

Table S27

male germline-List of genes identified as follows:

one-tailed t-test male vs tudor male ( $P < .01$  and male data > male tudor data)

genes in both male and female germline are excluded from this list

CG12756+ unknown \* gene product(aa) \* 8e-09 hypothetical protein \* \* CG12756 LD42148 64E3-64E3 ID:101C5  
 CG15634+ unknown \* CG15634 LD42284 25A4-25A4 ID:101D10  
 + enzyme \* unknown(aa) \* PROBABLE GMP SYNTHASE (GLUTAMINE-HYDROLYSING) (GLUTAMINE AMIDOTRANSFERASE)  
 (GMP SYNTHETASE)(aa) \* guanine-monophosphate synthetase; GM [CPSGATASE // GMP\_synt\_C // ANTSNTHASEII] CG9242  
 CG9242 LD42771 39B4-39B4 dup:2/2 ID:101G2  
 CG11770+ unknown \* CG11770 LD43682 44F9-44F9 dup:2/2 ID:102E12  
 CG17260+ nucleic\_acid\_binding \* [ZF\_RING] CG17260 LD44813 23C5-23C5 ID:103F8  
 + endopeptidase \* energy-dependent regulator of proteolysis(aa) \* 9e-61 YB77\_YEAST HYPOTHETICAL 57.9 KD PROTEIN IN  
 CG4538 PDB1-ABD1 INTERGENIC REGION \* 1e-104 Similarity to [AAA // ATP\_GTP\_A] CG4538 LD45279 92B9-92B9 dup:3/3 ID:104B5  
 + enzyme \* similar to tumor suppressor p33ING1; similar to \* Unknown protein(aa) \* 5e-17 YNJ7\_YEAST HYPOTHETICAL 37.0 KD  
 CG9293 PROTEIN IN RAS2-YPT53 INTERGENIC REGI [PHD // NLS\_BP] CG9293 LD46333 34B6-34B6 ID:105C2  
 + qkr58E-3RNA\_binding \* QKR58E-3(aa) \* qkr58E-3 \* 7e-13 hypothetical protein YLR116w - yeast (Saccharomyces cerevisiae) ( \* 5e-21  
 CG3584 similar to GAP-associated tyrosine phosph [KH-domain // KH\_DOMAIN] CG3584 LD46502 58D7-58D8 ID:105D8  
 + motor\_protein \* DMBNBR\_2 bnb \* mu2 \* 1e-07 RRP1\_DROME RECOMBINATION REPAIR PROTEIN (DNA-(APURINIC OR  
 CG14896 APYRIMIDINIC SITE) L \* 2e-21 C. elegans UNC-89 CG14896 LD46725 89C4-89C4 dup:1/3 ID:105F5  
 + 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  
 + peptidase \* VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR(aa) \* Probable serine-type carboxypeptidase (EC 3.4.16.1);  
 Ybr139wp(aa) \* Similarity to Human lysosomal pro [CARBOXYPEPT\_SER\_SER // CARBOXYPEPT\_SER\_] CG4572 LD47549 92B6-  
 CG4572 92B6 ID:106F2  
 CG12104+ unknown \* 4e-11 protein \* protein \* CAGF9 \* [HMG // HMG\_box] CG12104 LP01188 62A-62A ID:107D7  
 + Cdlc2 motor\_protein \* 8kd dynein light chain(aa) \* Cdlc1 \* dynein light chain 5(aa) \* 1e-21 DYLL1\_YEAST DYNEIN LIGHT CHAIN 1,  
 CG5450 CYTOPLASMIC dynein lig [Dynein\_light // DYNEIN\_LIGHT\_1] CG5450 LP02196 22A-22A ID:108A1  
 + receptor \* putative mitochondrial inner membrane protein import receptor(aa) \* MITOCHONDRIAL IMPORT INNER MEMBRANE  
 CG11779 TRANSLOCASE SUBUNIT TIM44 PRECURSOR(aa) \* P CG11779 91F4-91F4 dup:1/2 ID:108A11  
 CG7484 + CG7484 ID:108A12  
 + 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  
 CG18317+ unknown \* CG18317 LP02521 22B1-22F3 ID:108B1  
 CG2147 + unknown \* [ATP\_GTP\_A] CG2147 LP02728 7D18-7D18 ID:108B10  
 + P5cr enzyme \* 6e-29 PROC\_YEAST PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) \* 1e-157 pyrroline  
 CG6009 5-carboxylate reductase \* 3e-52 similar to pyrroline-5- [P5CR] CG6009 LP02537 91E4-91E4 ID:108B2

+ sktl enzyme \* phosphatidylinositol 4-phosphate 5-kinase(aa) \* skittles \* 7e-28 'multicopy suppressor of stt4 mutation (MSS4)' cerev \*  
 CG9985 phosphatidylinositol 4-phosp [NLS\_BP] CG9985 LP03320 57B6-57B6 dup:2/2 ID:108E11  
 + enzyme \* contains similarity to enoyl-CoA hydratases/isomerases Score=59.1, E=3.3e-16, N=1)(aa) \* 3e-51 Similar to enoyl-coA  
 CG5844 hydratase \* 2e-15 ECH1\_MOUSE PRO [ECH] CG5844 LP03547 87B15-87B15 ID:108F9  
 + chaperone \* DMTIDT4M\_4 l(2)tid \* 1e-22 MDJ1\_YEAST MDJ1 PROTEIN PRECURSOR heat shock protein MDJ1 \* 2e-42 Tid56  
 protein \* 2e-42 YLW5\_CAEEL HYPOTHETICAL 105.9 K[DnaJ\_CXXCXGXG // DNAJ\_1 // DnaJ // DNAJ] CG7387 LP05202 66B13-66B13  
 CG7387 dup:1/2 ID:109C10  
 + 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-  
 CG10764 54C3 ID:109D4  
 + transcription\_factor \* DMBTDGN\_2 btd \* 3e-18 ODD\_DROME ODD-SKIPPED PROTEIN odd \* 5e-19 Similarity to Drosophila  
 scratch neuronal zinc-finger transcriptio \* 2e-35 Z13 prote [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG6911 LP05442 4D1-4D1  
 CG6911 ID:109D5  
 + RNA\_binding \* ventral antigen 1(aa) \* astrocytic NOVA-like RNA-binding protein(aa) \* 0.00000003\* 2e-13 similar to RNA binding  
 CG8144 protein; cDNA EST comes from th [KH-domain // KH\_DOMAIN // ANTIFREEZEI] CG8144 LP05458 85D-85D ID:109D7  
 + ppl enzyme \* predicted using Genefinder(aa) \* 5e-19 GCSH\_YEAST GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR F  
 CG7758 \* 3e-28 predicted using Genefinder \* 7e-32 glycine c [LIPOYL] CG7758 LP05579 78C8-78C8 dup:2/2 ID:109E4  
 + 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[CYTCHRMEDIAB // cytochrome\_c // CYTOCHR] CG13263 LP05614 36A7-  
 CG13263 36A7 dup:2/2 ID:109E5  
 + actin\_binding \* 5e-06 alternatively spliced form \* 9e-06 alpha-actinin \* protein \* 9e-06 alpha-actinin - rabbit (fragment) muscle alp  
 CG11685[CH\_DOMAIN] CG11685 LP05986 85F7-85F7 ID:109F10  
 CG6968 + unknown \* [NLS\_BP] CG6968 LP06178 78D-78D dup:1/3 ID:109G3  
 + PpN58A protein\_phosphatase \* serine-threonine protein phosphatase(aa) \* PpN58A \* 1e-108 PP12\_YEAST SERINE/THREONINE  
 PROTEIN PHOSPHATASE PP1-2 pho \* 1e-174 serine-threonine prot[PHOSPHO\_ESTER // STPHPHTASE // SER\_THR\_] CG3245  
 CG3245 SD01703 58B1-58B1 ID:113A9  
 + transcription\_factor \* DMADF1A\_2 Adf1 \* 6e-05 ADF1\_DROME TRANSCRIPTION FACTOR ADF-1 (ADH DISTAL FACTOR 1) \*  
 CG9437 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  
 CG13714+ unknown CG13714 SD02453 ID:114B7  
 + transcription\_factor\_binding \* conserved hypothetical protein.(aa) \* predicted using Genefinder; Similarity to Human erythrocyte  
 CG2970 band integral membrane protein (SW:BAN7\_HUMAN)(aa [Band\_7 // STOMATIN] CG2970 SD03319 60A12-60A13 dup:2/2 ID:115E8  
 + Es2 enzyme \* HYPOTHETICAL 58.3 KD PROTEIN F42H10.7 IN CHROMOSOME III(aa) \* ES2 protein(aa) \* ES2 protein(aa) \* Es2  
 CG1474 CG1474 SD03464 7E7-7E7 ID:115G8  
 CG10192+ translation\_factor CG10192 SD03848 ID:116C4  
 CG11807+ CG11807 SD03973 dup:1/2 ID:116E2.2  
 CG1472 + unknown CG1472 SD04292 dup:2/2 ID:117A12.2

