

Table S5

genes with four expression peaks

CG5857	+ unknown * CG5857 LD42327 95C-95C dup:2/2 ID:101E3 + Grip91 cytoskeletal_structural_protein * gamma-tubulin interacting protein(aa) * gamma-tubulin ring protein Dgrip91(aa) * 1e-123 spindle pole body protein spindle pole body protein spc98[DEHYDRATASE_SER_THR] CG10988 LD42379 12B7-12B7 dup:3/4
CG10988	ID:101E5 + unknown * 6e-08 No definition line found * 1e-13 signal peptidase:SUBUNIT=12kD * 3E-97* 1e-07 No definition line found
CG2310	[ATP_GTP_A] CG2310 LD43791 99B3-99B3 ID:102F8 + BG:BACR48E02.4 cell_adhesion * Ras suppressor protein 1(aa) * 3e-07 adenylate cyclase * 3e-06 CHAO_DROME CHAOPTIN PRECURSOR (PHOTORECEPTOR CELL-SPECIFIC MEMBRANE PROTEIN) * 3e-63 [LRR // LEURICHRPT] CG9031 LD43891
CG9031	36E3-36E3 ID:102G5 + SPT4 enzyme * 3e-13 SPT4_YEAST TRANSCRIPTION INITIATION PROTEIN SPT4 SPT4 pro * 6e-30 contains similarity to
CG12372	Saccharomyces cerevisiae Spt4 * 7e-39 unknown * 1e-39 CG12372 LD44495 49B5-49B5 ID:103D2 + sut1 transporter * metabolite transport protein(aa) * membrane transporter like protein(aa) * ERD6 protein(aa) * solute carrier family (facilitated glucose transport)[SUGRTRANSPORT // SUGAR_TRANSPORT_2 // su] CG8714 LD44652 44A4-44A4 dup:4/4
CG8714	ID:103E4 + unknown * HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME II(aa) * 1e-19 hypothetical protein YDR492w
CG7530	- yeast (Saccharomyces cerevisiae) (U * 5e-26 C43G2 CG7530 LD44720 88D2-88D2 dup:3/3 ID:103E8 + 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 + EG:34F3.8 transporter * /match=(desc;; /match=(desc;; /match=(desc;; /match=(desc;; /motif=(desc;; the EST /match=(desc;;
CG7359	/match=(desc;; /match=(desc;; /match=(desc;; /mot [SYNAPTOBREVIN // synaptobrevin] CG7359 LD45288 1C2-1C2 ID:104B6 + enzyme * 1e-45 ESTs and come from this gene. th * unknown * BIOC_SERMA BIOTIN SYNTHESIS PROTEIN BIOC the p *
CG8067	CG8067 LD45826 50C22-50C23 ID:104F9 + ash2 transcription_factor * ash2 * trithorax protein ASH2 * 6e-83 Y17G7B.2a * 1e-134 similar to Drosophila ash2
CG6677	[SPRY_DOMAIN // NLS_BP] CG6677 LD46053 96A17-96A17 ID:104H8 + unknown * 2e-16 YKJ2_CAEEL HYPOTHETICAL 36.9 KD PROTEIN C02D5.2 IN CHROMOSOME III * 1e-05 INIP_HUMAN
CG9796	GAMMA-INTERFERON-INDUCIBLE PROTEIN IP-30 PRECURSOR * 4e-1 CG9796 LD47508 87E10-87E10 dup:3/3 ID:106E4 + cell_cycle_regulator * sorting nexin 9(aa) * 2e-11 YJD6_YEAST HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION * 5e-74 similar to PhoX homologous domain, pres[PX // BEM_DOMAIN // SH3DOMAIN // SH3] CG6757
CG6757	LD47602 67B13-67B13 ID:106F10 + peptidase * [pdb]1AYE Human Procarboxypeptidase A2(aa) * CARBOXYPEPTIDASE B(aa) * 3e-37 YHT2_YEAST HYPOTHETICAL 49.8 KD PROTEIN IN ACT3-YCK1 INTERGENIC REGION [CARBOXYPEPT_ZN_1 // CRBOXYPTASEA // Zn_]
CG3108	CG3108 LP01044 5B6-5B8 ID:107D1 + unknown * 3e-53 YEF1_YEAST HYPOTHETICAL 55.9 KD PROTEIN IN GDA1-UTR2 INTERGENIC REGION * 1e-115
CG6145	dJ283E3.6.1 (PUTATIVE novel protein similar to many (archae)ba CG6145 LP03268 50B4-50B5 dup:2/2 ID:108E7
CG10840	+ translation_factor * kDa protein; Fun12p(aa) * 1e-120 YAD5_YEAST 112.3 KD PROTEIN IN PYK1-SNC1 INTERGENIC

