

Table S10

Genes that display a significant change in expression during adult stages 0-30 day (ANOVA, $P < 0.001$)

Gene ID mixed annotation (+ indicates sequence confirmation)

CG12505+ unknown * CG12505 LD41905 50F6-50F6 ID:101A2
+ Pi3K21B signal_transduction * p60(aa) * DMPIK57 Pi3K21B * p60 p * 2e-08 similar to vav proto-oncogene [PI3KINASEP85 //
CG2699 SH2DOMAIN // SH2] CG2699 LD42724 21B7-21B7 dup:2/2 ID:101F10
+ 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
+ structural_protein * 6E-55* 1e-06 R02F2.4 gene product * 2e-06 peritrophin * 7e-35 Gasp CG17052 LD43683 19C1-19C1
CG17052 dup:1/2 ID:102F1
+ 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
CG4353 ID:105E10
+ structural_protein * 6e-14 CUP7_DROME PUPAL CUTICLE PROTEIN EDG-78 PRECURSOR ecdyson * 2e-28
CUD4_LOCM1 ENDOCUTICLE STRUCTURAL GLYCOPROTEIN (ABD-4A) g * 7e-16 DMEDG78B_2 [CUTICLE // insect_cuticle]
CG8505 CG8505 49A3-49A3 ID:105F10
+ nucleic_acid_binding * 2e-08 SFP1 * 3e-06 zinc-finger protein Pur-1 - mouse * 3e-06 MAZ * 3e-06 serum amyloid A-
CG12054 activating factor SAF-8 [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG12054 LD46863 100B9-100B9 dup:1/2 ID:105G10
+ chaperone * TFIIIC alpha subunit(aa) * 1e-07 precursor TRG1 protein * 6e-17 D-ERp60=protein disulphide isomerase
CG7099 isoform/multifunctional endoplasmic retic * 2e- CG7099 34B6-34B6 ID:105G9
CG8320 + CG8320 ID:105H9
+ Cht3 enzyme * chitinase(aa) * 2e-22 probable membrane protein YDR371w - yeast (Saccharomyces cerevisiae) * 2e-63
CG18140 chitinase * 1e-44 CHIT_CAEEL PUTATIVE ENDOCHITIN CG18140 LP01426 40D5-40D5 dup:4/4 ID:107E10
CG1153 + unknown * CG1153 LP01348 83E2-83E2 dup:2/2 ID:107E8
+ 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
CG3711 ID:107E9
+ receptor * 4e-06 LDL receptor-like repeat; orfla * 2e-47 coded for by C. elegans cDNA yk9e10.5; coded for by C. elegans
CG8756 cDNA yk9e10.3; mu * 3e-07 very low dens [LDLRA_2 // ldl_recept_a // LDLRA_1] CG8756 LP01646 76C-76C ID:107F11
+ 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 CG3097 LP01667 5B6-5B6 ID:107G1
+ 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
CG18317+ unknown * CG18317 LP02521 22B1-22F3 ID:108B1