CG5417 + CG5417 SD04331 dup:2/2 ID:117B6.2  
 + enzyme \* 7e-08 RECQ helicase homolog \* 2e-25 TNR3\_SCHPO THIAMIN PYROPHOSPHOKINASE (TPK) (THIAMIN KINASE) \*  
 CG14721 putative thiamin pyrophosphokinase \* YloS protein CG14721 SD04406 86F6-86F6 dup:2/3 ID:117C3  
 CG9531 + CG9531 SD04586 dup:3/3 ID:117E5  
 CG14800+ no blast hits pioneer protein? CG14800 SD04906 dup:1/2 ID:118A8  
 CG2385 + CG2385 SD05054 dup:1/2 ID:118C5  
 CG13223+ transporter CG13223 SD05296 dup:2/2 ID:118F1.2  
 CG10254+ enzyme CG10254 SD05555 dup:4/4 ID:119A2.2  
 + 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-  
 CG1512 39E5 dup:3/3 ID:119B10  
 + signal\_transduction \* AND-1 protein(aa) \* bgr;Cop \* 6e-29 Met30p \* 3e-28 Slimb [GPROTEINBRPT // GPROTEINB //  
 CG17437WD40\_REGIO] CG17437 3A8-3A8 dup:3/3 ID:119D12.2  
 CG7958 + unknown CG7958 SD05917 dup:2/2 ID:119E12  
 CG11526+ pioneer protein with human homolog (KIAA1170) CG11526 SD05886 dup:2/2 ID:119E8  
 CG18019+ CG18019 SD06401 dup:2/2 ID:119G12.2  
 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 52C4-52C5  
 CG12305 dup:7/8 ID:119H8  
 CG2103 + enzyme CG2103 SD10722 dup:1/2 ID:125F3.2  
 CG8979 + enzyme\_inhibitor \* 7e-15 proteasome inhibitor hPI31 subunit \* \* CG8979 GH01278 48D7-48D7 ID:30B10  
 + motor\_protein \* limited similarity with some myosins; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA  
 CG5886 EST yk392c1.3 comes from this gene; cDNA ES [NLS\_BP] CG5886 GH01188 96F5-96F5 ID:30B6  
 CG10589+ unknown \* [NLS\_BP] CG10589 GH01788 78A-78A ID:30F11  
 + unknown \* dipeptidyl peptidase III(aa) \* 1e-109 hypothetical protein YOL057w - yeast (Saccharomyces cerevisiae) \* 1e-105 similar  
 CG7415 to WD domain, G-beta repeat; CG7415 GH01916 84F14-84F15 dup:1/2 ID:30G7  
 CG12860+ unknown \* [NLS\_BP] CG12860 GH02210 51B11-51B11 ID:31A8  
 + enzyme \* hypothetical protein(aa) \* TUBULIN--TYROSINE LIGASE (TTL)(aa) \* Ybr094wp(aa) \* 2e-10 ORF2 [NLS\_BP] CG11201  
 CG11201 GH02545 27A1-27A1 ID:31C9  
 + unknown \* actin-fragmin kinase(aa) \* putative protein kinase(aa) \* HYPOTHETICAL 143.1 KD PROTEIN F33C8.1 IN  
 CG6758 CHROMOSOME X PRECURSOR(aa) \* 4e-10 YG52\_YEAST HYP [FBOX\_DOMAIN] CG6758 GH02866 58C5-58C5 dup:2/2 ID:31E7  
 + translation\_factor \* Eif4E \* 1e-23 IF4E\_YEAST EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA  
 CG8023 CA \* 2e-56 IF4E\_DROME EUKARYOTIC TRANSLATION INITIATION [IF4E] CG8023 GH04024 66C-66C ID:32D6  
 + metabolism \* 1e-47 PNPH\_YEAST PROBABLE PURINE NUCLEOSIDE PHOSPHORYLASE (INOSINE PHOSPHORYLASE) (PN  
 CG16758 \* 3e-51 similar to purine nucleoside phosphorylases \* 4e-73 pu [Mtap\_PNP] CG16758 GH04159 62E6-62E6 dup:5/5 ID:32E5

+ apoptosis\_inhibitor \* 2e-81 SINA\_DROME DEVELOPMENTAL PROTEIN SEVEN IN ABSENTIA devel \* 8e-67 seven-in-absentia  
 CG13030 protein homologue-1 \* 2e-73 siah-1A protein - mouse siah-1A [ZF\_RING] CG13030 GH04279 73D1-73D1 ID:32F2  
 + unknown \* 1e-26 VP28\_YEAST VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS28 \* 3e-40 putative protein \* 3e-  
 CG12770 76 inserted at base Both 5' and 3' ends of P elemen CG12770 GH04443 44A4-44A4 ID:32G10  
 CG6405 + unknown \* CG6405 GH04442 33D5-33D5 ID:32G9  
 + transporter \* 4e-41 similar to matrin F/G containing C4-type zinc-fingers \* 4e-79 PGT\_HUMAN PROSTAGLANDIN  
 CG3811 TRANSPORTER (PGT) prostaglandin tr \* 2e-76 PGT\_RAT PROST CG3811 GH04717 30B10-30B10 ID:33A7  
 + transcription\_factor \* HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III(aa) \* 7e-22 YN66\_YEAST  
 HYPOTHETICAL 39.2 KD PROTEIN IN EGT2-KRE1 INTERGENIC REGION \* 7e-13 pr [ZF\_DHHC] CG1407 GH04905 46D4-46D6  
 CG1407 dup:2/4 ID:33C1  
 + 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 61C8-61C8  
 CG12189 dup:2/2 ID:33E10  
 + unknown \* 9E-24\* 4e-21 0.9-kb RNA transcript \* 6e-21 DMRNAPER\_2 anon-3B1.2 \* per circadian controlled protein precursor -  
 CG11853 fruit fly (Drosophila mela CG11853 GH05615 96C4-96C4 ID:33G6  
 + motor\_protein \* 7e-15 cytoplasmic dynein intermediate chain isoform DIC2b \* 7e-15 similar to the beta transducin family \* 3e-14  
 CG9313 cytoplasmic dynein intermediate chai [NLS\_BP // WD40] CG9313 GH05829 57B14-57B14 ID:33H12  
 + transcription\_factor \* CCR4-ASSOCIATED FACTOR (CAF1)(aa) \* 5e-52 POP2 protein \* 1e-64 CAF1\_CAEEL CCR4-  
 CG5684 ASSOCIATED FACTOR (CAF1) cCAF1 protein \* 1e-100 POP2 (yeast homolog) CG5684 GH06247 68E4-68F ID:34D3  
 CG5538 + unknown \* [NLS\_BP] CG5538 87C-87C dup:1/3 ID:34G11  
 + 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  
 CG5555 ID:35A7  
 CG8701 + unknown \* CG8701 GH07855 44B9-44B9 ID:35G4  
 + motor\_protein \* very strong similarity to C. elegans myosin heavy chain B \* 6e-09 MYS1\_YEAST MYOSIN-1 ISOFORM (TYPE II  
 CG6059 MYOSIN) myosin heavy \* 1e-12 nonmuscle myosin [PEROXIDASE\_3] CG6059 GH07888 97E8-97E8 dup:1/2 ID:35G7  
 + CH4 \* COP9 complex subunit 4(aa) \* COP9 complex homolog subunit DCH4(aa) \* 5e-12 hypothetical protein YDL147w - yeast  
 CG8725 (Saccharomyces cerevisiae) \* 7e-13 [PCI\_DOMAIN // PCI] CG8725 43F8-43F8 dup:1/2 ID:37A9  
 + motor\_protein \* signaling molecule(aa) \* contains similarity to Mus musculus tumor susceptibility protein TSG101 \* tumor  
 CG9712 susceptibility protein TSG101(aa) \* 4e-11 [TPR\_REPEAT] CG9712 GH09529 73C4-73C4 ID:37B1  
 + norpA enzyme \* contains similarity to phophatidylinositol-specific phosphlipase C, X domains (Pfam: PI-PLC-X.hmm, score:  
 CG3620 200.23)(aa) \* phospholipase C beta-4(aa) \* CG3620 GH10316 4B6-4B6 dup:2/2 ID:37G8  
 CG3074 + endopeptidase similar to cysteine protease Peptidase\_C1, THIOL\_PROTEASE\_HIS CG3074 GH10620 dup:1/3 ID:38B6  
 CG9133 + unknown \* CG9133 GH10732 61F4-61F4 dup:1/3 ID:38C6  
 CG7148 + unknown \* CG7148 GH10766 79A4-79A5 dup:1/2 ID:38C9  
 CG4000 + unknown \* [PRO\_RICH] CG4000 GH10972 92F2-92F2 dup:3/3 ID:38E6

