

Table S6

genes with five and six expression peaks

+ 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
CG8351 85E9-85E9 ID:106C10
CG10283+ unknown * CG10283 LD47881 36F8-36F9 ID:107A11
+ BcDNA:LD28120 transporter * similar to the monocarboxylate transporter family(aa) * Yol119cp(aa) * contains similarity to
CG8062 monocarboxylate transporters(aa) * MONOCARBOXYLATE TRA CG8062 LP01259 18C2-18C2 dup:3/5 ID:107D11
+ unknown * Ypr147cp(aa) * 1e-11 probable membrane protein YPR147c - yeast (Saccharomyces cerevisiae) * 1e-20
CG9186 predicted using Genefinder; Similarity to C.elegan [ESTERASE // LIPASE_SER] CG9186 LP01162 62B4-62B4 dup:2/2 ID:107D5
+ enzyme * HemE homolog(aa) * uroporphyrinogen decarboxylase; Hem12p(aa) * UROPORPHYRINOGEN
DECARBOXYLASE (UPD)(aa) * UROPORPHYRINOGEN DECARBOXYLASE (URO-D)(a [UROD_1 // UROD_2 // URO-D]
CG1818 CG1818 LP03960 45F4-45F4 ID:108H1
+ 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
CG6339 + motor_protein CG6339 SD05424 ID:118G5
+ 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
CG8439 GH10122 48F1-48F1 ID:37F2
+ 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
+ unknown * ring finger protein 13(aa) * RING zinc finger protein(aa) * 2e-09 GOLI_DROME GOLIATH PROTEIN (G1
PROTEIN) regulatory protei * 6e-24 similar to Zinc [GRAM_POS_ANCHORING // zf-C3HC4 // CYTOC] CG10277 GH06194 84A4-
CG10277 84A4 dup:2/2 ID:58F6
+ 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
+ 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
+ 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 // TCOMPLEXT] CG7033 GH15038
CG7033 8C13-8C13 dup:2/2 ID:67B3
+ 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

+ ribosomal_protein * predicted using Genefinder; Similarity to Prototheca mitochondiral ribosomal protein S11
 CG5184 (SW:RT11_PROWI); cDNA EST yk372e6.3 comes from this gene; [Ribosomal_S11] CG5184 GM13519 89E13-89E13 ID:83A11
 + transporter * DMC171D11 * DMMDR49_2 Mdr49 * multidrug resistance protein (MRP2)(aa) * multidrug resistance protein
 CG6214 (ABCC3)(aa) [ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG6214 LD28149 33F2-33F3 ID:87C10
 CG10428+ RCC1_2, SAM_BIND CG10428 dup:3/5 ID:89B11
 + 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
 + enzyme * acyl-CoA oxidase (EC 1.3.3.6), peroxisomal - human(aa) * 6e-52 CAO_YEAST ACYL-COENZYME A OXIDASE
 CG9709 (ACYL-COA OXIDASE) ac * 1e-111 similar to ACYL-COEN CG9709 LD30186 57D12-57D12 dup:2/2 ID:89F10
 + 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
 + 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
 + 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
 CG9165 61F7-61F7 dup:2/2 ID:97D8
 + 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
 CG1951 ID:98F2