, vit-5 (Spieth et al., NAR \* 4e-07 prepro-vWF (aa -22 to 137 [vwd // Vitellogenin\_N // NLS\_BP] CG11064 GH18004 102F4-102F4 ID:70A10

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

CG8278 + enzyme \* 1e-05 cyclophilin Dicyp-2 \*\* [PRENYLATION] CG8278 GH17930 44F2-44F2 ID:70A2

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

CG4983 + DNA\_repair\_protein \* CG4983 GH17939 33A5-33A5 ID:70A4

CG9363 + enzyme \* MALEYLACETOACETATE ISOMERASE (MAAI)(aa) \* glutathione transferase zeta 1(aa) \* 6e-50 similar to glutathione S-transferase \* 3e-05 GTC\_MOUSE GLUTATHI [GST] CG9363 GH17960 85D18-85D18 ID:70A5

CG7925 + tko ribosomal\_protein \* 2e-21 YN8K\_YEAST PUTATIVE 40S MITOCHONDRIAL RIBOSOMAL PROTEIN YNR036C \* 2e-76 RT12\_DROME MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S12 PRECURSOR (TECHNICA [RIBOSOMAL\_S12 // Ribosomal\_S12 // RIBOS] CG7925 GH17961 3A2-3A2 ID:70A6

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

CG1600 + enzyme \* 3e-53 Weak similarity to Potato alcohol dehydrogenase (SW:ADH\_SULSO); cD \* 7e-06 QOR\_MOUSE QUINONE OXIDOREDUCTASE (NADPH:QUINONE REDUCTASE) (ZETA-CR [adh\_zinc] CG1600 GH18014 43D3-43D3 ID:70B1

CG3492 + chaperone \* [CSA\_PPIASE\_2 // PRENYLATION] CG3492 GH18016 60D2-60D2 ID:70B2

CG3835 + EG:87B1.3 actin\_binding \* alkylglycerone phosphate synthase precursor(aa) \* DMC87B1 CG3835 GH18028 2D4-2D6 ID:70B4

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

CG18403 + very low density lipoprotein receptor - mouse CG18403 ID:70B7

CG9573 + unknown \* Ynl288wp(aa) \* hypothetical protein(aa) \* protein involved in sexual development(aa) \* 2e-61 YN28\_YEAST HYPOTHETICAL 41.2 KD PROTEIN IN PLC1-SEC21 CG9573 GH18039 29F8-29F8 ID:70B8

CG2930 + BcDNA:GH06717 transporter \* OLIGOPEPTIDE TRANSPORTER, KIDNEY ISOFORM (PEPTIDE TRANSPORTER 2) (KIDNEY H+/PEPTIDE COTRANSPORTER)(aa) \* OLIGOPEPTIDE TRANSPORTER, KIDNEY ISOFORM (P [PTR2 // PTR2\_1 // PTR2\_2] CG2930 GH18049 4A1-4A1 dup:2/3 ID:70B9

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

CG6614 + unknown \* [TPR\_REGION // NLS\_BP // ATP\_GTP\_A] CG6614 GH18077 33A5-33A5 ID:70C2

CG15444 + ine neurotransmitter\_transporter \* ine \* DMROSA\_2 rosA \* neurotransmitter transporter \* 1e-119 Similarity to Human Na(+)/Cl(-)-dependent GABA transporter (SW:NTG [NANEUSMPORT // SNF] CG15444 GH18083 24F6-24F6 ID:70C4

+ enzyme\_inhibitor \* RNase L inhibitor (clone 8) - human(aa) \* probable membrane protein YDR091c - yeast (Saccharomyces cerevisiae) \* 3e-07 P-glycoprotein/multidrug resi [fer4 // ATP\_GTP\_A2 // ABC\_TRANSPORTER /] CG5651 GH18088 66E5-66E5 ID:70C5  
 CG5651  
 + function\_unknown \* 4e-66 probable membrane protein YLL031c - yeast (Saccharomyces cerevisiae) \* 2e-53 No definition  
 CG12263 line found \* 4E-86\* 2e-63 ORF YLL031c CG12263 GH18119 55C11-55C11 dup:1/2 ID:70C6  
 + 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  
 CG14813 GH18123 2B12-2B13 ID:70C8  
 + peptidase \* 5e-60 putative metalloprotease; Method: conceptual translation supplied by author \* 1e-23 coded for by C. elegans cDNA yk27b10.3; coded for by C. el [PEPDIPTASEA // Peptidase\_M2] CG8196 GH18145 45A6-45A6 ID:70D1  
 CG8196 + RpL7A \* DMRPL7A\_2 RpL7A \* 6e-69 RL4A\_YEAST 60S RIBOSOMAL PROTEIN L7A-2 (L4-2) (YL5) (RP6) \* 1e-132  
 CG3314 RL7A\_DROME 60S RIBOSOMAL PROTEIN L7A ribosoma \* 5e-07 NHP [RIBOSOMAL\_L7AE // Ribosomal\_L7Ae // L7A] CG3314 6B1-6B1 dup:2/2 ID:70D12  
 + msta unknown \* /match=(desc:(aa) \* map\_position:2E3 \* 7e-06 t-BOP \* 5e-13 putative Bop-like zinc finger protein CG18033  
 CG18033 GH18166 2E2-2E2 dup:2/2 ID:70D4  
 + \* NADP-dependent isocitrate dehydrogenase(aa) \* 1e-148 IDHP\_YEAST ISOCITRATE DEHYDROGENASE (NADP), MITOCHONDRIAL PRECURSOR (OXALOSUCCIN \* 1e-180 simil [IDH\_IMDH // isodh] CG7176 66C8-66C8 dup:3/4 ID:70D6  
 CG7176 + actin\_binding \* protein(aa) \* Similarity to Drosophila ring canal protein cDNA EST comes from this gene; cDNA EST comes from this gene(aa) \* 1e-116 kelch protein, I [BTB // KELCHREPEAT // Kelch] CG15097 GH18278 55F2-55F3 dup:2/2 ID:70E1  
 CG15097 + defense/immunity\_protein \* 3e-13 peptidoglycan recognition protein precursor \* 4e-17 TNF superfamily, member (LTB)-like (peptidoglycan recognition \* 8e-17 cuticular molt prote CG4384 67A8-67A8 dup:3/3 ID:70E2  
 CG4384  
 CG18568 + unknown \* CG18568 GH18325 50C21-50C21 dup:2/2 ID:70E3  
 + RNA\_binding \* putative RNA binding protein(aa) \* 3e-05 TUD\_DROME MATERNAL TUDOR PROTEIN posterior-group protein t \* 8e-07 YQK1\_CAEEL HYPOTHETICAL 55.9 KD PROTEIN [KH-domain // KH\_DOMAIN // TUDOR] CG7082 GH18329 23D1-23D1 dup:3/3 ID:70E4  
 CG7082  
 CG9520 + unknown CG9520 dup:5/5 ID:70E7  
 CG5835 + unknown \* CG5835 GH18370 91F4-91F4 dup:2/2 ID:70E9  
 CG18539 + unknown \* CG18539 GH18493 55C4-55C4 ID:70F10  
 + serpin \* 2e-30 Similar to serine protease inhibitor \* 1e-33 serine proteinase inhibitor \* 5e-42 SCC2\_HUMAN SQUAMOUS CELL CARCINOMA ANTIGEN (SCCA-2) (LEUPIN) [serpin // SERPIN] CG7722 GH18514 47C7-47C7 dup:2/4 ID:70F12  
 CG7722  
 CG6882 + unknown \* CG6882 GH18452 65A3-65A3 ID:70F7  
 + unknown \* 4e-05 BE46\_MOUSE BRAIN PROTEIN E46 gene E46 protein - mouse \* \* CG4975 GH18454 54E5-54E5 ID:70F8  
 CG4975  
 + RNA\_binding \* mus308 \* Ygr271wp(aa) \* similar to Helicases conserved C-terminal domain; cDNA EST comes from this gene; cDNA EST yk430a5.5 comes from this gene; cD [HELICASE // DEAD // ATP\_GTP\_A] CG5205 GH18520 88F6-88F6 ID:70G1  
 CG5205  
 + enzyme \* ubiquitin fusion degradation protein; Ufd1p(aa) \* UBIQUITIN FUSION DEGRADATION PROTEIN HOMOLOG (UB FUSION PROTEIN 1)(aa) \* 2e-47 UFD1\_YEAST UBIQUITI CG6233 GH18603 70E3-70E3 ID:70G10  
 CG6233

+ endopeptidase \* serine protease 18D(aa) \* 4e-36 SNAK\_DROME SERINE PROTEASE SNAKE PRECURSOR serine  
 proteina \* 2e-15 similar to peptidase family S1 (trypsin family) \* [trypsin // CHYMOTRYPSIN // TRYPSIN\_SER ] CG11842 GH18608  
 CG11842 98F10-98F10 ID:70G11  
 + unknown \* [NLS\_BP // ATP\_GTP\_A] CG8838 GH18521 25A1-25A1 ID:70G2  
 + enzyme \* secretory component(aa) \* mollusk-derived growth factor; MDGF \* AGSA\_APLCA ATRIAL GLAND-SPECIFIC  
 CG10143 ANTIGEN PRECURSOR (AGSA) \* [NLS\_BP // A\_deaminase] CG10143 GH18530 51B10-51B10 ID:70G4  
 + enzyme \* F08F3.4 gene product(aa) \* 2e-06 GALX\_YEAST UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) /  
 CG5955 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  
 CG12022 + unknown \* CG12022 GH18574 62E1-62E1 ID:70G8  
 + Cyp28a5 cytochrome\_P450 \* CYP6A2(aa) \* cytochrome P450 monooxygenase CYP28A1(aa) \* 6e-37 YS24\_CAEEL PUTATIVE  
 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  
 CG3342 + unknown \* 1e-05 protein \* CG3342 GH18625 6A4-6A4 ID:70H2  
 CG15891 + unknown \* CG15891 GH18658 5E1-5E1 ID:70H6  
 + glycerol\_kinase \* 1e-83 GLPK\_YEAST GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE)  
 (GLYCEROKINASE) ( \* 1e-116 similar to glycerol kinase \* 1e-147 GLPK\_MOUSE G[FGGY\_KINASES\_1 // FGGY\_KINASES\_2 //  
 CG7995 FGG] CG7995 GH18690 62B1-62B1 dup:2/3 ID:70H9  
 + translation\_factor \* GTP binding protein similar to S. cerevisiae HBS1(aa) \* elongation factor alpha(aa) \* Elf \* DMEF1AF2\_8  
 CG1898 Ef1 agr;100E [ELONGATNFCT // GTP\_EFTU // ATP\_GTP\_A] CG1898 GH18819 62E3-62E3 ID:71A1  
 CG1468 + unknown \* CG1468 GH18955 9A2-9A2 dup:2/2 ID:71A12  
 + unknown \* T03G11.3 gene product(aa) \* CGI-62 protein(aa) \* 1e-16 T03G11.3 gene product \* CG10999 GH18838 83C3-  
 CG10999 83C3 dup:1/2 ID:71A3  
 + 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  
 CG4951 + unknown \* CG4951 GH18902 98B2-98B3 ID:71A8  
 + unknown \* 4e-29 YO87\_CAEEL HYPOTHETICAL 28.5 KD PROTEIN IN CHROMOSOME III \* 6e-18 putative protein \*  
 CG5862 [PCI\_DOMAIN // NLS\_BP] CG5862 GH18921 95F5-95F5 dup:1/2 ID:71A9  
 + transcription\_factor\_binding \* 2e-47 WEB1\_YEAST WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31) \* 2e-07  
 fizzy-related protein \* 9e-37 predicted using Genefinder; Similarity to Yeas [WD40\_REGION // WD40] CG8266 GH19061 44F7-  
 CG8266 44F8 dup:1/3 ID:71B11  
 CG15772 + unknown \* 1E-141 \* CG15772 GH18971 5B3-5B4 ID:71B2  
 CG16783 + signal\_transduction fizzy-related protein FIZZY\_DOMAIN, WD40 CG16783 ID:71B5  
 + endopeptidase \* DMSTUBBLE\_1 Sb \* caldecrin=serum calcium-decreasing factor pancreas, Peptide, \* 7e-36  
 STUB\_DROME SERINE PROTEINASE STUBBLE (STUBBLE-STUBBLOID PROTEI [trypsin // CHYMOTRYPSIN // TRYPSIN\_HIS  
 CG5390 ] CG5390 31D5-31D6 dup:2/2 ID:71B8

+ transmembrane\_receptor \* DMEMP\_3 emp \* 3e-53 epithelial membrane protein - fruit fly (*Drosophila melanogaster*) \* 5e-24  
 CG3829 predicted using Genefinder; similar to CD36 family; cD [CD36] CG3829 GH19047 60E8-60E8 ID:71B9  
 CG1979 + BG:DS00464.1 transmembrane\_receptor \* unknown(aa) \* \* CG1979 GH19145 84C1-84C1 dup:1/2 ID:71C10  
 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  
 + unknown \* 5e-05 unknown \* 6e-16 unknown protein \* YDOC\_SCHPO HYPOTHETICAL 13.4 KD PROTEIN C15A10.12C IN  
 CG9067 CHROMOSOME I \* CG9067 GH19135 47E3-47E3 ID:71C7  
 + cell\_adhesion \* 7e-06 NTRI\_RAT NEUOTRIMIN PRECURSOR (GP65) neurotrimin - rat \* \* [ig] CG10946 GH19181 7C8-  
 CG10946 7C8 ID:71D1  
 + 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  
 + transporter \* mitochondrial carrier protein-like; similar to \* 4e-13 probable membrane protein YPR011c - yeast  
 CG2616 (*Saccharomyces cerevisiae*) \* 6e-11 colt \* 3e-61 YQ [mito\_carr // MITOCH\_CARRIER] CG2616 GH19222 84D10-84D10 ID:71D5  
 + enzyme \* 1e-05 GCST\_YEAST AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T  
 PROTEIN) \* 1e-10 partial CDS, \* 4e-08 sarcosine oxidase \* sarcosine deh [FAD\_Gly3P\_dh // NAD\_BINDING] CG6385 GH19226  
 CG6385 54E7-54E8 ID:71D6  
 + endopeptidase \* DMSNAKE\_2 snk \* gd \* Tequila \* zgr;Try [trypsin // CHYMOTRYPSIN // TRYPSIN\_HIS ] CG9649  
 CG9649 GH19262 88B3-88B3 ID:71D8  
 CG9130 + unknown \* CG9130 GH19274 61F4-61F4 dup:2/3 ID:71D9  
 + transmembrane\_receptor \* patched (*Drosophila*) homolog(aa) \* PATCHED PROTEIN HOMOLOG (PTC1) (PTC)(aa) \* similar  
 to drosophila membrane protein PATCHED \* 1e-26 probable m[PHOSPHOPANTETHEINE // 5TM\_BOX] CG11212 GH19449  
 CG11212 42A10-42A10 dup:2/2 ID:71E10  
 CG7224 + unknown \* CG7224 GH19363 30C1-30C1 dup:3/3 ID:71E4  
 + peptidase \* 1e-34 YHT2\_YEAST HYPOTHETICAL 49.8 KD PROTEIN IN ACT3-YCK1 INTERGENIC REGION  
 PRECURSOR \* 3e-44 similar to zinc carboxypeptidases (Pfam: Zn\_carbOpept [CARBOXYPEPT\_ZN\_1 // CRBOXYPTASEA // Zn\_] CG12374  
 CG12374 GH19395 49C2-49C2 dup:2/2 ID:71E6  
 + signal\_transduction \* rab11 binding protein(aa) \* 5e-41 YMZ2\_YEAST HYPOTHETICAL 94.3 KD TRP-ASP REPEATS  
 CONTAINING PROTEIN IN SNZ1-YPK2 \* 1e-07 transcription initiati[GPROTEINBRPT // WD40\_REGION // WD40] CG7814  
 CG7814 GH19431 99C7-99C7 dup:2/2 ID:71E8  
 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



CG12173 + protein\_phosphatase \* enolase-phosphatase E-1(aa) \* Similarity to klebsiella oxytoca E-1 enzyme (TREMBL ID \* 1e-24 UTR4\_YEAST UTR4 PROTEIN (UNKNOWN TRANSCRIPT PROTEIN) U [Hydrolase // HADHALOGNASE] CG12173 GH19505 83A1-83A1 ID:71F4

CG9075 + eIF-4a translation\_factor \* DMEIF4A\_3 Eif4a \* EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)(aa) \* EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) (STIMULATOR FACTOR I KD COMPONENT) [helicase\_C // HELICASE // DEAD // DEAD\_] CG9075 GH19518 26B1-26B1 dup:3/5 ID:71F5

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

CG7766 + 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 8C13-8C14 dup:1/2 ID:71F8

CG4679 + unknown \* CG4679 GH19550 49F14-49F15 ID:71F9

CG5839 + peptidase \* 3e-78 aminopeptidase yscII \* 9e-93 Similarity to Human aminopeptidase N (SW:AMPN\_HUMAN); cDNA EST EMB \* 1e-102 AMPN\_MOUSE AMINOPEPTIDASE N (MICROSOM [ALADIPTASE // Peptidase\_M1 // ZINC\_PROT] CG5839 GH19677 93F4-93F6 dup:3/7 ID:71G10

CG2196 + transporter \* unknown(aa) \* anon-100EF-D3 \* 1e-20 Similarity to Salmonella sodium/proline symporter (SW:PUTP\_SALTY); \* 1e-33 sodium iodide symporter [SSF // NA\_SOLUTE\_SYMP\_3] CG2196 GH19680 100E2-100E3 ID:71G12

CG13319 + unknown \* 1E-158\* \* CG13319 GH19585 49E1-49E1 ID:71G2

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

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

CG1744 + chp cell\_adhesion \* DMCOP10\_2 chp \* 2e-11 CYAA\_YEAST ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) \* CHAO\_DROME CHAOPTIN PRECURSOR (PHOTORECEPTOR CELL [ARM\_REPEAT // LRR // LEURICHRPT] CG1744 GH19649 100B8-100B9 ID:71G7

CG15208 + unknown \* 1e-24 YLS5\_CAEEL HYPOTHETICAL 55.1 KD PROTEIN F09G8.5 IN CHROMOSOME III \* 2e-25 c21ORF-HumF09G8.5 \* 5e-08 outer arm dynein light chain reinhar \* 2e- CG15208 GH19655 9F12-9F12 ID:71G8

CG14408 + unknown \* 2e-22 similarity to C. elegans protein C01C10.4 \* 1e-36 SH3-domain binding protein \* 1e-36 SH3 binding protein SH3 binding protein sapien \* YKL4\_CA CG14408 GH19670 12F7-13A1 ID:71G9

CG8774 + 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 GH19688 87E5-87E5 ID:71H1

CG14740 + enzyme \* citrate synthase(aa) \* CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR(aa) \* PROBABLE CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR(aa) \* citrate synthase. Nu [citrate\_synt // CITRATE\_SYNTHASE // CIT] CG14740 GH19789 87B1-87B1 ID:71H12

CG17485 + CG17485 GH19718 ID:71H3

CG1824 + transporter \* DMC171D11 \* DMMDR65\_2 Mdr65 \* 8e-46 STE6\_YEAST MATING FACTOR A SECRETION PROTEIN STE6 (MULTIPLE DRUG RESISTANCE PROT \* 4e-86 MDR4\_DROME MULTIDRUG RE [ATP\_GTP\_A2 // ABC\_TRANSPORTER //

ABC\_tr] CG1824 GH19726 11B12-11B12 ID:71H4

+ Eaat2 neurotransmitter\_transporter \* EXCITATORY AMINO ACID TRANSPORTER (SEAAT1)(aa) \* glutamate transporter 2B(aa) \* CeGlt-2(aa) \* predicted using Genefinder; Similarity to Yeast [SDF // EDTRNSPORT // NA\_DICARBOXYL\_SYMP] CG3159 GH19729 21D1-21D1 dup:2/4 ID:71H5

CG3159 + enzyme \* 1e-133 SYLM\_YEAST LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (LEUCINE--TRNA LIGASE \* 1e-08 predicted using Genefinder; Similarity to Yeast [tRNA-synt\_1 // TRNASYNTHLEU // AA\_TRNA\_] CG7479 64C-64C ID:71H7

CG7479 + ribosomal\_protein Ribosomal protein S28B Ribosomal\_S28e CG2998 ID:72A2

CG2998 + enzyme \* putative ribitol dehydrogenase(aa) \* coded for by C. elegans cDNA CEESL70F; similar to protochlorophyllide oxidoreductases(aa) \* CGI-82 protein(aa [GDHRDH // adh\_short] CG11200 GH19857 56F17-56F17 ID:72A6

CG11200 + transporter \* Similarity to sugar transporters(aa) \* DMORCT2\_2 Orct \* 2e-08 HXT5\_YEAST PROBABLE GLUCOSE TRANSPORTER HXT5 hexose trans \* 3e-90 putative organic ca [SUGAR\_TRANSPORT\_1 // sugar\_tr] CG6126 89B13-89B13 dup:1/4 ID:72A7

CG6126 + CG3195 ID:72B11

CG3195 + unknown \* 1E-160\* \* [COPPER\_BLUE] CG13458 GH20023 71B2-71B2 ID:72B12

CG13458 + endopeptidase \* neuropsin(aa) \* TRYPSIN BETA PRECURSOR(aa) \* zgr;Try \* 4e-27 TRYA\_DROME TRYPSIN ALPHA PRECURSOR trypsin-like proteinase ( [trypsin // CHYMOTRYPSIN // TRYPSIN\_HIS ] CG1497 GH20003 19F1-19F1 ID:72B8

CG1497 + Mst98Cb unknown \* CG18396 GH20038 98C2-98C2 ID:72C1

CG18396 + peptidase \* 1e-30 YHT2\_YEAST HYPOTHETICAL 49.8 KD PROTEIN IN ACT3-YCK1 INTERGENIC REGION PRECURSOR \* 7e-06 carboxypeptidase precursor \* 4e-52 similar to zinc ca [CRBOXYPTASEA // Zn\_carbOpept] CG8560 GH20109 65F7-65F8 ID:72C10

CG8560 + Hs2st enzyme \* DMSD\_2 Sd \* SEGREGATION DISTORTER PROTEIN(aa) \* 2e-74 cDNA EST yk273d10.3 comes from this gene; cDNA EST yk273d10.5 come \* 1e-101 heparan sulfate 2- CG10234 GH20044 37E3-37E3 ID:72C3

CG10234 + RNA\_binding \* Similarity to Human hnRNP F protein (PIR Acc. No. cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA [RBD // rrm // PRO\_RICH] CG8205 GH20047 52B5-52C1 ID:72C4

CG8205 + unknown \* 1e-05 hypothetical protein \* \* [lactamase\_B] CG12375 GH20064 28E-28E ID:72C5

CG12375 + unknown \* [PRO\_RICH] CG10209 GH20077 51D1-51D1 ID:72C8

CG10209 + enzyme \* polyketide synthase(aa) \* 1e-68 CEM1\_YEAST SYNTHASE HOMOLOG (BETA-KETOACYL-ACP \* 1e-69 similar to beta-ketoacyl synthase \* 3e-92 putative 3-oxoacyl [B\_KETOACYL\_SYNTHASE // PPTA // ketoacyl] CG12170 GH20093 83B6-83B6 ID:72C9

CG12170 + Gl 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 ID:72D10

CG7672 + transporter \* BLASTX 2.0E-28 Human sodium iodide symporter mRNA, complete cds.(dna) \* 4e-36 unknown \* 2e-17 Similarity to Salmonella sodium/proline symporter (SW: [NA\_SOLUTE\_SYMP\_3] CG7720 GH20226 93F9-91C7 ID:72D11

CG7720 + 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

CG6045 + enzyme \* aldehyde oxidase(aa) \* DMXDH\_4 ry \* xanthine dehydrogenase(aa) \* XANTHINE DEHYDROGENASE (XD) (ROSY LOCUS PROTEIN)(aa) [dehydrog\_molyb // Ald\_Xan\_dh\_C // fer2] CG6045 GH20168 88F8-88F8 ID:72D2

CG18042 + unknown \* predicted using hexExon; MAL3P6.28 Hypothetical protein, len: aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S. CG18042 GH20177 31B1-31B1 ID:72D3

CG9483 + unknown \* CG9483 GH20208 29F3-29F3 ID:72D7

CG1865 + serpin \* 3e-34 Similar to serine protease inhibitor \* 6e-38 proteinase inhibitor Spi3 - mouse serine proteinase inhib \* 1e-35 cytoplasmic antiproteinase, CAP [serpin // SERPIN] CG1865 GH20213 42F1-42F1 ID:72D9

+ unknown \* weak similarity with B1-hordein (Swiss Prot accession number cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this [SAM\_DOMAIN // SAM // PRO\_RICH] CG7915 GH20255 66B7-66B7 dup:4/4 ID:72E4

CG7915 + Cyp12c1 cytochrome\_P450 \* CYTOCHROME P450 CYP12A2(aa) \* 1e-08 ERG5\_YEAST CYTOCHROME P450 (C-22 STEROL DESATURASE) \* 2e-24 cytochrome P450 cytochrome P4 \* 5e-21 YRV8\_CAEEL[EP450II // p450 // P450 // MITP450 // C] CG4120 GH20281 75D2-75D2 dup:2/2 ID:72E6

CG4120 + unknown \* 1e-39 /match=(desc;; /ma \* 3e-06 F20D6.5 gene product \* predicted using Genefinder \* cDNA EST yk381e5.3 comes from this gene [NLS\_BP] CG10514 GH20308 96C7-96C7 dup:2/2 ID:72E7

CG10514 + Myosin-heavy-chain-like motor\_protein \* nonmuscle myosin II heavy chain A(aa) \* nonmuscle myosin heavy chain-A(aa) \* myosin heavy chain nonmuscle form A - human(aa) \* 2e-97 m[myosin\_head // IQ // MYOSINHEAVY] CG10218 GH20309 89B7-89B7 dup:4/4 ID:72E8

CG10218 + enzyme \* similar to aspartate aminotransferase(aa) \* 1e-99 aspartate aminotransferase cerevisiae, Peptide Partial, \* 1e-157 similar to aspartate aminotransfe [aminotran\_1 // AA\_TRANSFER\_CLASS\_1 // T] CG4233 GH20337 22B8-22B8 dup:2/2 ID:72F2

CG4233 + Taf30alpha transcription\_factor \* 9e-08 hypothetical protein YDR145w - yeast (Saccharomyces cerevisiae) \* 2e-59 T2DA\_DROME TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUNIT ALPHA/22 K [HIST\_TAF] CG17358 GH20363 86F1-86F1 dup:1/3 ID:72F4

CG17358 CG17822 + transcription\_factor CG17822 GH20378 ID:72F5

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

+ enzyme \* Yjr105wp(aa) \* 9e-49 ADK\_YEAST PUTATIVE ADENOSINE KINASE ribokinase homolog \* 2e-78 Similarity to Human adenosine kinase cDNA EST EMBL:Z1 \* 2e-50 AD [ADENOKINASE // MITOCH\_CARRIER // HELIX\_] CG3809 GH20396 87B5-87B5 ID:72F8

CG3809 CG3557 + unknown \* CG3557 GH20409 23E4-23E4 ID:72F9

CG3557 CG10494 + unknown \* CG10494 GH20554 57E-57E dup:2/2 ID:72G12

CG10494 CG12089 + unknown \* 7e-07 beaten path precursor \* 9e-09 beat \* \* CG12089 GH20456 98D1-98D1 ID:72G2

+ chaperone \* KD CHAPERONIN, CHLOROPLAST PRECURSOR (PROTEIN CPN10) (PROTEIN GROES)(aa) \* chaperonin 10(aa) \* 6e-17 CH10\_YEAST KD HEAT SHOCK PROTEIN, MITOCHONDRIA [CHAPERONIN10 // cpn10] CG9920 GH20473 88A10-88A10 ID:72G3

CG9920 CG5946 + electron\_transfer \* unknown(aa) \* NITRATE REDUCTASE (NAD(P)H) (NR)(aa) \* nitrate reductase NR1 (393 AA)(aa) \* 2e-

86 PP11\_YEAST SERINE/THREONINE PROTEIN PHOSPHATASE [oxidoreductase // FPNCR // PHEHYDRYLASE /] CG5946 GH20485  
68D3-68D3 dup:1/2 ID:72G4