REGION * 1e-11 waclaw * 3e-18 similar to initiation factor IF-[ELONGATNFCT // NLS_BP // GTP_EFTU // AT] CG10840 LP03795
 63D2-63D2 ID:108G5
 + serpin * SQUAMOUS CELL CARCINOMA ANTIGEN (SCCA-2) (LEUPIN)(aa) * ALPHA-1-ANTIPROTEINASE PRECURSOR
 CG6687 (ALPHA-1-ANTITRYPSIN) (ALPHA-1-PROTEINASE INHIBITOR)(aa) * [serpin] CG6687 LP04383 88E7-88E7 ID:108H12
 + mas endopeptidase * mas * masquerade precursor - fruit fly (Drosophila melanogaster) * 5e-30 similar to peptidase family S1
 (trypsin family) * 4e-38 KAL_MOUSE PLASMA KA [trypsin // CHYMOTRYPSIN // TRYPSIN_HIS] CG15002 LP06006 64A12-64A12
 CG15002 ID:109F11
 CG4449 + unknown * CG4449 LP06117 97B1-94E9 ID:109G2
 + Khc motor_protein * DMKINHCA_2 Khc * cos * KINESIN HEAVY CHAIN(aa) * recombinant kinesin heavy chain(aa) [kinesin //
 CG7765 KINESIN_MOTOR_DOMAIN1 // KIN] CG7765 SD02406 53A-53A dup:1/2 ID:114A9
 + transcription_factor * ovo * zinc-finger-motif-protein * zinc finger protein, subfamily 1A, (Ikaros)(aa) * DMSPALTR_3 salr
 CG11247 [ZINC_FINGER_C2H2 // zf-C2H2 // ZINC_FIN] CG11247 SD02478 78F4-79A ID:114B9
 + transcription_factor_binding * ESC virilis, Peptide, * extra sex combs protein - fruit fly (Drosophila melanogaster)(aa) * BLASTX
 CG5202 7.9E-26 Precis coenia transcription[GPROTEINBRPT // WD40_REGION // WD40] CG5202 SD02661 33B9-33B9 dup:2/2 ID:114E4
 + unknown * coded for by C. elegans cDNA cm04e9; coded for by C. elegans cDNA CESAC59F(aa) * unknown(aa) * *
 CG18112 CG18112 SD03121 99C5-99C5 ID:115C3
 + I(2)not transmembrane_receptor * DMNOTB_2 I(2)not * Not22(aa) * putative Dol-P-Man dependent alpha(1-3) mannosyltransferase
 CG4084 involved in the biosynthesis of the lipid-linked oligosac CG4084 SD03142 59F5-59F5 ID:115C6
 + transcription_factor transcription factor involved in DNA packaging MBD, NLS_BP, ZINC_FINGER_C2H2 CG10042 SD03893
 CG10042 dup:1/2 ID:116D1
 CG14971 + unknown Homo sapiens CGI-15 protein CG14971 SD04505 ID:117D9
 CG7623 + transporter CG7623 SD04658 dup:1/2 ID:117F5
 108000000+ GTP_binding 108000000 SD05004 ID:118C1
 CG4141 + Pi3K92E enzyme 1-phosphatidylinositol 3-kinase PI3K-C2, PI3K-rbd, PI3Ka, PI3-PI4-kinase CG4141 SD05105 ID:118C9
 CG17148 + enzyme CG17148 SD05284 ID:118E10.2
 + eIF-4E translation_factor * Eif4E * 2e-28 IF4E_YEAST EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E)
 CG4035 (MRNA CA * 1e-121 IF4E_DROME EUKARYOTIC TRANSLATION INITIATION CG4035 SD05406 67B2-67B2 dup:3/4 ID:118G2.2
 CG10254 + enzyme CG10254 SD05555 dup:4/4 ID:119A2.2
 CG8877 + CG8877 SD05715 dup:2/2 ID:119C11.2
 CG11874 + enzyme CG11874 SD05769 dup:3/3 ID:119D7.2
 CG12016 + enzyme * [ATP_GTP_A] CG12016 SD05789 63C5-63C5 dup:1/3 ID:119D9
 CG1553 + CG1553 SD06318 dup:4/5 ID:119G2.2
 CG11844 + unknown CG11844 SD06613 dup:1/2 ID:120A6.2
 + unknown * 2e-83 inserted at base 5' end of P element Inverse PCR * 1e-124 inserted at base Both 5' and 3' ends of P element
 CG2765 Inverse PCR * CG2765 SD07219 60E5-60E5 dup:3/5 ID:120G10.2
 CG12397 + transcription_factor * crol * 1e-32 CROL ALPHA * 1e-17 final three exons similar to C2H2-type zinc finger * 1e-31 kruppel-type