CG6456 + unknown \* 9e-07 prepro-APGWamide \* APGWamide \* [NLS\_BP] CG6456 GH11008 74B-74B dup:2/2 ID:38E7  
 CG17567 + unknown \* 1E-78\* \* CG17567 GH11551 37C-37C ID:39A10  
 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  
 CG3825 + unknown \* CG3825 GH11727 60A14-60A14 dup:1/3 ID:39C1  
 + unknown \* HSPC017(aa) \* 5e-35 YOY9\_CAEEL PUTATIVE UBIQUINONE BIOSYNTHESIS METHYLTRANSFERASE ZK652.9 \*  
 CG12162 4e-17 apaG protein \* APAG\_ECOLI APAG PROTEIN apaG prote CG12162 GH11824 83A8-83A9 ID:39C7  
 CG9284 + unknown \* CG9284 GH11908 58A2-58A2 ID:39D1  
 CG10841 + unknown \* CG10841 GH12158 87F6-87F6 dup:2/2 ID:39E9  
 + peptidase \* PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III(aa) \* Chain A, Bovine Lens Leucine Aminopeptidase  
 CG4750 Complexed With L-Leucine Phosphonic Acid(aa) \* [Peptidase\_M17] CG4750 GH12543 53C-53C ID:39G10  
 CG6087 + unknown \* [NLS\_BP] CG6087 GH12689 34A3-34A3 ID:40A9  
 + transporter \* similar to ADP/ATP translocase(aa) \* 2e-17 probable membrane protein YPL134c - yeast (Saccharomyces  
 CG4995 cerevisiae) \* 1e-32 colt \* 1e-58 similar to mito [mito\_carr // MITOCARRIER // MITOCH\_CARR] CG4995 GH13054 31D8-31D8 ID:40C11  
 CG6306 + unknown \* CG6306 GH12946 17B1-17B1 ID:40C7  
 + peptidase \* Chain A, Bovine Lens Leucine Aminopeptidase Complexed With L-Leucine Phosphonic Acid(aa) \* 6e-20  
 YOJ6\_CAEEL PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROM [LAMNOPPTDASE // Peptidase\_M17] CG6372 GH13022 68C1-  
 CG6372 68C1 dup:2/2 ID:40C9  
 + RNA\_binding \* 3e-16 RNA-binding protein cabeza - fruit fly (Drosophila melanogaster) ( \* 4e-14 EWS\_MOUSE RNA-BINDING  
 CG14718 PROTEIN EWS RNA-binding protein E \* 2e-15 TLS [RBD // zf-RanBP // rrm // ZF\_RANBP] CG14718 GH13594 86F1-86F1 ID:40G5  
 CG2046 + unknown \* CG2046 GH13924 83C-83C ID:41A10  
 + protein\_kinase \* serine/threonine protein kinase; Cdc7p(aa) \* protein kinase Cdc7(aa) \* DMSTPK Pk61C \* HsCdc7(aa)  
 CG5790 [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG5790 GH13884 36F-36F ID:41A7  
 + 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  
 CG9010 ID:41A8  
 CG7251 + unknown \* [NLS\_BP] CG7251 GH13914 27D1-27D1 ID:41A9  
 + Rca1 unknown \* Rca1 \* Rca1 \* Rca1 \* 6e-25 inserted at base 5' end of P element Inverse PCR [NLS\_BP] CG10800 GH14043 27C-  
 CG10800 27C ID:41B8  
 CG7131 + unknown \* CG7131 GH14048 90F7-90F7 ID:41B9  
 + Mvl unknown \* MALVOLIO PROTEIN(aa) \* Mvl \* 7e-42 SMF1\_YEAST TRANSPORTER PROTEIN SMF1/ESP1 vacuolar trans \* 1e-  
 CG3671 140 similar to M. musculus transport system membrane [NATRESASSCMP // ATP\_GTP\_A] CG3671 GH14215 93B5-93B7 ID:41C8  
 + unknown \* Ylr193cp(aa) \* bromodeoxyuridine-sensitive transcript protein - chicken(aa) \* hypothetical protein(aa) \* CGI-107  
 CG9131 protein(aa) CG9131 GH14384 26B2-26B3 ID:41D12  
 CG7567 + unknown \* CG7567 GH14364 99B5-99B5 ID:41D8

+ 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 // thioed] CG3315 GH14562 4F2-4F2 ID:41F1  
 + 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  
 + BG:DS00797.2 unknown \* 6e-38 YMY9\_YEAST HYPOTHETICAL 34.0 KD PROTEIN IN CTF13-YPK2 INTERGENIC REGION \* 3e-35  
 CG9008 putative protein \* AAPC\_PENCL POSSIBLE APOSPORY-ASSOCIATED PR CG9008 GH14910 34D1-34D1 ID:41H8  
 CG8136 + unknown \* CG8136 GH14973 85B2-85B2 dup:1/2 ID:42A2  
 + unknown \* Sui1 homolog(aa) \* 3e-30 SUI1\_YEAST PROTEIN TRANSLATION FACTOR SUI1 translation in \* 2e-10 coded for by  
 CG17737 C. elegans cDNA cm16g2; weakly similar to pr [SUI1 // SUI1\_2] CG17737 GH15018 64A3-64A3 ID:42A3  
 + 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  
 CG7220 ID:42A5  
 CG8601 + unknown \* [ATP\_GTP\_A] CG8601 GH15104 65F2-65F2 ID:42A9  
 CG2149 + unknown \* [NLS\_BP] CG2149 GH15120 44B9-44B9 dup:1/2 ID:42B2  
 CG2127 + unknown \* [EF\_HAND // NLS\_BP] CG2127 GH15271 44B9-44B9 ID:42C3  
 + unknown \* myelodysplasia/myeloid leukemia factor 1(aa) \* Y17G7B.17(aa) \* 6e-27 myeloid leukemia factor myelodysplasia/myel  
 CG8295 \* t(3;5)(q25.1;p34) fusion gene CG8295 LD22883 52D11-52D11 dup:2/2 ID:43D3  
 CG2862 + enzyme\_inhibitor protein kinase C inhibitor HISTRIAD, HIT CG2862 LD22892 dup:2/2 ID:43D6  
 + cell\_cycle\_regulator \* lipoic acid synthase; Lip5p(aa) \* LIPOIC ACID SYNTHETASE PRECURSOR(LIP-SYN)(aa) \* similar to lipoic  
 CG5231 acid synthase; cDNA EST yk283b6.3 comes from th CG5231 LD24887 77C1-77C1 ID:43G10  
 + unknown \* 4e-21 YS48\_CAEEL HYPOTHETICAL 66.5 KD PROTEIN ZK177.8 IN CHROMOSOME II (U \* 2e-20 MG11\_MOUSE  
 CG9670 INTERFERON-GAMMA INDUCIBLE PROTEIN MG11 unkn \* 4e-20 hy CG9670 LD25913 76A5-76A6 dup:3/3 ID:44B11  
 + Klp67A motor\_protein kinesin family protein 3B ATP\_GTP\_A, KINESINHEAVY, KINESIN\_MOTOR\_D] CG10923 LD27326 dup:2/2  
 CG10923 ID:44H12  
 + BcDNA:LD22910 endopeptidase \* reserved(aa) \* 1e-12 UBP9\_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (UBIQUITIN THIOLESTERASE 9) (\* 1e-08 UBPX\_CAEEL PROBABLE UBIQUITIN CARBOXYL[UCH\_2\_2 // UCH\_2\_3 // PRO\_RICH // UCH-2]  
 CG15817 CG15817 99A5-99A5 dup:2/2 ID:45A6  
 + 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  
 CG8073 + enzyme CG8073 ID:46D3  
 + RhoGEF3 signal\_transduction RHO guanyl-nucleotide exchange factor ATP\_GTP\_A, GRF\_DBL, RhoGEF, SH3 CG1225 LD29915  
 CG1225 dup:1/2 ID:46F8  
 CG12306 + protein\_kinase CG12306 ID:47A2  
 CG18683 + unknown \* CG18683 LD30576 99C6-99C6 ID:47B8  
 CG4968 + unknown \* predicted using Genefinder; cDNA EST comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA

EST yk278a11.5 comes from this gene; cDNA CG4968 LD30683 31D6-31D6 ID:47C3

+ cytoskeletal\_structural\_protein \* actin-like protein; (2 actin domains)(aa) \* 2e-71 ARP5\_YEAST ACTIN-LIKE PROTEIN ARP5  
CG7940 probable nuclear pro \* 3e-18 ACTU\_DROME ACTIN-LIKE PROTEIN 13E [NLS\_BP // actin] CG7940 90E5-90E6 dup:1/2 ID:47D6

CG9288 + unknown \* [PYRUVATE\_KINASE] CG9288 LD32260 87F13-87F13 ID:48B5

+ 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

+ ligand\_binding\_or\_carrier \* 2e-05 odorant-binding protein Rpal2' palmaru \*\* [PBP\_GOBP] CG13421 GH01026 57A6-57A6  
CG13421 ID:54A2

+ unknown \* 3e-80 YKL6\_CAEEL HYPOTHETICAL 103.8 KD PROTEIN C03C10.6 IN CHROMOSOME III \* E03A3.6 \* E03A3.7 \*  
CG5237 [AA\_TRNA\_LIGASE\_II\_2 // PRO\_RICH // CYTO] CG5237 GH01039 91F10-91F11 ID:54A4

CG14981 + unknown \* CG14981 GH01116 63F6-63F6 dup:2/2 ID:54B1

+ 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

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

+ unknown \* PROTEIN 22A3(aa) \* 8e-46 YL22\_YEAST HYPOTHETICAL 28.3 KD PROTEIN IN PPR1-SNF7 INTERGENIC  
CG8549 REGION \* 4e-56 YOM4\_CAEEL HYPOTHETICAL 29.1 KD PROTEIN W06E [UPF0023] CG8549 GH01786 66D10-66D10 ID:54G12

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

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

+ unknown \* 4e-11 YMH6\_CAEEL HYPOTHETICAL 19.1 KD PROTEIN F58A4.6 IN CHROMOSOME III \*\* CG12123 GH02722  
CG12123 7E6-7E6 ID:55D12

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 Mcd4p  
CG6790 homolog \* 1e-18 hypothetical protein \* unknown protein CG6790 GH02677 86E15-86E15 ID:55D6

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

+ 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

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

+ transcription\_factor \* LTG19 - human(aa) \* BLASTX 1.2E-10 Caenorhabditis elegans cosmid ZK354.(dna) \* 1e-11 YNK7\_YEAST  
CG4913 HYPOTHETICAL 26.0 KD PROTEIN IN CYB5-LEU4 INTERGENIC [NLS\_BP] CG4913 GH03493 90E1-90E1 dup:1/2 ID:55H10