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

CG3790 + transporter \* DMORCT2\_2 Orct \* organic cationic transporter-like 1(aa) \* 9e-08 ITR2\_YEAST MYO-INOSITOL  
TRANSPORTER myo-inositol transp \* 6e-75 putative organic ca [SERPIN // sugar\_tr] CG3790 GH20501 49D-49D ID:72G6

CG11703 + transporter \* 3e-19 nervous system antigen nerv \* 5e-06 Similarity to Shrimp sodium/potassium-transporting ATPase beta  
cha \* 7e-10 ATNB\_MOUSE SODIUM/POTASSIUM-TRA CG11703 GH20514 91F10-91F10 ID:72G7

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

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

CG14021 + unknown \* CG14021 GH20612 25D5-25D6 dup:2/2 ID:72H2

+ 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

CG15892 + CG15892 ID:72H4

CG10408 + enzyme CG10408 ID:72H5

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

+ unknown \* /match=(desc:; /match=(desc:(aa) \* 1e-77 /match=(desc:; /ma \* 1e-05 E02C12.6 gene product \* 1E-151 CG9497  
GH20717 26C4-26C4 ID:73A1

CG9497

CG1521 + transporter homology to uncharacterized human and C.elegans proteins MgtE CG1521 GH20809 ID:73A10

CG1648 + unknown \* 2e-12 inserted at base 5' end of P element Inverse PCR \* \* CG1648 GH20817 46B10-46B10 dup:2/3 ID:73A11

+ enzyme \* Similar to glycogenin.(aa) \* GLYCOGENIN(aa) \* 1e-27 GLG2\_YEAST GLYCOGEN SYNTHESIS INITIATOR

CG9480 PROTEIN GLG2 hy \* 7e-67 Similar to glycogenin. CG9480 GH20752 57C7-57C7 dup:1/2 ID:73A3

+ transcription\_factor \* BLASTX 1.3E-19 Human super cysteine rich protein mRNA, partial cds.(dna) \* GAGA factor class A-  
isoform(aa) \* 8e-32 alternatively spliced form \* 8e- [BTB // zf-C2H2 // ZINC\_FINGER\_C2H2] CG12236 GH20830 5C6-5C6 ID:73B1

CG12236 + structural\_protein \* 4e-07 CUP8\_DROME PUPAL CUTICLE PROTEIN EDG-84 PRECURSOR ecdyson \* 3e-08  
CU19\_LOCFMI 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

+ unknown \* density regulated protein drp1(aa) \* 2e-08 YJY4\_YEAST HYPOTHETICAL 22.5 KD PROTEIN IN SPC1-ILV3

CG9099 INTERGENIC REGION \* 4e-13 hypothetical protein \* 8e- [SUI1\_2 // NLS\_BP] CG9099 GH20858 15B1-15B1 ID:73B7

- Ket cytoskeletal\_structural\_protein \* BM KETTIN(aa) \* titin(aa) \* titin [ig // AA\_TRNA\_LIGASE\_II\_1 // SH3 // NLS]

CG1915 CG1915 GH20861 62C2-62C3 dup:2/2 ID:73B8

+ transporter \* pot. w(+) polypeptide(aa) \* WHITE PROTEIN HOMOLOG(aa) \* Active transport ATPase; Adp1p(aa) \* BROWN  
PROTEIN(aa) [ATP\_GTP\_A2 // ABC\_TRANSPORTER // ABC\_tr] CG3327 GH20863 25A1-25A1 ID:73B9

CG3327 + BcDNA:GH02901 enzyme \* hypothetical protein(aa) \* 5e-11 LCFA\_HAEIN LONG-CHAIN-FATTY-ACID--COA LIGASE (LONG-  
CHAIN ACYL-COA SYNTHETASE) > \* LCFA\_ECOLI LONG-CHAIN-FATTY-ACID CG9009 GH20984 13A5-13A5 dup:2/4

CG9009

ID:73C10

CG7583 + CtBP enzyme \* CtBP \* C-terminal binding protein CtBP2(aa) \* C-terminal binding protein(aa) \* similar to the D-isomer specific 2-hydroxyacid dehydrogenases family [2-Hacid\_DH] CG7583 GH20987 87D9-87D11 dup:1/2 ID:73C12

CG6661 + enzyme \* UNKNOWN(aa) \* 7e-63 PUT2\_YEAST DELTA-1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE PRECURSOR (P5C DEHYDROG \* 8e-11 alternatively spliced form; /prediction [aldedh] CG6661 GH20963 70C11-70C11 ID:73C5

CG2750 + enzyme \* No definition line found(aa) \* \* [ATP\_GTP\_A] CG2750 GH20980 11A7-11A7 ID:73C8

+ peptidase \* 1e-24 YBY9\_YEAST PUTATIVE SERINE CARBOXYPEPTIDASE IN ESR1-IRA1 INTERGENIC REGION \* 2e-83 similar to BPTI/KUNITZ inhibitor domain; cDNA EST come \* 8e [ESTERASE // serine\_carbpept // CRBOXYPT] CG3344 GH21114 61C9-61C9 ID:73D10

CG3344 + 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 + defense/immunity\_protein \* 1e-28 peptidoglycan recognition protein precursor \* 1e-28 TNF superfamily, member (LTB)-like (peptidoglycan recognition protein) (AF0 \* 2e-28 peptid CG14704 GH21008 86E-86E ID:73D2

CG14704 (peptidoglycan recognition protein) (AF0 \* 2e-28 peptid CG14704 GH21008 86E-86E ID:73D2

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 GH21048 18D8-18D8 ID:73D5

CG10752 + unknown \* CG10752 GH21086 69E8-69E8 ID:73D8

+ Hr46 steroid\_hormone\_receptor \* DMDHR3A\_2 Hr46 \* HR3\_DROME PROBABLE NUCLEAR HORMONE RECEPTOR HR3 (DHR3) st \* 4e-67 CHR3 gene product \* 2e-71 ROR1\_MOUSE NUCLEAR RECEPTOR ROR-A[STROIDFINGER // hormone\_rec // THYROIDH] CG11823 GH21112 46F4-46F ID:73D9

CG11823 + ribosomal\_protein \* ribosome recycling factor(aa) \* RRF\_HAEIN RIBOSOME RECYCLING FACTOR (RIBOSOME RELEASING FACTOR) (RRF) \* RRF\_CLOPE RIBOSOME RECYCLING FACTOR (RIBOS CG4447 GH21184 67B1-67B1 dup:2/2 ID:73E11

CG4447 ID:73E11

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 comes from this gene(aa) \* 5e-30 YE06\_YEAST HYPOTHETICAL [ATP\_GTP\_A] CG6204 GH21168 95E5-95E5 dup:2/2 ID:73E5

CG6204 from this gene(aa) \* 5e-30 YE06\_YEAST HYPOTHETICAL [ATP\_GTP\_A] CG6204 GH21168 95E5-95E5 dup:2/2 ID:73E5

CG6740 + unknown \* CG6740 GH21172 67C-67C dup:2/2 ID:73E7

+ Cyp4p2 cytochrome\_P450 \* DMC152A3 \* DMCYP4D2\_12 Cyp4d2 \* 6e-09 CP56\_YEAST CYTOCHROME P450-DIT2 (CYTOCHROME P450 56) cyt \* 3e-53 cytochrome P450 cytochrome P4 [EP450II // p450 // P450 // MITP450 // C] CG1944 GH21174 45C-45C dup:2/2 ID:73E8

CG1944 GH21174 45C-45C dup:2/2 ID:73E8

CG8918 + enzyme \* similar to tubulin tyrosine ligase; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST

comes from this gene; cDNA EST comes from CG8918 GH21352 15E5-15E5 ID:73F10

CG8086 + structural\_protein \* 6e-22 NSP1\_YEAST NUCLEOPORIN NSP1 (NUCLEAR PORE PROTEIN NSP1) (NUCLEOSKELETAL-LIKE PRO \* 5e-08 C. elegans DNA-directed RNA polymerase II large subun CG8086 GH21437 29A1-29A1 dup:3/4 ID:73F12

CG12449 + Gfat enzyme \* glucosamine--fructose-6-phosphate aminotransferase(aa) \* 1e-155 GFA1\_YEAST GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (HEX \* g [GATase\_2 // SIS] CG12449 GH21229 cyto\_unknown dup:2/2 ID:73F3

CG5411 + enzyme \* cAMP-specific phosphodiesterase 8B; PDE8B1; 3',5'-cyclic nucleotide phosphodiesterase(aa) \* phosphodiesterase 8(aa) \* 7e-16 cAMP phosphodiesterase [PDEase // PDIESTERASE1 // PAS\_REPEAT //] CG5411 GH21295 59F-59F4 dup:2/2 ID:73F7

CG5627 + 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

CG7045 + DNA\_binding \* DMHMGDA\_2 HmgD \* HIGH MOBILITY GROUP PROTEIN Z (HMG-Z)(aa) \* 2e-11 HMGD\_DROME HIGH MOBILITY GROUP PROTEIN D (HMG-D) high mob \* 2e-05 SSRP\_CAEEL PROB [HIGHMOBLTY12 // HMG\_box] CG7045 GH21448 94B4-94B4 ID:73G1

CG11961 + function\_unknown \* 2e-19 YBS4\_YEAST HYPOTHETICAL 47.8 KD PROTEIN IN HSP26-TIF32 INTERGENIC REGION \* 8e-90 YP67\_CAEEL HYPOTHETICAL 98.3 KD PROTEIN IN CHROMOSOME II (U2 CG11961 GH21451 56D2-56D2 ID:73G2

CG7803 + CG7803 ID:73G3

CG7388 + unknown \* 2e-06 hypothetical protein \* hypothetical protein \* UVS2\_NEUCR UVS-2 PROTEIN uvs2 protein - Neurospora crassa \* [GLYCOSYL\_HYDROL\_F5 // zf-C3HC4 // ZINC\_] CG7388 GH21463 66A12-66A12 dup:1/3 ID:73G4

CG6484 + transporter \* 5e-27 HXT0\_YEAST HEXOSE TRANSPORTER HXT10 hexose transport pro \* 9e-42 GTRL\_DROME GLUCOSE TRANSPORTER-LIKE PROTEIN glucose transpo \* 4e-22 predicted [SUGRTRNSPORT // SUGAR\_TRANSPORT\_1 // SU] CG6484 GH21490 54D2-54D2 ID:73G7

CG7216 + 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

CG7571 + transporter \* 2e-64 coded for by C. elegans cDNA yk54h9.5; coded for by C. elegans cDNA yk54h9.3; si \* 4e-70 PGT\_HUMAN PROSTAGLANDIN TRANSPORTER (PGT) prostagland CG7571 GH21536 74D1-74D1 dup:2/2 ID:73H1

CG14209 + transporter \* 8e-32 YG5F\_YEAST PUTATIVE MITOCHONDRIAL CARRIER YGR257C hypot \* 2e-06 phosphate transporter precursor melanogas \* 2e-53 YQ51\_CAEEL PUTATIVE MITOCHON [mito\_carr // MITOCH\_CARRIER] CG14209 GH21653 18D8-18D8 ID:73H12

CG10193 + motor\_protein \* 3e-05 F35D11.11 gene product \* 2e-06 hyaluronan receptor - human \* 3e-06 tetravalent M protein=hybrid molecule containing amino-terminal subuni \* Si [PRO\_RICH] CG10193 GH21577 95C3-95C3 dup:2/2 ID:73H4

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

CG3455 + Rpt4 endopeptidase \* 26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED ATPASE DOMAIN PROTEIN 44)(aa) \* Pros45 proteosome subunit homolog(aa) \* 1e-134 SUG2\_YEAST PROB CG3455 GH21618 5E1-5E1 dup:2/2 ID:73H8

CG6652 + motor\_protein \* 6e-13 unknown \* \* [NLS\_BP] CG6652 GH21622 73E4-73E4 dup:2/2 ID:73H9

+ Orct transporter \* DMORCT2\_2 Orct \* 3e-10 YGK4\_YEAST PROBABLE METABOLITE TRANSPORT PROTEIN YGL104C \*  
 CG6331 putative organic cation transporter [sugar\_tr] CG6331 GH21655 95F2-95F2 ID:74A1  
 + unknown \* 2e-07 /match=(desc: \* 3e-08 MPV1\_MOUSE MPV17 PROTEIN mpv17 protein - mouse \* 1e-07 MpV17  
 CG12355 transgene, murine homolog, glomerulosclerosis \* 1e-06 PMP2\_ CG12355 GH21685 75F9-75F9 ID:74A4  
 + ligand\_binding\_or\_carrier \* 4e-59 62D9.a \* 1e-09 cellular retinaldehyde-binding protein; CRALBP \* 3e-14 tocopherol (alpha)  
 CG3091 transfer protein (ataxia (Friedreich-like) with \* 3e- [CRAL\_TRIO] CG3091 GH21689 2F1-2F1 ID:74A6  
 + corto nucleic\_acid\_binding \* corto \* CENTROSOMAL AND CHROMOSOMAL FACTOR (CCF) (CHROMOCENTROSOMIN)(aa)  
 CG2530 \* CP-1(aa) \* inserted at base Both 5' and 3' ends of P element Inverse PCR CG2530 GH21787 82F5-82F5 ID:74B1  
 + EG:4F1.1cell\_adhesion \* /match=(desc:; /match=(desc:(aa) \* sarcoglycan, delta (35kD dystrophin-associated glycoprotein)(aa) \*  
 CG14808 4e-06 delta sarcoglycan \* 9e-05 delta-sarcogl CG14808 GH21860 2B8-2B9 ID:74B10  
 + motor\_protein \* mutated in colorectal cancers(aa) \* 3e-05 myosin heavy chain, MHC CCl4-cirrhotic liver fat-storing cell I \* 2e-  
 CG6156 06 DMMHC\_2 Mhc \* myosin heavy chain I CG6156 GH21874 88F1-88F1 dup:2/2 ID:74B12  
 + unknown \* POLYPOSIS LOCUS PROTEIN (TB2 PROTEIN)(aa) \* pathogenicity protein(aa) \* 2e-09 YSV4\_CAEEL  
 CG5539 HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III (U CG5539 GH21788 60A2-60A2 ID:74B2  
 + unknown \* 1e-23 hypothetical protein YDL219w - yeast (Saccharomyces cerevisiae) \* 3e-32 predicted using Genefinder \* 5e-  
 CG5270 27 SPAC8C9.05, len:149aa; similarity: [FYVE\_DOMAIN // FYVE] CG5270 GH21817 86E5-86E5 ID:74B5  
 + BcDNA:GH04802 ion\_channel \* 5e-05 TOK1\_YEAST OUTWARD-RECTIFIER POTASSIUM CHANNEL TOK1 (TWO-DOMAIN  
 OUTWARD RECTIFIE \* 1e-18 C24H11.8 \* 8e-06 TWIK-related acid-sensitive K+ chann [CHANNEL\_PORE\_K] CG1688 46B4-  
 CG1688 46B5 dup:2/2 ID:74B7  
 + metabolism \* 3601, 14-kDa protein subunit of reductase complex(aa) \* ubiquinol-cytochrome c reductase binding protein(aa)  
 CG3560 \* UBIQUINOL-CYTOCHROME C REDUCTASE COMP CG3560 GH21854 14B12-14B12 ID:74B9  
 + unknown \* 2e-52 gene C35D10.2 protein - Caenorhabditis elegans similar to \* 3e-81 RGS-GAIP interacting protein GIPC  
 CG11546 GLUT1 \* 7e-81 RGS-GAIP interacting protein [PDZ] CG11546 GH21964 44A8-44B dup:1/2 ID:74C11  
 + weak homology to leucine carboxyl methyltransferase [Homo sapiens] and receptor protein kinase-like protein [Arabidopsis  
 CG14768 thaliana] CG14768 GH21888 ID:74C2  
 + unknown \* /match=(desc:; /match=(desc:(aa) \* 4e-77 /match=(desc:; /ma \* 7e-06 No definition line found \* No definition line  
 CG7135 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  
 CG2457 + inaF ion\_channel \* INAF protein(aa) \* 1e-115 INAF protein \* \* CG2457 GH21930 10D5-10D6 dup:1/2 ID:74C7  
 + enzyme \* 7e-97 ALAM\_YEAST PUTATIVE ALANINE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR  
 (GLUTAMIC \* 1e-159 Similar to alanine aminotransferase; coded for by C. [aminotran\_1 // ACCSYNTHASE] CG1640 GH21936  
 CG1640 11E9-11E10 dup:2/3 ID:74C8  
 + receptor \* 3e-10 tolloid related-1 \* 5e-17 similar to CUB domain (2 domains), Low-density lipoprotein recepto \* 8e-15  
 BMP1\_MOUSE BONE MORPHOGENETIC PROTEIN PRE [LDLRA\_2 // CUB // ldl\_recept\_a // PRO\_R] CG5449 GH21941 94A3-  
 CG5449 94A3 ID:74C9  
 + rux unknown \* CELL CYCLE NEGATIVE REGULATOR ROUGHSEX(aa) \* rux \* 1e-170 rux \* [NLS\_BP] CG4336 GH22074 5D1-  
 CG4336 5D1 ID:74D12

+ transcription\_factor \* TRANSCRIPTION FACTOR ADF-1 (ADH DISTAL FACTOR 1)(aa) \* DMADF1A\_2 Adf1 \* 3e-07 cDNA  
 CG10949 EST comes from this gene; cDNA EST yk319a3.5 come [NLS\_BP // ATP\_GTP\_A] CG10949 GH22016 38C9-38C9 ID:74D3  
 CG10693 + CG10693 GH22026 ID:74D5  
 + kls unknown \* klarsicht protein(aa) \* 8e-06 protein \* hypothetical protein \* protein [NLS\_BP // SUGAR\_TRANSPORT\_1]  
 CG17046 CG17046 GH22034 61C3-61C7 dup:5/6 ID:74D8  
 + transporter \* similar to Mitochondrial carrier proteins (2 domains); cDNA EST yk309c6.5 comes from this gene; cDNA EST  
 yk309c6.3 comes from this gene; cDNA EST [mito\_carr // MITOCARRIER // MITOCH\_CARR] CG5805 GH22160 98E1-98E1  
 CG5805 dup:2/2 ID:74E10  
 CG3246 + unknown \* CG3246 25A3-25A3 dup:2/2 ID:74E11  
 + 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  
 CG7365 dup:2/2 ID:74E2  
 CG6684 + CG6684 dup:2/2 ID:74E3  
 + enzyme \* carnitine racemase - Escherichia coli(aa) \* ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR  
 (SHORT CHAIN ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATA [GRAM\_POS\_ANCHORING // ECH] CG6984  
 CG6984 GH22096 53F10-53F10 dup:2/2 ID:74E5  
 + 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-  
 CG4096 5B1 dup:3/3 ID:74E6  
 + jdp chaperone \* 1e-11 SCJ1\_YEAST SCJ1 PROTEIN SCJ1 protein - yeast (Saccharomyce \* 1e-09 DNJ1\_DROME DNAJ  
 PROTEIN HOMOLOG (DROJ1) droj1 \* 1e-10 YRY1\_CAEEL HYPOTHETIC [GRAM\_POS\_ANCHORING // DnaJ // DNAJPROTE]  
 CG2239 CG2239 GH22106 99F8-99F10 dup:3/3 ID:74E7  
 CG2233 + unknown \* CG2233 GH22123 7D5-7D5 dup:5/5 ID:74E8  
 + transporter \* MITOCHONDRIAL FAD CARRIER PROTEIN FLX1(aa) \* UCP2(aa) \* 5e-26 YIA6\_YEAST PUTATIVE  
 MITOCHONDRIAL CARRIER YIL006W probabl \* 4e-09 ADT\_DROME ADP,ATP CA [mito\_carr] CG8026 GH22139 45B4-45B5  
 CG8026 dup:2/2 ID:74E9  
 + protein\_kinase \* coded for by C. elegans cDNA CEESC01F; coded for by C. elegans cDNA cm11b7; coded for by C. elegans  
 CG10737 cDNA cm11b8; Similar to protein kinase.(aa) \* 1e [DAG\_PE\_BINDING\_DOMAIN // DAG\_PE-bind //] CG10737 56B6-56C ID:74F1  
 + cell\_adhesion \* Down syndrome cell adhesion molecule(aa) \* 3e-66 neuroglian \* 1e-58 predicted protein contains a large  
 CG17800 number of Ig superfamily repeat \* 2e-39 PTPT9 [ig // PRO\_RICH // fn3] CG17800 GH22207 43B1-43B2 dup:3/4 ID:74F3  
 + chitinase \* dJ73M23.3 \* 1E-137\* 9e-06 chitinase protein precursor \* similar to similar to [EGF\_2] CG7565 GH22222 66B6-  
 CG7565 66B6 ID:74F4  
 CG11737 + unknown \* 3e-24 K02G10.3 gene product \* \* CG11737 GH22337 85A5-85A5 ID:74G2  
 + enzyme \* 3-hydroxy-3-methylglutaryl-CoA-synthase(aa) \* Similar to hydroxymethylglutaryl-CoA synthase; coded for by C.  
 elegans cDNA cm01e7(aa) \* 3-hydroxy-3- [HMG\_CoA\_synt // HMG\_COA\_SYNTHASE] CG4311 GH22436 53A5-53B1 dup:2/4  
 CG4311 ID:74G8



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

CG4321 + Cyp4d8 cytochrome\_P450 \* DMLCYP6A9 Cyp6a9 \* DMCYTO\_2 Cyp4d1 \* DMCYP4D2\_12 Cyp4d2 \* cytochrome P450(aa) [EP450II // p450 // P450 // MITP450 // B] CG4321 GH22459 66A1-66A1 ID:74H1

CG10833 + Cyp28d1 cytochrome\_P450 \* cytochrome P450 monooxygenase CYP28A2(aa) \* 8e-48 CYP6A2 \* 2e-32 YRVA\_CAEEL PUTATIVE CYTOCHROME P450 T10B9.10 IN CHROMOSOME II \* 3e-49 cytochrome P4 [EP450II // p450 // P450 // MITP450 // C] CG10833 GH22460 25C9-25C9 ID:74H2

CG9336 + unknown \* CG9336 GH22472 38F1-38F1 ID:74H4

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

CG10704 + transcription\_factor \* eyg \* 9e-46 Eyegone \* 1e-38 similar to 'Paired box' domain, homeobox protein (paired subfamily \* 2e-41 PAX3\_MOUSE PAIRED BOX PROTEIN PAX-3 pax-3 p[PAX // HOMEBOX\_1 // homeobox // HOMEOB] CG10704 GH22493 69B3-69B4 ID:74H8

CG5001 + \* DnaJ-1 \* heat shock protein dnaJ homolog - human(aa) \* similar to DNAJ protein; cDNA EST comes from this gene; cDNA 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

CG6716 + prd transcription\_factor \* SEGMENTATION PROTEIN PAIRED(aa) \* DMPRD\_5 prd \* 3e-58 similar to 'Paired box' domain, homeobox protein (paired subfamily \* 2e-87 PAX3\_MOUSE PAIRE[PAX // HOMEBOX\_1 // homeobox // HOMEOB] CG6716 GH22686 33B14-33B14 ID:75B4

CG10291 + Abdominal B transcription\_factor HOMEBOX, HOMEBOX\_1, HOMEBOX\_2, HTHREP] CG10291 GH22693 dup:4/5 ID:75B6

CG12177 + enzyme \* 6e-06 YD40\_YEAST HYPOTHETICAL 42.3 KD PROTEIN IN YTA2-DIT1 INTERGENIC REGION \* 4e-33 predicted using Genefinder; similar to Inosine-uridine preferri [IU\_nuc\_hydro] CG12177 GH22706 12B1-12B1 ID:75B7

CG1942 + unknown \* 1e-35 probable membrane protein YOR245c - yeast (Saccharomyces cerevisiae) \* 3e-58 K07B1.4 gene product \* 9e-21 hypothetical protein \* predicted usi CG1942 GH22719 43E11-43E11 ID:75B9

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

CG12316 + unknown \* BLASTX 2.0E-06 Theileria parva schizont/sporozyte surface protein gene, partial cds.(dna) \* \* [NLS\_BP]

CG12316 GH22749 71B2-71B2 ID:75C3  
+ Flo-2 unknown \* 1e-176 flotillin-2 \* 1e-114 epidermal surface antigen \* 1e-114 flotillin epidermal surface antigen - human \* 1e-114 growth-associated protein [NLS\_BP] CG11547 GH22754 13A3-13A4 ID:75C4

CG11547  
+ unknown \* CG8960 GH22765 62D2-62D2 ID:75C5

CG8960  
+ transcription\_factor \* [PRO\_RICH] CG8991 GH22790 48C-48C ID:75C6

CG8991  
+ unknown \* CG10311 GH22794 89B22-89B22 ID:75C7

CG10311  
+ enzyme \* 1e-151 GLS1\_CAEEL PUTATIVE GLUTAMINASE DH11.1 (GLS) (L-GLUTAMINE AMIDOHYDROLASE) \* 1e-170 protein \* 1e-171 GLSK\_RAT GLUTAMINASE, KIDNEY ISOFORM PREC [ANK\_REP // ank // ANK\_REP\_REGION] CG8772 GH22838 49B8-49B8 dup:2/2 ID:75D1

CG8772  
+ bt protein\_kinase \* projectin - fruit fly (*Drosophila melanogaster*)(aa) \* bt \* similar to Fibronectin type III domain (31 domains), IG (immunoglobulin) superfamily [PROTEIN\_KINASE\_ST // FNTYPEIII //] CG1479 GH22863 102D6-102E1 dup:1/2 ID:75D11

CG1479  
+ Fragile-X-related RNA\_binding \* FRAGILE X MENTAL RETARDATION SYNDROME RELATED PROTEIN 1(aa) \* Fxr2h(aa) \* protein isoform d(aa) \* 6e-81 FMR1\_MOUSE FRAGILE X MENTAL RETARDATION [KH-domain // TONB\_DEPENDENT\_REC\_1 // KH] CG6203 GH22839 85F10-85F11 ID:75D2

CG6203  
+ 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

CG10561  
+ unknown \* CG3330 GH22851 97F8-97F8 ID:75D7

CG3330  
+ enzyme \* probable membrane protein YPR184w - yeast (*Saccharomyces cerevisiae*) \* similar to Alpha amylase; cDNA EST yk217a9.5 comes from this gene; \* amylo-1, [ISOCITRATE\_LYASE] CG9485 GH22856 57D4-57D5 dup:3/4 ID:75D8

CG9485  
+ unknown CG3770 dup:2/2 ID:75E10

CG3770  
+ unknown \* CG11388 GH22974 60B1-60B1 dup:2/2 ID:75E11

CG11388  
+ electron\_transfer \* GEC-3(aa) \* 3e-43 coded for by *C. elegans* cDNA yk51h9.5; coded for by *C. elegans* cDNA yk117c2.5; c \* 1e-64 quiescin Q6 quiescin \* 2e-66 GEC-3 [THIOREDOXIN\_2] CG17843 GH22889 96B6-96B6 dup:2/2 ID:75E2

CG17843  
+ unknown \* CG2081 GH22911 10A3-10A3 dup:2/2 ID:75E4

CG2081  
+ unknown \* CG7905 GH22919 66B6-66B7 dup:2/2 ID:75E5

CG7905  
+ cell\_adhesion \* 2e-11 CHAO\_DROME CHAOPTIN PRECURSOR (PHOTORECEPTOR CELL-SPECIFIC MEMBRANE PROTEIN) \* 3e-06 Similarity to Rat insulin-like growth factor binding prote [LRR // LEURICHRPT // NLS\_BP] CG15658 GH22922 57C7-57C7 dup:2/2 ID:75E6

CG15658  
+ neurotransmitter\_transporter \* SerT \* glycine transporter type-2(aa) \* SODIUM- AND CHLORIDE-DEPENDENT GABA TRANSPORTER 3(aa) \* hypothetical protein T23G5.5 - *Caenor[NA\_NEUROTRAN\_SYMP\_1 // NANEUSMPORT // N]* CG8380 GH22929 53C-53C dup:2/2 ID:75E8

CG8380  
+ enzyme \* PHOSPHOMANNOMUTASE (PMM)(aa) \* 2e-91 YM8L\_YEAST HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION \* 1e-114 similar to Phosphoglucomutase a [PGM\_PMM // PGMPMM] CG10202 GH22984 51C5-51C5 ID:75F1

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

CG12789

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

CG10126 + ligand\_binding\_or\_carrier \* calcyphosine(aa) \* CRUSTACEAN CALCIUM-BINDING PROTEIN (CCBP-23 PROTEIN)(aa) \* 1e-10 predicted using Genefinder; Similarity to Human calmodulin (SW:P [EF\_HAND // efhand // EF\_HAND\_2] CG10126 GH22994 87D3-87D3 ID:75F5