zinc finger protein [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG12397 GH01265 42B3-42B3 ID:30B9

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

CG5629 + BcDNA:GH03502 unknown * unknown(aa) * 3e-55 YII3_YEAST HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION * 1e-75 inserted at base Both 5' and 3' ends of P element CG5629 GH03502 91F4-91F4 dup:1/2 ID:32A8

+ Lim1 transcription_factor * HOMEODOMAIN PROTEIN LIM-1(aa) * Lim3 * 7e-20 LIM homeodomain transcription factor * 9e-30 homeotic protein lin-11 - Caenorhabditis elegans (fragment) [HOMEODOMAIN_1 // homeobox // HTHREPRESSR /] CG11354 GH04929

CG11354 8A4-8B1 ID:33C4

+ 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

CG4918 + CG4918 dup:1/2 ID:35A5

+ protein_kinase * DMDFR2_2 btl * 3e-43 ABL_DROME TYROSINE-PROTEIN KINASE DASH/ABL protein-tyrosine * 7e-41 Tyrosine-protein kinase ABL-1; cDNA EST comes from th[PROTEIN_KINASE_TYR // TYRKINASE // PROT] CG17309 GH10267

CG17309 86E18-86E19 dup:1/2 ID:37G1

+ BcDNA:GH08860 * 9e-86 cif1 * 1e-37 predicted using Genefinder; similar to trehalose phosphate synthase * 4e-86 TPS1_KLULA

CG4104 ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (U [TrehaloseP_syn] CG4104 24F1-24F1 dup:1/3 ID:37G7

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

CG3620 + T-cp1 chaperone * DMTCP1_2 T-cp1 * T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA)(aa) * 1e-178 T complex protein (put.); putative * similar to T-complex [TCP1_1 // TCP1_2 // TCP1_3 // TCOMPLEX] CG5374 GH10347 94B4-94B4 ID:37H1

CG5374 + unknown * 1e-07 cDNA clone for has a 574-bp insertion at position * BLASTX 8.8E-06 SRP40|Suppressor of mutant AC40 subunit of RNA polymerase * [PRO_RICH // NLS_BP] CG9056 GH10459 13F7-13F8 dup:1/2 ID:38A3

CG9056 + tumor_suppressor * 3e-09 /match=(desc; /ma * 3e-16 predicted using Genefinder; Similarity to Human leukocyte surface * 4e-26 CD82_MOUSE CD82 ANTIGEN (INDUCIBLE MEMBRANE [transmembrane4 // TMFOUR // TM4_2] CG4999 GH11168 66E3-66E3 ID:38F10

CG4999 + transcription_factor * zinc finger protein(aa) * patched related protein translocated in renal cancer(aa) * protein(aa) * required to degrade misfolded ER lumenal and [zf-C3HC4 // PRO_RICH // ZF_RING] CG1937 GH11117 100E3-100E3 dup:1/2 ID:38F5