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

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

CG9803 + unknown \* [PRO\_RICH] CG9803 GH03629 59D6-59D6 ID:56B1  
 CG3124 + unknown \* CG3124 GH03736 59D4-59D4 ID:56B12  
 CG9861 + DNA\_binding \* [NLS\_BP] CG9861 GH03827 59D6-59D6 ID:56C11  
 + bol RNA\_binding \* bol \* 3e-06 NAB4\_YEAST NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4 \* 3e-85 boule protein  
 CG4760 - fruit fly (Drosophila melanogaster) boul \* 3e-15 YSO5 [RBD // rrm] CG4760 GH03796 66F5-66F5 dup:1/2 ID:56C6  
 + BcDNA:GH07626 enzyme \* p270(aa) \* Similar to polyketide synthase.(aa) \* FK506 polyketide synthase(aa) \* [adh\_zinc //  
 CG3523 Thioesterase // ACP\_DOMAIN ] CG3523 GH03816 23D-23D dup:4/9 ID:56C9  
 CG15608+ unknown \* 2e-06 CGI-62 protein \* \* [NLS\_BP] CG15608 GH03957 53F6-53F7 dup:1/3 ID:56D12  
 CG6541 + Mst33A unknown \* [NLS\_BP] CG6541 GH04277 33A3-33A3 ID:56G4  
 + 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  
 CG12028 ID:57C3  
 + 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  
 + 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  
 CG5071 GH04969 96E6-96E6 dup:2/2 ID:57E3  
 CG15867+ unknown CG15867 GH05072 ID:57F2  
 none + none GH05253 ID:57G7  
 + transcription\_factor\_binding \* oxidoreductase(aa) \* 3e-20 YULF\_BACSU HYPOTHETICAL 36.5 KD PROTEIN IN GBSA-TLPB  
 INTERGENIC REGION \* YMO1\_RHIME HYPOTHETICAL 36.4 KD PROTEIN IN MOC [GFO\_IDH\_MocA] CG13280 GH05468 36A9-  
 CG13280 36A10 dup:2/2 ID:57H11  
 CG5073 + CG5073 ID:57H3  
 CG9136 + CG9136 GH05420 ID:57H7  
 + RNA\_binding \* No definition line found(aa) \* qrk58E-3 \* KEP1(aa) \* 8e-05 hypothetical protein YLR116w - yeast (Saccharomyces  
 CG9337 cerevisiae) ( [KH\_DOMAIN] CG9337 GH05725 38F1-38F1 ID:58B8  
 + sm RNA\_binding \* DMSMOOTH\_2 sm \* 4e-20 homologous to human hnRNP L \* 5e-22 DMSMOOTH\_2 sm \* [RBD] CG9218  
 CG9218 GH05823 56D11-56E1 dup:1/2 ID:58C12  
 + 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 CG2830 GH05807 21D1-21D1 ID:58C8  
 + unknown \* K10D2.3 gene product(aa) \* 3e-14 hypothetical protein YOL102c - yeast (Saccharomyces cerevisiae) \* 4e-07  
 CG7163 /match=(desc: \* 4e-12 The gene is expresse [PAP // ZINC\_FINGER\_C2H2] CG7163 GH05885 66C11-66C11 dup:1/3 ID:58D3  
 + enzyme \* by content; by match; 2-match\_description=4-NITROPHENYLPHOSPHATASE.; 2-match...(aa) \* similar to N-acetyl-  
 CG2077 glucosamine catabolism(aa) \* Similar to CG2077 GH05933 63B3-63B3 ID:58D8



+ cell\_adhesion \* sdk \* DMNRGAA\_3 Nrg \* fra \* 8e-23 LAR\_DROME PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR  
 CG8619 (PROTEIN-TYROSINE-PHOSPHAT [ig // FNTYPEIII // fn3] CG8619 GH06134 65E7-65E7 dup:2/2 ID:58F1  
 + unknown \* predicted using Genefinder; cDNA EST yk268h6.5 comes from this gene; cDNA EST yk465f2.5 comes from this gene;  
 CG10512 cDNA EST yk393g7.5 comes from this gen CG10512 GH06154 78C3-78C4 ID:58F3  
 + transcription\_factor \* 6e-06 TF3A\_YEAST TRANSCRIPTION FACTOR IIIA (TFIIIA) transcriptio \* 2e-11 zinc finger motif protein \*  
 CG10631 5e-09 similar to Zinc finger, C2H2 typ[zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN] CG10631 GH06278 38A2-38A dup:1/3 ID:58G1  
 + transporter \* organic anion transporter-K2(aa) \* solute carrier family (prostaglandin transporter), member 2(aa) \* SODIUM-  
 CG3380 INDEPENDENT ORGANIC ANION TRANSPORTER (O CG3380 GH06385 58D1-58D1 dup:1/2 ID:58G11  
 + EG:BACN32G11.3 unknown \* BACN32G11.f \* 1e-29 L130\_HUMAN KD LEUCINE-RICH PROTEIN (LRP 130) (GP130) le \* leucine-rich  
 CG14786 protein - human leucine-rich protein sa \* BACN32G11.l CG14786 GH06301 2B1-2B1 ID:58G4  
 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  
 CG7557 + unknown \* [ATP\_GTP\_A] CG7557 GH07076 68C3-68C3 ID:59C11  
 + transporter \* 9e-43 hypothetical protein YLR348c - yeast (Saccharomyces cerevisiae) (U \* 1e-74 Oxoglutarate/malate carrier  
 CG4323 protein - Caenorhabditis elegans \* 8e-2 [mito\_carr // MITOCARRIER // MITOCH\_CARR] CG4323 GH07093 92E7-92E7 ID:59D2  
 + RNA\_binding \* spn-E \* 1e-111 hypothetical protein YLR419w - yeast (Saccharomyces cerevisiae) (U \* 1e-120 MLE\_DROME  
 DOSAGE COMPENSATION REGULATOR (MALE-LESS PROTEI [ZF\_CCCH // HELICASE // zf-CCCH // ATP\_G] CG1582 GH07148  
 CG1582 9F11-9F12 ID:59D5  
 + \* TRIACYLGLYCEROL LIPASE (LIPASE, PANCREATIC)(aa) \* 2e-16 VIT1\_DROME VITELLOGENIN I PRECURSOR (YOLK  
 CG10116 PROTEIN 1) vitell \* 2e-19 LIPL\_MOUSE LIPOPROTEIN L [lipase] CG10116 73D5-73D5 dup:2/2 ID:59D6  
 + enzyme \* DMADHA1\_9 Adh \* DMSCU scu \* 7e-17 SP19\_YEAST SPORULATION PROTEIN SPS19 (SPORULATION-SPECIFIC  
 PROTEIN SPX19) \* 4e-05 3-hydroxyacyl-CoA dehydrogenase [CPSASE\_2 // adh\_short\_C2 // GDHRDH // a] CG2907 GH07691 83B6-  
 CG2907 83B6 ID:59H8  
 CG3092 + unknown \* CG3092 GH07743 59D-59D dup:1/2 ID:60A5  
 CG16887 + BG:DS00941.11 unknown \* AAs(aa) \* AAs(aa) \* CG16887 GH07914 34D4-34D4 dup:2/3 ID:60B12  
 CG6332 + unknown \* [NLS\_BP] CG6332 GH07879 93F14-93F14 dup:1/2 ID:60B8  
 + endopeptidase \* coded for by C. elegans cDNA CEESC71F; similar to the S25B family of peptidases(aa) \* PROTEASOME  
 COMPONENT C7-I (MACROPAIN SUBUNIT C7-I) (MULTI[PROTEASOME\_B // PROTEASOME\_PROTEASE // ] CG17302 GH07971  
 CG17302 23A3-23A3 dup:1/3 ID:60C10  
 CG11018 + unknown \* [DNA\_LIGASE\_A1] CG11018 GH07940 56E2-56E2 dup:1/2 ID:60C2  
 + 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  
 + endopeptidase \* 3e-11 TBP6\_YEAST PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG 6) \* 3e-08  
 CG14183 MEI1\_CAEEL MEIOTIC SPINDLE FORMATION PROTEIN MEI-1 mei-1 \* 0.000 CG14183 GH08353 76E3-76E4 dup:3/3 ID:60E12

+ 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  
 CG6255 GH08383 92A6-92A6 dup:2/4 ID:60F3  
 CG7669 + unknown \* [NLS\_BP] CG7669 GH08407 91A-91A dup:1/2 ID:60F7  
 CG11656+ unknown \* CG11656 GH08448 87D9-87D9 dup:1/2 ID:60F9  
 + 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 CG17336 GH08705 13F13-13F13 ID:60H3  
 + enzyme \* \* 6e-25 nuclear binding protein - yeast (Saccharomyces cerevisiae) \* 5e-24 MRPL\_CAEEL MRP-FAMILY PUTATIVE  
 CG3262 NUCLEOTIDE-BINDING PROTEIN F10G8.6 \* 9e-2 [fer4\_NifH // MRP // ATP\_GTP\_A] CG3262 GH09040 40D2-40D2 dup:1/2 ID:61C8  
 CG7841 + unknown \* CG7841 GH09068 71C4-71C4 dup:1/2 ID:61D1  
 CG6304 + unknown \* [NLS\_BP] CG6304 GH09088 36A14-36A14 dup:2/3 ID:61D2  
 + unknown \* 5e-07 YNK8\_YEAST HYPOTHETICAL 30.7 KD PROTEIN IN CYB5-LEU4 INTERGENIC REGION \* 4e-46 T07F12.1  
 CG13604 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 // CHYMOTRYPSIN //  
 CG4653 TRYPSIN\_HIS ] CG4653 GH09333 15A1-15A1 ID:61F1  
 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-  
 CG9314 158 catalase (EC 1.11.1.6) - Caenorhabditis [CATALASE // catalase // CATALASE\_1] CG9314 GH09387 29E4-29E4 dup:1/2 ID:61F8  
 CG4891 + BG:DS04095.1 unknown \* CG4891 GH09478 35F1-35F1 dup:1/2 ID:61G1  
 + DNA\_binding \* pNORF1(aa) \* NAM7\_YEAST NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-  
 CG1559 FRAMESHIFT \* nonsense-mediated mRNA decay trans-acting factor \* 3 [ATP\_GTP\_A] CG1559 GH09524 10F6-10F7 dup:1/2 ID:61G7  
 + enzyme \* 7e-62 SYWM\_YEAST TRYPTOPHANYL-TRNA SYNTHETASE, MITOCHONDRIAL (TRYPTOPHAN--TRNA LIGASE) \*  
 1e-60 SYWM\_CAEEL PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE, MIT [TRNASYNTHTRP // tRNA-synt\_1b // AA\_TRNA]  
 CG7441 CG7441 GH09538 75A4-75A4 dup:1/3 ID:61G8  
 + transporter \* DMORCT2\_2 Orct \* 5e-13 putative organic cation transporter \* 4e-09 similar to C. elegans protein and to rat synaptic  
 CG7448 vesicle protein (PIR:S3 \* 2e-13 CG7448 GH09791 79B2-79B2 dup:1/2 ID:61H11  
 CG11074+ unknown \* [NLS\_BP] CG11074 GH09884 42F2-42F2 ID:62A8  
 + \* neural precursor cell expressed developmentally downregulated Nedd9(aa) \* 1e-37 Crk-associated substrate \* 6e-36 enhancer  
 CG1212 of filamentation Crk-assoc [SH3DOMAIN // SH3] CG1212 61A4-61A5 dup:2/4 ID:62B1  
 + metabolism \* NADH-UBIQUINONE OXIDOREDUCTASE SGD1 SUBUNIT PRECURSOR (COMPLEX I-SGDH) (CI-SGDH)(aa) \*  
 CG9762 NADH dehydrogenase (ubiquinone) beta subcomplex, (16kD, SGD1) CG9762 GH10129 68F5-68F5 ID:62C1  
 + motor\_protein \* myosin heavy chain(aa) \* ORF 73, contains large complex repeat CR sarcoma-associated \* 7e-06 YIO9\_YEAST  
 CG3213 HYPOTHETICAL 195.1 KD PROTEIN IN DNA43-UBI1 [PRO\_RICH // RIBOSOMAL\_S14] CG3213 GH10403 23F5-23F5 ID:62D11  
 CG6980 + chaperone \* 5e-06 YB05\_YEAST HYPOTHETICAL 44.1 KD PROTEIN IN RPB5-CDC28 INTERGENIC REGION \* 1e-10