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

CG1090 + transporter \* retinal rod Na/Ca+K exchanger(aa) \* Na/Ca,K-exchanger(aa) \* 2e-06 probable membrane protein YDL206w - yeast (Saccharomyces cerevisiae) \* 1e-05 Na/C CG1090 GH23040 82B1-82B1 ID:75G4

CG1303 + agt DNA\_repair\_protein \* O-6-alkylguanine-DNA alkyltransferase(aa) \* agt \* 3e-16 MGMT\_YEAST METHYLATED-DNA-- PROTEIN-CYSTEINE METHYLTRANSFERASE (6-O-METHYLGUANINE \* 2e-10 MGM [Methyltransf\_1 // MGMT] CG1303 GH23047 84C4-84C4 ID:75G5

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

CG18102 + shi enzyme \* dynamin(aa) \* DMDDYN4\_2 shi \* dynamin II - human(aa) \* dynamin-like protein - fruit fly (Drosophila melanogaster)(aa) CG18102 GH23121 13F9-13F10 dup:1/2 ID:75H1

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

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

CG13787 + It has been mapped cytologically to 28A1 CG13787 GH23165 ID:75H7

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:76A2

CG13832 + enzyme \* 5e-20 T10H10.3 gene product \* 9e-07 ubiquitin protein ligase \* 3e-07 WWP1 \* 1e-05 S-SCAM beta [WW\_rsp5\_WWP // WW\_DOMAIN\_2] CG13832 GH23265 94D13-94D13 ID:76A4

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

CG7962 + CG7962 GH23282 ID:76A8

CG10377 + Hrb27C RNA\_binding \* DMHRP481\_2 Hrb27C \* HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1)(aa) \* 2e-36 NAB4\_YEAST NUCLEAR POLYADENYLATED RNA-BINDING PROTE [RNP\_1 // RBD // rrm] CG10377 27C-27C dup:6/8 ID:76B1

CG6028 + unknown \* 2e-22 YNQ8\_YEAST HYPOTHETICAL 28.8 KD PROTEIN IN PSD1-SKO1 INTERGENIC REGION \* 2e-27 YO23\_CAEEL HYPOTHETICAL 23.3 KD PROTEIN ZK688.3 IN CHROMOSOME I [ATP\_GTP\_A] CG6028 GH23390 93F14-93F14 ID:76B10

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

CG1121 + alpha-Est8 enzyme \* agr;-Est8 \* alpha esterase(aa) \* agr;-Est3 \* alpha esterase [CARBOXYLESTERASE\_B\_1 // CARBOXYLESTERAS] CG1121 GH23353 85A1-84D5 ID:76B3

CG11856 + structural\_protein \* Ran/TC4-binding nucleopore protein(aa) \* RanBP2 protein - mouse (fragment)(aa) \* RAN binding protein 2; nucleoporin 358(aa) \* HTF9-A protein[GRAM\_POS\_ANCHORING // zf-RanBP // ZF\_RA] CG11856 GH23370 96C4-96C5 dup:2/4 ID:76B5

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

CG3348 + unknown \* CG3348 GH23384 97F6-97F6 ID:76B8

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

CG5670 + Atpalpatransporter \* 3e-78 ATC1\_YEAST CALCIUM-TRANSPORTING ATPASE (GOLGI CA2+-ATPASE) \* ATNA\_DROME SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA CHAIN (SODIUM PUMP) (NA+/ [NAKATPASE // Na\_K\_ATPase\_C // ATPASE\_E1] CG5670 GH23483 93B-93B dup:2/3 ID:76C12

CG8054 + transporter \* 3e-69 predicted using Genefinder; cDNA EST comes from this g \* 3e-07 tetracycline resistance protein \* similar to translocase \* contains similarity [PRO\_RICH // NLS\_BP] CG8054 GH23453 45B1-45B1 ID:76C6

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

CG1760 + protein\_kinase \* bt \* hep \* 8e-21 SPK1\_YEAST PROTEIN KINASE SPK1 (SERINE-PROTEIN KINASE 1) \* 2e-20 p90 ribosomal S6 kinase [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG1760 GH23573 10C3-10C3 ID:76D10

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

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

CG13551 + GH20780 CG13551 GH23524 ID:76D4

CG6942 + ion\_channel \* 1e-15 chloride channel protein CLC-1 - yeast (Saccharomyces cerevisiae) \* 1e-108 similar to T. marmorata chloride channel protein (SP:ClCH\_TORMA, \* [CLCHANNEL // CBS // voltage\_CLC] CG6942 GH23529 86F9-86F9 ID:76D5

CG5201 + Dad transcription\_factor \* Dad \* DAD polypeptide \* 2e-18 similar to ZK370.2 \* 2e-40 Smad6 [Dwarfin // PRO\_RICH // NLS\_BP] CG5201 GH23534 89E12-89E13 dup:3/4 ID:76D6

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

CG4848 + transporter \* 4e-12 IdlBp \* \* CG4848 GH23636 87B6-87B6 dup:3/3 ID:76E12

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

CG9396 + unknown \* 0-44 PROTEIN(aa) \* HYPOTHETICAL 14.6 KD PROTEIN IN REC104-SOL3 INTERGENIC REGION(aa) \* HYPOTHETICAL 16.3 KD PROTEIN F53F10.3 IN CHROMOSOME I(aa) \* h CG9396 GH23618 86C3-86C3 dup:2/2 ID:76E7

+ 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  
 CG9519  
 + endopeptidase \* DMSTUBBLE\_1 Sb \* zgr;Try \* 2e-22 TRYI\_DROME TRYPSIN IOTA PRECURSOR iota trypsin \* 2e-15 kallikrein [trypsin // CHYMOTRYPSIN // TRYPSIN\_CATA] CG9898 GH23641 59B8-59B8 ID:76F1  
 CG9898  
 + enzyme \* fructose-1,6-bisphosphatase; Fbp1p(aa) \* fructose-bisphosphatase 1(aa) \* fructose-1,6-bisphosphatase precursor(aa) \* fructose-1,6-bisphosphatase ho [FBPASE // FBpase // INFBPHPTASE // FBP] CG10611 38A-38A dup:3/3 ID:76F10  
 CG10611  
 + unknown \* growth factor-responsive protein, vascular smooth muscle - rat(aa) \* 3e-47 Weak similarity with apoptosis protein RP-8; cDNA EST \* SM-20 \* CG1114 GH23732 83A1-83A1 ID:76F11  
 CG1114  
 + pyd enzyme \* DMD477 pyd \* TamA(aa) \* 1e-16 coded for by C. elegans cDNA yk25e5.3; coded for by C. elegans cDNA yk25e5.5; si \* 1e-138 ZO1\_MOUSE TIGHT JUNCTION PRO [Guanylate\_kin // GUANYLATE\_KINASE\_2 // ] CG9763 GH23642 85B4-85B5 ID:76F2  
 CG9763  
 + enzyme \* 1e-31 pdb|1SDY|A Saccharomyces cerevisiae Saccharomyces cerevisiae \* 1e-34 SODC\_DROME SUPEROXIDE DISMUTASE (CU-ZN) superoxide dismuta \* 5e-38 SODE\_C [CUZNDISMUTASE // SOD\_CU\_ZN\_1 // SOD\_CU\_Z] CG9027 47F6-47F7 ID:76F8  
 CG9027  
 + 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  
 CG7628  
 + endopeptidase \* mas \* DMSE1\_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  
 CG6467  
 + chaperone \* DMCYP1\_2 Cyp1 \* 4e-41 CYPH\_YEAST PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) \* 1e-36 CYPH\_DROME PEPTIDYL-PROLYL CIS-TRANS [pro\_isomerase // CSA\_PPIASE\_1 // CSA\_PP] CG1866 GH23813 98C3-98C3 dup:1/4 ID:76G11  
 CG1866  
 + Arr2 unknown \* DMPPP\_2 Arr2 \* ARRB\_DROME PHOSRESTIN I (ARRESTIN B) (ARRESTIN 2) (49 KD ARRESTIN-LIKE PROTEIN) \* 2e-73 ARRB\_CAEEL PROBABLE BETA-ARRESTIN coded for [ARRESTIN // arrestin // ARRESTINS] CG5962 GH23741 66D-66D dup:4/5 ID:76G2  
 CG5962  
 + unknown \* CG17549 GH23745 37E1-37E1 dup:2/2 ID:76G4  
 CG17549  
 + unknown \* 1e-05 NIPM\_BOVIN NADH-UBIQUINONE OXIDOREDUCTASE KD SUBUNIT (COMPLEX I-15 KD) (CI-15 \* \* CG11455 GH23780 21B2-21B2 ID:76G6  
 CG11455  
 + rha motor\_protein \* RADHA protein(aa) \* 1e-10 similar to C. elegans UNC-89 and titins \* 3e-07 ORF 73, contains large complex repeat CR sarcoma-associated herpesv \* YL CG11908 GH23783 96D-96D ID:76G7  
 CG11908  
 + rdgA enzyme \* DMDKA\_1 rdgA \* KDGE\_DROME EYE-SPECIFIC DIACYLGLYCEROL KINASE (RETINAL DEGENERATION A PROTEIN) ( \* DMDKA\_1 rdgA \* [ANK\_REP // DAGKa // ank // DAGKc // ANK] CG10966 GH23785 8C4-8C7 ID:76G8  
 CG10966  
 + BcDNA:GH05095 motor\_protein \* 8e-34 protein \* \* [NLS\_BP] CG6424 GH23788 54E3-54E4 dup:1/3 ID:76G9  
 CG6424  
 + transmembrane\_receptor \* CG7655 GH23865 90C-90C ID:76H10  
 CG7655  
 + unknown \* [ABC\_TRANSPORTER] CG9780 GH23891 82A4-82A4 ID:76H12  
 CG9780

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

CG10585 + enzyme \* hexaprenyl pyrophosphate synthetase; Coq1p(aa) \* 9e-26 COQ1\_YEAST HEXAPRENYL PYROPHOSPHATE SYNTHETASE PRECURSOR (HPS) \* 9e-13 trans-prenyltransferase [ATP\_GTP\_A] CG10585 GH23839 78A6-78A6 ID:76H7

CG3192 + CG3192 ID:76H8

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

CG8866 + protein\_kinase \* DMSTPK Pk61C \* DMFUSED\_2 fu \* similar to the CDF-1/PDGF receptor family of tyrosine protein kinases(aa) \* DMRSK\_2 S6kII [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

CG10131 + enzyme \* 3-hydroxyacyl-CoA dehydrogenase (hbd-8)(aa) \* 9e-14 HCD1\_CAEEL PROBABLE 3-HYDROXYACYL-COA DEHYDROGENASE F54C8.1 \* 1e-54 lambda-crystallin \* 3e-74 C [3HCDH // NAD\_BINDING // NLS\_BP] CG10131 GH23990 51B7-51B7 dup:2/2 ID:77B1

CG6043 + unknown \* [PRO\_RICH] CG6043 GH24071 34A11-34B1 ID:77B11

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

CG17534 + enzyme \* DMGST\_3 GstD1 \* 2e-44 unknown \* 1e-13 GTT1\_MOUSE GLUTATHIONE S-TRANSFERASE THETA (CLASS-THETA) \* 6e-16 glutathione S-transferase theta GLUTATHIONE S [GST] CG17534 55C9-55C9 dup:4/4 ID:77B3

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 // ehand // EF\_HAND\_2] CG16932 60D14-60D15 dup:2/4 ID:77B5

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

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

CG7529 + enzyme \* DMGLUTAC\_9 Glt \* LIPASE PRECURSOR(aa) \* GLUTACTIN PRECURSOR(aa) \* 1e-42 EST1\_CAEEL GUT ESTERASE PRECURSOR (NON-SPECIFIC CARBOXYLESTERASE) [CARBOXYLESTERASE\_B\_1 // ESTERASE // COe] CG7529 GH24077 78D7-78D7 ID:77C1

+ transcription\_factor \* zinc finger protein 37(aa) \* hkb \* 2e-17 AZF1\_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN  
 CG8367 AZF1 fin \* 4e-47 zinc finger motif protein [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG8367 GH24215 50E4-50E4 ID:77C11  
 + unknown \* 5e-11 HST2\_YEAST HST2 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 2) \* 1e-09 SIR2 \* 1e-48 similar to  
 CG3187 SIR; cDNA EST yk300f10.3 comes from this gene \* 3e-49 u CG3187 GH24142 5A12-5A12 ID:77C5  
 + transcription\_factor \* DMSUHW\_6 su(Hw) \* crol \* zf43C \* 7e-08 zinc finger 30C [zf-C2H2 // ZINC\_FINGER\_C2H2 //  
 CG7101 ZINC\_FIN] CG7101 GH24178 17E1-17E1 ID:77C7  
 + transporter \* DMWHITER\_2 w \* WHITE PROTEIN HOMOLOG(aa) \* hypothetical protein \* 3e-39 ORF YOL075c  
 CG9663 [ATP\_GTP\_A2 // ABC\_TRANSPORTER // ABC\_tr] CG9663 GH24286 25A1-25A1 ID:77D10  
 + 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 //  
 CG7788 CASPASE\_P20 /] CG7788 GH24292 99C4-99C4 ID:77D11  
 + unknown \* R01H10.7(aa) \* inositol polyphosphate 4-phosphatase, type II(aa) \* inositol polyphosphate 4-phosphatase type  
 CG1846 II-alpha(aa) \* 4e-58 inositol polypho [PH\_DOMAIN] CG1846 GH24251 12E1-12E1 dup:2/2 ID:77D3  
 + Cyp4ac1 cytochrome\_P450 \* 2e-75 /motif=(desc:; /ma \* 3e-80 similar to Cytochrome P450 \* 1e-54 cytochrome P450 Cyp4a -  
 CG14032 mouse \* 2E-56 [EP450II // p450 // P450 // MITP450 // C] CG14032 GH24257 25D2-25D2 ID:77D4  
 + enzyme \* flavin containing monooxygenase 3(aa) \* T3P18.10(aa) \* similar to Flavin-binding monooxygenase-like(aa) \*  
 CG3006 similar to flavin-containing monooxygena [ADXRDTASE // FADPNR // FMO-like // PNDR] CG3006 GH24271 60A13-60A13 ID:77D7  
 + signal\_transduction \* EPHRIN-B1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 2) (LERK-2)  
 (ELK LIGAND PRECURSOR) (ELK-L) (XLERK)(aa) \* 4e-13 cek5 receptor ligand [Ephrin] CG1862 GH24276 102C5-102C5  
 CG1862 ID:77D9  
 + transcription\_factor \* ORFveg132; similar to Caenorhabditis elegans ORF F59B10.1 encoded by EMBL Accession Number \*  
 CG3328 protein(aa) \* 2e-70 similarity to a transmembranous of [CASPASE\_HIS] CG3328 GH24458 60B9-60B10 dup:3/3 ID:77E12  
 + phyl signal\_transduction \* phyl \* 1e-175 phyllopod \* phyllopod - fruit fly (Drosophila melanogaster) ORF \* phyllopod [NLS\_BP]  
 CG10108 CG10108 GH24326 51A-51A2 dup:2/2 ID:77E4  
 + az2 transcription\_factor \* zf43C \* 2e-09 AZF1\_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin \* putative zinc  
 CG1605 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  
 + enzyme \* CYSTEINYL-TRNA SYNTHETASE (CYSTEINE--TRNA LIGASE) (CYSRS)(aa) \* 5e-52 YNY7\_YEAST PUTATIVE  
 CYSTEINYL-TRNA SYNTHETASE C29E6.06C (CYSTEINE--TRNA LIGASE [TRNASYNTHCYS // tRNA-synt\_1e] CG8257  
 CG8257 GH24360 50E2-50E2 dup:3/3 ID:77E7  
 + unknown \* 6e-43 COX11 (AA 1-277) \* 2e-44 cDNA EST comes from this gene; cDNA EST co \* 1e-124 protein \* 3e-51  
 CG6922 component involved in Haem biosynthesis americana CG6922 GH24534 25E6-25E6 ID:77F11  
 CG11440 + wunen \* similarity to phosphatidic acid phosphatase PA\_PHOSPHATASE CG11440 ID:77F12  
 CG1888 + unknown \* [NLS\_BP] CG1888 GH24468 45F1-45F1 ID:77F2  
 + transmembrane\_receptor \* DMLRR47\_3 Lrr47 \* 8e-06 LRR47 protein - fruit fly (Drosophila melanogaster) ( \* 6e-06 Ras-  
 CG2143 binding protein SUR-8 leuc \* 6e-06 Ras-binding protein SUR [LRR // LEURICHRPT] CG2143 GH24470 9C2-9C2 ID:77F3  
 CG10137 + unknown \* glycine-, glutamate-, thienylcyclohexylpiperidine-binding protein(aa) \* 1e-59 protein \* 1E-170\* CG10137 37F1-

37F1 ID:77F4

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

CG9245 + enzyme \* phosphatidylinositol synthase; Pis1p(aa) \* phosphatidylinositol synthase(aa) \* phosphatidylinositol synthase(aa) \* 2e-31 PIS\_YEAST CDP-DIACYLGLYCERO [CDP\_ALCOHOL\_P\_TRANSF // CDP\_ALCOHOL\_P\_T] CG9245 GH24502 13E14-13E14 ID:77F7

CG1782 + Uba1 enzyme \* ubiquitin-activating enzyme \* ubiquitin activating enzyme \* predicted using Genefinder; Similarity to Mouse ubiquitin-activati \* UBA1\_MOUSE UBIQUIT [UBA\_NAD // ThiF\_family // UBIQUITIN\_ACT] CG1782 GH24511 46A1-46A1 dup:3/3 ID:77F8

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

CG12800 + Cyp6d4 cytochrome\_P450 \* THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)(aa) \* Similar to cytochrome P450(aa) \* cytochrome P450(aa) \* CYTOCHROME P450 4A11 PRECURSOR (CYP1A11) [EP450II // p450 // P450 // MITP450 // B] CG12800 GH24669 94C4-94C4 ID:77G11

CG3239 + endopeptidase \* 2e-11 similar to Zinc-binding metalloprotease; cDNA EST come \* 3e-14 NEP\_MOUSE NEPRILYSIN (NEUTRAL ENDOPEPTIDASE) (NEP) (ENKEPHALINASE) (CD10) \* 2e[NEPRILYSIN // PRENYLATION // ZINC\_PROTE] CG3239 GH24674 5A1-5A1 dup:1/3 ID:77G12

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

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

CG7106 + ligand\_binding\_or\_carrier \* Acp29AB \* mannan-binding lectin; collectin(aa) \* 2e-16 accessory gland protein Acp29AB \* 4e-08 FCE2\_MOUSE LOW AFFINITY IMMUNOGLOBULIN EPSILON FC [lectin\_c // C\_TYPE\_LLECTIN\_2] CG7106 GH24720 28D3-28D3 dup:1/2 ID:77H5

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

CG6518 + inaC protein\_kinase \* protein kinase C (EC 2.7.1.-) beta-II - rat(aa) \* DMPKCR\_2 Pkc53E \* DMPKC53E\_2 inaC \* 5e-78 KPC1\_YEAST PROTEIN KINASE C-LIKE (PKC 1) serine/threoni [DAG\_PE\_BINDING\_DOMAIN // PROTEIN\_KINASE] CG6518 GH24781 53E1-53E2 ID:77H9

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

CG5453



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

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

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

+ unknown \* ATP(GTP)-binding protein(aa) \* HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III(aa) \* weak similarity to ATPases(aa) \* Yor262wp(aa) [ATP\_GTP\_A] CG10222 GH25024 70A7-70A7 ID:78B10

CG10222

CG10553 + unknown CG10553 ID:78B2

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

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

CG3795 + \* 2e-67 MAZS\_YEAST PROBABLE ALPHA-GLUCOSIDASE FSP2 (MALTASE) (FLOCCULENT SPECIFIC PROTE \* 1e-154 MAL2\_DROME POSSIBLE MALTASE PRECURSOR (LARVAL VISCERA [ALPHAAMYLASE // PRENYLATION // alpha-am]

CG14935 CG14935 33B2-33B2 dup:1/2 ID:78C1

+ SP2523 motor\_protein \* 1e-05 YM96\_YEAST HYPOTHETICAL 113.1 KD PROTEIN IN PRE5-FET4 INTERGENIC REGION \* \* CG7493 CG7493 GH25141 66A8-66A8 dup:2/3 ID:78C11

+ transporter \* 3e-11 aquaporin \* 4e-15 BIB\_DROME NEUROGENIC PROTEIN BIG BRAIN bib protein - frui \* 6e-15 similar to CG4019 MIP protein \* 1e-28 MIP\_MOUSE LENS FIBER MAJOR [MINTRINSICP // MIP] CG4019 GH25142 59F1-59F2 ID:78C12

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

CG5813

CG17450 + unknown \* CG17450 GH25094 cyto\_unknown ID:78C5

+ 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

CG14026

CG8444 + CG8444 ID:78D12

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

CG4059 + transporter \* peroxisomal Ca-dependent solute carrier(aa) \* Similarity to N.crassa ADP/ATP carrier protein (SW:ADT\_NEUCR)(aa) \* 1e-38 probable membrane protein [mito\_carr // MITOCARRIER // ADPTRNSLCAS] CG4392 GH25190 69B3-69B3 dup:2/2 ID:78D7

CG4392

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

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

+ Cyp4d21 cytochrome\_P450 \* DMC152A3 \* Cyp4e2 \* DMCYP4D2\_12 Cyp4d2 \* 1e-112 cytochrome P450 cytochrome P4 CG6730 GH25251 28A6-28B1 dup:2/2 ID:78E3

CG6730

CG6470 + transcription\_factor \* [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG6470 GH25257 17B5-17B5 dup:2/2 ID:78E4

+ unknown \* 6e-32 antigen 5-related \* 1e-19 antigen 5-related protein \* 6e-34 Ag5r2 \* VA3\_SOLIN VENOM ALLERGEN III (ALLERGEN SOL I 3) (SOL I III) CG17210 GH25284 86D8-86D8 dup:2/2 ID:78E5

CG17210

+ enzyme \* thioredoxin peroxidase (antioxidant enzyme)(aa) \* 2e-58 TSA1\_YEAST THIOL-SPECIFIC ANTIOXIDANT  
 CG1274 PROTEIN (PRP) thiol \* 3e-72 similar to M. musculus MER [AhpC-TSA] CG1274 GH25379 63B5-63B5 ID:78F1  
 + enzyme \* 8e-11 YGA1\_YEAST PUTATIVE BETA-HYDROXYSTEROID DEHYDROGENASE/DELTA 5-->4-ISOMERASE ( \*  
 CG7724 2e-12 weakly similar to dihydrokaempferol 4-reductase \* 2e-21 [3Beta\_HSD] CG7724 GH25466 73E5-73E5 dup:2/2 ID:78F12  
 + Ork1 ion\_channel \* potassium channel, subfamily K, member (TASK-2); TASK-2(aa) \* two P domain potassium channel  
 CG1615 ORK1(aa) \* Ork1 \* BLASTX 8.1E-08 Mus musculus TREK-1 K [CHANNEL\_PORE\_K] CG1615 GH25390 9F8-9F10 ID:78F2  
 + transporter \* sodium-dicarboxylate cotransporter SDCT1(aa) \* 8e-08 YJT8\_YEAST HYPOTHETICAL 97.7 KD MEMBRANE  
 CG4961 PROTEIN IN PRP21-UBP12 INTERGENIC REGIO \* 4e-29 YKG6\_C CG4961 GH25396 92C4-92C4 dup:2/2 ID:78F3  
 CG1835 + unknown \* [NLS\_BP] CG1835 GH25431 19E2-19E2 ID:78F5  
 + Pk92B protein\_kinase \* coded for by C. elegans cDNA CEESN53F; similar to protein kinases including CDC15 in yeast(aa) \*  
 DMPK92B\_4 Pk92B \* 8e-43 protein kinase \* protei[PROTEIN\_KINASE\_ST // TYRKINASE // PROTE] CG4720 GH25453 92B8-  
 CG4720 92B8 dup:2/3 ID:78F7  
 none + none GH25455 ID:78F8  
 + sut2 transporter \* GLUCOSE TRANSPORTER TYPE 7, HEPATIC MICROSOMAL(aa) \* Contains similarity to Pfam domain:  
 CG17975 (sugar\_tr), Score=356.0, E-value=1.3e-103, N=1(aa) \* solute CG17975 GH25507 44A4-44A4 dup:2/2 ID:78G4  
 + cell\_adhesion \* similar to the BPTI/Kunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor  
 CG1540 (TFPI)(aa) \* similar to Kunitz/Bovine [ig // EGF\_1 // BPTI\_KUNITZ // Kunitz\_BP] CG1540 GH25513 98D2-98D2 dup:1/3 ID:78G5  
 + transcription\_factor \* interleukin enhancer binding factor 2, 45kD(aa) \* 2e-37 predicted using Genefinder; Similarity to Human  
 CG5641 NF45 protein (TR:Q \* 5e-19 zinc finger RNA b [25A\_SYNT\_2] CG5641 GH25564 87B15-87B15 ID:78H1  
 + Pu enzyme \* 4e-52 GCH1\_YEAST GTP CYCLOHYDROLASE I (GTP-CH-I) GTP cyclohyd \* 1e-133 GCH1\_DROME GTP  
 CYCLOHYDROLASE I (GTP-CH-I) (PUNCH PROTEIN) \* 2e-67 GCH1\_CAEEL [GTP\_cyclohydrol // GTP\_CYCLOHYDROL\_1\_1 ]  
 CG9441 CG9441 GH25630 57C5-57C6 dup:3/3 ID:78H12  
 CG5677 + CG5677 dup:2/2 ID:78H3  
 + signal\_transduction \* actin-filament binding protein Frabin(aa) \* DMD547\_2 still-life \* 2e-14 still life type \* 1e-34 guanine  
 CG7511 nucleotide exchange factor UNC-73A [GRF\_DBL // RhoGEF // PH\_DOMAIN] CG7511 GH25579 66A7-66A7 ID:78H4  
 + 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  
 CG2677 ID:78H7  
 + Myo61F motor\_protein \* Myo61F \* Myo31DF \* 1e-143 YMZ9\_YEAST HYPOTHETICAL MYOSIN-LIKE PROTEIN IN ILV2-ADE17  
 INTERGENIC REGION \* myosin IB - fruit fly (Drosophila melanoga[myosin\_head // IQ // MYOSINHEAVY // ATP] CG9155 GH25605  
 CG9155 62B4-62B4 dup:3/3 ID:78H8  
 + BcDNA:GH06348 enzyme \* predicted using Genefinder; Similarity to Human pyruvate carboxylase cDNA EST comes from this  
 CG1516 gene; cDNA EST comes from this gene; cDNA EST comes f [CPSase\_L\_chain] CG1516 GH25836 46B14-46C1 dup:5/8 ID:79B10  
 + \* Chain B, \* 305aa long hypothetical \* lysosomal \* PUTATIVE N4-(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE  
 CG1827 PRECURSOR (GLYCOSYLASPARAGINASE) (ASPARTYLG [Asparaginase\_2] CG1827 45F4-45F4 dup:2/2 ID:79B3  
 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