CG1937 + Rpt5 endopeptidase * contains similarity to the AAA family of ATPases (Pfam; AAA, score; 259.07); most similar to human probable 26S protease subunit TBP-1 * putative [AAA // MITOCH_CARRIER // ATP_GTP_A] CG10370 GH12068 95B7-95B7 ID:39D12

CG10370 + bw transporter * BROWN PROTEIN(aa) * DMBROWN_1 bw * brown protein(aa) * BROWN PROTEIN(aa) [ATP_GTP_A2 // ABC_tran // DA_BOX] CG17632 GH12107 59E-59E3 dup:2/2 ID:39E3

CG17632 + unknown * protein(aa) * lml1p(aa) * 9e-46 YJ9G_YEAST HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6

CG12090 INTERGENIC REGION * 4e-75 Proline rich domain; cDNA EST comes CG12090 GH12915 62A5-62A6 dup:3/3 ID:40C3

+ chaperone * t-complex polypeptide 20(aa) * 1e-142 TCPZ_YEAST T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) * 7e-46 CCT-gamma protein * 1e-178 TCPZ_ [TCP1_1 // TCP1_2 // TCP1_3 // TCOMPLEX] CG8231 GH13725

CG8231 13E17-13E17 ID:40G12

+ unknown * TRANSMEMBRANE PROTEIN PFT27(aa) * probable membrane protein; Ybr187wp(aa) * 5e-34 YB37_YEAST
 CG4196 HYPOTHETICAL 30.3 KD PROTEIN IN MBA1-RPS13 INTERGENIC R [UPF0016] CG4196 GH14710 88E7-88E7 ID:41G4
 + unknown * 4e-21 YS48_CAEEL HYPOTHETICAL 66.5 KD PROTEIN ZK177.8 IN CHROMOSOME II (U * 2e-20
 MG11_MOUSE INTERFERON-GAMMA INDUCIBLE PROTEIN MG11 unkn * 4e-20 hy CG9670 LD25913 76A5-76A6 dup:3/3
 CG9670 ID:44B11
 + unknown * Putative homolog of subunit of bovine prefoldin, a chaperone comprised of six subunits; Gim5p(aa) * c-myc binding
 CG7048 protein MM-1(aa) * 4e-21 YMJ4_YEAS CG7048 LD25740 94B4-94B4 ID:44B4
 + endopeptidase serine proteinase [Anopheles gambiae] CHYMOTRYPSIN, TRYPSIN_CATAL, TRYPSIN_HIS] CG11836
 CG11836 LD25830 dup:2/2 ID:44B8
 CG2994 + CG2994 LD26546 dup:4/4 ID:44E6
 + signal_transduction homology to actin interacting protein 1 and WD repeat-containing protein 1 GPROTEINBRPT, WD40,
 CG10724 WD40_REGION CG10724 LD27045 dup:2/3 ID:44G2
 + Dp1 DNA_binding * 2e-44 SCP160 * 4e-09 KH-domain putative RNA binding protein * 951003: Homology with human
 lipoprotein-binding protein (PIR Acc. * high density lipop [KH-domain // KH_DOMAIN // NLS_BP] CG5170 LD29992 55C10-55C11
 CG5170 dup:1/5 ID:46G2
 + SNF4Agamma protein_kinase * SNF4A ggr; * protein kinase protein serine/threonine kinase) map_position:93C * 8e-29
 SNF4_YEAST NUCLEAR PROTEIN SNF4 (REGULATORY PROTEIN CAT3) * 1 [CBS // SNF4_REP // NLS_BP] CG17299 LD30628
 CG17299 93C4-95F5 dup:1/11 ID:47C1
 + unknown * xenotropic and polytropic murine leukemia virus receptor X3(aa) * polytropic murine leukemia virus receptor
 CG7536 SYG1(aa) * predicted using Genefinder; CG7536 LD30826 16F7-16F7 ID:47D1
 + mub RNA_binding * DMMUB_6 mub * PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X)
 (CBP)(aa) * nucleic acid binding protein(aa) * 4e-13 YB83_YEAST HYPOTHETI [KH-domain // KH_DOMAIN] CG7437 LD32520
 CG7437 79B1-79B1 ID:48C7
 + electron_transfer * 1e-11 C05E11.1 gene product * 2e-07 hypothetical protein * 3e-45 inserted at base Both 5' and 3' ends of P
 CG8735 element Inverse PCR * [CYTOCHROME_C] CG8735 LD34731 44D-44D2 dup:3/3 ID:49E11
 CG10671 + unknown * cDNA EST yk481g5.5 comes from this gene(aa) * * CG10671 GH01192 64C12-64C12 ID:54B9
 CG15217 + transmembrane_receptor * CG15217 GH01875 40C2-40C2 ID:54H7
 + unknown * 4e-11 YMH6_CAEEL HYPOTHETICAL 19.1 KD PROTEIN F58A4.6 IN CHROMOSOME III * * CG12123
 CG12123 GH02722 7E6-7E6 ID:55D12
 + enzyme * Sar oxidase(aa) * * 7e-63 cDNA EST comes from this gene; cDNA EST co * 2e-41 unknown protein CG3270
 CG3270 GH02863 42C6-42C6 dup:2/2 ID:55E5
 + transporter * 8e-16 GPI-anchored protein - mouse (fragment) hum * 2e-16 P137_HUMAN GPI-ANCHORED PROTEIN P137
 CG4144 GPI-anchored prote * 2e-17 gram negative binding prot CG4144 GH02872 75D2-75D2 dup:3/3 ID:55E6
 CG5914 + unknown * 1E-179 * * CG5914 GH03315 5D2-5D2 ID:55H6
 CG4782 + unknown * CG4782 GH03334 86D6-86D6 ID:55H7
 CG9162 + unknown * CG9162 GH05093 26B3-26B4 ID:57F4