Hsp70/Hsp90 organizing protein homolog \* 1e-08 coded for by C. [TPR\_REGION] CG6980 GH10293 98E1-98E1 ID:62D2

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) (isoform

CG17238 1) \* c431H6.1.3 (PUTATIVE novel prot CG17238 GH10365 87E1-87E1 dup:2/2 ID:62D8

+ 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

CG16979+ unknown \* 3e-61 F38A5.1 gene product \* 1e-40 putative protein \* CG16979 GH10640 71D3-71D3 ID:62F11

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

+ acj6 DNA\_binding \* DMIPOU\_2 acj6 \* POU domain transcription factor(aa) \* INHIBITORY POU PROTEIN (I-POU) (ABNORMAL CHEMOSENSORY JUMP PROTEIN)(aa) \* 1e-152 PP12\_YEAST SE [HOMEBOX\_1 // homeobox // HOMEBOX\_2 //] CG9151

CG9151 GH10637 13C1-13C4 ID:62F9

+ unknown \* 1e-36 predicted using Genefinder; Similarity to Human leukocyte surface \* 7e-22 CD63\_MOUSE CD63 ANTIGEN

CG10742 CD63/ME491 antigen homolog - mou \* 3e-44 tet [transmembrane4 // TMFOUR // TM4\_2] CG10742 GH10778 3A9-3A9 dup:1/2 ID:62G10

+ metabolism \* xylulokinase (H. influenzae) homolog(aa) \* xylulose kinase(aa) \* xylulokinase(aa) \* HYPOTHETICAL 60.3 KD

CG3544 PROTEIN R08D7.7 IN CHROMOSOME III(aa) [FGGY] CG3544 GH10780 21E1-21E1 ID:62G11

+ cell\_adhesion \* DMARTAN\_7 trn \* kek1 \* tartan protein(aa) \* 5e-16 CYAA\_YEAST ADENYLATE CYCLASE (ATP

CG11280 PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) [LRR // LEURICHRPT // LRRCT] CG11280 GH10871 69F5-69F5 ID:62H10

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

+ enzyme \* intermediate chain 1(aa) \* nm23-H7(aa) \* NUCLEOSIDE DIPHOSPHATE KINASE (NDK) (NDP KINASE)(aa) \* 1e-06

CG8362 type nucleoside diphosphate kinase NM23-H6 CG8362 GH10857 85E4-85E4 ID:62H9

+ enzyme \* 1e-09 URE2\_YEAST URE2 PROTEIN glutathione transferase homolog U \* 4e-78 glutathione transferase (EC 2.5.1.18)

CG10091 D1 - fruit fly (Drosophila melanogaste [GST] CG10091 GH11034 87B12-87B12 ID:63B3

+ transcription\_factor \* scr1 \* Similarity to Drosophila scratch neuronal zinc-finger transcription factor \* 9e-05 RIM1 \* 7e-73 neuron

CG12605 specific zinc finger transcription[zf-C2H2 // ZINC\_FINGER\_C2H2 // ATP\_GTP\_] CG12605 GH11439 64A1-64A1 ID:63D10

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

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

+ srp transcription\_factor \* GATA factor(aa) \* DMGATAFAC\_2 srp \* 3e-12 GAT1\_YEAST GAT1 PROTEIN probable membrane

protein YFL02 \* 2e-18 ELT1\_CAEEL TRANSCRIPTION FACTOR[GATAZNFINGER // LECTIN\_LEGUME\_BETA // G] CG3992 GH11649

CG3992 89B3-89B4 dup:2/5 ID:63F10

+ cytoskeletal\_structural\_protein \* DMTUBA1\_2 agr;Tub84B \* 1e-117 TBA1\_YEAST TUBULIN ALPHA-1 CHAIN tubulin alpha-1

CG7794 chain \* 1e-132 TBA1\_DROME TUBULIN ALPHA-1 CHAIN tubulin alpha-1 chain [tubulin] CG7794 GH11574 90D2-90D2 ID:63F2

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

CG1324 + unknown \* [ATP\_GTP\_A] CG1324 GH11587 19E3-19E3 ID:63F6

CG16959+ unknown \* [EGF\_2] CG16959 GH11627 71B2-71B2 dup:2/2 ID:63F7  
 + 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  
 CG1340 ID:63G10  
 CG14355+ unknown \* CG14355 GH11706 88A12-88B1 ID:63G5  
 CG11404+ unknown \* CG11404 GH11730 79E-79E ID:63G9  
 CG7886 + signal\_transduction \* 2e-15 IP63 protein \* \* CG7886 GH12083 88C10-88C10 ID:64B9  
 CG4375 + unknown \* CG4375 GH12486 21E2-21E2 dup:2/2 ID:64E10  
 + enzyme \* DMPAH Hn \* 1e-114 phenylalanine hydroxylase \* 1e-117 tryptophan hydroxylase \* 1e-149 TR5H\_MOUSE  
 TRYPTOPHAN 5-MONOOXYGENASE (TRYPTOPHAN 5-HYDROXYLASE [FYWHYDRXLASE // bioppterin\_H // BIOPTERI] CG9122  
 CG9122 GH12537 61F3-61F3 ID:64F2  
 CG11146+ signal\_transduction Shb=Src homology 2 protein ANTIFREEZE1, SH2 CG11146 ID:64F5  
 + 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 GH12763 38E5-38E5  
 CG9323 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  
 + protein\_phosphatase \* DMPP1A1\_2 Pp1 agr;-96A \* serine-threonine protein phosphatase(aa) \* type 1-related protein  
 phosphatase(aa) \* 1e-110 PP12\_YEAST SERINE/THREONINE PR[PHOSPHO\_ESTER // STPHPTASE // SER\_THR\_] CG10138  
 CG10138 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  
 + signal\_transduction \* F35A5.8 gene product(aa) \* endophilin III(aa) \* contains similarity to scr homology domain (SH3) (PFam:  
 CG14296 SH3.hmm, score: 63.24)(aa) \* DMSHPSP\_3 drk [SH3DOMAIN // SH3 // NLS\_BP] CG14296 GH12907 91D4-91D4 dup:1/2 ID:65A4  
 + transcription\_factor\_binding \* coded for by C. elegans cDNA yk131g12.5(aa) \* Rack1 \* transcription initiation factor IID-associated  
 CG6734 protein, 80K - fruit fly (Drosophil[WD40\_REGION // BEACH\_DOMAIN // IG\_MHC /] CG6734 GH12955 33B10-33B11 ID:65A8  
 + unknown \* FLAGELLAR RADIAL SPOKE PROTEIN 4(aa) \* radial spokehead(aa) \* 9e-13 predicted using Genefinder; similar to  
 CG3121 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  
 + unknown \* No definition line found(aa) \* 4e-06 probable membrane protein YPR091c - yeast (Saccharomyces cerevisiae) \* 6e-43  
 CG5741 No definition line found \* 3e-05 h CG5741 GH13177 66E4-66E4 ID:65C6  
 CG15086+ unknown \* 4e-05 immunogenic secreted protein precursor \* \* CG15086 GH13187 55E6-55E8 ID:65C7  
 + enzyme \* 5e-49 IDH1\_YEAST ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT PRECURSOR (IS \* 6e-57  
 CG3483 IDHA\_CAEEL PROBABLE ISOCITRATE DEHYDROGENASE (NAD), MIT [isodh] CG3483 GH13226 60D2-60D2 ID:65C9  
 + \* ribokinase(aa) \* ribokinase RbsK(aa) \* DMC115C2 \* 1e-71 /match=(desc:; /ma [pfkB // PRO\_RICH // RIBOKINASE] CG17010  
 CG17010 33D3-33D3 dup:2/2 ID:65D12