+ ligand\_binding\_or\_carrier \* GTP binding protein, almost identical to Gsp1p; Gsp2p(aa) \* 3e-70 GSP2\_YEAST GTP-BINDING  
 NUCLEAR PROTEIN GSP2/CNR2 GTP-bind \* 3e-23 rab11 \* 6e[ras // GTPRANTC4 // ATP\_GTP\_A // RASTRN] CG7815 GH25818  
 75F9-75F9 ID:79B9  
 CG7815  
 + unknown \* No definition line found(aa) \* 6e-23 No definition line found \* No definition line found \* No definition line found  
 CG11473 5A9-5A9 ID:79C12  
 CG11473  
 + enzyme \* 1e-19 probable membrane protein YLR070c - yeast (Saccharomyces cerevisiae) \* 8e-40 sorbitol dehydrogenase \*  
 5e-39 similar to sorbitol dehydrogenase; [adh\_zinc // NLS\_BP] CG4836 GH25858 92C-92C dup:1/4 ID:79C3  
 CG4836  
 CG13515  
 + unknown \* CG13515 GH25860 58F4-58F4 ID:79C4  
 CG13515  
 + unknown \* hypothetical 43.2 kDa protein(aa) \* predicted using Genefinder; Similarity to Yeast hypothetical protein YAE2  
 (SW:YAE2\_YEAST); cDNA EST comes from t CG7011 GH25868 71B3-71B3 dup:2/2 ID:79C6  
 CG7011  
 + 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  
 CG5186  
 + 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  
 CG8888  
 CG17470  
 + unknown \* CG17470 GH26094 38E-38E dup:2/2 ID:79E10  
 CG17470  
 + enzyme\_activator \* HYPOTHETICAL 45.1 KD PROTEIN IN IMP2-DNA43 INTERGENIC REGION(aa) \* phosphotyrosyl  
 phosphatase activator(aa) \* similar to phosphotyrosyl phosphatase CG8509 GH26069 13F1-13F1 dup:2/2 ID:79E2  
 CG8509  
 + unknown \* hypothetical protein(aa) \* Hrt2p(aa) \* F31D4.2(aa) \* hypothetical protein(aa) [NLS\_BP] CG11475 GH26080  
 58C1-58C1 dup:2/2 ID:79E5  
 CG11475  
 + 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  
 CG9848  
 + transcription\_factor \* segmentation protein hairy - fruit fly (Drosophila melanogaster)(aa) \* DMHAIRG\_5 h \* 3e-07 lin-22 \* 2e-  
 18 HES1\_MOUSE TRANSCRIPTION FACTOR HES-1 (HAI [HLH // HELIX\_LOOP\_HELIX\_2] CG10446 37B10-37B10 dup:2/2  
 ID:79F1  
 CG10446  
 + 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  
 CG10842  
 + motor\_protein \* homeotic most like HMPB\_DROME: homeotic proboscipedia protein(aa) \* 1e-05 neurofilament triplet H1  
 protein - rabbit (fragment) neuro \* \* [GRAM\_POS\_ANCHORING // NLS\_BP] CG12105 GH26183 62A-62A dup:2/2 ID:79F12  
 CG12105  
 + 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  
 CG7227  
 + transporter \* aquaporin 2(aa) \* 1e-07 YFF4\_YEAST HYPOTHETICAL 70.5 KD PROTEIN IN AGP3-DAK3 INTERGENIC  
 REGION \* 8e-05 BIB\_DROME NEUROGENIC PROTEIN BIG BRAIN bib pr [MINTRINICP // MIP] CG5398 GH26134 59F1-59F1  
 ID:79F5  
 CG5398  
 CG18316  
 + \* CG18316 44A4-44A4 dup:2/3 ID:79F6  
 CG18316  
 + 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 REGION[SET\_DOMAIN // SET // PHD // NLS\_BP] CG9007  
 GH26152 70C9-70C10 dup:2/2 ID:79F7  
 CG9007

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

CG12136 + unknown \* [AA\_TRNA\_LIGASE\_I // NLS\_BP] CG12136 GH26280 8D10-8D10 ID:79G11

CG6836 + unknown \* CG6836 GH26215 75E6-75E6 ID:79G4

CG17012 + Caenorhabditis elegans 'similar to peptidase family S1 (trypsin family)' EMBL:U58751 CG17012 ID:79G7  
+ BG:DS01068.2 unknown \* hypothetical protein(aa) \* 1e-98 R08F11.1 gene product \* 7e-50 putative protein \* unknown [HMG\_COA\_REDUCTASE\_2] CG7469 GH26380 34F5-34F5 dup:2/2 ID:79H12

CG7469

CG12423 + actin\_binding \* 1e-05 contains similarity to the kelch/MIPP family \* 1e-06 Keap1 \* 1e-07 The gene product is related to Drosophila melanogaster ri \* 1e-06 kelch pro [BTB] CG12423 GH26310 cyto\_unknown ID:79H3

CG10365 + unknown \* contains similarity to E. coli cation transport protein \* 6e-16 YEZ3\_YEAST HYPOTHETICAL 26.3 KD PROTEIN IN RAD4-CHD1 INTERGENIC REGION \* 3e-22 cont CG10365 GH26317 95B5-95B5 ID:79H4

CG6094 + unknown \* 5e-07 hypothetical protein YOL114c - yeast (Saccharomyces cerevisiae) \* 2e-17 R02F2.2 gene product \* 3e-23 immature colon carcinoma transcript prote [NLS\_BP] CG6094 GH26345 31E5-31E5 ID:79H6

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

CG7300 + unknown \* CG7300 GH26358 32A-32A ID:79H9

CG18350 + Sxl RNA\_binding \* DMSX1PS1\_2 Sxl \* 7e-15 PABP\_YEAST POLYADENYLATE-BINDING PROTEIN, CYTOPLASMIC AND NUCLEAR (PABP) (ARS CO \* 1e-158 sex-lethal sex determination protei CG18350 sxl-male 6F5-6F5 dup:6/7 ID:8-31 cntrlBA10  
+ da transcription\_factor \* TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-[HLH // HELIX\_LOOP\_HELIX // PEROXIDASE\_1] CG5102 da 31E1-31E1 dup:3/3 ID:8-31 cntrlBA11

CG5102

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

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

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

CG3772 + Cry photoreceptor \* cry \* 4e-13 photolyase (EC 4.1.99.3) \* blue-light receptor (AF0 \* 3e-99 photolyase/blue-light receptor homolog [DNA\_photolyase // DNAPHOTLYASE] CG3772 cyr 94B1-94B1 dup:4/4 ID:8-31 cntrlBB4  
+ 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

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

CG1378 + tll steroid\_hormone\_receptor CG1378 tll dup:2/2 ID:8-31 cntrlBC1  
+ 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

CG1856 + ttk transcription\_factor \* DNA-binding protein ttk - fruit fly (*Drosophila melanogaster*)(aa) \* DMDNABPMR\_2 ttk \* DNA binding protein \* 3e-06 contains sim[BTB // zf-C2H2 // ZINC\_FINGER\_C2H2 // Z] CG1856 HK or ttk 100E1-100E1 dup:5/7 ID:8-31 cntrlBC2

CG1539 + spdo actin\_binding \* sanpodo protein(aa) \* 1e-179 sanpodo protein \* 8e-47 Similar to tropomodulin; coded for by *C. elegans* cDNA yk88e7.5; coded for by *C. elegans* \* 6e-47 TMOD\_MO CG1539 sanpodo 100A-100A dup:3/3 ID:8-31 cntrlBC5

CG17348 + drl CG17348 drl dup:2/2 ID:8-31 cntrlBC8

CG1374 + tsh transcription\_factor CG1374 tsh dup:3/3 ID:8-31 cntrlBD3

+ inv transcription\_factor \* SEGMENTATION POLARITY PROTEIN ENGRAILED(aa) \* DMINVR\_2 inv \* INVECTED PROTEIN(aa) \* 2e-29 HM16\_CAEEL HOMEODOMAIN PROTEIN ENGRAILED-LIKE CEH-16 homology CG17835 inv 47F17-48A

CG17835 dup:3/4 ID:8-31 cntrlBD4

+ pros transcription\_factor \* DMPROS\_3 pros \* PRO\_DROME PROTEIN PROSPERO homeotic protein prospero - f \* 4e-58 HM26\_CAEEL HOMEODOMAIN PROTEIN CEH-26 K12H4.1 protein - *Caen* \* 2e-50 [PRO\_RICH] CG17228 pros p'3' 3211 86E2-86E2

CG17228 dup:4/4 ID:8-31 cntrlBD7

CG4354 + slbo CG4354 slbo dup:2/2 ID:8-31 cntrlBD9

+ Antp transcription\_factor \* DMANTPG5\_7 Antp \* 1e-159 HMAN\_DROME HOMEOTIC ANTENNAPEDIA PROTEIN homeotic protein \* 7e-23 DNA-binding protein mab5 \* 5e-34 HXB7\_MOUSE HOMEODOMAIN PROTEIN CG1028 ANTP 84B-84D11 dup:3/3 ID:8-31 cntrlBE12

CG1028

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 // HOMEODOMAIN\_1 // homeobox] CG10619 islet 37B5-37B5 dup:3/3 ID:8-31 cntrlBF7

CG10619

CG2956 + twist transcription\_factor CG2956 twist dup:3/5 ID:8-31 cntrlBG3

CG10325 + abdA transcription\_factor CG10325 abdA dup:4/4 ID:8-31 cntrlBH1

CG7902 + Bap transcription\_factor CG7902 Bap dup:6/6 ID:8-31 cntrlBH11

CG1133 + opa transcription\_factor CG1133 opa dup:4/4 ID:8-31 cntrlBH4

CG2328 + eve transcription\_factor CG2328 eve dup:2/2 ID:8-31 cntrlBH7

+ 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 RLM1 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

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

CG9392

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  
CG8358 85E4-85E4 ID:80C1  
+ unknown \* polytropic murine leukemia virus receptor SYG1(aa) \* 3e-32 SYG1\_YEAST SYG1 PROTEIN SYG1 protein -  
CG10483 yeast (Saccharomy \* 1e-150 predicted using Genefin [CRYSTALLIN\_BETAGAMMA] CG10483 GH26628 64F5-64F5 ID:80C8  
+ actin\_binding \* 4e-21 alternatively spliced form \* 2e-31 similar to actin binding domain of alpha-actinin and spectra beta chain  
CG3960 \* 6e-30 mouse smoothelin, large iso [CH\_DOMAIN // CH] CG3960 GH26714 6B3-6C1 dup:3/3 ID:80D12  
+ enzyme \* dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) precursor - Arabidopsis thaliana (fragment)(aa) \*  
CG5261 Dihydrolipoamide acetyltransferase component (E [LIPOYL // 2-oxoacid\_dh // biotin\_lipoyl] CG5261 27F7-27F7 ID:80D4  
CG11700 + CG11700 dup:1/2 ID:80D5  
CG5755 + transporter \* TB1(aa) \* \* [mito\_carr] CG5755 GH26696 36E-36E ID:80D7  
CG4669 + unknown \* [PRO\_RICH] CG4669 GH26702 64D1-64D1 ID:80D8  
+ unknown \* HYPOTHETICAL 90.9 KD PROTEIN C08B11.4 IN CHROMOSOME II(aa) \* weak similarity to nodulation protein X  
CG11353 (probable sugar acetylase) (Swiss Prot accessio CG11353 GH26735 64B13-64B14 dup:3/3 ID:80E2  
+ motor\_protein \* APXL(aa) \* 2e-23 APXL \* 2e-23 apical protein, Xenopus laevis-like \* [PRO\_RICH] CG8603 GH26744 50F6-  
CG8603 50F6 dup:4/4 ID:80E4  
CG5758 + unknown \* CG5758 GH26746 36E-36E dup:2/2 ID:80E5  
+ Rpl23a ribosomal\_protein \* ribosomal protein L23a(aa) \* 5e-38 RL25\_YEAST 60S RIBOSOMAL PROTEIN L25 (YL25) (RP61L)  
rib \* 5e-38 RL2C\_CAEEL PROBABLE 60S RIBOSOMAL PROTEIN L23A ([Ribosomal\_L23 // RIBOSOMAL\_L23 // NLS\_B] CG7977  
CG7977 62A11-62A11 dup:3/3 ID:80E8  
+ fln cytoskeletal\_structural\_protein \* DMFLIGHT\_2 fln \* FLIGHTIN (MUSCLE PROTEIN 27)(aa) \* 2e-19 CMP-N-  
CG7445 acetylneuraminic acid synthetase \* myofibrillar protein flightin - fruit fly (Drosop CG7445 GH26786 76E2-76E2 dup:3/3 ID:80E9  
+ fu12 enzyme \* 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE(aa) \* PUTATIVE 1-ACYL-SN-GLYCEROL-3-  
PHOSPHATE ACYLTRANSFERASE T06E8.1 (1- AGP ACYLTRANSFERASE) (1-AG [GLYCEROL\_ACYLTRANS] CG17608  
CG17608 GH26888 29C4-29C4 ID:80F12  
+ Cyp9f2 cytochrome\_P450 \* CYP9 cytochrome P450(aa) \* 3e-18 CYP6A2 \* 2e-10 similar to cytochrome P450 \* 5e-16  
CG11466 cytochrome P450 3A11 - mouse cytochrome P-45 [EP450II // p450] CG11466 GH26796 87B14-87B14 ID:80F2  
+ cell\_adhesion \* yl \* 9e-73 YL\_DROME PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL) puta \* 1e-96 contains  
similarity to EGF-like domains \* 1e-132 AM2 receptor [LDLRA\_2 // LDLRECEPTOR // EGF\_2 // EGF\_] CG4823 GH26833 96F1-  
CG4823 96F1 dup:2/2 ID:80F6  
+ 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-  
CG7675 91A2 dup:2/4 ID:80F8  
+ transporter \* protein(aa) \* BLASTX 3.6E-09 Plasmodium falciparum protein gene, complete cds.(dna) \* rab3 effector(aa) \*  
CG7321 4e-11 SY65\_DROME SYNAPTOTAGMIN (P65) syna [C2 // C2\_DOMAIN\_2 // PDZ] CG7321 GH26867 90C7-90C7 ID:80F9

CG13130 + unknown \* 1E-38\* 9e-24 inserted at base Both 5' and 3' ends of P element Inverse PCR \* CG13130 GH26896 30F4-30F4 ID:80G1

CG17137 + ion\_channel \* Vdac \* DMMITPORN\_2 porin \* 1e-09 POR2\_YEAST OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION \* 3e-66 voltage dependent anion-sele [Euk\_porin // EUKARYTPORIN] CG17137 GH26967 32B3-32B3 ID:80G10

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 Yeast LPG22P protein cDNA EST EMBL:T0 \* CG15433 GH27091 26A1-26A1 ID:80H11

CG15084 + unknown \* 3e-12 YKJ5\_YEAST 32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION \* 1e-64 YS19\_CAEEL HYPOTHETICAL 42.1 KD PROTEIN IN CHROMOSOME III \* 1e-17 unknown \* CG15084 GH26994 55F4-55F4 ID:80H2

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

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

CG7920 + enzyme \* 2e-08 ACH1\_YEAST ACETYL-COA HYDROLASE (ACETYL-COA DEACYLASE) (ACETYL-COA ACYLASE) \* 1e-136 coded for by C. elegans cDNA yk20f6.3; coded for by C. el [ATP\_GTP\_A] CG7920 GH27164 99D4-99D4 dup:2/2 ID:81A11

CG17765 + endopeptidase \* SORCIN(aa) \* 8e-12 YG25\_YEAST HYPOTHETICAL 38.4 KD PROTEIN IN MUP1-SPR3 INTERGENIC REGION \* 1e-15 CAN\_DROME CALPAIN (CALCIUM-ACTIVATED NEUTRAL PROTE [EF\_HAND // efhand // EF\_HAND\_2] CG17765 47A9-47A9 dup:3/3 ID:81A2

CG17369 + Vha55 enzyme \* ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2(aa) \* H+-ATPase beta subunit(aa) \* PROBABLE VACUOLAR [ATP-synt\_ab] CG17369 GH27148 87C5-87C5 dup:3/3 ID:81A7

CG2913 + yin transporter \* opt1 long(aa) \* 8e-17 PTR2\_YEAST PEPTIDE TRANSPORTER PTR2 (PEPTIDE PERMEASE PTR2) \* 8e-74 high-affinity peptide transporter \* 2e-06 cAMP inducible p [PTR2 // PTR2\_1 // PTR2\_2] CG2913 GH27264 4A1-4A1 dup:2/2 ID:81B12

CG1607 + transporter \* amino acid transporter chain (AmAt-L-1c) ASUR4(aa) \* Similarity to Human membrane protein E16 (SW:E16\_HUMAN); cDNA EST comes from this gene; cDNA ES [AROMATIC\_AA\_PERMEASE\_2 // aa\_permeases ] CG1607 GH27380 100C-100C ID:81C11

CG8861 + unknown \* CG8861 GH27383 85D7-85D7 ID:81C12

CG11625 + unknown \* CG11625 GH27289 92A4-92A4 dup:2/2 ID:81C4

CG2968 + CG2968 ID:81C7

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

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

+ Cyp305a1cytochrome\_P450 \* CYTOCHROME P450 76C4(aa) \* cytochrome P450 epoxygenase(aa) \* cinnamate 4-hydroxylase(aa) \* Cytochrome P-450 2A14(aa) [EP450II // p450 // P450 // MITP450 // B] CG8733 GH27419 76D3-76D3 ID:81D5  
 CG8733 + cell\_adhesion \* DMARTAN\_7 trn \* 4e-35 KEK1 \* 3e-06 contains similarity to leucine-rich repeats (LRR) \* 8e-12 neurogenic  
 CG9431 extracellular slit protein [ig // LRR // LRRCT] CG9431 GH27420 34A10-34A10 ID:81D6  
 CG4841 + unknown \* [NLS\_BP] CG4841 GH27425 36A11-36A11 ID:81D7  
 + unknown \* 2e-11 cDNA EST CEMSB78F comes from this gene; cDNA EST yk293d9.3 comes \* 2e-10 Unknown \* CG12118  
 CG12118 GH27430 8D2-8D2 dup:3/4 ID:81D8  
 + enzyme \* phosphodiesterase 6B, cGMP-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant);  
 PDEB(aa) \* 7e-45 YBZJ\_CAEEL PROBABLE 3 [PDEase // PDIESTERASE1 // PDEASE\_I // P] CG8279 GH27433 89E3-88C6  
 CG8279 dup:2/2 ID:81D9  
 + protein\_kinase \* similar to serine/threonine kinase(aa) \* 3e-37 hypothetical protein YPL236c - yeast (Saccharomyces  
 cerevisiae) \* 2e-17 SNF1A/AMP-activated protein k [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG1227 84C7-84C7  
 CG1227 dup:3/3 ID:81E11  
 CG6503 + CG6503 dup:2/2 ID:81E12  
 + unknown \* 7e-07 probable membrane protein YOL031c - yeast (Saccharomyces cerevisiae) \* 1e-11 SLS1\_YARLI SLS1  
 CG10420 PROTEIN PRECURSOR Sls1 protein precursio \* 7e-83 i CG10420 GH27496 96C3-96C3 dup:3/4 ID:81E3  
 + enzyme \* 1e-43 CCR4\_YEAST GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL  
 CG5534 EFFECTOR (C \* 2e-07 ANGEL \* 3e-86 predicted using Genefinder; Similarity CG5534 GH27503 95E6-95E6 dup:2/2 ID:81E4  
 + unknown \* 1e-16 No definition line found \* W06B11.1 gene product \* 1e-16 No definition line found \* W06B11.1 gene product  
 CG3967 CG3967 GH27541 67B2-67B3 dup:2/2 ID:81E6  
 CG11595 + unknown \* CG11595 GH27568 12D5-12D5 dup:2/2 ID:81E9  
 + \* 1e-15 YMB8\_YEAST HYPOTHETICAL 43.7 KD PROTEIN IN OST6-PSP2 INTERGENIC REGION \* 7e-23 No definition  
 CG8195 line found \* 2e-19 hypothetical protein \* hypothe CG8195 52A13-52A13 ID:81F1  
 + ligand\_binding\_or\_carrier \* verprolin(aa) \* mucin (clone PGM-2A) - pig(aa) \* Sec23-interacting protein p125(aa) \*  
 CG8552 DMCLPTN\_6 Cpn [GRAM\_POS\_ANCHORING] CG8552 GH27701 28E-28E9 dup:3/3 ID:81F10  
 + enzyme \* 2e-32 YPT6\_YEAST GTP-BINDING PROTEIN YPT6 YPT6 protein - yeas \* 2e-34 rab6 \* 3e-53 similar to ras-  
 related protein \* 9e-34 RB17\_MOUSE RAS-RELATED PRO [ALDEHYDE\_DEHYDR\_CYS // ras // ATP\_GTP\_A] CG17515  
 CG17515 GH27649 cyto\_unknown ID:81F2  
 + Cyp6u1 cytochrome\_P450 \* PUTATIVE CYTOCHROME P450 T10B9.7 IN CHROMOSOME II(aa) \* similar to cytochrome  
 P450(aa) \* DMCYP6A2A\_5 Cyp6a2 \* 3e-16 CP51\_YEAST CYTOCHROME P450 (CYP [EP450II // p450 // P450 // MITP450 // C]  
 CG3567 CG3567 GH27663 42D4-42D4 ID:81F6  
 CG15131 + unknown \* CG15131 GH27691 36A10-36A10 ID:81F9  
 + protein\_phosphatase \* similar to glycogen-binding subunit protein phosphatase-1(aa) \* smooth muscle protein phosphatase  
 CG9619 type 1-binding subunit(aa) \* protein phosphatase CG9619 GH27769 76A4-76A5 ID:81G10  
 + enzyme \* threonyl-tRNA synthetase(aa) \* threonyl-tRNA synthetase (aa 1-734) \* SYTC\_CAEEL PROBABLE THREONYL-  
 TRNA SYNTHETASE, CYTOPLASMIC (THREONINE--TRNA LIG [TRNASYNTHTHR // tRNA-synt\_2b // AA\_TRNA] CG5353  
 CG5353 GH27773 33C1-33C1 ID:81G11



+ \* UDP-GLUCURONOSYLTRANSFERASE 2B13 PRECURSOR, MICROSOMAL (UDPGT)(aa) \* UDP-  
 GLUCURONOSYLTRANSFERASE 2B20 PRECURSOR, MICROSOMAL (UDPGT)(aa) \* similar t [UDPGT] CG17323 37B3-37B3  
 CG17323 dup:1/2 ID:81G12  
 CG14735 + unknown \* CG14735 GH27720 87A10-87A10 ID:81G2  
 CG8813 + transcription\_factor \* CG8813 GH27752 23B5-23B5 dup:1/2 ID:81G5  
 CG4955 + RNA\_binding \* CG4955 GH27756 15D1-15D1 ID:81G7  
 + Cyp4d20 cytochrome\_P450 \* /motif=(desc;; /match=(desc;; /match=(desc;; /match=(desc;; /motif=(desc:(aa) \* 1e-70 similar to  
 cytochrome P450; cDNA EST CEMSH91R comes from this [EP450II // p450 // P450 // MITP450 // B] CG16761 GH27758 62E5-  
 CG16761 62E5 ID:81G8  
 CG15360 + unknown \* CG15360 GH27779 22B3-22B3 ID:81H1  
 CG5048 + unknown \* CG5048 GH27783 70F1-70F1 ID:81H2  
 + Gel actin\_binding \* DMGELS\_2 Gel \* gelsolin, secreted form precursor - fruit fly (Drosophila melanogaster) \* 2e-73 similar to  
 CG1106 gelsolin; cDNA EST comes from this gene \* [GELS // GELSOLIN // Gelsolin] CG1106 GH27784 82A2-82A3 ID:81H3  
 CG2865  
 + \* caltractin (20kD calcium-binding protein)(aa) \* Calmodulin; Cmd1p(aa) \* 7e-09 CALM\_YEAST CALMODULIN calmodulin -  
 CG17272 yeast (Saccharomyces cere \* 1e-09 C [EF\_HAND\_2] CG17272 92F13-92F13 dup:2/2 ID:81H6  
 + enzyme \* G4 nucleic acid binding protein, involved in tRNA aminoacylation; Arc1p(aa) \* PROBABLE METHIONYL-TRNA  
 CG8235 SYNTHETASE (METHIONINE--TRNA LIGASE) (METRS)(a CG8235 GH27932 44F9-44F9 ID:82A6  
 + glaikit unknown \* Contains similarity to Pfam domain: (PLDc), Score=13.8, E-value=0.2, N=1(aa) \* \* CG8826 GH27933 23D4-  
 CG8826 23D4 ID:82A7  
 CG10630 + RNA\_binding \* CG10630 GH28067 64E-64E ID:82B10  
 + unknown \* 2e-19 YIC3\_YEAST HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION \* 4e-37 cDNA  
 CG7816 EST comes from this gene; cDNA EST co \* 3e-39 KE4 \* 1e-38 CG7816 GH28072 99C7-99C7 dup:2/2 ID:82B11  
 + structural\_protein \* Gasp precursor(aa) \* 1e-09 Gasp precursor \* 3e-07 R02F2.4 gene product \* 9e-13 insect intestinal mucin  
 CG4948 IIM22 CG4948 GH28017 66F4-66F4 dup:3/3 ID:82B4  
 + RNA\_binding \* protein(aa) \* 2e-49 ovarian protein - fruit fly (Drosophila melanogaster) s \* 8e-75 YLF1\_CAEEL  
 HYPOTHETICAL 42.4 KD PROTEIN C40H1.1 IN CHROMOSOME II [RNP\_1 // RBD // PFKB\_KINASES\_1 // rrm] CG5735  
 CG5735 GH28038 66E4-66E4 dup:2/3 ID:82B7  
 + transcription\_factor \* hepatocyte nuclear factor alpha(aa) \* Contains similarity to Pfam domain: (homeobox), Score=20.5,  
 N=1(aa) \* onecut 2(aa) \* coded for by C. elegans [homeobox // HOMEBOX\_2 // NLS\_BP] CG1922 GH28062 102C6-102C6  
 CG1922 ID:82B9  
 + nucleic\_acid\_binding \* unknown(aa) \* weak similarity with BRKA gene from Bordetella Pertussis; cDNA EST comes from  
 CG4405 this gene; cDNA EST comes from this gene(aa) \* 2e-52 (P CG4405 GH28348 30B11-30B12 dup:2/3 ID:82C11  
 + ligand\_binding\_or\_carrier \* 16k antigen precursor - nematode (Onchocerca volvulus)(aa) \* phosphatidylethanolamine binding  
 CG6180 protein Ovd1 - nematode (Onchocerca volvulus) (fragmen [PBP] CG6180 33F2-33F2 dup:1/2 ID:82C12  
 CG17034 + 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  
+ RNA\_binding \* hypothetical protein(aa) \* heterogeneous nuclear ribonucleoprotein R(aa) \* 1e-08 RN15\_YEAST MRNA 3'-  
END PROCESSING PROTEIN RNA15 RNA15 pro \* 6e-16 p [RBD // rrm // NLS\_BP] CG17838 GH28335 92F10-92F10 dup:2/5  
ID:82C6  
CG17838 + 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\_SER  
CG1773 ] CG1773 GH28342 46A3-46A3 ID:82C7  
+ endopeptidase \* Ser12 \* DMEAST\_4 ea \* Ser6 \* DMSTUBBLE\_1 Sb [trypsin // CHYMOTRYPSIN // TRYPSIN\_HIS ]  
CG9676 CG9676 15A1-15A1 dup:1/3 ID:82C8  
CG7206 + unknown \* CG7206 GH28353 16F7-16F7 dup:2/2 ID:82D1  
+ unknown \* CGI-05 protein(aa) \* 7e-23 YQT5\_CAEEL HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III  
CG6550 (U \* 1e-65 432aa long hypothetical protein \* conserved [UPF0004] CG6550 GH28477 54C1-54C1 ID:82D10  
CG8854 + unknown \* CG8854 GH28507 48F3-48F3 ID:82D12  
+ AcCoAS enzyme \* DMACOASYN\_2 AcCoAS \* 1e-154 ACS2\_YEAST ACETYL-COENZYME A SYNTHETASE (ACETATE--COA  
LIGASE 2) (ACYL-ACTIVAT \* acetyl-CoA synthetase - fruit fly (Droso [AMP\_BINDING // AMPBINDING // AMP-bindin] CG9390  
CG9390 78C7-78C7 ID:82D4  
+ enzyme \* phosphoglyceromutase - fruit fly (Drosophila melanogaster)(aa) \* DMPGLY\_4 Pglym78 \* 3e-72 PMG1\_YEAST  
PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE 1 [PGAM // PG\_MUTASE] CG17645 GH28416 87B7-87B7  
CG17645 ID:82D6  
+ Galpha49B signal\_transduction \* 7e-50 GBA2\_YEAST GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-2 SUBUNIT (GP2-  
ALPHA) \* 1e-169 GBQ3\_DROME GUANINE NUCLEOTIDE-BINDING PROTEIN G(Q), ALPH[GPROTEINA // G-alpha //  
CG17759 GPROTEINAQ // G] CG17759 GH28437 49B3-49B5 ID:82D7  
+ transporter \* similar to C. elegans protein and to rat synaptic vesicle protein \* putative integral membrane transport  
CG8654 protein(aa) \* HYPOTHETICAL 84.8 KD PROTEIN [sugar\_tr] CG8654 GH28654 56F-56F dup:2/2 ID:82E12  
CG11347 + unknown \* [NLS\_BP] CG11347 GH28550 64B11-64B11 dup:2/2 ID:82E4  
CG7093 + unknown \* [PRO\_RICH] CG7093 GH28569 28D5-28D5 dup:2/2 ID:82E6  
CG6908 + unknown \* 6e-20 /match=(desc;; /ma \*\* CG6908 GH28576 86F1-86F1 dup:2/2 ID:82E7  
+ igl ligand\_binding\_or\_carrier \* ligand binding or carrier calmodulin binding ) map\_position:51E \* 6e-51 growth-associated  
CG18285 protein GAP-43 homolog=igloo-L melanogas \* 6e-53 igl \* gro [IQ] CG18285 GH28577 51A4-51E7 dup:2/2 ID:82E8  
+ Rh5 G\_protein\_linked\_receptor \* Rh5 \* DMNKDTACH\_2 Takr86C \* OPSIN RH4 (INNER R7 PHOTORECEPTOR CELLS  
OPSIN)(aa) \* short wavelength-sensitive opsin; ultraviolet-sensi[GPCRRHODOPSN // OPSIN // G\_PROTEIN\_RECE] CG5279  
CG5279 GH28578 33B10-33B10 dup:2/2 ID:82E9  
+ unknown \* clot.599(dna)\* 1e-104 l(3)j1D5 l(3)j1D5 inserted at base Both 5' and 3' ends of P element Inverse PCR \*  
CG8588 CG8588 GH28656 65F4-65F4 dup:3/4 ID:82F1  
+ unknown \* protein(aa) \* 5e-16 SSM4\_YEAST SSM4 PROTEIN SSM4 protein - yeast (Saccharomy \* 2e-08 predicted using  
CG1317 Genefinder \* 2e-37 putative protein [PRO\_RICH] CG1317 GH28722 62E-62E ID:82F10