CG11344 + unknown * CG11344 GH05223 21E2-21E2 ID:57G3
+ ana unknown * ana * neuroblast proliferation inhibitor ana - Drosophila(aa) * ana * neuroblast proliferation inhibitor=ana eye disc,
CG8084 Peptide, [WW_DOMAIN_1] CG8084 GH07389 45A9-45A10 ID:59F6
CG14689 + unknown CG14689 GH07528 ID:59G5
CG8568 + unknown * 4e-05 C09D4.2 gene product * * [NLS_BP] CG8568 GH07892 16A4-16A5 dup:1/2 ID:60B9
+ ligand_binding_or_carrier * DMC30B8 * retinaldehyde-binding protein 1(aa) * tocopherol (alpha) transfer protein (ataxia
(Friedreich-like) with vitamin E deficiency)(aa) * 62D[CRETINALDHBP // CRAL_TRIO] CG10237 GH08711 37E3-37E3 dup:2/3
CG10237 ID:60H5
CG7841 + unknown * CG7841 GH09068 71C4-71C4 dup:1/2 ID:61D1
+ enzyme * sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)(aa) * SPHINGOMYELIN
PHOSPHODIESTERASE PRECURSOR (ACID SPHINGOMYELINASE)(aa [PHOSPHO_ESTER // SAP_B] CG3376 GH09489 60C1-
CG3376 60C2 dup:2/5 ID:61G4
+ BcDNA:GH07066 enzyme * 8e-47 PLSB_CAEEL PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR
(GPAT) * 6e-77 PLSB_MOUSE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (G [GLYCEROL_ACYLTRANS]
CG5508 CG5508 GH11892 98B2-98B2 dup:2/2 ID:63H8
+ unknown * 4e-14 probable membrane protein YOL084w - yeast (Saccharomyces cerevisiae) * 1e-103 protein * 6e-17
CG11210 hypothetical protein * 3e-54 inserted at base Bo CG11210 GH13794 44A4-44A4 ID:65F9
+ transporter * UDP-galactose transporter related(aa) * 4e-18 probable membrane protein YPL244c - yeast (Saccharomyces
CG5802 cerevisiae) * 2e-16 No definition line found CG5802 95F1-95F1 dup:2/3 ID:66F5
CG8420 + * [ER_TARGET] CG8420 85D2-85D3 dup:3/3 ID:67F12
+ BcDNA:GH06717 transporter * OLIGOPEPTIDE TRANSPORTER, KIDNEY ISOFORM (PEPTIDE TRANSPORTER 2) (KIDNEY
H+/PEPTIDE COTRANSPORTER)(aa) * OLIGOPEPTIDE TRANSPORTER, KIDNEY ISOFORM (P [PTR2 // PTR2_1 // PTR2_2]
CG2930 CG2930 GH18049 4A1-4A1 dup:2/3 ID:70B9
+ function_unknown * 4e-66 probable membrane protein YLL031c - yeast (Saccharomyces cerevisiae) * 2e-53 No definition line
CG12263 found * 4E-86* 2e-63 ORF YLL031c CG12263 GH18119 55C11-55C11 dup:1/2 ID:70C6
+ RNA_binding * putative RNA binding protein(aa) * 3e-05 TUD_DROME MATERNAL TUDOR PROTEIN posterior-group
protein t * 8e-07 YQK1_CAEEL HYPOTHETICAL 55.9 KD PROTEIN [KH-domain // KH_DOMAIN // TUDOR] CG7082 GH18329
CG7082 23D1-23D1 dup:3/3 ID:70E4
+ translation_factor * GTP binding protein similar to S. cerevisiae HBS1(aa) * elongation factor alpha(aa) * Elf * DMEF1AF2_8
CG1898 Ef1 agr;100E [ELONGATNFCT // GTP_EFTU // ATP_GTP_A] CG1898 GH18819 62E3-62E3 ID:71A1
+ transcription_factor_binding * 2e-47 WEB1_YEAST WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31) * 2e-07
fizzy-related protein * 9e-37 predicted using Genefinder; Similarity to Yeas [WD40_REGION // WD40] CG8266 GH19061 44F7-44F8
CG8266 dup:1/3 ID:71B11
CG13458 + unknown * 1E-160* * [COPPER_BLUE] CG13458 GH20023 71B2-71B2 ID:72B12
CG10494 + unknown * CG10494 GH20554 57E-57E dup:2/2 ID:72G12
CG9009 + BcDNA:GH02901 enzyme * hypothetical protein(aa) * 5e-11 LCFA_HAEIN LONG-CHAIN-FATTY-ACID--COA LIGASE (LONG-