+ endopeptidase serine proteinase (EC 3.4.21.-) 2 precursor - fruit fly CHYMOTRYPSIN,TRYPSIN_CATAL, TRYPSIN_SER,]
 CG10475 CG10475 ID:108C1
 + SA unknown * nuclear protein SA(aa) * SA * 2e-15 unknown * 1e-160 cDNA EST comes from this gene; cDNA EST co
 CG3423 [NLS_BP] CG3423 LP03425 27C6-27C6 ID:108F2
 + 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
 CG9701 ID:109C4
 + Neurotactin cell adhesion axon, ocellar nerve, ventral nerve cord CARBOXYLESTERASE_B_2, COesterase, ESTERA] CG9704
 CG9704 LP05519 ID:109D11
 CG13598 + sba unknown * DMTF125_2 Tf125 * type I(aa) * [MBD] CG13598 LP05532 95C9-95C11 ID:109D12
 + BG:DS09217.1 unknown * 1e-14 predicted using Genefinder; cDNA EST comes from this g * * CG13240 GH01660 35D6-35D6
 CG13240 dup:2/2 ID:30E12
 CG15387 + CG15387 ID:31A6
 CG9759 + unknown * CG9759 GH02603 87F-87F ID:31D2
 + structural_protein * 2e-05 CUP7_DROME PUPAL CUTICLE PROTEIN EDG-78 PRECURSOR ecdyson * 8e-06
 CU26_ARADI ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 12.6 (ACP 12.6) * 2e-07 DM [CUTICLE // insect_cuticle] CG12045
 CG12045 GH03728 100B-100B ID:32B12
 CG7738 + CG7738 dup:2/2 ID:32C2
 CG6186 + CG6186 dup:2/2 ID:32G1
 + 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
 + 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
 + BcDNA:GH12144 unknown * Contains similarity to Pfam domain: (TPR), Score=38.0, E-value=6.9e-08, N=6(aa) * weakly similar
 CG4341 to E. nidulans bimA gene product * * [TPR_REGION // TPR_REPEAT] CG4341 GH12144 21D4-21E dup:3/3 ID:39E7
 CG4929 + CG4929 dup:2/2 ID:39E8
 + cher actin_binding * contains similarity to the x aa approximate repeats found in human filamin * filamin, Mueller cell -
 chicken(aa) * filamin (actin-binding protein[Filamin // FILAMIN_REPEAT // GRAM_POS_A] CG3937 GH12209 92D1-92D1 dup:2/5
 CG3937 ID:39F1
 + chaperone * embryonal lethal (2)13-1 (el(2)13-1) - fruit fly (Drosophila melanogaster)(aa) * 4e-16 HS27_DROME HEAT
 CG4461 SHOCK PROTEIN heat shock protein - f * 9e-10 [HSP20] CG4461 GH12586 67B1-67B1 ID:39H6
 + unknown * insect intestinal mucin IIM22(aa) * putative cell surface glycoprotein; Sed1p(aa) * 71(aa) * GLYCOPROTEIN X
 CG7874 PRECURSOR(aa) CG7874 GH13361 18B6-18B6 dup:2/2 ID:40E12
 CG1721 + Pglym78 enzyme * phosphoglyceromutase - fruit fly (Drosophila melanogaster)(aa) * DMPGLY_4 Pglym78 * 7e-48 pdb|4PGM|A

Chain A, *Saccharomyces Cerevisiae* Phosphoglycer [PGAM // PG_MUTASE] CG1721 GH13304 99A1-99A1 dup:2/2 ID:40E5

CG10513+ unknown * /match=(desc:; /match=(desc:(aa) * 1e-36 /match=(desc:; /ma * * CG10513 GH13495 96C7-96C7 ID:40F11
+ cytoskeletal_structural_protein * similar to Probable rabGAP domains; cDNA EST comes from this gene; cDNA EST comes

CG7324 from this gene; cDNA EST comes from this gene; cDNA EST comes fro [TBC] CG7324 GH15186 78D-78D dup:2/4 ID:42B8
+ enzyme * coded for by *C. elegans* cDNA yk16b2.3; coded for by *C. elegans* cDNA yk16b2.5; Similar to amidase.(aa) *
PUTATIVE AMIDASE AMIA2(aa) * 3364, putative [CRYSTALLIN_BETAGAMMA // Amidase] CG7910 GH15201 84E10-84E10

CG7910 ID:42B9
+ 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

CG17903 36A7-36A7 ID:43F5

CG16944+ sesB transporter ADP/ATP translocase ADPTRNSLCASE, MITOCARRIER CG16944 ID:46A4
+ TFIIS transcription_factor * 2e-20 DST1 DNA strand transferase alpha * 1e-124 TFS2_DROME TRANSCRIPTION
ELONGATION FACTOR S-II (RNA POLYMERASE II ELONGATION FA * 3e-42 TFS2_CAEEL [TFIIS] CG3710 LD34766 35C1-

CG3710 35C1 ID:49F1
+ 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
+ Bc larval_serum_protein * pro-phenol oxidase A1 * pro-phenol oxidase subunit 1; proPO-p1 * DMORA_2 Bc *

CG5779 prophenoloxidase [TYROSINASE_2 // hemocyanin // HEMOCYANI] CG5779 GH04080 55A1-55A1 dup:2/2 ID:56E11
+ unknown * 1e-35 hypothetical protein YDR531w - yeast (*Saccharomyces cerevisiae*) (U * 3e-27 No definition line found *

CG5725 5e-42 putative protein * coded for by *C. elegans* CG5725 GH04001 77B6-77B6 dup:3/3 ID:56E4
+ unknown * antigen 5-related 2(aa) * antigen 5-related protein(aa) * Ag5r2 * 7e-12 predicted using Genefinder; Similarity to