CG14996 + 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

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

CG17492 + cytoskeletal\_structural\_protein \* erythroid ankyrin(aa) \* DMCCTUSB\_8 cact \* 1e-07 probable membrane protein YOR034c - yeast (Saccharomyces cerevisiae) [ANK\_REP // ank // ANK\_REP\_REGION // ZF\_] CG17492 GH28686 37B10-37B11 dup:5/6 ID:82F5

CG12040 + unknown similar to GTPase-activating (rhoGAP) like protein CRAL\_TRIO CG12040 GH28696 dup:2/2 ID:82F6

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

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

CG17342 + Lk6 protein\_kinase \* 7e-51 LK6 protein kinase \* 2e-06 similar to serine/threonine kinase; cDNA EST comes from \* 2e-11 map kinase interacting kinase \* 3e-12 Putative map k [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG17342 GH28825 86F7-86F7 ID:82G11

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

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

CG4088 + lat DNA\_replication\_factor \* recognition complex subunit mela \* 8e-92 recognition complex subunit \* 9e-95 recognition complex associated protein p81 \* 2e-92 inserted at base Bot [NLS\_BP // ATP\_GTP\_A] CG4088 GH28787 49F10-49F10 dup:1/2 ID:82G4

CG13316 + \* 0.000000002 \* CG13316 3F2-3F2 ID:82G7

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

CG17676 + CG17676|unknown|CT39055 ID:82H3

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

CG8857 + ribosomal\_protein \* 5e-46 RS41\_YEAST 40S RIBOSOMAL PROTEIN RP41 (YS12) (S18A / S18B) \* 4e-56 Similarity to Human 40S ribosomal protein S11 (SW:RS11\_HUMAN); cDN \* [RIBOSOMAL\_S17 // Ribosomal\_S17 // RIBOS] CG8857 GH28880 48F1-48F1 dup:2/2 ID:82H8

CG14226 + protein\_phosphatase \* 3e-10 PTP9\_DROME PROTEIN-TYROSINE PHOSPHATASE 99A PRECURSOR (RECEPTOR-LINKED PROTEIN-T \* 1e-10 myotactin form A \* 1e-08 protein tyrosine phosphatase [fn3] CG14226 GM13503 18D13-18D13 ID:83A10

CG5184 + ribosomal\_protein \* predicted using Genefinder; Similarity to Prototheca mitochondiral ribosomal protein S11 (SW:RT11\_PROWI); cDNA EST yk372e6.3 comes from this gene; [Ribosomal\_S11] CG5184 GM13519 89E13-89E13 ID:83A11

CG4466 + Hsp27 chaperone \* DMHSP27G\_3 Hsp27 \* 1e-118 HS27\_DROME HEAT SHOCK PROTEIN heat shock protein - f \* 3e-13 Contains similarity to Pfam domain: (HSP20), Score=130.7, \* 2 [TONB\_DEPENDENT\_REC\_1 // HSP20 // ACRYST] CG4466

GM13686 67B2-67B2 ID:83A12

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

CG9140 + enzyme \* NADH:ubiquinone dehydrogenase kDa subunit(aa) \* similar to NADH-ubiquinone oxidoreductase; cDNA EST comes from this gene; cDNA EST comes from this [COMPLEX1\_51K\_1 // COMPLEX1\_51K\_2] CG9140 GM14163 26B3-26B3 ID:83B12

CG12740 + ribosomal\_protein \* 2e-08 predicted using Genefinder; Similarity to Human 60S ribosomal prot \* 1e-22 RL28\_MOUSE 60S RIBOSOMAL PROTEIN L28 ribosomal protein L \* 1e-22 ri CG12740 GM13756 64A3-64A3 ID:83B2

CG14080 + protein\_phosphatase \* 4e-11 PVH1\_YEAST PROTEIN-TYROSINE PHOSPHATASE YVH1 (PTPASE YVH1) \* 5e-22 puckered protein \* 3e-32 Similar to protein-tyrosine phosphatase \* 1e-26 DU [DSPc] CG14080 GM13896 75F5-75F5 ID:83B6

CG1583 + \* similar to Gila monster phospholipase A2; similar to \* 2e-22 phospholipase A2 (EC 3.1.1.4) Pa5 - Gila monster phosp \* 8e-89 inserted at base Both 5' [PA2\_HIS] CG1583 7D14-7D15 dup:2/2 ID:83B8

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

CG2151 + Gr enzyme \* 4e-59 glutathine reductase \* GSHR\_DROME GLUTATHIONE REDUCTASE (GR) (GRASE) glutathione \* 1e-125 TRXB\_CAEEL PROBABLE THIOREDOXIN REDUCTASE Similar t [HGRDTASE // FADPNR // pyr\_redox // PYRI] CG2151 GM14215 7D18-7D18 ID:83C1

CG6544 + fau unknown \* CG6544 HL07933 86C4-86C4 dup:1/2 ID:83C11

CG12775 + ribosomal\_protein \* 60S RIBOSOMAL PROTEIN L21(aa) \* 7e-46 R21A\_YEAST 60S RIBOSOMAL PROTEIN L21E A ribosomal protein \* 5e-50 RL21\_CAEEL PROBABLE 60S RIBOSOMAL PROTEIN L2 [RIBOSOMAL\_L21E // Ribosomal\_L21e] CG12775 GM14242 40D2-40D2 ID:83C2

CG6050 + translation\_factor CG6050 GM14682 ID:83C4

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

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

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

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

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

CG9578 + CG9578 ID:83D8

CG2287 + hk ion\_channel \* 3e-38 Hk protein \* 4e-09 potassium channel beta subunit \* 8e-09 potassium channel beta subunit \* 4e-09 alpha-dendrotoxin-sensitive potassium channel CG2287 HL08167 9B7-9B8 ID:83D9

CG9089 + chaperone \* HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR(aa) \* DNAJ PROTEIN HOMOLOG (DROJ1)(aa) \* 1e-06 SCJ1\_YEAST SCJ1 PROTEIN SCJ1 protein [DnaJ // DNAJ\_2] CG9089 LD21896 15B4-15B4 dup:2/2 ID:83E11

CG9300 + unknown \* [SUGAR\_TRANSPORT\_2] CG9300 76B8-76B8 dup:2/2 ID:83E12

CG17064 + motor\_protein \* HYPOTHETICAL PROTEIN \* PSD-95 binding protein(aa) \* 2e-08 PSD-95/SAP90-associated protein-1 \* 2e-

70 inserted at base Both 5' and 3' ends of P elemen [NLS\_BP] CG17064 LD21642 50B1-50B2 dup:3/3 ID:83E2

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

+ Ank cytoskeletal\_structural\_protein \* DMANKY\_5 Ank \* 8e-16 YIL2\_YEAST HYPOTHETICAL 123.6 KD PROTEIN IN POR2-  
 CG1651 COX5B INTERGENIC REGION \* ankyrin ankyrin m \* AO13 ankyrin [ank // ZU5] CG1651 LD21682 101F1-101F1 dup:3/4 ID:83E5

+ swa RNA\_binding \* SWA\_DROME SWALLOW PROTEIN gene swallow protein - fruit fl \* DMSWAL\_3 swa \* \* [NLS\_BP]  
 CG3429 LD21771 5E6-5E7 dup:2/2 ID:83E6

+ Bsg25D motor\_protein \* BSG2\_DROME BLASTODERM SPECIFIC PROTEIN 25D bsg25D protein \* 1e-05 contains similarity to  
 CG14025 kinesin (PFam: kinesin.hmm, score: 10.52 and 16.62) \* 6e-1 CG14025 LD21844 25D2-25D2 dup:2/2 ID:83E8

CG3416 + translation\_factor CG3416 LD22193 dup:2/2 ID:83F10

CG18282 + unknown \* CG18282 LD22270 5E1-5E1 ID:83F11

+ 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

+ unknown \* BRcore-Q1-Z1 protein - fruit fly (Drosophila melanogaster)(aa) \* BROAD-COMPLEX CORE-TNT1-Q1-Z1  
 CG5166 PROTEIN (BRCORE-TNT1-Q1-Z1) (CONTAINS: BROAD-COMPLEX CG5166 LD22183 88F-88F dup:3/3 ID:83F9

+ transporter \* 1e-28 ZRC1\_YEAST ZINC/CADMIUM RESISTANCE PROTEIN heavy metal \* 2e-10 cDNA EST comes from  
 CG17723 this gene elegans \* 3e-31 zinc transporter ZnT-1 - mouse ZnT CG17723 LD22804 63C4-63C5 ID:83G10

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

+ 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

+ nucleic\_acid\_binding \* 3e-09 GOLI\_DROME GOLIATH PROTEIN (G1 PROTEIN) regulatory protei \* 1e-10 contains similarity  
 to C3HC4-type zinc fingers (Pfam; zf-C3HC4.hmm, score; [zf-C3HC4 // PRO\_RICH // NLS\_BP // ZF\_RI] CG6923 LD22771 86F6-  
 CG6923 86F6 ID:83G8

+ protein\_kinase mitotic checkpoint control protein kinase B-like PROTEIN\_KINASE\_ATP CG14030 LD22858 dup:1/2  
 CG14030 ID:83H1

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

+ zf30C transcription\_factor \* leukemia/lymohoma related factor cLRF(aa) \* zf30C \* 4e-17 YJF6\_YEAST HYPOTHETICAL 98.9  
 KD ZINC FINGER PROTEIN IN BTN1-PEP8 INTERGENIC REG \* zinc f[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG3998  
 CG3998 LD23102 30D1-30D1 ID:83H12

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

+ B4 unknown \* No definition line found(aa) \* No definition line found \* 1e-16 inserted at base 5' end of P element Inverse PCR \*  
 CG9239 [NLS\_BP] CG9239 LD22933 36D1-36D1 dup:4/5 ID:83H6  
 + 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  
 CG7946 + unknown CG7946 ID:84A8  
 + 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  
 + RNA\_binding \* 4e-55 SUV3\_YEAST MITOCHONDRIAL ATP-DEPENDENT RNA HELICASE SUV3 PRECURSOR \* 1e-151  
 CG9791 Similarity to Yeast ATP-dependent RNA helicase (SW:SUV3\_YEAST); cD [helicase\_C] CG9791 LD23445 82A5-82A5 ID:84B12  
 + \* Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST comes from this gene; cDNA EST  
 CG2221 comes from this gene; cDNA EST CG2221 9B14-9B14 dup:3/3 ID:84B2  
 + RpL27A ribosomal\_protein \* ribosomal protein L27a.e - yeast (Saccharomyces cerevisiae)(aa) \* RpL27Ab \* 2e-71  
 CG15442 RL2B\_DROME 60S RIBOSOMAL PROTEIN L27A RpL27a \* 2e-44 RL2A\_MOUSE 60 [L15] CG15442 24F5-24F5 dup:6/6 ID:84B6  
 CG6712 + unknown NLS\_BP CG6712 LD23405 dup:2/2 ID:84B8  
 + metastasis-associated-1-like-protein unknown \* metastasis associated gene 1-like 1(aa) \* 3e-74 similar to metastasis-associated  
 CG2244 protein mta-1 (GB:U0 \* 1e-128 metastasis associat[ELM2 // myb\_DNA-binding // zf-C2H2 // Z] CG2244 LD24461 83B6-83B6  
 ID:84C10  
 + La RNA\_binding \* LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)(aa) \* La \*  
 CG10922 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  
 + unknown \* dJ633O20.1 (similar to Bos taurus P14)(aa) \* M01E11.2(aa) \* 1e-84 dJ633O20.1 (similar to Bos taurus P14) \*  
 CG11964 7e-20 P14 CG11964 LD23493 85C2-85C2 ID:84C3  
 + TfiIB transcription\_factor \* TfiIB \* 3e-43 TF2B\_YEAST TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) (TRANSCRIPTION  
 FACTOR E) \* 1e-174 TF2B\_DROME TRANSCRIPTION INITIATION FACTOR I[TIFACTORIIB // transcript\_fac2 // TFIIB] CG5193  
 CG5193 LD24035 33D1-33D1 ID:84C6  
 CG11403 + DNA\_repair\_protein CG11403 LD24267 dup:2/2 ID:84C8  
 + DNA\_replication\_factor \* replication control protein 1(aa) \* CDC6 protein(aa) \* 7e-31 CC6\_YEAST CELL DIVISION  
 CG5971 CONTROL PROTEIN cell division \* 3e-30 recognition complex subu [AAA // ATP\_GTP\_A] CG5971 LD25083 66D-66D ID:84D11  
 + unknown \* 1e-133 inserted at base Both 5' and 3' ends of P element Inverse PCR \* 1e-133 inserted at base Both 5' and 3'  
 CG2446 ends of P element Inverse PCR \* CG2446 LD24866 10D4-10D5 dup:2/2 ID:84D4  
 + enzyme \* 1e-171 CTP synthase (EC 6.3.4.2) URA8 - yeast (Saccharomyces cerevisiae) \* 1e-147 similar to CTP SYNTHASE  
 CG6854 (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP \* [GATase // GATASE\_TYPE\_I] CG6854 LD25005 71B2-71B2 dup:2/6 ID:84D5  
 + transcription\_factor \* TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD(aa) \* TAFII60(aa) \*  
 CG10390 8e-48 transcription factor TFIID \* 2e-15 contain CG10390 LD25013 83B2-83B2 ID:84D6  
 CG10267 + transcription\_factor CG10267 dup:2/2 ID:84E4  
 + unknown \* NY-REN-18 antigen(aa) \* BS4 PROTEIN(aa) \* 3e-35 hypothetical protein \* BS4 [UBA] CG15445 19E7-19E7  
 CG15445 dup:2/3 ID:84E5

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

CG2275 LD25202 46E2-46E2 dup:2/2 ID:84E7  
+ Paps enzyme \* 3-prime-phosphoadenosine 5-prime-phosphosulfate synthase 1(aa) \* DMPAPSSYN\_2 Paps \* 7e-54  
KAPS\_YEAST ADENYLYLSULFATE KINASE (APS KINASE) (ATP ADENOS [ATP\_GTP\_A] CG8363 LD25351 76D4-76D5

CG8363 ID:84F7  
+ mnd transporter \* minidisks(aa) \* 1e-23 MUP1\_YEAST HIGH AFFINITY METHIONINE PERMEASE methionine \* 1e-105 strong similarity to Schistosoma amino acid permease \* 1e-120 [aa\_permeases // AMINO\_ACID\_PERMEASE\_2] CG3297 LD25378 71A2-71A3 ID:84F8

CG3297 + transcription\_factor \* C43H6.7 gene product(aa) \* HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II(aa) \* hypothetical protein(aa) \* 5e-15 probable membrane protei [ZF\_DHHC] CG5880 LD25420 97E8-97E8 ID:84F9

CG5880 + unknown CG13345 dup:2/3 ID:84H11  
CG13345 + RNA\_binding \* DMMLE\_2 mle \* protein(aa) \* PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE C04H5.6(aa) \* PR22\_YEAST PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 PRP [DEAH\_ATP\_HELICASE // HELICASE // ATP\_GT] CG10689 LD25692 37C1-37C1 ID:84H6

CG10689 + unknown \* 5e-37 protein \* \* [FBOX\_DOMAIN] CG11866 46E4-46E4 dup:2/2 ID:84H7  
CG11866 + enzyme \* 1e-82 Similar to NADH-ubiquinone oxidoreductase kd subunit; coded for by C. elegans \* 4e-88 NADH dehydrogenase (ubiquinone) Fe-S protein (30kD) (NAD [complex1\_30Kd] CG12079 63B11-63B11 dup:2/2 ID:84H8

CG12079 + numb unknown \* NUMB PROTEIN(aa) \* DMNUMB\_2 numb \* 3e-42 similar to Phosphotyrosine interaction domain (PTB/PID).; cDNA EST \* 8e-67 m-Numb [PTB\_DOMAIN // PID // NLS\_BP // ATP\_GTP\_] CG3779 LD25907 30B5-30B6 dup:1/3 ID:85A11

CG3779 + \* [NLS\_BP] CG17159 cyto\_unknown dup:2/3 ID:85A4  
CG17159 + 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

CG9509 + transcription\_factor \* zinc finger protein(aa) \* ZINC FINGER PROTEIN 184(aa) \* protein(aa) \* [zf-C2H2 // ZINC\_FINGER\_C2H2\_2] CG5135 LD25880 86D8-86D8 dup:3/3 ID:85A9

CG5135 + 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

CG8525 + 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

CG12894 + Pros45 endopeptidase \* Ug \* 1e-157 PRS8\_YEAST 26S PROTEASE REGULATORY SUBUNIT HOMOLOG (SUG1 PROTEIN) (CIM3 PROTE \* Pros45 proteosome subunit homolog \* 1e-176 similar to AT [AAA // ATP\_GTP\_A] CG1489 LD26005 19F2-19F2 ID:85B12

CG1489 + glu DNA\_binding \* 1e-123 hypothetical protein YLR086w - yeast (Saccharomyces cerevisiae) ( \* 2e-34 Cap \* 1e-100 Similarity

CG11397

with the yeast chromosome segregation prot[ATP\_GTP\_A2 // DA\_BOX // NLS\_BP // ATP\_G] CG11397 LD25919 36A7-36A7  
dup:3/3 ID:85B2

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

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

CG14233 + meso18E unknown \* meso18E\* CG14233 LD26007 18E2-18E3 ID:85C1

CG2190 + unknown \* [PRENYLATION] CG2190 LD26151 11D5-11D5 ID:85C10

CG10281 + TfiIFalpha transcription\_factor \* DMTFAC5\_2 TfiIF agr; \* coded for by C. elegans cDNA yk79f12.5; coded for by C. elegans cDNA  
cm17c10; coded for by C. elegans cDNA yk98e4.5; coded fo [NLS\_BP] CG10281 LD26157 84A4-84A4 ID:85C11

CG2835 + G-alpha60A signal\_transduction \* DMGNB\_2 G-o agr;47A \* 2e-39 GBA1\_YEAST GUANINE NUCLEOTIDE-BINDING PROTEIN  
ALPHA-1 SUBUNIT (GP1-ALPHA) \* GBS1\_DROME GUANINE NUCLEOTIDE-BINDIN[GPROTEINA // G-alpha // GPROTEINAQ // G]  
CG2835 LD26182 60A12-60A12 ID:85C12

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

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

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

CG17255 + unknown \* 2e-05 BAT2 \* 2e-05 BAT2 \* CG17255 LD26094 9C2-9C2 dup:2/4 ID:85C6

CG10591 + unknown \* [COLLAGEN\_REP // PRO\_RICH] CG10591 LD26105 64E-64E3 ID:85C7

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

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

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

CG9972 + signal\_transduction \* 3e-07 secreted polypeptide spatzle precursor - fruit fly (Drosophila melanogaster) \* 3e-07  
SPZ\_DROME SPAETZLE PROTEIN PRECURSOR \* 4e-09 spz \* CG9972 LD26258 63A-63E4 ID:85D5

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

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

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

CG8290 + motor\_protein \* 7e-07 No definition line found \* 1e-15 ATRX protein \* 2e-15 X-linked nuclear protein \* 6e-06 putative protein  
[NLS\_BP // CYTOCHROME\_C] CG8290 48D7-48D8 dup:3/3 ID:85E2

CG12737 + CRAG ligand\_binding\_or\_carrier \* CRAG protein \* 1e-145 contains similarity to human MAP kinase-activating death domain \*  
1e-120 protein \* 3e-16 Rab3 GDP/GTP exchange protein [DENN\_DOMAIN // CYTOCHROME\_C] CG12737 LD26363 7F4-7F4



dup:6/6 ID:85E3  
 + transcription\_factor \* pipsqueak(aa) \* 8e-29 BTB domain \* 2e-07 contains similarity to the kelch/MIPP family \* 7e-07 BAZF  
 CG3726 [BTB] CG3726 LD26392 5C8-5C8 dup:2/2 ID:85E5  
 + unknown \* 2e-40 No definition line found \* 2e-09 hypothetical protein \* 1E-180\* Hypothetical protein [NLS\_BP] CG8352  
 CG8352 LD26402 65B4-65B5 dup:4/4 ID:85E6  
 + structural\_protein \* 7e-06 bK217C2.1 (Rat RTP60 (nuclear pore complex protein Npap60) isolog) \* 4e-11 RTP60 \*  
 CG2158 [Ran\_BP1 // RAN\_BP1 // RANBP1\_WASP] CG2158 LD26583 44A7-44A7 dup:3/3 ID:85F12  
 CG17018 + unknown CG17018 LD26456 dup:1/2 ID:85F2  
 CG10609 + Or83b signal\_transduction (Odorant receptor 83b ) olfactory receptor CG10609 LD26485 ID:85F4  
 + e(y)1 transcription\_factor \* TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUNIT (TAFII-42) (TAFII40) (P42)  
 (ENHANCER OF YELLOW PROTEIN)(aa) \* e(y)1 \* 2e-12 YM75\_YEAST HYPOTHETICAL [HIST\_TAF] CG6474 LD26511 16D4-  
 CG6474 16D5 ID:85F5  
 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\_BP]  
 CG11371 CG11371 LD26519 21A5-21A5 dup:3/4 ID:85F7  
 CG12234 + unknown exportin CG12234 LD26789 dup:1/2 ID:85G12  
 + enzyme \* Similar to carbonic anhydrase; coded for by C. elegans cDNA yk72d10.3; coded for by C. elegans cDNA  
 CG6906 yk119b1.3; coded for by C. elegans cDNA cm18b8; [carb\_anhydrase] CG6906 LD26647 68F7-68F7 dup:2/2 ID:85G2  
 CG7824 + unknown \* unknown(aa) \* 2e-14 unknown \* \* [PPASE // NLS\_BP] CG7824 LD26655 99C6-99C7 ID:85G3  
 + exu RNA\_binding \* Exuperantia (exu) protein - fruit fly (Drosophila melanogaster)(aa) \* exu \* 1e-158 exuperantia protein - fruit  
 CG8994 fly (Drosophila virilis) \* exu [LECTIN\_LEGUME\_BETA] CG8994 LD26657 57B2-57B2 ID:85G4  
 + transcription\_factor \* 2e-11 AZF1\_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin \* Zinc finger-AT hook  
 protein \* 3e-15 contains multiple of strong similarity to C2H2[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG10274 LD26701  
 CG10274 65A6-65A6 ID:85G6  
 + protein\_kinase \* 1e-07 probable membrane protein YDL146w - yeast (Saccharomyces cerevisiae) \* 3e-09 hypothetical  
 CG2258 protein \* [SH3] CG2258 LD26707 7D9-7D9 dup:1/3 ID:85G7  
 + unknown \* 1e-35 YNU1\_YEAST HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION \* 1e-118 No  
 CG9351 definition line found \* 3e-51 hypothetical protein \* 5e-50 [RANBP1\_WASP] CG9351 LD26904 87F8-87F9 dup:3/4 ID:85H10  
 + EcR steroid\_hormone\_receptor \* ECDYSONE RECEPTOR (ECDYSTEROID RECEPTOR) (20-HYDROXY-ECDYSONE  
 RECEPTOR) (20E RECEPTOR)(aa) \* DMECR\_4 EcR \* 8e-14 ecdysteroid receptor \* 6e-51 [STROIDFINGER // hormone\_rec // zf-  
 CG1765 C4 //] CG1765 LD26915 42A7-42A8 ID:85H12  
 CG10016 + transcription\_factor ZINC\_FINGER\_C2H2, ZINC\_FINGER\_C2H2\_2, zf] CG10016 LD26791 dup:2/2 ID:85H2  
 CG8580 + \* 1e-155 inserted at base Both 5' and 3' ends of P element Inverse PCR \* \* [NLS\_BP] CG8580 65F4-65F5 dup:2/2 ID:85H4  
 + enzyme \* ACONITATE HYDRATASE, MITOCHONDRIAL PRECURSOR (CITRATE HYDRO-LYASE) (ACONITASE)(aa) \*  
 ACON\_YEAST ACONITATE HYDRATASE, MITOCHONDRIAL PRECURSOR (CITRA [ACONITASE\_2 // Aconitase\_C //  
 CG9244 THIOLASE\_] CG9244 LD26837 39B3-39B3 dup:3/3 ID:85H6

CG14100 + unknown \* 6e-11 hypothetical protein \* hypothetical protein \* YG73\_SYNY3 HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE \* [SpoU\_methylase] CG14100 LD26903 76B9-76B9 dup:1/2 ID:85H9

CG5640 + function\_unknown \* coded for by C. elegans cDNA yk36f5.3; coded for by C. elegans cDNA yk36f5.5; similar to glucose repression mediator protein (SP:CYC8\_YEAST, \* ubiqu [TPR\_REGION // TPR\_REPEAT // TPR] CG5640 LD27005 31C7-31D1 dup:2/2 ID:86A10

CG17540 + RNA\_binding \* 2e-14 predicted using Genefinder; Similarity to Arabidopsis DNA-damage-r \* 8e-43 splicing factor (45kD); SPF 45kDa splicing factor; SPF \* 2e-17 D111 [D111\_DOMAIN] CG17540 LD27025 cyto\_unknown ID:86A12

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

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

CG10038 + unknown \* 1e-29 predicted using Genefinder \* 1e-33 unknown \* 1e-29 predicted using Genefinder \* 1e-33 unknown [ESTERASE] CG10038 LD26985 87B11-87B11 ID:86A6

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

CG1034 + bcd transcription\_factor \* DNA-binding-protein,transcription-factor(aa) \* DMBCDG\_3 bcd \* 1e-125 bcd protein \* 8e-52 homeotic protein bicoid - fruit fly (Drosophila ps[RNP\_1 // HOMEBOX\_1 // homeobox // HOME] CG1034 LD27003 84D1-84D1 dup:1/2 ID:86A8

CG18362 + cell\_cycle\_regulator \* protein(aa) \* HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III(aa) \* 5e-05 USF2\_MOUSE UPSTREAM STIMULATORY FACTOR (UPSTREAM TRANSCRIPT[HLH // HELIX\_LOOP\_HELIX\_2 // NLS\_BP] CG18362 LD27073 39D1-39D2 dup:3/4 ID:86B10

CG7843 + arsenate resistance protein ARS2 CG7843 LD27090 dup:2/2 ID:86B12

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

CG10171 + unknown \* CG10171 LD27069 70A5-70A5 ID:86B8

CG10602 + peptidase \* insulin-regulated membrane aminopeptidase IRAP(aa) \* LEUKOTRIENE A-4 HYDROLASE (LTA-4 HYDROLASE) (LEUKOTRIENE A(4) HYDROLASE)(aa) \* LEUKOTRIENE A-4 [ALADIPTASE // Peptidase\_M1 // ZINC\_PROT] CG10602 LD27070 37B4-37B5 ID:86B9

CG5452 + dnk enzyme \* 1e-145 deoxynucleoside kinase \* 2e-31 DCK\_MOUSE DEOXYCYTIDINE KINASE (DCK) deoxycytidine kina \* 1e-49 thymidine kinase \* 2e-30 DCK\_RAT DEOXYCYTIDINE [ATP\_GTP\_A] CG5452 94A3-94A3 dup:2/2 ID:86C1