CHAIN ACYL-COA SYNTHETASE) > * LCFA_ECOLI LONG-CHAIN-FATTY-ACID CG9009 GH20984 13A5-13A5 dup:2/4 ID:73C10
+ ribosomal_protein * ribosome recycling factor(aa) * RRF_HAEIN RIBOSOME RECYCLING FACTOR (RIBOSOME
CG4447 RELEASING FACTOR) (RRF) * RRF_CLOPE RIBOSOME RECYCLING FACTOR (RIBOS CG4447 GH21184 67B1-67B1 dup:2/2
ID:73E11
+ unknown * 2e-52 gene C35D10.2 protein - Caenorhabditis elegans similar to * 3e-81 RGS-GAIP interacting protein GIPC
CG11546 GLUT1 * 7e-81 RGS-GAIP interacting protein [PDZ] CG11546 GH21964 44A8-44B dup:1/2 ID:74C11
+ transporter * similar to Mitochondrial carrier proteins (2 domains); cDNA EST yk309c6.5 comes from this gene; cDNA EST
CG5805 yk309c6.3 comes from this gene; cDNA EST [mito_carr // MITOCARRIER // MITOCH_CARR] CG5805 GH22160 98E1-98E1 dup:2/2
ID:74E10
+ transcription_factor * eyg * 9e-46 Eyegone * 1e-38 similar to 'Paired box' domain, homeobox protein (paired subfamily * 2e-41
CG10704 PAX3_MOUSE PAIRED BOX PROTEIN PAX-3 pax-3 p[PAX // HOMEBOX_1 // homeobox // HOMEBOX] CG10704 GH22493 69B3-
69B4 ID:74H8
+ unknown * BLASTX 2.0E-06 Theileria parva schizont/sporozoite surface protein gene, partial cds.(dna) * * [NLS_BP]
CG12316 CG12316 GH22749 71B2-71B2 ID:75C3
+ electron_transfer * GEC-3(aa) * 3e-43 coded for by C. elegans cDNA yk51h9.5; coded for by C. elegans cDNA yk117c2.5; c *
CG17843 1e-64 quiescin Q6 quiescin * 2e-66 GEC-3 [THIOREDOXIN_2] CG17843 GH22889 96B6-96B6 dup:2/2 ID:75E2
+ enzyme * 5e-20 T10H10.3 gene product * 9e-07 ubiquitin protein ligase * 3e-07 WWP1 * 1e-05 S-SCAM beta
CG13832 [WW_rsp5_WWP // WW_DOMAIN_2] CG13832 GH23265 94D13-94D13 ID:76A4
+ transporter * 3e-69 predicted using Genefinder; cDNA EST comes from this g * 3e-07 tetracycline resistance protein * similar
CG8054 to translocase * contains similarity [PRO_RICH // NLS_BP] CG8054 GH23453 45B1-45B1 ID:76C6
CG4848 + transporter * 4e-12 ldlBp * * CG4848 GH23636 87B6-87B6 dup:3/3 ID:76E12