CG9400 Human testis-specific pr [SCP // GATASE_TYPE_II] CG9400 GH04057 12E2-12E2 dup:2/2 ID:56E9

CG4962 + unknown * CG4962 GH04593 72E2-72E2 ID:57B2
+ Scp2 ligand_binding_or_carrier * 6e-95 calcium-binding protein Cex C * 1e-15 YSO6_CAEEL HYPOTHETICAL CALCIUM-
BINDING PROTEIN F56D1.6 IN CHROMOSOME II * 2e-33 calexcitin * 7[EF_HAND // EF_HAND_2 // ATP_GTP_A] CG14904

CG14904 GH06666 92A1-89D4 dup:2/4 ID:59B6
+ defense/immunity_protein * 2e-33 peptidoglycan recognition protein precursor * 7e-37 TNF superfamily, member (LTB)-like

CG8577 (peptidoglycan recognition * 1e-33 peptidoglycan recogn CG8577 GH07464 44D8-44D8 ID:59F11
+ enzyme * DIHYDROFOLATE REDUCTASE(aa) * 6e-10 hypothetical protein YOR280c - yeast (*Saccharomyces cerevisiae*)

CG5412 * 6e-31 Similarity to *S.pombe* dihydrofolate redu CG5412 GH07367 92E11-92E11 ID:59F2
+ 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
+ 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

CG13432+ unknown CG13432 GH08941 dup:1/2 ID:61B12
+ 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
+ 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
+ unknown * 6e-05 transmembrane protein * 2e-12 Similarity to C.elegans cuticulin (SW:CUT1_CAEEL) * 7e-07 DMDUSKY_1
CG3541 dy * similar to cuticlin CG3541 GH12163 60D7-60D8 dup:1/2 ID:64C4
+ 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 CG7651 GH12627 79F3-79F3 ID:64F10
CG6123 + unknown * [NLS_BP] CG6123 GH13094 17A7-17A7 ID:65B9
CG15390+ unknown * CG15390 GH14074 22E-22E ID:65H11
+ 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
+ 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] [CYTOCHROME_B5 // CYTOCHROME B5 // CYTOCH]
CG2140 CG2140 GH15091 43D-43D dup:3/3 ID:67B9
+ Scp1 ligand_binding_or_carrier * calcium-binding protein alpha-a chain - penaeid shrimp (Penaeus sp.)(aa) * Scp1 * 5e-94
CG15848 calcium-binding protein * 2e-43 SCPB_PENSP SARCOPLASMIC CALC CG15848 GH15296 cyto_unknown ID:67D6
+ 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
CG16820+ unknown * CG16820 GH15921 34A11-34A11 dup:2/2 ID:68B9
+ unknown * 5e-08 myosin phosphatase, target subunit (A * 1e-07 PP1M M21 subunit=protein phosphatase 1M kda regulatory
CG5600 subunit * myosin phosphatase, target subu CG5600 GH16214 72D3-72D4 dup:2/4 ID:68D7
+ protein_kinase * protein kinase C, mu(aa) * DMPKC98F_2 Pkc98E * protein kinase C, mu(aa) * 6e-42 DUN1_YEAST DNA
DAMAGE RESPONSE PROTEIN KINASE DUN1 protei [DAG_PE_BINDING_DOMAIN // PROTEIN_KINASE] CG7125 GH16373
CG7125 90F8-90F9 dup:3/3 ID:68E7
CG18403+ very low density lipoprotein receptor - mouse CG18403 ID:70B7
+ unknown * 4e-05 BE46_MOUSE BRAIN PROTEIN E46 gene E46 protein - mouse * * CG4975 GH18454 54E5-54E5
CG4975 ID:70F8
+ 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
+ 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

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

CG1744 LEURICHRPT] CG1744 GH19649 100B8-100B9 ID:71G7
+ 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

CG8560 GH20109 65F7-65F8 ID:72C10
+ serpin * 3e-34 Similar to serine protease inhibitor * 6e-38 proteinase inhibitor Spi3 - mouse serine proteinase inhib * 1e-35

CG1865 cytoplasmic antiproteinase, CAP [serpin // SERPIN] CG1865 GH20213 42F1-42F1 ID:72D9

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

CG1521 + transporter homology to uncharacterized human and C.elegans proteins MgtE CG1521 GH20809 ID:73A10
+ transcription_factor * BLASTX 1.3E-19 Human super cysteine rich protein mRNA, partial cds.(dna) * GAGA factor class A-