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

CG6673 + glutathione\_transferase \* 1e-24 contains similarity to glutathione S transferases \* 2e-26 glutathione-S-transferase homolog \* 2e-30 glutathione-S-transferase like glutathion [GST] CG6673 LD27185 66D4-66D5 ID:86C12

CG7586 + 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

CG9660 + toc motor\_protein \* map\_position:23D4 \* 6e-30 Toucan protein \* 8e-32 DMToc toc \* map\_position:23D4 CG9660 LD27161 23D-23D3 dup:1/2 ID:86C6

CG11471 + 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  
 + fidipidine cytoskeletal\_structural\_protein homology to sarcolemmal-associated protein (SLAP-2) [Homo sapiens] and latent  
 CG7773 nuclear antigen [Kaposi's sarcoma-associated herpesvirus] NLS\_BP CG7773 LD27169 dup:2/2 ID:86C8  
 + dco protein\_kinase \* serin/threonin-kinase(aa) \* dbt \* Ckl agr; \* DMDG2CD5\_3 for [PROTEIN\_KINASE\_ST //  
 CG2048 PROTEIN\_KINASE\_DOM] CG2048 LD27173 100B-100B ID:86C9  
 CG9028 + unknown \* 2e-15 inserted at base 5' end of P element Inverse PCR \* CG9028 LD27194 70C8-70C9 dup:2/2 ID:86D1  
 CG6005 + NLS\_BP CG6005 LD27322 dup:2/2 ID:86D10  
 + pescadillo [Homo sapiens] (widely expressed in embryogenesis of zebrafish, high in liver) BRCT, BRCT\_DOMAIN, NLS\_BP  
 CG4364 CG4364 LD27336 dup:2/2 ID:86D12  
 CG7396 + unknown \* [PPASE // NLS\_BP] CG7396 LD27215 71E1-71E1 dup:2/2 ID:86D3  
 CG8237 + Autosomal Highly Conserved Protein CG8237 LD27256 dup:2/2 ID:86D5  
 CG4790 + unknown \* CG4790 LD27288 5C8-5C9 ID:86D8  
 + transporter \* 2e-14 aquaporin \* 5e-22 BIB\_DROME NEUROGENIC PROTEIN BIG BRAIN bib protein - frui \* 6e-22 similar to  
 CG7777 MIP transmembrane protein; cDNA EST yk459g7.3 c [MINTRINSICP // MIP] CG7777 LD27313 47F13-47F13 ID:86D9  
 + RNA\_binding \* 6e-05 NOP3\_YEAST NUCLEOLAR PROTEIN (MITOCHONDRIAL TARGETING SUPPRESSOR PROTEIN) \*  
 CG13298 1e-32 contains similarity to RNA recognition motifs (RNP) \* 2e-50 C [RNP\_1 // RBD // rrm] CG13298 LD27466 65A6-65A6 dup:2/2  
 ID:86E10  
 + UbcD4 enzyme \* 3e-33 UBC1\_YEAST UBIQUITIN-CONJUGATING ENZYME E2-24 KD (UBIQUITIN-PROTEIN LIGASE) (UBI \*  
 CG8284 1e-107 ubiquitin conjugating enzyme \* 7e-54 contains simila [UBA // UBIQUITIN\_CONJUGAT // UQ\_con // ] CG8284 LD27480  
 67B12-67B12 dup:2/2 ID:86E11  
 + poly-U-binding-splicing-factor RNA\_binding \* siah binding protein 1(aa) \* 4e-13 PABP\_YEAST POLYADENYLATE-BINDING  
 CG12085 PROTEIN, CYTOPLASMIC AND NUCLEAR (PABP) (ARS CO \* 3e-14 polyadenylate-bind[RNP\_1 // RBD // rrm] CG12085 LD27486  
 62A4-62A4 dup:2/2 ID:86E12  
 + Similar to a hydrophilic protein that is peripherally associated with the late Golgi in yeast. Homology to uncharacterized  
 CG3338 proteins in Arabidopsis, h CG3338 LD27356 dup:3/3 ID:86E2  
 + unknown \* 8e-15 YKK3\_CAEEL HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III >g \*  
 CG10795 YJ05\_CAEEL HYPOTHETICAL 85.1 KD NUCLEASE C41D11.5 simila \* CG10795 LD27358 57D11-57D11 dup:2/2 ID:86E3  
 CG1444 + enzyme PUTATIVE STEROID DEHYDROGENASE ADH\_SHORT, GDHRDH, adh\_short CG1444 LD27387 dup:3/3 ID:86E5  
 + Aats-pheenzyme \* 8e-84 mitochondrial phenylalanyl-tRNA synthetase alpha subunit precursor \* 1e-125 phenylalanine-tRNA  
 CG13348 synthetase \* phenylalanyl tRNA synthetase \* Aat [AA\_TRNA\_LIGASE\_II\_1 // AA\_TRNA\_LIGASE\_I] CG13348 LD27389 50C20-  
 50C20 dup:2/2 ID:86E6  
 + chaperone \* 9e-13 XDJ1 protein - yeast (Saccharomyces cerevisiae) Xdj1p: H \* 4e-09 DNJ1\_DROME DNAJ PROTEIN  
 CG8531 HOMOLOG (DROJ1) droj1 \* 1e-46 contains strong similar [DnaJ // DNAJ\_2] CG8531 LD27406 50E9-50E9 dup:2/2 ID:86E7  
 + function\_unknown \* 5e-09 cDNA EST yk293f3.3 comes from this gene \* 5e-05 Y0DG\_MYCTU HYPOTHETICAL 17.3 KD  
 CG8079 PROTEIN CY1A11.16C (Z \* cDNA EST yk331d5.3 comes from thi[FHA\_DOMAIN // D111\_DOMAIN // NLS\_BP // ] CG8079

LD27413 51E9-51E9 dup:2/2 ID:86E8

CG5868 + CG5868 dup:2/2 ID:86E9

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

CG5466 + unknown CG5466 LD27620 dup:2/2 ID:86F11

CG1716 + transcription\_factor ATP\_GTP\_A, DEAD\_ATP\_HELICASE, NLS\_BP, PR] CG1716 LD27627 ID:86F12

+ enzyme (L76944) calmodulin-dependent cyclic nucleotide phosphodiesterase [Mus musculus] HELIX\_LOOP\_HELIX,

CG14940 PDEASE\_I, PDEase, PDIE] CG14940 LD27504 dup:2/2 ID:86F3

+ Cdk8 protein\_kinase \* Cdk8(aa) \* 3e-67 cyclin-dependent kinase chain SRB10 - yeast (Saccharomyces cerevisiae) \* Cdk8 \* 1e-127 Similarity to Human cell division protein ki [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG10572 LD27520 69D3-69D3 ID:86F4

CG10572 + unknown \* predicted using Genefinder; Similarity in 3' end to Human protein cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from CG9986 LD27564 98D4-98D4 ID:86F8

CG9986 + transporter \* 8e-11 syntaxin \* 3e-17 hypothetical protein \* 2e-17 syntaxin \* 1e-19 inserted at base 5' end of P element

CG11278 Inverse PCR [T\_SNARE // Syntaxin] CG11278 LD27581 69F2-69F2 ID:86F9

+ protein\_phosphatase \* PROTEIN PHOSPHATASE 2C GAMMA ISOFORM (PP2C-GAMMA) (FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 13) (FIN13)(aa) \* PROTEIN PHOSPHATASE 2C GAMMA ISOFORM [PP2C\_1 // PP2C // PP2C\_2]

CG10417 CG10417 LD27655 41D1-41D1 ID:86G1

+ 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

CG10120 + NTPase enzyme \* NTPase \* 3e-37 GDA1\_YEAST GUANOSINE-DIPHOSPHATASE (GDPASE) guanosine-dip \* NTPase \* 2e-56 similar to GDA1/CD39 (nucleoside phosphatase) family; cDNA [NLS\_BP // GDA1\_CD39] CG3059 LD27725 23B5-23B6 ID:86G12

CG3059 + transmembrane\_receptor \* contains similarity to M. musculus patched \* 1e-21 No definition line found \* [PEROXIDASE\_1 // 5TM\_BOX // NLS\_BP] CG2019 LD27661 83C4-83C4 dup:3/4 ID:86G4

CG2019 + unknown \* CG8229 LD27667 44F12-45A1 dup:2/2 ID:86G5

CG8229 + 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

CG17520 + enzyme GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERAS Epimerase CG12030 LD27852 dup:2/2 ID:86H11

CG12030 + BG:DS01219.1 unknown \* 1e-20 YKQ3\_CAEEL HYPOTHETICAL 42.1 KD PROTEIN C06E1.3 IN CHROMOSOME III (L1 \* \* CG4482 LD27791 35B9-35B9 ID:86H4

CG4482 + unknown \* CG4710 21E-21E dup:2/2 ID:86H5

CG4710 + transcription\_factor \* CROL ALPHA(aa) \* zinc finger protein 207(aa) \* predicted using Genefinder; similar to Zinc finger, C2H2 type; cDNA EST comes from this gene; cDNA E CG17912 LD27810 36A7-36A8 dup:3/3 ID:86H6

CG17912 + RNA\_binding CG9680 ID:86H8

CG9680 + GAP signal\_transduction \* Cdc42 GTPase-activating protein(aa) \* Rga1p (Dbm1p)(aa) \* DMC23E12 \* ABR protein - human(aa)

CG10538

[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

CG3102 + protein\_phosphatase \* 7e-33 protein-tyrosine phosphatase; PTPase; MPTP-MEG2 \* 1e-32 protein tyrosine phosphatase, non-receptor type \* 7e-40 protein-tyrosine-phosphatase ( [G\_PROTEIN\_RECEPTOR // CRAL\_TRIO] CG3102 LD27988 8F2-8F2 ID:87A10

CG1836 + Rad23 DNA\_repair\_protein \* DHR23(aa) \* 2e-30 UV excision repair protein UV exci \* 9e-05 ubiquitin / ribosomal protein S27a - fruit fly (Drosophila melanogaster) \* 4e-38 Simila [UBA // ubiquitin // UBIQUITIN\_2] CG1836 102A8-102A8 dup:1/3 ID:87A11

CG1976 + ion\_channel \* similar to S. cerevisiae HAP4 transcriptional activator (SP:HAP4\_YEAST, similar to regulatory domain of PI3-kinase P85-alpha subunit (phosphatidylin [PDZ] CG1976 LD28013 100F1-100F2 ID:87A12

CG4200 + sl enzyme \* 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) gamma-D - fruit fly (Drosophila melanogaster)(aa) \* DMCS\_2 sl \* phospholipa [PHPLIPASEC // SH2DOMAIN // C2 // PIPLC] CG4200 LD27939 14B18-14C1 ID:87A7

CG3279 + receptor \* 4e-16 VTI1\_YEAST VESICLE TRANSPORT V-SNARE PROTEIN VTI1 proba \* 3e-27 cDNA EST yk433f11.3 comes from this gene; cDNA EST yk433f11.5 come \* 3e-32 put CG3279 LD27967 61C9-61C9 dup:1/3 ID:87A9

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

CG3249 + enzyme\_activator \* 1e-29 YQK1\_CAEEL HYPOTHETICAL 55.9 KD PROTEIN C56G2.1 IN CHROMOSOME III (U \* 6e-32 AKAP121 \* 9e-33 A kinase anchor protein, 149kD \* 9e-35 A-kinase a [TUDOR] CG3249 LD28079 4F8-4F9 dup:2/3 ID:87B11

CG9924 + actin\_binding CG9924 LD28030 dup:2/2 ID:87B2

CG12052 + lola transcription\_factor \* DMPIPSQ1\_3 psq \* BtbV \* lola \* 1e-171 LOLS\_DROME LOLA PROTEIN, SHORT ISOFORM (LONGITUDINALS LACKING PROTEIN) [BTB] CG12052 LD28033 47A-47A ID:87B3

CG10702 + transmembrane\_receptor \* InR \* INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)(aa) \* 2e-52 INSR\_DROME INSULIN-LIKE RECEPTOR PRECURSOR insulin recep[Recep\_L\_domain // Furin-like] CG10702 LD28036 37B13-37B13 dup:2/3 ID:87B4

CG5809 + CaBP1 chaperone protein disulfide isomerase ER\_TARGET, THIOREDOXIN CG5809 LD28038 dup:2/2 ID:87B5

CG17454 + unknown \* splicing factor 30, survival of motor neuron-related; SPF 30(aa) \* SMN gene \* CG17454 LD28068 cyto\_unknown ID:87B8

CG6214 + transporter \* DMC171D11 \* DMMDR49\_2 Mdr49 \* multidrug resistance protein (MRP2)(aa) \* multidrug resistance protein (ABCC3)(aa) [ATP\_GTP\_A2 // ABC\_TRANSPORTER // ABC\_tr] CG6214 LD28149 33F2-33F3 ID:87C10

CG2218 + unknown \* 1e-21 protein \* \* [ZINC\_FINGER\_C3HC4] CG2218 LD28173 99F6-99F6 ID:87C11

CG6963 + protein\_kinase \* CASEIN KINASE I, GAMMA ISOFORM (CKI-GAMMA 1)(aa) \* CASEIN KINASE I, ALPHA ISOFORM (CKI-ALPHA)(aa) \* 1e-89 CK12\_YEAST CASEIN KINASE I HOMOLOG casein [pkinase] CG6963 LD28216 89B17-89B19 ID:87C12

CG10898 + DNA\_repair\_protein \* 5e-20 predicted using Genefinder; similar to MUTT protein like; cDNA EST \* 9e-05 YZGD\_BACSU HYPOTHETICAL 45.4 KD PROTEIN IN THIAMINASE I 5'REGION \* [MUTT // mutT // MUTTDOMAIN] CG10898 LD28119 86E13-86E13 ID:87C5

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

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

CG4082 + Mcm5 DNA\_replication\_factor \* Mcm5 \* 1e-176 MCM5\_YEAST MINICHROMOSOME MAINTENANCE PROTEIN (CELL DIVISION CONTROL PROTEIN \* MCM5 homolog \* MCM5\_CAEEL DNA REPLICATION LICENSIN[MCM // MCM\_1 // MCM\_2 // NLS\_BP] CG4082 LD28351 86C5-86C5 dup:3/5 ID:87D11

CG1578 + unknown \* 1e-05 HR12\_MOUSE HEAT-RESPONSIVE PROTEIN heat-responsive prot \* 7e-05 UK14\_HUMAN 14.5 KD TRANSLATIONAL INHIBITOR PROTEIN (P14.5) (UK114 ANTIGEN H [UPF0076 // PROTEIN\_KINASE\_ATP] CG1578 LD28359 10E3-10E4 dup:4/5 ID:87D12

CG2061 + BcDNA:LD28247 G protein-coupled receptor 69A CRYSTALLIN\_BETAGAMMA CG2061 LD28247 dup:2/3 ID:87D2

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

CG10593 + Acer peptidase \* DMACERMET\_2 Acer \* dipeptidyl carboxypeptidase I converting enzyme)(aa) \* metallopeptidase(aa) \* enzyme-like protein(aa) [PEPDIPTASEA // Peptidase\_M2 // ZINC\_PRO] CG10593 LD28328 31B1-31B1 ID:87D9

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

CG16972 + motor\_protein \* [NLS\_BP] CG16972 LD28380 34A9-34A9 dup:4/4 ID:87E5

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

CG1065 + Scsalphaenzyme \* succinyl-CoA synthetase alpha subunit(aa) \* 7e-75 SUCA\_YEAST PROBABLE SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN PRECURSOR (S \* 8e-41 succinyl c CG1065 64C4-64C4 dup:2/4 ID:87F1

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

CG6988 + CG6988 dup:1/3 ID:87F2

CG9208 + trio cytoskeletal\_structural\_protein huntingtin-associated protein interacting protein CRAL\_TRIO, GRF\_DBL, PH\_DOMAIN, RhoGEF, S] CG9208 LD28463 dup:2/3 ID:87F3

CG6961 + RNA\_binding \* dJ222E13.3.2 (PUTATIVE partial isoform 2)(aa) \* DMBNBR\_2 bnb \* CG6961 LD28479 17D5-17D5 dup:3/4 ID:87F6

CG10627 + CG10627 ID:87F7

CG3634 + CG3634 LD28488 dup:1/2 ID:87F8

CG11486 + protein\_kinase \* 5e-49 PAN3\_YEAST PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN3 (PAB1P-DEPEN \* 2e-92 YOT7\_CAEEL HYPOTHETICAL 76.2 KD PROTEIN ZK632.7 IN CH [AA\_TRNA\_LIGASE\_II\_2 // ANTIFREEZEI] CG11486 63F4-63F4 dup:1/6 ID:87G3

CG10346 + chaperone \* CG10346 37A4-37A4 dup:1/3 ID:87G7  
 + Qm ribosomal\_protein 60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) RIBOSOMAL\_L10E, Ribosomal\_L10e  
 CG17521 CG17521 ID:87H3  
 CG12134 + CG12134 ID:87H4  
 CG6407 + signal\_transduction CG6407 dup:3/3 ID:87H5  
 CG17870 + unknown CG17870 dup:3/4 ID:87H7  
 CG17033 + CG17033 ID:87H8  
 CG1218 + CG1218 ID:87H9  
 CG1542 + CG1542 ID:88A10  
 + wal electron\_transfer \* 2e-61 ETFA\_YEAST PROBABLE ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT  
 PRECURSOR (ALP \* 1e-106 ETFA\_CAEEL PROBABLE ELECTRON TRANSFER FLAVOPROTEIN AL [ETF\_alpha // ETF\_ALPHA]  
 CG8996 ETF\_ALPHA] CG8996 48B6-48B6 dup:1/3 ID:88A12  
 CG3876 + unknown CG3876 ID:88A4  
 + unknown \* rap55(aa) \* 2e-07 SCD6\_YEAST SCD6 PROTEIN SCD6 protein - yeast (Saccharom \* 2e-19 predicted using  
 CG10686 Genefinder; cDNA EST yk343c12.5 comes from this \* CG10686 69C3-69C3 dup:1/3 ID:88A5  
 CG5821 + RNA\_binding CG5821 ID:88A7  
 + sop ribosomal\_protein \* Ribosomal protein S2 (S4) (rp12) (YS5); Rps2p(aa) \* sop \* 2e-73 RS4\_YEAST 40S RIBOSOMAL  
 PROTEIN S4 (OMNIPOTENT SUPPRESSOR PROTEIN SUP44) (RP12) ( \* 1 [Ribosomal\_S5 // RIBOSOMAL\_S5] CG5920 33A1-  
 CG5920 33A1 dup:1/2 ID:88A8  
 + chaperone \* 1e-14 embryonal lethal (2)13-1 (el(2)13-1) - fruit fly (Drosophila melanogaster) \* 4e-41 similar to small heat  
 CG14207 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  
 + unknown \* contains similarity to a BR-C/TTK domain(aa) \* 5e-10 kelch protein, long form - fruit fly (Drosophila melanogaster)  
 CG1826 \* 7e-12 Kelch motif containing [BTB // PROTEIN\_SPLICING // NLS\_BP] CG1826 9E2-9E2 dup:2/2 ID:88B4  
 CG9216 + unknown \* [NLS\_BP] CG9216 14A6-14A8 ID:88B5  
 CG18041 + CG18041 ID:88B6  
 CG12081 + unknown CG12081 ID:88C3  
 CG12132 + unknown \* 7e-30 C34G6.1 gene product \* CG12132 8D8-8D8 dup:1/3 ID:88C6  
 CG11177 + CG11177 ID:88C8  
 CG3661 + \* 2e-47 precursor TRG1 protein \* D-ERp60=protein disulphide isomerase isoform/multifunctional endoplasmic retic \* 1e-136  
 CG8983 predicted using Genefinder; S [THIOREDOXIN // THIOREDOXIN\_2 // thioered] CG8983 48D1-48D1 dup:3/4 ID:88D12  
 + \* EPIDIDYMAL SECRETORY PROTEIN E1 PRECURSOR (CE1)(aa) \* 4e-22 epididymal secretory protein \* 9e-23  
 CG7291 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

CG8116 + unknown \* 1e-108 inserted at base 3' end of P element Inverse PCR \*\* CG8116 85B2-85B2 dup:1/2 ID:88D7  
+ Ugt enzyme \* Ugt \* UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)(aa) \* 8e-19  
KRE5\_YEAST KILLER TOXIN-RESISTANCE PROTEIN PRECURSOR \* coded for by [NLS\_BP] CG6850 79E3-79E3 dup:5/7

CG6850 ID:88D8

CG7407 + CG7407 dup:1/2 ID:88D9  
+ apoptosis\_inhibitor \* DIHA(aa) \* lap2 \* 3e-07 inhibitor of apoptosis protein \* 8e-06 coded for by C. elegans cDNA yk27g3.5;  
CG17019 coded for by C. elegans cDNA yk27g3.3; Si [NLS\_BP // ZF\_RING] CG17019 49E1-49E1 dup:6/6 ID:88E10

CG13849 + unknown CG13849 dup:2/2 ID:88E12  
+ unknown \* histone acetyltransferase 1(aa) \* histone acetyltransferase; Hat1p(aa) \* weak similarity with SINR protein (Swiss  
CG2051 Prot accession number cDNA EST co [NLS\_BP] CG2051 83C-83C dup:2/3 ID:88F12

CG18858 + CG18858 ID:88F6  
+ ion\_channel \* NY-REN-45 antigen(aa) \* contains similarity to the A-type potassium current class of channel proteins(aa) \*  
CG9467 /match=(desc;; /match=(desc;; /match=(d [BTB // GAPDH // WD\_REPEATS] CG9467 85E10-85E10 dup:3/5 ID:88F9  
+ BcDNA:GH02636 transporter \* 1e-134 putative open reading frame \* 1e-133 P protein \* 2e-30 arsA \* P protein, truncated

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

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

CG16901 + CG16901 ID:88G12  
+ structural\_protein \* 0.000000000006\* 2e-06 nonmuscle myosin-II heavy chain \* 2e-07 Identity to myosin heavy chain C  
CG12702 (SW:MYSC\_CAEEL); cDNA EST EMBL:M8 \* 0.0000001 CG12702 18F1-18F2 dup:1/3 ID:88G4

CG1596 + CG1596[unknown]CT3517 ID:88G5  
+ Rpl140 enzyme \* polymerase (RNA) II (DNA directed) polypeptide B (140kD)(aa) \* DNA-DIRECTED RNA POLYMERASE  
SUBUNIT B'(aa) \* second largest subunit of RNA polymerase [RNA\_pol\_B // RNA\_POL\_BETA] CG3180 88A10-88A11 dup:2/3  
ID:88G9

CG3180

CG7471 + enzyme CG7471 ID:88H1  
+ RNA\_binding \* pre-mRNA cleavage factor Im (68kD)(aa) \* 2e-16 Similarity to Brassica glycine-rich RNA-binding protein  
CG7185 (SW:GR10\_B \* 2e-29 HPBR11-7 protein - human H [RBD // rrm // PRO\_RICH // NLS\_BP] CG7185 66C6-66C7 dup:3/5 ID:88H10  
+ EG:EG0007.12 unknown \* by content; by motif; 2-match\_description=ATP/GTP-binding site motif A (P-I...(aa) \* by content; 1-meth  
CG4857 \* by content; 1-meth \* CG4857 4B1-4B2 dup:3/3 ID:88H5

CG11723 + transcription\_factor \* [AA\_TRNA\_LIGASE\_II\_1] CG11723 22C3-22C3 dup:2/2 ID:88H7

CG5094 + chaperone CG5094 dup:2/2 ID:88H9  
+ \* 6e-24 predicted using Genefinder; similar to zinc-finger protein; cDNA E \* 8e-05 DNA-binding protein BZP - golden  
CG1244 hamster DNA-binding prot \* 2e-06 z [zf-C2H2 // ZINC\_FINGER\_C2H2 // PRO\_RICH] CG1244 62F2-62F2 dup:2/5 ID:89A1

CG9172 + enzyme CG9172 ID:89A10

CG9277 + betaTub56D cytoskeletal\_structural\_protein beta-1 tubulin TUBULIN, TUBULIN\_B\_AUTOREG, tubulin CG9277 ID:89A3

CG16812 + unknown \* predicted using Genefinder(aa) \* 3e-12 predicted using Genefinder \* \* [SAM\_DOMAIN] CG16812 34A10-34A10



dup:1/4 ID:89A4  
 + Ef1alpha48D ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (50 KD FEMALE-SPECIFIC PROTEIN ATP\_GTP\_A, EFACTOR\_GTP, ELONGATNFCT, GTP] CG8280 dup:2/2 ID:89B10  
 CG8280  
 + RCC1\_2, SAM\_BIND CG10428 dup:3/5 ID:89B11  
 CG10428  
 + protein\_kinase CG8789 dup:2/2 ID:89B2  
 CG8789  
 + CG17678 dup:2/2 ID:89B3  
 CG17678  
 + \* C15H9.5 gene product(aa) \* 5e-05 by content; 1-meth \* 5e-70 C15H9.5 gene product \* 1e-05 NEUM\_MOUSE  
 CG12121 NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (P CG12121 8D4-8D5 dup:2/3 ID:89B4  
 CG12269  
 + enzyme \* coded for by C. elegans cDNA yk4d2.3; coded for by C. elegans cDNA yk4d2.5; coded for by C. elegans cDNA yk109a1.5; similar to protein tyrosine phos [PHOSPHOPANTETHEINE // PDZ // PRO\_RICH] CG16757 62E7-62E7 dup:5/6  
 CG16757 ID:89B7  
 + RpS3 \* Ribosomal protein S3 (rp13) (YS3); Rps3p(aa) \* 40S RIBOSOMAL PROTEIN S3(aa) \* DMRPS3\_2 RpS3 \* 8e-82 RS3\_YEAST 40S RIBOSOMAL PROTEIN S3 (YS3) (RP13) [KH-domain // RIBOSOMAL\_S3 // Ribosomal\_] CG6779 94F1-94F1 dup:2/2 ID:89B9  
 CG6779  
 + homolog of a human hypothetical protein DKFZp434D1319.1 NLS\_BP CG2186 LD29862 dup:1/2 ID:89C10  
 CG2186  
 + P34-ARC actin\_binding PROBABLE ARP (actin related protein) 2/3 COMPLEX 34 KDA SUBUNIT CG10954 LD29815 dup:2/3 ID:89C2  
 CG10954  
 + transcription\_factor \* 4e-30 alternatively spliced form \* 4e-07 BAC1\_MOUSE TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) \* 2e-07 actin binding protein MAYV [BTB] CG8924 LD29820 13F14-13F14 ID:89C4  
 CG8924  
 + \* VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33)(aa) \* 2e-09 SCS2\_YEAST SCS2 PROTEIN SCS2 protein - yeast (Saccharomy \* 6e [MSP\_domain // MSP\_DOMAIN] CG5014 4A2-4A2 dup:2/3 ID:89D12  
 CG5014  
 + BcDNA:LD29885 unknown \* coatomer protein complex, subunit epsilon(aa) \* PROBABLE COATOMER EPSILON SUBUNIT (EPSILON-COAT PROTEIN) (EPSILON-COP)(aa) \* COATOMER EPSILON SUBUNI CG9543 LD29885 26D7-26D7 dup:1/2 ID:89D2  
 CG9543  
 + Nop60B enzyme \* CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5)(aa) \* major low affinity kDa Centromere/microtubu CG3333 LD30073 60B10-60B10 dup:4/4 ID:89E9  
 CG3333  
 + 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  
 CG7022  
 + enzyme \* acyl-CoA oxidase (EC 1.3.3.6), peroxisomal - human(aa) \* 6e-52 CAO\_YEAST ACYL-COENZYME A OXIDASE (ACYL-COA OXIDASE) ac \* 1e-111 similar to ACYL-COEN CG9709 LD30186 57D12-57D12 dup:2/2 ID:89F10  
 CG9709  
 + RpP0 \* DMAP3A\_2 RpP0 \* ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG (L10E) (RIBOSOMAL PROTEIN L10)(aa) \* 60S ACIDIC RIBOSOMAL PROTEIN P0 (DEOXYRIBONUCLEASE (APURINI [60s\_ribosomal // Ribosomal\_L10] CG7490 79C3-79C3 dup:3/3 ID:89F5  
 CG7490