+ enzyme \* 1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (P5C DEHYDROGENASE)(aa) \* UNKNOWN(aa) \* Similar to  
 CG6670 aldehyde dehydrogenase; coded for by C. elegans cDNA cm1 [aldehy // NLS\_BP] CG6670 GH13449 93F-93F10 dup:2/2 ID:65D9  
 + cytoskeletal\_structural\_protein \* 2e-47 dystrophin \* 1e-117 unnamed protein product \* 1e-143 dystrobrevin dystrobrevin \* 1e-143  
 CG8529 dystrobrevin B [ZF\_ZZ // ZZ // CYTOCHROME\_C] CG8529 GH13689 49A6-49A7 dup:2/2 ID:65E12  
 CG1314 + unknown \* CG1314 GH13802 19E4-19E4 ID:65F10  
 + structural\_protein \* 8e-30 YLS5\_CAEEL HYPOTHETICAL 55.1 KD PROTEIN F09G8.5 IN CHROMOSOME III \* 2e-07 B7 \* 6e-36  
 CG14995 chromosome open reading frame 28.3 KD PROTEIN C21OR \* 8e- [LRR] CG14995 GH13848 64A7-64A8 dup:3/3 ID:65F12  
 + unknown \* SMC2orf(aa) \* CD2 antigen (cytoplasmic tail)-binding protein 2(aa) \* 1e-08 YHV6\_YEAST HYPOTHETICAL 40.4 KD  
 CG5198 PROTEIN IN SPO16-REC104 INTERGENIC REGIO CG5198 GH13760 33D1-33D1 ID:65F7  
 + signal\_transduction \* cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene;  
 CG8683 cDNA EST comes from this gene; cDNA EST comes from thi CG8683 GH13975 28E5-28E6 dup:2/3 ID:65G12  
 + rb chaperone \* beta3 \* Beta3 protein(aa) \* 2e-50 beta-adaptin protein \* 2e-78 cDNA EST yk288h5.5 comes from this gene; cDNA  
 CG11427 EST yk288f1.5 comes CG11427 GH14079 4C4-4C4 ID:66A1  
 + 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  
 + 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  
 + translation\_factor \* HYPOTHETICAL 64.2 KD PROTEIN R08D7.3 IN CHROMOSOME III(aa) \* UNKNOWN(aa) \* eIF3 p66(aa) \*  
 CG4810 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 GH14476  
 CG3565 60D8-60D8 ID:66D8  
 + E(Pc) unknown \* 3e-15 YFC4\_YEAST HYPOTHETICAL 96.7 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION \* enhancer of  
 CG7776 polycomb \* 2e-67 enhancer of polycomb \* E(Pc) [NLS\_BP] CG7776 GH14582 47F15-47F15 dup:5/6 ID:66E10  
 + 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  
 CG1394 + unknown \* CG1394 GH14622 10A11-10A11 ID:66F4  
 CG12699 + unknown \* CG12699 GH14656 54B7-54B7 ID:66F9  
 + 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  
 + And ligand\_binding\_or\_carrier \* similar to calmodulin-like protein.(aa) \* Homo sapiens(aa) \* CALMODULIN(aa) \* Eip63F-1 [efhand //  
 CG17769 EF\_HAND\_2] CG17769 GH15245 99D1-99D1 ID:67D2  
 CG1999 + unknown \* CG1999 GH15272 7A4-7A4 ID:67D3  
 + protein\_kinase \* DMDOA\_2 Doa \* Mpk2 \* DMDC2\_2 Pka-C3 \* 2e-70 KM65\_YEAST PROBABLE SERINE/THREONINE-PROTEIN  
 CG8565 KINASE YMR216C [PROTEIN\_KINASE\_ST // PROTEIN\_KINASE\_DOM] CG8565 GH15551 13F3-13F4 ID:67G7

+ motor\_protein \* 6e-31 tektin \* 3e-54 testicular tektin B1-like protein \* 4e-52 tektin B1 \* tektin A1 - sea urchin (Strongylocentrotus  
 CG3085 purpuratus) [TEKTIN] CG3085 GH15825 59C3-59C3 dup:2/4 ID:68A12  
 CG7742 + unknown \* [TBC // RAB\_GAP] CG7742 GH15768 25C9-25C9 ID:68A4  
 + enzyme \* Chain A, Crystal Structure Of Recombinant Human Brain Hexokinase Type I Complexed With Glucose And Glucose-6-  
 CG5443 Phosphate(aa) \* hexokinase-like protei [HEXOKINASES // hexokinase // HEXOKINASE] CG5443 GH15883 100A5-97B2 ID:68B3  
 CG14891+ unknown \* CG14891 GH16156 92A1-92A1 ID:68C12  
 CG17349+ unknown \* E04F6.2 gene product(aa) \* 1E-130\* CG17349 GH16267 37D6-37D7 ID:68D11  
 + \* 3e-30 No definition line found \* 5e-48 SCF complex protein Skp2 \* 1e-42 S-phase kinase-associated protein (p45) cyclin  
 CG9772 A/CDK2-associate \* YKK7\_CAEE FBOX\_DOMAIN CG9772 ID:68F1  
 + BG:DS02252.2 cytoskeletal\_structural\_protein \* 2e-48 tektin \* 2e-34 testicular tektin B1-like protein \* 3e-59 tektin A1 - sea urchin  
 CG4767 (Strongylocentrotus purpuratus) \* tektin C1 [TEKTIN] CG4767 GH16413 35E-35E ID:68F2  
 + unknown \* 9e-36 by content; 1-meth \* 1e-43 YS15\_CAEL HYPOTHETICAL 41.1 KD PROTEIN IN CHROMOSOME II \* 1e-42  
 CG3881 Sqv-8-like protein \* 7e-47 UDP-glucuronyltransfera CG3881 GH16433 30C2-30C2 ID:68F5  
 none + none GH16763 ID:68H11  
 CG8278 + enzyme \* 1e-05 cyclophilin Dicyp-2 \* \* [PRENYLATION] CG8278 GH17930 44F2-44F2 ID:70A2  
 + unknown \* conserved hypothetical protein(aa) \* CGI-111 protein(aa) \* predicted using Genefinder; Similarity to E.coli hypothetical  
 CG3663 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  
 + enzyme \* MALEYLACETOACETATE ISOMERASE (MAAI)(aa) \* glutathione transferase zeta 1(aa) \* 6e-50 similar to glutathione  
 CG9363 S-transferase \* 3e-05 GTC\_MOUSE GLUTATHI [GST] CG9363 GH17960 85D18-85D18 ID:70A5  
 CG3492 + chaperone \* [CSA\_PPIASE\_2 // PRENYLATION] CG3492 GH18016 60D2-60D2 ID:70B2  
 + unknown \* Ynl288wp(aa) \* hypothetical protein(aa) \* protein involved in sexual development(aa) \* 2e-61 YN28\_YEAST  
 CG9573 HYPOTHETICAL 41.2 KD PROTEIN IN PLC1-SEC21 CG9573 GH18039 29F8-29F8 ID:70B8  
 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\_CAEL HYPOTHETICAL 55.9 KD PROTEIN [KH-domain // KH\_DOMAIN // TUDOR] CG7082 GH18329 23D1-23D1  
 CG7082 dup:3/3 ID:70E4  
 + serpin \* 2e-30 Similar to serine protease inhibitor \* 1e-33 serine proteinase inhibitor \* 5e-42 SCC2\_HUMAN SQUAMOUS CELL  
 CG7722 CARCINOMA ANTIGEN (SCCA-2) (LEUPIN) [serpin // SERPIN] CG7722 GH18514 47C7-47C7 dup:2/4 ID:70F12  
 CG8838 + unknown \* [NLS\_BP // ATP\_GTP\_A] CG8838 GH18521 25A1-25A1 ID:70G2  
 CG15891+ unknown \* CG15891 GH18658 5E1-5E1 ID:70H6  
 + unknown \* T03G11.3 gene product(aa) \* CGI-62 protein(aa) \* 1e-16 T03G11.3 gene product \* CG10999 GH18838 83C3-83C3  
 CG10999 dup:1/2 ID:71A3  
 CG16783+ signal\_transduction fizzy-related protein FIZZY\_DOMAIN, WD40 CG16783 ID:71B5  
 CG1979 + BG:DS00464.1 transmembrane\_receptor \* unknown(aa) \* \* CG1979 GH19145 84C1-84C1 dup:1/2 ID:71C10  
 CG9067 + unknown \* 5e-05 unknown \* 6e-16 unknown protein \* YDOC\_SCHPO HYPOTHETICAL 13.4 KD PROTEIN C15A10.12C IN

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

+ transporter \* mitochondrial carrier protein-like; similar to \* 4e-13 probable membrane protein YPR011c - yeast (Saccharomyces cerevisiae) \* 6e-11 colt \* 3e-61 YQ [mito\_carr // MITOCH\_CARRIER] CG2616 GH19222 84D10-84D10 ID:71D5

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

+ peptidase \* PROBABLE 55.1 KD PEPTIDASE C12B10.05(aa) \* Xaa-Pro dipeptidase; peptidase D; prolidase; imidodipeptidase; CG9581 proline dipeptidase(aa) \* 2e-59 YEQ8\_YEAST [Peptidase\_M24 // MAPEPTIDASE] CG9581 GH19483 19C1-19C1 ID:71F2

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

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

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

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

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

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

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

+ alpha-Est6 enzyme \* agr;-Est6 \* enzyme carboxyesterase ) map\_position:84D4 \* alpha esterase(aa) \* agr;-Est7 [ESTERASE // CG1108 COesterase] CG1108 GH20431 84D5-84D5 ID:72F11

+ 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 CG3809 ID:72F8

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

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

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

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

CG15892 + CG15892 ID:72H4

+ enzyme \* UNKNOWN(aa) \* 7e-63 PUT2\_YEAST DELTA-1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE PRECURSOR CG6661 (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