CG12236 isoform(aa) * 8e-32 alternatively spliced form * 8e- [BTB // zf-C2H2 // ZINC_FINGER_C2H2] CG12236 GH20830 5C6-5C6 ID:73B1
+ 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 //

CG6305 insect_cuticle] CG6305 GH20904 50C9-50C11 ID:73B10
+ 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
+ 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
+ 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

CG6335 GH22474 17B5-17B5 ID:74H5
+ unknown * 1e-05 NIPM_BOVIN NADH-UBIQUINONE OXIDOREDUCTASE KD SUBUNIT (COMPLEX I-15 KD) (CI-15 * *

CG11455 CG11455 GH23780 21B2-21B2 ID:76G6

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

CG2555 11B10-11B10 ID:77A6
+ e enzyme * ebony(aa) * e * ebony * 1e-56 bacitracin synthetase 3; BacC [AMP_BINDING // ACP_DOMAIN // AMP-bindin]

CG3331 CG3331 GH24002 93D2-93D2 dup:2/2 ID:77B2
+ 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

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

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

+ 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

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

CG7300 + unknown * CG7300 GH26358 32A-32A ID:79H9

+ spdo actin_binding * sanpodo protein(aa) * 1e-179 sanpodo protein * 8e-47 Similar to tropomodulin; coded for by C. elegans

CG1539 cDNA yk88e7.5; coded for by C. * 6e-47 TMOD_MO CG1539 sanpodo 100A-100A dup:3/3 ID:8-31 cntrlBC5

+ pros transcription_factor * DMPROS_3 pros * PRO_DROME PROTEIN PROSPERO homeotic protein prospero - f * 4e-58 HM26_CAEEL HOMEBOX PROTEIN CEH-26 K12H4.1 protein - Caen * 2e-50 [PRO_RICH] CG17228 pros p'3' 3211 86E2-

CG17228 86E2 dup:4/4 ID:8-31 cntrlBD7

+ unknown * 7e-12 M03A8.2 gene product * 4e-07 inserted at base Both 5' and 3' ends of P element Inverse PCR * CG1241

CG1241 GH26553 63A1-63D3 ID:80B11

CG8154 + unknown * [NLS_BP] CG8154 GH26521 67C2-67C2 ID:80B9

+ 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

+ 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

+ unknown * hypothetical protein(aa) * hypothetical protein YPL086c - yeast (Saccharomyces cerevisiae) (* Similarity to

CG15433 Yeast LPG22P protein cDNA EST EMBL:T0 * CG15433 GH27091 26A1-26A1 ID:80H11

+ 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

CG15520+ * CG15520 99D-99D dup:1/2 ID:82C1

+ 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

+ unknown * CUTICLE PROTEIN (BC-NCP1)(aa) * BLASTX 1.2E-10 Theileria parva schizont/sporozyte surface protein

CG8736 gene, partial cds.(dna) * CG8736 HL08183 44D-44D ID:83D10

+ 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

+ 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

CG1578 10E3-10E4 dup:4/5 ID:87D12

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*
 CG1826 *melanogaster*) * 7e-12 Kelch motif containing [BTB // PROTEIN_SPLICING // NLS_BP] CG1826 9E2-9E2 dup:2/2 ID:88B4
 CG18041 + CG18041 ID:88B6
 CG3661
 + 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
 + * 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
 + 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
 + 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
 + 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
 + RasGAP signal_transduction * RasGap protein(aa) * 2e-16 BUD2_YEAST INHIBITORY REGULATOR PROTEIN BUD2/CL2
 GTPase- * RasGap protein * 1e-40 similar to GTPase-activating p[RAS_GTPASE_ACTIV_2 // SH2DOMAIN // C2 /] CG9209
 CG9209 LD38909 14A1-14A1 dup:1/2 ID:98B8
 + unknown * 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-
 CG8483 87E3 ID:98C2
 + unknown * 3e-21 hypothetical protein YOR289w - yeast (*Saccharomyces cerevisiae*) * 1e-43 R166.3 * 3e-45 unknown
 CG5902 protein * Y810_METJA HYPOTHETICAL PROTEIN hypo CG5902 97F1-97F1 dup:1/6 ID:98G6
 CG9432 + CG9432 G041 dup:1/4 ID:Farhad's BC7