+ transcription\_factor neural zinc finger factor 3; NZF-3 [Rattus norvegicus] ATPASE\_ALPHA\_BETA, zf-C2HC CG4985  
 CG4985 LD30401 dup:2/2 ID:89H10  
 CG12050 + unknown unknown protein [Arabidopsis thaliana] NLS\_BP, WD40\_REGION CG12050 LD30416 dup:2/2 ID:89H12  
 + transcription\_factor \* fruitless protein(aa) \* fruitless class I male isoform(aa) \* 3e-21 LOLS\_DROME LOLA PROTEIN,  
 SHORT ISOFORM (LONGITUDINALS LACKING PROTEIN) \* 2e-06 co [BTB // HTH\_FIS\_FAMILY // NLS\_BP] CG7230 56C-56C  
 CG7230 dup:6/10 ID:89H5  
 CG4602 + CG4602 dup:3/4 ID:89H6  
 CG4488 + protein\_kinase CG4488 ID:89H8  
 CG7065 + unknown \* [NLS\_BP] CG7065 LD35502 8C17-8C17 ID:95A12  
 CG6241 + unknown \* 8e-07 TAFI68 \* 7e-06 transcription factor SL1 \* [NLS\_BP] CG6241 LD35363 85F13-85F13 ID:95A2  
 + ribosomal\_protein \* cDNA EST yk433f11.3 comes from this gene; cDNA EST yk433f11.5 comes from this gene(aa) \* 9e-05  
 CG5108 YJ83\_YEAST PUTATIVE 40S RIBOSOMAL PROTEIN YJR113C pro [Ribosomal\_S7] CG5108 LD35371 31D11-31D11 ID:95A3  
 + unknown \* hypothetical protein(aa) \* 2e-19 probable membrane protein YPR105c - yeast (Saccharomyces cerevisiae) \* 2e-  
 CG7456 40 contains similarity to Arabidopsis me CG7456 LD35507 31E4-31E4 dup:2/2 ID:95B1  
 + \* Anchor protein. Mediates attachment of autophagosomes to microtubules.; Aut2p(aa) \* similar to Histidine acid  
 CG4428 phosphatases; cDNA EST yk432a1.3 come CG4428 21E2-21E2 dup:4/4 ID:95B10  
 + unknown \* Similarity to Yeast SOH-1 protein \* CGI-125 protein(aa) \* 2e-19 YB78\_YEAST HYPOTHETICAL 35.9 KD  
 CG1057 PROTEIN IN PCS60-ABD1 INTERGENIC REGION CG1057 LD35644 82D2-82D2 ID:95B11  
 + unknown \* 1e-52 NUC1\_YEAST MITOCHONDRIAL NUCLEASE nuclease NUC1 (EC 3.1.30 \* 5e-77 YJ05\_CAEEL  
 HYPOTHETICAL 85.1 KD NUCLEASE C41D11.5 simila \* 2e-68 NUCG\_MOUSE [NUCLEASE\_NON\_SPEC // Endonuclease]  
 CG8862 CG8862 LD35517 48F1-48F1 ID:95B2  
 + actin\_binding \* erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)(aa) \* DMP41A\_4 cora \* 2e-55 product of  
 CG9764 alternative splicing; homologue to membra [BAND\_41\_1 // Band\_41 // BAND41 // BAND\_] CG9764 LD35542 89A1-89A1 ID:95B4  
 + \* canalicular multispecific organic anion transporter (ABC superfamily)(aa) \* cadmium resistance protein YCF1 - yeast  
 CG10441 (Saccharomyces cerevisiae) \* 1e- [ATP\_GTP\_A2 // ABC\_TRANSPORTER // ABC\_tr] CG10441 37B9-37B9 dup:1/2 ID:95C1  
 CG5456 + unknown \* CG5456 LD35728 94A3-94A3 ID:95C10  
 + RNA\_binding \* splicing factor (CC1.3)(aa) \* 5e-12 polyadenylated RNA-binding protein PUB1 - yeast (Saccharomyces  
 cerevisiae) >g \* 7e-11 RNA-binding protein \* 1e-1 [RNP\_1 // RBD // rrm // NLS\_BP] CG11266 LD35730 27D-27D3 dup:1/2  
 CG11266 ID:95C11  
 + E2f transcription\_factor \* E2f \* E2F \* 1e-19 predicted using Genefinder; cDNA EST comes from this \* 5e-35 E2F3\_MOUSE  
 CG6376 TRANSCRIPTION FACTOR E2F3 (E2F-3) transcripti [NLS\_BP] CG6376 LD35741 93F1-93F1 dup:2/3 ID:95C12  
 + unknown \* BLASTX 1.2E-22 Human YL-1 mRNA for YL-1 protein (nuclear protein with DNA-binding ability), complete  
 CG4621 cds.(dna) \* transcription factor-like 1(aa) \* t [NLS\_BP] CG4621 LD35676 34A3-34A3 ID:95C3  
 CG7705 + unknown \* CG7705 LD35690 91B7-91B8 ID:95C5  
 + CycC cell\_cycle\_regulator \* DMCYCLCG\_2 CycC \* cyclin C(aa) \* cyclin C protein(aa) \* cyclin C(aa) CG7281 LD35705 88D8-  
 CG7281 88D8 dup:3/3 ID:95C8

+ Arp66B cytoskeletal\_structural\_protein \* DMACTR66B\_2 Arp66B \* 1e-126 ARP3\_YEAST ACTIN-LIKE PROTEIN ARP3 actin homolog YJR065 \* ARP3\_DROME ACTIN-LIKE PROTEIN (ACTIN-LIKE PROTEIN 66B) (ACTIN [ACTINS\_ACT\_LIKE // actin])  
 CG7558 LD35711 66B8-66B8 ID:95C9  
 + CDC45L DNA\_replication\_factor \* CDC45L \* 2e-31 Cdc45p: assembles into a complex with Cdc46p/Mcm5p \* CDC45L \* 1e-30  
 CG3658 predicted using Genefinder; cDNA EST yk307h3.3 comes from this ge CG3658 LD35753 1E1-1E1 ID:95D1  
 + unknown \* 8e-73 YIJ1\_YEAST HYPOTHETICAL 84.0 KD PROTEIN IN SGA1-KTR7 INTERGENIC REGION \* 1e-119  
 CG3735 dJ434O14.5 (novel PUTATIVE protein similar to YIL091C yeast hy CG3735 LD35854 60A11-60A11 ID:95D10  
 + RNA\_binding \* HYPOTHETICAL PROTEIN \* 3e-23 YKB7\_YEAST HYPOTHETICAL 78.3 KD PROTEIN IN RAM2-ATP7 INTERGENIC REGION \* 9e-11 cDNA EST yk384f3.5 comes from this gene; [zf-CCCH] CG9425 LD35863 70F6-70F6 dup:3/3 ID:95D12  
 CG9425 + EG:114E2.2 \* MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT)(aa) \* MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT)(aa) \* by content; by mat [THIOLASE\_3 // HLH // HELIX\_LOOP\_HELIX\_2] CG2856 3F2-3F2 dup:2/2 ID:95D2  
 CG2856 + Rad51 DNA\_repair\_protein \* DMDMRBA\_1 Rad51 \* 2e-97 RA51\_YEAST DNA REPAIR PROTEIN RAD51 RAD51 protein - yeast \* 1e-176 RA51\_DROME DNA REPAIR PROTEIN RAD51 HOMOLOG (RECA PROTEIN [HHH // RECA\_1 // RECA\_2 // ATP\_GTP\_A] CG7948 LD35801 99D5-99D6 ID:95D3  
 CG7948 + Bub1 enzyme \* Bub1 \* 4e-75 hypothetical protein YLR419w - yeast (Saccharomyces cerevisiae) (U \* DDX9\_CAEEL PROBABLE ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HEL [PROTEIN\_KINASE\_ST // pkinase // PROTEIN] CG7838 LD35813 42A1-42A1 ID:95D5  
 CG7838 + motor\_protein \* 1e-34 cDNA EST comes from this gene; cDNA EST co \* 3e-61 protein \* 4e-19 SAD1\_SCHPO SPINDLE POLE BODY ASSOCIATED PROTEIN SAD1 sp \* 4e-29 inserted at CG3287 LD35815 42D1-42D1 dup:2/2 ID:95D6  
 CG3287 + cos motor\_protein \* cos \* 3e-20 YGW6\_YEAST PUTATIVE KINESIN-LIKE PROTEIN YGL216W hypoth \* kinesin-related protein; KRP; Costal2 \* 1e-21 Similarity to Mouse kinensin-lik [kinesin // KINESIN\_MOTOR\_DOMAIN2 // KIN] CG1708 LD35834 43B2-43B2 ID:95D7  
 CG1708 + defense/immunity\_protein \* 1e-101 inserted at base Both 5' and 3' ends of P element Inverse PCR \* \* CG8187 LD35843 52A10-52A10 ID:95D8  
 CG8187 CG15435 + nucleic\_acid\_binding \* [ZINC\_FINGER\_C2H2 // ZINC\_FINGER\_C2H2\_2] CG15435 LD35850 24F5-24F5 ID:95D9  
 + lace enzyme \* 1e-107 LCB2\_YEAST SERINE PALMITOYLTRANSFERASE (LONG CHAIN BASE BIOSYNTHESIS PROTEIN \* 2e-24 delta-aminolevulinate synthase \* 1e-128 Similar to serin [aminotran\_2 // AA\_TRANSFER\_CLASS\_2 // N] CG4162 LD36009 35D3-35D3 dup:2/2 ID:95E11  
 CG4162 + RNA\_binding \* 8e-06 hypothetical protein YPR112c - yeast (Saccharomyces cerevisiae) (U \* 1e-05 similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); c [RBD // rrm // NLS\_BP] CG3594 LD36016 60D15-60D15 dup:2/2 ID:95E12  
 CG3594 + protein\_kinase \* DMRNASTK\_2 mnb \* protein kinase Dyrk1B(aa) \* MNB(aa) \* SRPK1(aa) [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG8174 LD35909 51F11-51F11 dup:3/3 ID:95E3  
 CG8174 + Sdic motor\_protein \* Sdic \* DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN)(aa) \* axonemal dynein intermediate chain Sdic(aa) \* 4e- [WD40] CG9580 LD35918 19C1-19C1 dup:2/2 ID:95E4  
 CG9580 CG11837 + unknown \* dimethylase(aa) \* 2e-97 DIM1\_YEAST DIMETHYLADENOSINE TRANSFERASE (S-ADENOSYLMETHIONINE-

6-N', N'-ADENOSY \* 4e-99 YQN1\_CAEEL HYPOTHETICAL 34.1 KD PROT [RnaAD // RRNA\_A\_DIMETH // SAM\_BIND] CG11837  
LD35950 98F9-98F9 dup:2/2 ID:95E6  
+ signal\_transduction \* 5e-11 CC4\_YEAST CELL DIVISION CONTROL PROTEIN cell division \* 8e-25 Lis1 homolog \* 1e-127  
YPR4\_CAEEL HYPOTHETICAL 77.0 KD TRP-ASP REPEATS CO[GPROTEINBRPT // WD40\_REGION // WD\_REPEA] CG9062  
CG9062 LD35961 47E3-47E3 dup:4/4 ID:95E7  
+ motor\_protein \* 6e-08 F35D11.11 gene product \* YL17\_CAEEL HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN  
CG17081 CHROMOSOME X ( \* [NLS\_BP] CG17081 LD35990 71B2-71B2 dup:3/3 ID:95E9  
+ Eip55E enzyme \* Yfr055wp(aa) \* ecdysteroid-inducible polypeptide EIP40(aa) \* 4e-99 CYS3\_YEAST CYSTATHIONINE  
GAMMA-LYASE (GAMMA-CYSTATHIONASE) \* 1e-133 CGL\_CAEEL PUT [Cys\_Met\_Meta\_PP] CG5345 LD36096 55E5-55E5  
CG5345 dup:2/2 ID:95F11  
+ Irp-1B RNA\_binding \* Irp-1B \* 9e-47 aconitase (ACO1) (EC 4.2.1.3) \* iron regulatory protein-1B \* ACOC\_CAEEL PROBABLE  
ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYA [ACONITASE\_2 // Aconitase\_C // aconitase] CG6342  
CG6342 LD36108 86A6-86A6 ID:95F12  
CG6398 + unknown \* 8e-16 coded for by C. elegans cDNA yk81c2.5 \* \* CG6398 LD36024 16D4-16D4 dup:2/2 ID:95F3  
+ nmo protein\_kinase \* nmo \* 2e-58 HOG1\_YEAST MITOGEN-ACTIVATED PROTEIN KINASE HOG1 (MAP KINASE HOG1)  
(OSMOSENSING \* nemo, form I - fruit fly (Drosophila melanogaster) [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG7892  
CG7892 LD36031 67D9-66B4 dup:2/2 ID:95F4  
CG1943 + unknown \* CG1943 LD36048 84C1-84C1 ID:95F5  
+ nucleic\_acid\_binding \* castor protein - fruit fly (Drosophila sp.)(aa) \* neuroblast cell lineage zinc finger protein ming - fruit fly  
CG2102 (Drosophila melan \* I(3)j1C2 I(3)j1C[CRYSTALLIN\_BETAGAMMA // ZINC\_FINGER\_C2H] CG2102 LD36057 83C1-83C1 ID:95F7  
+ ubiquitin \* BAT3(aa) \* 2e-05 ubiquitin-like protein DSK2 - yeast (Saccharomyces cerevisiae) \* 3e-14 BAT3 \* 2e-15 Scythe  
CG7546 [UBIQUITIN\_1 // ubiquitin // UBIQUITIN\_2] CG7546 LD36241 67B10-67B10 dup:1/2 ID:95G12  
CG4454 + unknown \* CG4454 LD36125 32A1-32A1 dup:2/3 ID:95G2  
CG8326 + motor\_protein \* CG8326 LD36157 16B10-16B10 ID:95G4  
+ Hsp67Bb chaperone \* DMHGS2\_7 Hsp67Bb \* 1e-14 hypothetical protein YOR285w - yeast (Saccharomyces cerevisiae) \* 5e-60  
HS6B\_DROME HEAT SHOCK PROTEIN 67B2 heat shock prot [Rhodanese // RHODANESE] CG4456 LD36162 67B1-67B1  
CG4456 ID:95G6  
CG5175 + CG5175 ID:95H10  
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  
C1A9 \* 6e-06 similar to 'chromo' (CHRromatin Organization MOfifier) do [chromo // CHROMO\_2 // NLS\_BP] CG8289 LD36501  
CG8289 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 ID:96A3  
 CG11798  
 + 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 LD36412 55E5-55E5 ID:96A4  
 CG5482  
 + unknown \* 2e-10 transmembrane protein \* 6e-12 weak similarity to plasminogens \* 2e-12 DMDUSKY\_1 dy \* similar to cuticlin [NLS\_BP] CG7802 LD36439 99C5-99C5 ID:96A7  
 CG7802  
 + enzyme \* bgr;ggt-l \* protein farnesyl transferase beta subunit(aa) \* farnesyl protein transferase subunit B(aa) \* predicted using Genefinder; Similarity t [prenyltrans] CG17565 LD36454 89C3-89C3 dup:1/2 ID:96A8  
 CG17565  
 CG1918 + \* [PHOSPHOPANTETHEINE // ANTIFREEZE] CG1918 43F4-43F4 ID:96A9  
 CG1918  
 + Dlc90F motor\_protein \* Tctex protein(aa) \* DMTCTEXPR\_2 Tctex \* 1e-61 Tctex protein \* 7e-14 predicted using Genefinder; cDNA EST yk460f12.5 comes from this ge CG12363 LD36705 90F7-90F7 ID:96B11  
 CG12363  
 + Sap47 unknown \* synapse associated protein sap47-2 - fruit fly (Drosophila melanogaster)(aa) \* DMSAP472\_2 Sap47 \* 1e-99 synapse-associated protein sap47-1 - fruit f CG8884 LD36546 89B1-89B2 ID:96B2  
 CG8884  
 + transcription\_factor \* ZINC FINGER PROTEIN GLI4 (NEURAL SPECIFIC DNA BINDING PROTEIN XGLI4) (XGLI-4)(aa) \* 4e-07 YJF6\_YEAST HYPOTHETICAL 98.9 KD ZINC FINGER PROTE[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG9403 LD36562 42B2-42B2 dup:1/2 ID:96B3  
 CG9403  
 + unknown \* HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III(aa) \* CGI-150 protein(aa) \* 3e-21 Similar to protein from Brassica oleracea which is simila [Glyoxalase] CG1532 LD36566 19E6-19E6 ID:96B4  
 CG1532  
 + EG:86E4.4 signal\_transduction \* /match=(desc;; /match=(desc;; /match=(de \* 2e-25 lin-9 protein - Caenorhabditis elegans \* 8e-21 protein \* 4e-07 inserted at base Both 5' and 3' ends CG3480 LD36606 2B16-2B16 ID:96B7  
 CG3480  
 + 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  
 CG6394  
 + Rpt1 endopeptidase \* 1e-166 PRS7\_YEAST 26S PROTEASE REGULATORY SUBUNIT HOMOLOG (CIM5 PROTEIN) (TAT-BINDING \* 4e-48 transitional endoplasmic reticulum ATPase TER94 \* PRS [AAA // ATP\_GTP\_A] CG1341 LD36653 43E6-43E6 dup:1/3 ID:96B9  
 CG1341  
 + electron\_transfer \* 2e-36 C561\_CAEEL PUTATIVE CYTOCHROME B561 (CYTOCHROME B-561) hy \* 6e-37 cytochrome B561 \* 4e-39 C561\_HUMAN CYTOCHROME B561 (CYTOCHROME B-561) cytoch CG1275 LD36721 62D4-62D5 dup:1/2 ID:96C1  
 CG1275  
 + 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  
 CG4612  
 + 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  
 CG7012  
 + \* 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  
 CG2858

+ Csp chaperone \* cysteine string protein 1(aa) \* 2e-16 MAS5\_YEAST MITOCHONDRIAL PROTEIN IMPORT PROTEIN MAS5  
 (PROTEIN YDJ1) \* 4e-19 similar to the DNA-J domain foun [4FE4S\_FERREDOXIN // DNAJ\_1 // DnaJ // D] CG6395 LD36856  
 CG6395 79E1-79E2 dup:1/4 ID:96C8  
 + unknown \* Yor240wp(aa) \* hypothetical protein(aa) \* \* 1e-56 probable membrane protein YOR240w - yeast  
 CG13929 (Saccharomyces cerevisiae) [MET\_TRANS // SAM\_BIND] CG13929 LD36863 62A10-62A10 ID:96C9  
 + 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  
 CG4831 32E4-32E4 ID:96D1  
 + thr unknown \* three rows protein \* thr \* THR\_DROME THREE ROWS PROTEIN chromosome disjunction prot [NLS\_BP]  
 CG5785 CG5785 LD37031 54F5-54F6 dup:2/2 ID:96D10  
 + unknown TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN)(aa) NLS\_BP CG11642  
 CG11642 LD36954 dup:2/2 ID:96D3  
 + l(2)k09913 unknown \* 1e-22 inserted at base Both 5' and 3' ends of P element Inverse PCR \* \* CG3082 LD36990 59C3-59C3  
 CG3082 dup:2/2 ID:96D4  
 CG4877 + unknown \* [NLS\_BP] CG4877 LD36996 72F1-72F1 dup:2/2 ID:96D5  
 CG13626 + unknown \* 1e-05 No definition line found \* [T\_SNARE] CG13626 LD37002 96A14-96A14 ID:96D6  
 + 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  
 CG9749 88A10-88A10 dup:2/2 ID:96D8  
 + unknown \* 1e-111 protein \* 1e-114 UNR\_RAT UNR PROTEIN probable unr protein - rat \* unknown [COLD\_SHOCK // CSD]  
 CG7015 CG7015 LD37025 66C13-66C13 dup:2/4 ID:96D9  
 + Ndr protein\_kinase \* DMPROKINX\_2 Ndr \* Ndr protein kinase(aa) \* 1e-128 KNQ1\_YEAST PROBABLE  
 SERINE/THREONINE-PROTEIN KINASE YNL161W \* 1e-175 coded for by C. elegans [PROTEIN\_KINASE\_ST //  
 CG8637 PROTEIN\_KINASE\_DOM] CG8637 LD37189 76D3-76D3 dup:2/2 ID:96E10  
 CG6144 + unknown \* predicted using Genefinder(aa) \* \* CG6144 LD37206 31E4-31E4 dup:2/2 ID:96E12  
 + EG:100G10.5 transporter \* by content; by match; 2-match\_description=UDP-GALACTOSE TRANSLOCATOR (UDP-...(aa) \* No  
 CG2675 definition line found(aa) \* 8e-71 Similarity to Mouse CMP-s CG2675 LD37122 3B5-3B5 dup:2/2 ID:96E3  
 + Noa36 nucleic\_acid\_binding \* nucleolar protein, putative(aa) \* 1e-111 cysteine-rich protein \* 1e-110 Zn finger factor \*  
 CG10009 [NLS\_BP] CG10009 LD37139 98D3-98D3 dup:2/2 ID:96E5  
 CG5541 + unknown \* [C\_TYPE\_LLECTIN\_1] CG5541 LD37145 13A8-13A8 dup:3/3 ID:96E6  
 + 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 //  
 CG4898 TROPOMYOSIN // PRO\_RICH] CG4898 LD37158 88E10-88E11 dup:4/4 ID:96E7  
 + pnut cytoskeletal\_structural\_protein \* pnut \* PEANUT PROTEIN(aa) \* 3e-82 cell division cycle protein \* 1e-134 CDC10  
 CG8705 [GTP\_CDC // NLS\_BP // ATP\_GTP\_A] CG8705 LD37170 44B3-44B4 dup:2/2 ID:96E9  
 CG13601 + unknown \* 7e-08 No definition line found \* \* CG13601 LD37258 95C-95C ID:96F10

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

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

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

CG3218 + fs(1)K10DNA\_binding \* regulatory protein K10, oocyte-specific - fruit fly (Drosophila melanogaster)(aa) \* DMK10G\_4 fs(1)K10 \*  
4e-58 K10\_DROME DNA-BINDING PROTEIN K10 \* 62 [PRO\_RICH] CG3218 LD37240 2F1-2F1 ID:96F7

CG11128 + transporter \* cationic amino acid transporter-1(aa) \* solute carrier family (cationic amino acid transporter, y+ system),  
member 1(aa) \* LOW-AFFINITY CATIONIC AMI [aa\_permeases // AMINO\_ACID\_PERMEASE\_2] CG11128 LD37241 79F5-79F6  
dup:2/2 ID:96F8

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

CG8949 + unknown \* 8e-08 predicted using Genefinder; similar to WW domain \* 1e-07 inserted at base Both 5' and 3' ends of P  
element Inverse PCR \* [WW\_rsp5\_WWP // WW\_DOMAIN\_1 // NLS\_BP //] CG8949 15D1-15D1 ID:96G10

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

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

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

CG5462 + ion\_channel \* outer membrane protein(aa) \* The gene product is related to adenylyl cyclase.(aa) \* 1e-18 DLG1\_DROME  
LETHAL(1)DISCS LARGE-1 TUMOR SUPPRESSOR PROTEIN [PDZ] CG5462 LD37377 100B1-97B9 dup:1/3 ID:96G9

CG10851 + B52 RNA\_binding \* transcription, DNA-dependent mRNA splicing ) RNA binding RNA binding ) nucleic acid binding pre-mRNA  
splicing factor ) \* DMB52\_2 B52 \* 52K active ch [RBD // rrm // NLS\_BP] CG10851 LD37428 87F7-87F7 ID:96H1

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

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

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

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

CG12878 + unknown \* 6e-10 MLN \* 1e-41 l(3)rL203 l(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

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

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

CG15100  
CG14442 + unknown \* 7e-05 unknown \* \* [MIP // NLS\_BP] CG14442 LD38069 6C7-6C8 dup:2/3 ID:97D2  
+ transcription\_factor \* Cys2/His2 zinc finger protein(aa) \* ovo \* fruit fly STS clone SP6(dna) \* zinc finger protein NY-REN-21

CG4639 antigen(aa) [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG4639 LD38072 94E-94E ID:97D4

CG8928 + unknown \* CG8928 LD38104 13F14-13F14 ID:97D7  
+ enzyme \* BLASTX 1.1E-34 Rattus sp. mRNA for hemC gene.(dna) \* BLASTX 1.1E-34 Rattus sp. mRNA for hemC gene.(dna) \* 7e-54 HEM3\_YEAST PORPHOBILINOGEN DEAMINASE [PORPHBDMNASE // Porphobil\_deam] CG9165 LD38107 61F7-61F7 dup:2/2 ID:97D8

CG9165  
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  
+ 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

CG5486  
CG5112 + enzyme \* coded for by C. elegans cDNA yk16b2.3; coded for by C. elegans cDNA yk16b2.5; Similar to amidase.(aa) \* 1e-23 putative yeast amidase \* 3e-21 coded f [Amidase // AMIDASES] CG5112 LD38433 99B4-99B4 ID:97F10

CG17170 + su(f) DNA\_binding \* 2e-47 RN14\_YEAST MRNA 3'-END PROCESSING PROTEIN RNA14 RNA14 p \* SUF\_DROME SUPPRESSOR OF FORKED PROTEIN gene su(f) protein \* cleavage stimulation fa [NLS\_BP] CG17170 LD38348 cyto\_unknown ID:97F2

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

CG1078 + unknown \* 5e-10 FIP1\_YEAST FIP1 PROTEIN FIP1 protein - yeast (Saccharom \* 3e-16 contains similarity to S. cerevisiae FIP1 \* 2e-13 YAAA\_SCHPO HYPOTHETICAL 37.3 [PRO\_RICH // NLS\_BP] CG1078 LD38592 82C2-82C2 dup:1/3 ID:97G11

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

CG8180 + unknown \* 1E-178\* \* [ANTIFREEZEI] CG8180 LD38554 52A4-52A4 dup:1/2 ID:97G8  
+ \* 2e-45 sulfate permease \* 1e-27 Similar to sulfate transporter. \* 9e-33 DTD\_MOUSE SULFATE TRANSPORTER (DIASTROPHIC DYSPLASIA PROTEIN HOMOLOG) (ST-OB) [Sulfate\_transp // SUGAR\_TRANSPORT\_2] CG5002 54E7-54E7 ID:97G9

CG5002  
CG6773 + BcDNA:LD03471 transcription\_factor\_binding \* SEC13-RELATED PROTEIN(aa) \* cytoplasmic protein involved in release of



transport vesicles from the ER; Sec13p(aa) \* PROTEIN TRANSPORT PROTEIN SEC13( [WD40\_REGION // WD40] CG6773 LD38669 94F1-94F1 ID:97H2

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

+ DNA\_binding \* 7e-32 NAM7\_YEAST NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT \* 1e-27 nonsense-mediated mRNA decay trans-acting factor \* 2[ZINC\_FINGER\_C2H2 // PRO\_RICH // ATP\_GTP] CG6701 LD38709 50C21-50C22 dup:2/2 ID:97H8

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

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

+ BcDNA:GH07910 protein\_kinase \* 7e-22 CC5\_YEAST CELL CYCLE PROTEIN KINASE CDC5/MSD2 protein ki \* 3e-12 p90 ribosomal S6 kinase \* 1e-121 YKT3\_CAEEL PUTATIVE SERINE/THREONINE-[PFKB\_KINASES\_1 // PROTEIN\_KINASE\_ST // ] CG2829 LD38852 3F4-3F6 dup:5/6 ID:98B2

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

+ RasGAP signal\_transduction \* RasGap protein(aa) \* 2e-16 BUD2\_YEAST INHIBITORY REGULATOR PROTEIN BUD2/CLA2 GTPase- \* RasGap protein \* 1e-40 similar to GTPase-activating p[RAS\_GTPASE\_ACTIV\_2 // SH2DOMAIN // C2 /] CG9209 LD38909 14A1-14A1 dup:1/2 ID:98B8

CG8441 + unknown \* 4e-14 YPT2\_CAEEL HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III \* 5e-05 unknown protein \* \* [NLS\_BP] CG8441 LD38910 52F7-52F7 dup:2/2 ID:98B9

CG18011 + nucleic\_acid\_binding \* CG18011 LD39136 46E8-46E8 ID:98C11

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

CG8483 + 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 LD39062 93F10-93F10 dup:2/2 ID:98C4

CG6678 + CytT cell\_cycle\_regulator \* CytT \* 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

CG6292 + unknown \* 1e-75 hypothetical protein \* repressor of the gab DTP gene cluster \* Y039\_MYCPN HYPOTHETICAL PROTEIN MG039 HOMOLOG glycerol- \* CG10639 LD39082 37B8-37B8 ID:98C7