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

CG14208 + 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

CG10752+ unknown \* CG10752 GH21086 69E8-69E8 ID:73D8  
+ enzyme \* similar to tubulin tyrosine ligase; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes fro CG8918 GH21352 15E5-15E5 ID:73F10  
CG8918 + 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  
CG7045 94B4-94B4 ID:73G1  
CG6652 + motor\_protein \* 6e-13 unknown \*\* [NLS\_BP] CG6652 GH21622 73E4-73E4 dup:2/2 ID:73H9  
+ endopeptidase \* DMEAST\_4 ea \* 3e-27 EAST\_DROME SERINE PROTEASE EASTER PRECURSOR serine protein \* 9e-13 similar to peptidase family S1 (trypsin family) \* 2e-20 serin [trypsin // CHYMOTRYPSIN // TRYPSIN\_SER ] CG8215 GH21666 52C-52C  
CG8215 ID:74A2  
+ corto nucleic\_acid\_binding \* corto \* CENTROSOMAL AND CHROMOSOMAL FACTOR (CCF) (CHROMOCENTROSOMIN)(aa) \* CP-1(aa) \* inserted at base Both 5' and 3' ends of P element Inverse PCR CG2530 GH21787 82F5-82F5 ID:74B1  
CG2530 + 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  
CG5539 + enzyme \* similar to GTP binding protein (YPT1 subfamily)(aa) \* 5e-36 YPT8\_YEAST GTP-BINDING PROTEIN YPT8 GTP-binding protein Y \* 1e-45 rab2 \* 1e-44 RAB2\_MOU [ras // ATP\_GTP\_A // RASTNSFRMNG] CG12156 GH21792 7B8-7B8 ID:74B3  
CG12156 + unknown \* 2e-52 gene C35D10.2 protein - Caenorhabditis elegans similar to \* 3e-81 RGS-GAIP interacting protein GIPC GLUT1 \* 7e-81 RGS-GAIP interacting protein [PDZ] CG11546 GH21964 44A8-44B dup:1/2 ID:74C11  
CG11546 + 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  
CG8772 49B8-49B8 dup:2/2 ID:75D1  
+ enzyme \* l(2)37Cs \* Cs protein \* 2e-19 No definition line found \* 4e-15 protein [NAD\_BINDING] CG10561 GH22841 37C1-37C1  
CG10561 dup:2/2 ID:75D3  
CG3330 + unknown \* CG3330 GH22851 97F8-97F8 ID:75D7  
+ enzyme \* PHOSPHOMANNOMUTASE (PMM)(aa) \* 2e-91 YM8L\_YEAST HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8  
CG10202 INTERGENIC REGION \* 1e-114 similar to Phosphoglucomutase a [PGM\_PMM // PGMPMM] CG10202 GH22984 51C5-51C5 ID:75F1  
CG10202 + 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  
CG10126 ID:75F5  
+ unknown \* hypothetical protein gs1.1.27.1(aa) \* 6e-26 hypothetical protein YPL020c - yeast (Saccharomyces cerevisiae) ( \* 1e-29  
CG11023 YRW3\_CAEEL HYPOTHETICAL 75.7 K CG11023 GH23213 21A3-21A3 dup:1/2 ID:75H9  
CG11023 + cytoskeletal\_structural\_protein \* p60 katanin(aa) \* katanin p60 subunit(aa) \* 4e-42 CC48\_YEAST CELL DIVISION CONTROL  
CG1193 PROTEIN cell divisi \* 3e-43 transitional endoplasmic reticulum A [AAA // NLS\_BP // ATP\_GTP\_A] CG1193 GH23455 83C-83C ID:76C7  
CG1193 + rha motor\_protein \* RADHA protein(aa) \* 1e-10 similar to C. elegans UNC-89 and titins \* 3e-07 ORF 73, contains large complex  
CG11908 repeat CR sarcoma-associated herpesv \* YL CG11908 GH23783 96D-96D ID:76G7



+ transcription\_factor \* DMSUHW\_6 su(Hw) \* crol \* zf43C \* 7e-08 zinc finger 30C [zf-C2H2 // ZINC\_FINGER\_C2H2 // ZINC\_FIN]  
 CG7101 CG7101 GH24178 17E1-17E1 ID:77C7  
 + 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 GH24360  
 CG8257 50E2-50E2 dup:3/3 ID:77E7  
 + unknown \* 4e-14 weak similarity to Bos taurus mitochondrial ATP synthase coupling factor B (SP \* 1e-11 unknown \* 8e-06  
 CG10731 ATPW\_BOVIN ATP SYNTHASE COUPLING FACTOR CG10731 GH24822 52F3-52F3 ID:77H11  
 + 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  
 CG9176 ID:77H7  
 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  
 + EG:9D2.4endopeptidase \* DMC9D2 \* /motif=(desc;; /motif=(desc;; /motif=(desc;; /match=(desc;; /m \* 2e-20 kallikrein \* 1e-28  
 CG3795 mesotrypsinogen mesotrypsino [trypsin // CHYMOTRYPSIN // TRYPSIN\_SER] CG3795 GH24985 2B8-2B8 ID:78B4  
 CG17450+ unknown \* CG17450 GH25094 cyto\_unknown ID:78C5  
 + ftz-f1 steroid hormone receptor steroid receptor beta FTZ-F1 [Drosophila melanogaster] NUCLEAR\_RECEPTOR, STRDHORMONER,  
 CG4059 STROIDFI] CG4059 GH25189 dup:3/3 ID:78D6  
 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  
 CG17210(ALLERGEN SOL I 3) (SOL I III) CG17210 GH25284 86D8-86D8 dup:2/2 ID:78E5  
 + Ork1 ion\_channel \* potassium channel, subfamily K, member (TASK-2); TASK-2(aa) \* two P domain potassium channel ORK1(aa) \*  
 CG1615 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  
 + 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 (TFPI)(aa) \*  
 CG1540 similar to Kunitz/Bovine [ig // EGF\_1 // BPTI\_KUNITZ // Kunitz\_BP] CG1540 GH25513 98D2-98D2 dup:1/3 ID:78G5  
 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  
 CG7815 75F9-75F9 ID:79B9  
 + enzyme \* 1e-19 probable membrane protein YLR070c - yeast (Saccharomyces cerevisiae) \* 8e-40 sorbitol dehydrogenase \* 5e-39  
 CG4836 similar to sorbitol dehydrogenase; [adh\_zinc // NLS\_BP] CG4836 GH25858 92C-92C dup:1/4 ID:79C3  
 CG4764 + unknown \* cDNA EST yk375c3.5 comes from this gene; cDNA EST yk375c3.3 comes from this gene(aa) \* conserved