CG10639 + transcription\_factor\_binding \* Ydr324cp(aa) \* 1e-25 hypothetical protein YDR324c - yeast (Saccharomyces cerevisiae) (U \* 3e-29 hypothetical protein \* 7e-05 DMENHSPA\_3 gro [WD40\_REGION] CG5018 LD39110 72D11-72D12 ID:98C8

CG5018 CG18533 + CG18533 LD39166 ID:98D1

CG18533 CG1624 + transcription\_factor \* 0.00000000006\* 9e-25 YMB4\_CAEEL HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN

CHROMOSOME III \* 4e-13 TIF1 protein - mouse TIF1 isoform Pepti \* 8e-24 brai [NHL] CG1624 LD39167 43C5-43C7 ID:98D2

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

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

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

CG14792 + sta ribosomal\_protein \* 6e-69 NABA\_YEAST 40S RIBOSOMAL PROTEIN SA HOMOLOG A (NUCLEIC ACID-BINDING PROTEIN NAB1 \* 1e-143 RSP4\_DROME 40S RIBOSOMAL PROTEIN SA (P40) (STUBARIST RIBOSOMALS2, RIBOSOMAL\_S2\_1 CG14792 ID:98D8

CG4502 + enzyme \* 9e-41 /match=(desc:; /ma \* 5e-35 cDNA EST comes from this gene; cDNA EST co \* 9e-06 Ubc84D \* contains similarity to ubiquitin-conjugatin enzymes (Pf [UQ\_con // UBIQUITIN\_CONJUGAT\_2] CG4502 LD39243 27E4-27E4 ID:98D9

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

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

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

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

CG3654 + DNA\_binding \* 2e-15 YJ89\_YEAST HYPOTHETICAL 85.0 KD PROTEIN IN STE24-ATP2 INTERGENIC REGION \* 8e-26 Similarity to Human XE169 protein (SW:XE169\_HUMAN); cDNA EST E [ARID // PRO\_RICH // NLS\_BP] CG3654 LD39559 67B5-67B5 dup:3/3 ID:98F11

CG1896 + unknown \* [NLS\_BP] CG1896 LD39576 100E2-100E2 dup:2/2 ID:98F12

CG1951 + protein\_kinase \* ZC581.9 gene product(aa) \* 4e-40 SCY1\_YEAST SCY1 PROTEIN SCY1 protein - yeast (Saccharom \* 8e-26 ZC581.9 gene product \* 3e-05 putative serine/threon [PROTEIN\_KINASE\_DOM // pkinase] CG1951 LD39455 98F-98F dup:2/2 ID:98F2

CG6141 + Rpl9 ribosomal\_protein 60S RIBOSOMAL PROTEIN L9 RIBOSOMAL\_L6\_2, Ribosomal\_L6 CG6141 ID:98F7

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

CG2050 + mod DNA\_binding \* DNA-BINDING PROTEIN MODULO(aa) \* DMLA9\_4 mod \* 3e-05 Similarity to Human spliceosome-associated protein SAP62 (PIR Acc. \* 5e-05 NUCL\_MOUSE NUCLEOLIN [RBD // rrm // NLS\_BP // ATP\_GTP\_A] CG2050 100F5-100F5 dup:3/3 ID:98F9

CG5720 + BcDNA:LD27873 actin\_binding \* 1e-06 RNA-binding protein \* 1e-06 NAB2\_YEAST NUCLEAR POLYADENYLATED RNA-

BINDING PROTEIN NAB2 \* 3e-88 inserted at base Both 5' and 3' ends of P eleme [NLS\_BP] CG5720 95F-98B1 dup:5/8 ID:98G12

CG11299 + cell\_cycle\_regulator \* non-p53 regulated PA26-T1 nuclear protein(aa) \* 2e-72 p53 regulated PA26-T3 nuclear protein \* p53 regulated PA26-T2 nuclear protein \* CG11299 LD39604 59F5-59F6 ID:98G2

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

CG4032 + Abl protein\_kinase \* DMTKABL3\_2 Abl \* Dsrc41(aa) \* TYROSINE-PROTEIN KINASE DASH/ABL(aa) \* 2e-16 SPK1\_YEAST PROTEIN KINASE SPK1 (SERINE-PROTEIN KINASE 1) [SH2DOMAIN // SH3DOMAIN // PRO\_RICH // P] CG4032 LD39618 77A3-73B1 ID:98G4

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

CG2712 + EG:95B7.7 transcription\_factor \* /motif=(desc;; /motif=(desc;; /motif=(desc;; /match=(desc:(aa) \* /motif=(desc;; /motif=(desc;; /motif=(de \* 3e-29 similar to Zinc finger, C2H2 type[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG2712 LD39664 3B6-3B6 ID:98G8

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

CG10944 + RpS6 ribosomal\_protein 40S RIBOSOMAL PROTEIN S6 NLS\_BP, RIBOSOMAL\_S6E CG10944 ID:98H3

CG4501 + enzyme CG4501 ID:98H6

CG14646 + unknown \* 2e-20 predicted using Genefinder; cDNA EST comes from this g \* \* CG14646 LD39811 82B2-82B3 ID:98H8

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

CG6222 + su(s) RNA\_binding \* DMSUSG\_16 su(s) \* su(s) homolog; similar to Drosophila melanogaster suppressor of sable (su(s)) pro \* DMSUSG\_16 su(s) \* SUS\_DROME SUPPRESSOR OF SAB [NLS\_BP] CG6222 LD39941 1B10-1B10 dup:2/3 ID:99A10

CG4654 + Dp transcription\_factor \* DMDPRTF\_2 Dp \* transcription factor \* 6e-59 similar to transcription factor DP-1; cDNA EST comes f \* 5e-72 TDP1\_MOUSE TRANSCRIPTION FACTOR DP-1 (E2F CG4654 LD39905 49F13-49F13 dup:2/2 ID:99A2

CG3303 + enzyme \* putative serine protease-like protein(aa) \* weakly similar to human placental protein precursor (SP:PP11\_HUMAN)(aa) \* placental protein (serine pro CG3303 LD39912 89A13-89B1 ID:99A3

CG2198 + Ama cell\_adhesion \* DMAMA\_5 Ama \* Immunoglobulin-C2-type-domain protein \* 1e-15 hemiceitin 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-&agr; CG8247 LD39926 44F9-44F9 ID:99A5

CG6542 + BcDNA:LD23181 protein\_phosphatase \* 1e-41 inserted at base Both 5' and 3' ends of P element Inverse PCR \* \* [TYR\_PHOSPHATASE\_1] CG6542 LD39930 54C1-54C3 ID:99A6

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  
 + unknown \* W06E11.6 gene product(aa) \* BRX protein(aa) \* W06E11.5 gene product CG5938 LD40095 97F5-97F5  
 CG5938 dup:2/2 ID:99B11  
 + enzyme \* 2e-45 acyl-coenzyme A oxidase \* 1e-100 Similarity to Rat Acyl-CoA oxidase I (SW:CAO1\_RAT); cDNA EST  
 CG4586 EMBL: \* 1e-116 peroxisomal acyl-CoA oxidase \* 1e CG4586 LD40103 6E4-6E4 ID:99B12  
 + protein\_kinase \* 9e-52 SSK2\_YEAST SERINE/THREONINE PROTEIN KINASE SSK2 (SUPPRESSOR OF SENSOR  
 CG7717 KINASE 2) \* 5e-34 protein kinase (EC 2.7.1.37) 2B - fruit fly (Drosop[PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG7717  
 LD39970 93F9-93F9 dup:3/5 ID:99B2  
 + Rab10 cell\_cycle\_regulator \* Rab1 \* 4e-56 SEC4\_YEAST RAS-RELATED PROTEIN SEC4 GTP-binding protein SE \* 1e-111  
 Rab10 \* 9e-80 strong similarity to the YPT1 sub-family of RAS pro[SIGMA54\_INTERACT\_1 // ras // ATP\_GTP\_A ] CG17060  
 CG17060 LD39986 19C1-19C2 ID:99B3  
 + EG:52C10.2 signal\_transduction \* 1e-100 by content; 1-meth \* 3e-43 YUE1\_CAEEL HYPOTHETICAL 19.6 KD PROTEIN  
 F16H9.1 IN CHROMOSOME X \* 2e-31 RGS5\_MOUSE REGULATOR OF G-PROTEIN SIGNALIN [GRK // RGS] CG5036 LD40005  
 CG5036 54F1-54F1 dup:2/3 ID:99B4  
 + chaperone \* M-phase phosphoprotein 11(aa) \* zuotin related factor 2(aa) \* strong similarity to mouse DNAJ-like protein  
 MTJ1 \* 6e-41 ZUO1\_YEAST ZUOTIN zuotin - [MYB\_3 // DnaJ // DNAJ\_2 // NLS\_BP] CG10565 LD40027 78C1-78C1 dup:2/2  
 CG10565 ID:99B6  
 CG1726 + unknown CG1726 LD40039 ID:99B7  
 + enzyme \* 5e-30 gliotactin precursor - fruit fly (Drosophila melanogaster) \* 8e-15 similar to carboxyesterase \* 7e-37  
 CG12869 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  
 CG6584 86C7-86C7 ID:99C11  
 + transcription\_factor \* 3e-09 TF3A\_YEAST TRANSCRIPTION FACTOR IIIA (TFIIIA) transcriptio \* 3e-15 CROL ALPHA \* 2e-  
 06 similar to Zinc finger, C2H2 type (3 domains)[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG12941 LD40262 47C6-47C6  
 CG12941 dup:1/2 ID:99C12  
 + \* similar to S. cerevisiae nitrogen permease regulator \* G21 protein(aa) \* homologous to yeast nitrogen permease  
 CG9104 (candidate tumor suppressor)(aa) \* 3e CG9104 15A11-15B1 dup:1/2 ID:99C3  
 CG9866 + unknown \* CG9866 LD40170 22E-22E ID:99C4  
 + unknown \* ilvB (bacterial acetolactate synthase)-like(aa) \* BLASTX 4.8E-22 YEL020C|Protein with similarity to oxalyl-CoA  
 CG11208 decarboxylase from Oxalobacter formig [TPP\_enzymes // TPP\_ENZYMES] CG11208 LD40177 56F14-56F14 ID:99C5  
 + gammaTub23C cytoskeletal\_structural\_protein \* similar to Tubulin (2 domains); cDNA EST CEMSG51F comes from this gene(aa)  
 \* gamma-tubulin 3(aa) \* TUBULIN ALPHA-4 CHAIN(aa) \* DMTUBA4\_2 agr;Tub67C [TUBULIN // tubulin] CG3157 LD40196 23C2-  
 CG3157 23C2 ID:99C6

CG8374 + dmt unknown \* [NLS\_BP] CG8374 LD40216 85E5-85E5 ID:99C7  
+ electron\_transfer \* Protein with glutaredoxin activity; Grx3p(aa) \* predicted using Genefinder; cDNA EST CEMSA40F comes from this gene; cDNA EST CEMSA40R comes from [AA\_TRNA\_LIGASE\_II\_2 // THIOREDOXIN\_2] CG6523 LD40224 34B6-34B6

CG6523 dup:1/2 ID:99C9  
+ endopeptidase \* 6e-15 UBPA\_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (UBIQUITIN THIOLESTERASE \* 2e-12 FAF\_DROME PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF [UCH\_2\_1 // UCH\_2\_2 // UCH\_2\_3 // UCH-1 ] CG5505 LD40339 66A5-66A5 ID:99D11

CG5505 + endopeptidase \* Herpes virus-associated ubiquitin-specific protease(aa) \* 1e-99 UBPF\_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (UBIQUITIN THIOLESTERASE \* 4e-40 UB [UCH\_2\_1 // UCH\_2\_2 // MATH // UCH\_2\_3 /] CG1490 LD40280 11A4-11A4 ID:99D2

CG1490 CG13840 + CG13840 LD40283 ID:99D4  
+ 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

CG11537 ID:99D5  
+ receptor \* 7e-05 CRM1\_YEAST CHROMOSOME REGION MAINTENANCE PROTEIN CRM1 \* 1e-120 protein \* 6e-28 inserted at base Both 5' and 3' ends of P element Inverse PCR \* [IBN\_NT] CG7212 LD40304 90E-90E5 dup:2/3 ID:99D6

CG7212 + transcription\_factor \* Yjr119cp(aa) \* XE169 PROTEIN (SMCX PROTEIN)(aa) \* T17H7.10(aa) \* JUMONJI PROTEIN(aa) [ARID // PHD] CG9088 LD40310 26B1-26B1 dup:2/2 ID:99D7

CG9088 + enzyme \* ubiquitin-conjugating enzyme E2-32k(aa) \* 2e-33 UBC7\_YEAST UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN LIGASE) (UBI \* 3e-24 UBC6\_DROME [UBIQUITIN\_CONJUGAT // UQ\_con // UBIQUIT] CG7656 LD40324 71D4-71E1 dup:3/3 ID:99D8

CG7656 + unknown \* DIMETHYLADENOSINE TRANSFERASE (S-ADENOSYLMETHIONINE-6-N', N'-ADENOSYL(RRNA) DIMETHYLTRANSFERASE) (16S RRNA DIMETHYLASE) (HIGH LEVEL KASUGAMYCIN RESI [RrnaAD] CG7319 LD40326 71C2-71C2 dup:2/2 ID:99D9

CG7319 + BcDNA:GH02220 enzyme \* OXA1 homolog - human(aa) \* 3e-25 OXA1\_YEAST CYTOCHROME OXIDASE BIOGENESIS PROTEIN OXA1 PRECURSOR \* 2e-29 Similarity to Human OXA1HS protein (cytochr CG6404 LD40470 67F4-67F4 dup:3/3

CG6404 ID:99E10  
+ RfC40 DNA\_replication\_factor \* 3e-99 RFC4\_YEAST ACTIVATOR KD SUBUNIT (REPLICATION FACTOR C KD SUBUNIT) \* AC14\_DROME ACTIVATOR KD SUBUNIT (REPLICATION FACTOR C KD SUBUNIT) (A1 \* 1 [ATP\_GTP\_A] CG14999 LD40483 64A10-64A10 dup:2/2 ID:99E11

CG14999 + fs(1)Ya cell\_cycle\_regulator \* mitosis initiation protein fs(1)Ya - fruit fly (Drosophila melanogaster)(aa) \* FSYA\_DROME MITOSIS INITIATION PROTEIN FS(1)YA fs(1)Ya prote \* DMFS1Y [ZINC\_FINGER\_C2H2] CG2707 LD40381 3B6-3B6 dup:2/2 ID:99E2

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

CG1911 + RpA-70 DNA\_replication\_factor \* DMRPA1\_3 RpA-70 \* REPLICATION PROTEIN A KD DNA-BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) CG9633 LD40420 84F-84F dup:4/4

CG9633 ID:99E5

+ unknown \* 2e-49 kraken \* 1e-19 dJ222E13.1 (N-terminal part of novel protein with some similarit \* 6e-12 TPES\_PSEPU  
 TROPINESTERASE (ATROPINESTERASE) (ATROPINE [ESTERASE // EF\_HAND // abhydrolase] CG11309 LD40450 78C8-  
 CG11309 78C9 dup:4/4 ID:99E7  
 + unknown \* 5e-70 weak similarity to HSP90 \* 1e-05 YXAQ\_BACSU HYPOTHETICAL 37.5 KD PROTEIN IN GNTR-HTPG  
 CG2982 INTERGENIC REGION \* CG2982 LD40453 4B5-4B5 dup:2/2 ID:99E8  
 + M(2)21ABenzyme \* 1e-88 METK\_YEAST S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE  
 CG2674 ADENOSYLTRANSFERASE 1) \* 1e-142 METK\_DROME S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE  
 [ADOMET\_SYNTHETASE\_1 // ADOMET\_SYNTHETAS] CG2674 LD40460 21B-21B dup:2/2 ID:99E9  
 + RNA\_binding \* DMB52\_2 B52 \* ASF/SF2 homolog(aa) \* nuclear phosphoprotein SRp55 - fruit fly (Drosophila  
 CG6987 melanogaster)(aa) \* dJ862K6.2.1 (splicing factor, (SRP55-1) [RBD // rrm] CG6987 LD40489 89B21-89B21 dup:2/3 ID:99F1  
 + for unknown \* CGMP-DEPENDENT PROTEIN KINASE, ISOZYME FORMS T1/T3 (CGK) (PROTEIN FORAGING)(aa) \* \*  
 CG10033 CG10033 LD40611 25B1-25B1 dup:3/4 ID:99F10  
 + ligand\_binding\_or\_carrier \* fast-twitch myosin light chain 1(aa) \* DMTNC41C\_2 TpnC41C \* 1e-35 CC31\_YEAST CELL  
 CG17493 DIVISION CONTROL PROTEIN cell division \* 5e-32 CALM\_DROME CALMO[EF\_HAND // efhand // EF\_HAND\_2] CG17493  
 LD40645 cyto\_unknown ID:99F11  
 + DNA\_binding \* 9e-09 ssrp2 \* 4e-09 contains similarity to HMG boxes \* 3e-19 mitochondrial transcription factor A \* 6e-27  
 CG4217 transcription factor 6-like (mitochondria [HMG // HMG\_box // NLS\_BP] CG4217 LD40493 92E11-92E11 ID:99F2  
 + unknown \* No definition line found(aa) \* 4e-13 No definition line found \* [WW\_rsp5\_WWP // NLS\_BP // WW\_DOMAIN\_2]  
 CG11820 CG11820 LD40504 98F6-98F6 dup:1/2 ID:99F5  
 + enzyme \* 3-KETOACYL-COA THIOLASE MITOCHONDRIAL (BETA-KETOTHIOLASE) (ACETYL-COA  
 CG4600 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  
 + RNA\_binding \* 2e-16 SME1\_YEAST SMALL NUCLEAR RIBONUCLEOPROTEIN E HOMOLOG SME1 \* 1e-27 predicted  
 CG7102 using Genefinder \* 1e-30 small nuclear ribonucleoprotein E \* 8e-33 [BTB // Sm] CG7102 LD40565 28D5-28D5 ID:99F7  
 CG9839 + unknown \* [CYTOCHROME\_C] CG9839 LD40589 85E9-85E9 ID:99F8  
 + signal\_transduction \* Caf1 \* Nle \* Taf80 \* 5e-13 T2D4\_YEAST TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUNIT  
 CG6724 (TAFII-90) [GPROTEINBRPT // WD40\_REGION // WD\_REPEA] CG6724 LD40657 32A5-32A5 ID:99G1  
 + unknown \* predicted using Genefinder; similar to Acetyltransferase (GNAT) family (2 domains); cDNA EST yk466g5.3 comes  
 CG1969 from this gene; cDNA EST yk255h7.3 come [Acetyltransf] CG1969 LD40766 99C1-99C1 ID:99G10  
 + BcDNA:LD34343 enzyme \* 1e-111 SCS1 product=suppressor of chaperonin sixty-1 cerevisi \* 1e-152 similar to RTS1 PROTEIN  
 CG5643 (SCS1 PROTEIN) \* 1e-149 protein phosphatase 2A subuni CG5643 LD40774 98A3-98A3 dup:2/3 ID:99G11  
 + RNA\_binding \* Bub3 \* WD-40 repeat protein(aa) \* HYPOTHETICAL 41.4 KD TRP-ASP REPEATS CONTAINING PROTEIN  
 F10G8.3 IN CHROMOSOME I(aa) \* HYPOTHETICAL RAE1-LIKE PROTE [GPROTEINBRPT // WD40\_REGION // WD\_REPEA]  
 CG9862 CG9862 LD40776 57F6-57F6 ID:99G12  
 + unknown \* HYPOTHETICAL 96.2 KD PROTEIN C08B11.4 IN CHROMOSOME II(aa) \* predicted using Genefinder(aa) \* 3e-  
 CG8185 05 /match=(desc: \* 7e-38 cDNA EST comes from this CG8185 LD40680 52A9-52A10 dup:1/2 ID:99G3  
 CG5589 + RNA\_binding \* 1e-89 ROK1\_YEAST ATP-DEPENDENT RNA HELICASE ROK1 ATP-dependen \* 1e-41 VASA\_DROME

VASA PROTEIN vasa mel \* 1e-81 similar to ATP dependent RNA helicase [helicase\_C // HELICASE // DEAD // NLS\_B] CG5589  
 LD40692 75A2-75A2 dup:1/3 ID:99G4  
 + transporter \* CGI-19 protein(aa) \* 5e-07 probable membrane protein YPL244c - yeast (Saccharomyces cerevisiae) \* 7e-83  
 CG7853 No definition line found \* 2e-40 putative pr CG7853 LD40702 73E4-73E4 ID:99G5  
 + unknown \* hypothetical protein(aa) \* 6e-71 inserted at base Both 5' and 3' ends of P element Inverse PCR \* [NLS\_BP]  
 CG2162 CG2162 LD40717 63B4-63B5 dup:2/2 ID:99G7  
 + enzyme \* Yjr084wp(aa) \* acyl-protein thioesterase(aa) \* 1e-22 probable membrane protein YLR118c - yeast  
 CG7351 (Saccharomyces cerevisiae) \* 3e-67 YPI7\_CAEEL HYPOTH [TNF\_1] CG7351 LD40777 68C10-68C10 dup:2/3 ID:99H1  
 + unknown \* 7e-41 SS72\_YEAST SSU72 PROTEIN hypothetical protein YNL222w - \* 7e-57 coded for by C. elegans cDNA  
 CG14216 yk10c10.3; coded for by C. elegans cDNA yk37e8.3; CG14216 LD40846 18D12-18D12 ID:99H10  
 + \* BLASTX 2.3E-13 TRA1|Homolog of human TR-AP which associates with a domain of c-Myc essential for cellular  
 CG2905 transformation(dna) \* predicted using Gen [PI3\_4\_KINASE\_3] CG2905 41A1-41A1 ID:99H3  
 + DNA\_repair\_protein \* DMDNAPOLD\_2 DNAPol- dgr; \* DNA polymerase zeta subunit; Rev3p(aa) \* 1e-152 DPOZ\_YEAST  
 DNA POLYMERASE ZETA CATALYTIC SUBUNIT DNA-dire \* 2e-69 DPOD\_D[DNAPOLB // DNA\_POLYMERASE\_B // DNA\_pol\_] CG1925  
 CG1925 LD40801 43E16-43E17 ID:99H4  
 CG1404 + enzyme CG1404 ID:99H5  
 + motor\_protein \* \* similar to S. pombe phosphoprotein \* BLASTX 2.1E-09 P.falciparum merozoite surface antigen (MSA-2)  
 CG8176 gene, complete cds.(dna) \* BLASTX 5.7E-22 Homo [ZINC\_PROTEASE] CG8176 LD40806 86C1-85D23 dup:3/3 ID:99H6  
 + sec23 unknown \* COPII protein, homolog of s. cerevisiae SEC23p(aa) \* SC23\_YEAST PROTEIN TRANSPORT PROTEIN  
 CG1250 SEC23 protein transpo \* S23A\_MOUSE PROTEIN TRANSPORT PRO CG1250 LD40826 83B6-83B6 dup:3/4 ID:99H8  
 CG12758 + unknown \* [NLS\_BP] CG12758 trimmed 55F8-55F13 dup:2/3 ID:Farhad's BA1  
 CG6044 + unknown \* CG6044 Igg2(4036) 58D7-58D7 dup:1/2 ID:Farhad's BA10  
 CG14709 + transporter CG14709 LD21507 ID:Farhad's BA11  
 CG10934 + CG10934 GH26058 dup:2/3 ID:Farhad's BA12  
 CG8633 + unknown CG8633 GJB.Hx4 dup:1/2 ID:Farhad's BA5  
 + BcDNA:LD24639 enzyme \* F17F8.28(aa) \* sperm associated antigen 2(aa) \* UDP-N-acetylglucosamine pyrophosphorylase;  
 Qri1p(aa) \* 3e-88 QRI1\_YEAST HYPOTHETICAL 53.5 KD PROTEIN [ATP\_GTP\_A] CG9535 LD24639 26D5-26D5 dup:2/3  
 CG9535 ID:Farhad's BB11  
 CG7873 + protein\_kinase CG7873 Src42 dup:2/3 ID:Farhad's BB12  
 CG4376 + Actn alpha-actinin (Flightless A) CG4376 GH06025 ID:Farhad's BB6  
 CG17682 + CG17682 LP04696 ID:Farhad's BB8  
 + transcription\_factor\_binding \* Fas-binding protein(aa) \* ETS1 associated protein EAP1/Daxx(aa) \* 2e-13 Fas-binding protein  
 CG9537 \* 9e-09 Fas-binding protein Daxx [NLS\_BP] CG9537 LD30183 26D6-26D7 dup:3/5 ID:Farhad's BB9  
 CG9432 + CG9432 G041 dup:1/4 ID:Farhad's BC7  
 CG2016 + unknown \* 0.0000000007\* 4e-10 0.9-kb RNA transcript \* CG2016 ck01170 82E7-82E7 dup:2/3 ID:Farhad's BD11  
 CG4267 + enzyme \* 2e-25 pancreatic lipase related protein \* 1e-26 pancreatic lipase-related protein \* 1e-31 phospholipase, GPL -

guinea pig \* LIP1\_HUMAN PANCREAT[DOLALLERGEN // TAGLIPASE // ESTERASE //] CG4267 ck01198 22D3-22D3 dup:2/2 ID:Farhad's BD12

+ BcDNA:GH02976 structural\_protein \* 5e-28 Gasp precursor \* 9e-11 cDNA EST comes from this gene; cDNA EST yk369a9.5 come \* 4e-08 peritrophin \* 6e-30 Gasp CG4778 ck00178 30F6-30F6 dup:3/3 ID:Farhad's BD2

CG4778 + transporter CG5772 ck00325 ID:Farhad's BD8

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

CG1124 + unknown \* [PRO\_RICH // NLS\_BP] CG13800 ck01201 62E-62E dup:2/2 ID:Farhad's BE1

CG13800 + W unknown \* W \* HEAD INVOLUTION DEFECTIVE PROTEIN (WRINKLED PROTEIN)(aa) \* 1e-148 W \* 6E-99 CG5123

CG5123 ck02091 75C-75C2 dup:2/4 ID:Farhad's BE10

+ nucleic\_acid\_binding \* protein(aa) \* 2e-23 F28F5.2 gene product \* zinc-finger domain-containing protein \* LIM domain only

CG1055 LIM domain only s [LIM\_DOMAIN\_1 // LIM // LIM\_DOMAIN\_2 // ] CG1055 ck02463 82D5-82D6 ID:Farhad's BE12

CG15288 + CG15288 ck01592 ID:Farhad's BE4

+ 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

CG7540 MEMBRANE GLYCOPROTEIN M6-A membrane glycoprote \* 3 [Myelin\_PLP] CG7540 ck01837 78D7-78D8 ID:Farhad's BE8

CG9503 + enzyme CG9503 ck02694 ID:Farhad's BF1

CG10130 + CG10130 sec61b ID:Farhad's BF2

CG4859 + unknown CG4859 dMMP dup:2/2 ID:Path + CtrlL1 + kras160

CG3619 + cell\_adhesion CG3619 Delta dup:2/4 ID:Path + CtrlL1 + kras195

CG5848 + cytoskeletal\_structural\_protein CG5848 cactus dup:3/4 ID:Path + CtrlL1 + kras198

CG6794 + transcription\_factor CG6794 dif dup:3/3 ID:Path + CtrlL1 + kras210

CG12763 + CG12763 Diptericin dup:2/3 ID:Path + CtrlL1 + kras244

+ N transmembrane\_receptor \* cell adhesion cell adhesion ) plasma membrane plasma membrane ) map\_position:3C7 \* NEUROGENIC LOCUS NOTCH PROTEIN PRECURSOR[ANK\_REP // EGFBLOOD // EGF\_1 // EGF //] CG3936 Notch 3C7-3C9

CG3936 dup:2/4 ID:Path + CtrlL1 + kras248

+ protein\_kinase \* DMFGFR1\_2 htl \* connectin/titin(aa) \* flt-1(aa) \* FTL4(aa) [ig // PROTEIN\_KINASE\_TYR // PROTEIN\_KIN]

CG8222 CG8222 VEGFR 78F1 28F4-28F5 dup:9/12 ID:Path + CtrlL1 + kras305

CG7939 + CG7939 RP49 dup:3/3 ID:Path + CtrlL1 + kras60

CG10810 + CG10816 drosocin dup:1/3 ID:Path + CtrlL1 + kras62