hypothetical protein(aa) \* Vps29(aa) \* PEP11 PROT [UPF0025] CG4764 GH25884 21E4-21E4 ID:79C7  
 CG17470+ unknown \* CG17470 GH26094 38E-38E dup:2/2 ID:79E10  
 + enzyme\_activator \* HYPOTHETICAL 45.1 KD PROTEIN IN IMP2-DNA43 INTERGENIC REGION(aa) \* phosphotyrosyl  
 CG8509 phosphatase activator(aa) \* similar to hosphotyrosyl phosphatase CG8509 GH26069 13F1-13F1 dup:2/2 ID:79E2  
 + unknown \* hypothetical protein(aa) \* Hrt2p(aa) \* F31D4.2(aa) \* hypothetical protein(aa) [NLS\_BP] CG11475 GH26080 58C1-  
 CG1147558C1 dup:2/2 ID:79E5  
 + transcription\_factor \* segmentation protein hairy - fruit fly (Drosophila melanogaster)(aa) \* DMHAIRG\_5 h \* 3e-07 lin-22 \* 2e-18  
 CG10446 HES1\_MOUSE TRANSCRIPTION FACTOR HES-1 (HAI [HLH // HELIX\_LOOP\_HELIX\_2] CG10446 37B10-37B10 dup:2/2 ID:79F1  
 + transporter \* aquaporin 2(aa) \* 1e-07 YFF4\_YEAST HYPOTHETICAL 70.5 KD PROTEIN IN AGP3-DAK3 INTERGENIC REGION  
 CG5398 \* 8e-05 BIB\_DROME NEUROGENIC PROTEIN BIG BRAIN bib pr [MINTRINSICP // MIP] CG5398 GH26134 59F1-59F1 ID:79F5  
 CG4715 + unknown \* CG4715 GH26159 21E-21E ID:79F9  
 CG12136+ unknown \* [AA\_TRNA\_LIGASE\_I // NLS\_BP] CG12136 GH26280 8D10-8D10 ID:79G11  
 + actin\_binding \* 1e-05 contains similarity to the kelch/MIPP family \* 1e-06 Keap1 \* 1e-07 The gene product is related to Drosophila  
 CG12423melanogaster ri \* 1e-06 kelch pro [BTB] CG12423 GH26310 cyto\_unknown ID:79H3  
 + unknown \* contains similarity to E. coli cation transport protein \* 6e-16 YEZ3\_YEAST HYPOTHETICAL 26.3 KD PROTEIN IN  
 CG10365RAD4-CHD1 INTERGENIC REGION \* 3e-22 cont CG10365 GH26317 95B5-95B5 ID:79H4  
 CG7895 + tin transcription\_factor CG7895 tin dup:5/6 ID:8-31 cntrlBG4  
 + motor\_protein \* BACR37P7.j(aa) \* MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) LINKER HISTONE  
 CG9392 PROTEINS ALPHA, BETA, DELTA AND \* \* CG9392 GH26462 76C1-76C1 ID:80B3  
 CG5755 + transporter \* TB1(aa) \* \* [mito\_carr] CG5755 GH26696 36E-36E ID:80D7  
 CG4669 + unknown \* [PRO\_RICH] CG4669 GH26702 64D1-64D1 ID:80D8  
 + 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  
 CG17137ID:80G10  
 + unknown \* 2e-11 cDNA EST CEMS78F comes from this gene; cDNA EST yk293d9.3 comes \* 2e-10 Unknown \* CG12118  
 CG12118GH27430 8D2-8D2 dup:3/4 ID:81D8  
 + 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  
 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  
 CG15360+ unknown \* CG15360 GH27779 22B3-22B3 ID:81H1  
 CG2865 unknown \* GH27792 81H4  
 + glaikit unknown \* Contains similarity to Pfam domain: (PLDc), Score=13.8, E-value=0.2, N=1(aa) \* \* CG8826 GH27933 23D4-23D4  
 CG8826 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 EST  
 CG7816 comes from this gene; cDNA EST co \* 3e-39 KE4 \* 1e-38 CG7816 GH28072 99C7-99C7 dup:2/2 ID:82B11  
 + RNA\_binding \* protein(aa) \* 2e-49 ovarian protein - fruit fly (Drosophila melanogaster) s \* 8e-75 YLF1\_CAEEL HYPOTHETICAL  
 42.4 KD PROTEIN C40H1.1 IN CHROMOSOME II [RNP\_1 // RBD // PFKB\_KINASES\_1 // rrm] CG5735 GH28038 66E4-66E4 dup:2/3  
 CG5735 ID:82B7  
 + 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  
 + RNA\_binding \* hypothetical protein(aa) \* heterogeneous nuclear ribonucleoprotein R(aa) \* 1e-08 RN15\_YEAST MRNA 3'-END  
 CG17838 PROCESSING PROTEIN RNA15 RNA15 pro \* 6e-16 p [RBD // rrm // NLS\_BP] CG17838 GH28335 92F10-92F10 dup:2/5 ID:82C6  
 + enzyme \* phosphoglyceromutase - fruit fly (Drosophila melanogaster)(aa) \* DMPGLY\_4 Pglym78 \* 3e-72 PMG1\_YEAST  
 CG17645 PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE 1 [PGAM // PG\_MUTASE] CG17645 GH28416 87B7-87B7 ID:82D6  
 + unknown \* cDNA EST comes from this gene; cDNA EST yk304g10.3 comes from this gene; cDNA EST yk304g10.5 comes from  
 CG11848 this gene(aa) \* 2e-16 ankyrin repeat-contai CG11848 GH28553 96B20-96B20 dup:2/2 ID:82E5  
 + peptidase \* leucyl aminopeptidase - like protein (partial)(aa) \* 1e-103 leucine aminopeptidase \* 1e-105 AMPL\_BOVIN CYTOSOL  
 AMINOPEPTIDASE (LEUCINE AMINOPEPTIDAS [LAMNOPPTDASE // CRYSTALLIN\_BETAGAMMA //] CG8040 GH28719 67D12-  
 CG8040 67D13 dup:3/3 ID:82F9  
 CG17884+ Snap25 synaptosome-associated\_protein Synapse protein 25 CG17884 GH28821 ID:82G10  
 CG8006 + unknown \* CG8006 GH28769 67E7-67E7 ID:82G2  
 + lat DNA\_replication\_factor \* recognition complex subunit mela \* 8e-92 recognition complex subunit \* 9e-95 recognition complex  
 CG4088 associated protein p81 \* 2e-92 inserted at base Bot [NLS\_BP // ATP\_GTP\_A] CG4088 GH28787 49F10-49F10 dup:1/2 ID:82G4  
 + ribosomal\_protein \* predicted using Genefinder; Similarity to Prototheca mitochondrial ribosomal protein S11 (SW:RT11\_PROWI);  
 CG5184 cDNA EST yk372e6.3 comes from this gene; [Ribosomal\_S11] CG5184 GM13519 89E13-89E13 ID:83A11  
 + endopeptidase \* valosin-containing protein homolog(aa) \* Sug2p(aa) \* 726aa long hypothetical transitional endoplasmic reticulum  
 CG6815 ATPase(aa) \* ATPase-like protein(a [AAA // ATP\_GTP\_A] CG6815 89B17-89B17 dup:2/2 ID:83F7  
 + motor\_protein \* DNA segment, single copy, probe pH4 (transforming sequence, thyroid-1,(aa) \* 1e-07 microtubule binding protein  
 CG6664 D-CLIP-190 \* 1e-20 YRU4\_CAEEL HYPOTHE CG6664 LD23434 73E2-73E3 dup:2/2 ID:84B11  
 CG15340+ CG15340 LD25626 ID:84G11  
 + GTP-binding protein ligand\_binding\_or\_carrier signal recognition particle receptor-like ATP\_GTP\_A, NLS\_BP, SRP54 CG2522  
 CG2522 LD25651 ID:84H2  
 + enzyme \* 7e-52 DEOC\_CAEEL PUTATIVE DEOXYRIBOSE-PHOSPHATE ALDOLASE (PHOSPHODEOXYRIBOALDOLASE) ( \*  
 CG8525 9e-69 CGI-26 protein \* 1e-26 2-deoxyribose 5-phosphate aldol CG8525 LD25963 49A4-49A5 ID:85B10  
 CG10609+ Or83b signal\_transduction (Odorant receptor 83b ) olfactory receptor CG10609 LD26485 ID:85F4  
 + protein\_kinase \* 1e-07 probable membrane protein YDL146w - yeast (Saccharomyces cerevisiae) \* 3e-09 hypothetical protein \*  
 CG2258 [SH3] CG2258 LD26707 7D9-7D9 dup:1/3 ID:85G7  
 CG9828 + chaperone DnaJ homolog 2 DNAJPROTEIN CG9828 LD27049 dup:2/2 ID:86B6  
 CG10171+ unknown \* CG10171 LD27069 70A5-70A5 ID:86B8

+ UbcD4 enzyme \* 3e-33 UBC1\_YEAST UBIQUITIN-CONJUGATING ENZYME E2-24 KD (UBIQUITIN-PROTEIN LIGASE) (UBI \* 1e-107 ubiquitin conjugating enzyme \* 7e-54 contains similar [UBA // UBIQUITIN\_CONJUGAT // UQ\_con // ] CG8284 LD27480 67B12-67B12 dup:2/2 ID:86E11  
 CG8284 + 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  
 PROTEIN CY1A11.16C (Z \* cDNA EST yk331d5.3 comes from thi[FHA\_DOMAIN // D111\_DOMAIN // NLS\_BP // ] CG8079 LD27413  
 CG8079 51E9-51E9 dup:2/2 ID:86E8  
 CG2061 + BcDNA:LD28247 G protein-coupled receptor 69A CRYSTALLIN\_BETAGAMMA CG2061 LD28247 dup:2/3 ID:87D2  
 + Acer peptidase \* DMACERMET\_2 Acer \* dipeptidyl carboxypeptidase I converting enzyme(aa) \* metallopeptidase(aa) \* enzyme-like  
 CG10593 protein(aa) [PEPDIPTASEA // Peptidase\_M2 // ZINC\_PRO] CG10593 LD28328 31B1-31B1 ID:87D9  
 CG16972 + motor\_protein \* [NLS\_BP] CG16972 LD28380 34A9-34A9 dup:4/4 ID:87E5  
 CG5094 + chaperone CG5094 dup:2/2 ID:88H9  
 + Sdic motor\_protein \* Sdic \* DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE  
 CG9580 CHAIN)(aa) \* axonemal dynein intermediate chain Sdic(aa) \* 4e- [WD40] CG9580 LD35918 19C1-19C1 dup:2/2 ID:95E4  
 + 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  
 + Hsp67Bb chaperone \* DMHGS2\_7 Hsp67Bb \* 1e-14 hypothetical protein YOR285w - yeast (Saccharomyces cerevisiae) \* 5e-60  
 CG4456 HS6B\_DROME HEAT SHOCK PROTEIN 67B2 heat shock prot [Rhodanese // RHODANESE] CG4456 LD36162 67B1-67B1 ID:95G6  
 + chaperone \* FKBP54(aa) \* 2e-11 FKBP\_YEAST FK506-BINDING PROTEIN (FKBP) (PEPTIDYL-PROLYL CIS-TRANS  
 ISOMERASE) (P \* 3e-08 FKB2\_DROME KD FK506-BINDING PROTEIN (FK [TPR\_REGION // FKBP\_PPIASE\_2 // FKBP\_PPI] CG5482  
 CG5482 LD36412 55E5-55E5 ID:96A4  
 + 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  
 CG1341 ID:96B9  
 + unknown \* 6e-07 No definition line found \* 8e-26 unknown protein \* [UX\_DOMAIN // UBX] CG5469 LD37137 55E6-55E6 dup:3/3  
 CG5469 ID:96E4  
 + unknown \* hypothetical protein(aa) \* Hrt2p(aa) \* F31D4.2(aa) \* hypothetical protein(aa) CG2921 LD38241 58C1-58C1 dup:2/2  
 CG2921 ID:97E5  
 + 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  
 CG7004 dup:3/3 ID:97G12  
 + chaperone \* possesses DNAJ-like domain; cDNA EST yk272a11.3 comes from this gene; cDNA EST yk272a11.5 comes from this  
 gene(aa) \* 2e-10 YNH7\_YEAST HYPOTHETICAL 5 [DNAJ\_1 // DnaJ // DNAJPROTEIN // DNAJ\_2] CG11035 LD38634 84E7-84E7  
 CG11035 ID:97H1  
 CG10639 + 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

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

+ transcription\_factor \* DMDORSAL\_2 dl \* EMBRYONIC POLARITY DORSAL PROTEIN(aa) \* 4e-37 KBF1\_MOUSE NUCLEAR  
FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FA[REL // REL\_2 // NFKBTNSCPFCT // RHD] CG6667 dorsal 36C2-36C2

CG6667 dup:3/4 ID:Path + Ctrl1 + kras11