+ unknown * growth factor-responsive protein, vascular smooth muscle - rat(aa) * 3e-47 Weak similarity with apoptosis protein
CG1114 RP-8; cDNA EST * SM-20 * CG1114 GH23732 83A1-83A1 ID:76F11
+ rdgA enzyme * DMDKA_1 rdgA * KDGE_DROME EYE-SPECIFIC DIACYLGLYCEROL KINASE (RETINAL DEGENERATION A
CG10966 PROTEIN) (* DMDKA_1 rdgA * [ANK_REP // DAGKa // ank // DAGKc // ANK] CG10966 GH23785 8C4-8C7 ID:76G8
+ 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
+ transcription_factor * DMSUHW_6 su(Hw) * crol * zf43C * 7e-08 zinc finger 30C [zf-C2H2 // ZINC_FINGER_C2H2 //
CG7101 ZINC_FIN] CG7101 GH24178 17E1-17E1 ID:77C7
+ signal_transduction * EPHRIN-B1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 2) (LERK-2)
CG1862 (ELK LIGAND PRECURSOR) (ELK-L) (XLERK)(aa) * 4e-13 cek5 receptor ligand [Ephrin] CG1862 GH24276 102C5-102C5 ID:77D9
CG1888 + unknown * [NLS_BP] CG1888 GH24468 45F1-45F1 ID:77F2
+ unknown * ATP(GTP)-binding protein(aa) * HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III(aa) * weak
CG10222 similarity to ATPases(aa) * Yor262wp(aa) [ATP_GTP_A] CG10222 GH25024 70A7-70A7 ID:78B10
+ unknown * hypothetical 43.2 kDa protein(aa) * predicted using Genefinder; Similarity to Yeast hypothetical protein YAE2
CG7011 (SW:YAE2_YEAST); cDNA EST comes from t CG7011 GH25868 71B3-71B3 dup:2/2 ID:79C6
CG11700 + CG11700 dup:1/2 ID:80D5

+ unknown * 1E-38* 9e-24 inserted at base Both 5' and 3' ends of P element Inverse PCR * CG13130 GH26896 30F4-30F4
 CG13130 ID:80G1
 + unknown * 7e-07 probable membrane protein YOL031c - yeast (*Saccharomyces cerevisiae*) * 1e-11 SLS1_YARLI SLS1
 CG10420 PROTEIN PRECURSOR Sls1 protein precursor * 7e-83 i CG10420 GH27496 96C3-96C3 dup:3/4 ID:81E3
 + * 1e-15 YMB8_YEAST HYPOTHETICAL 43.7 KD PROTEIN IN OST6-PSP2 INTERGENIC REGION * 7e-23 No definition line
 CG8195 found * 2e-19 hypothetical protein * hypothe CG8195 52A13-52A13 ID:81F1
 + enzyme * 2e-32 YPT6_YEAST GTP-BINDING PROTEIN YPT6 YPT6 protein - yeas * 2e-34 rab6 * 3e-53 similar to ras-related
 protein * 9e-34 RB17_MOUSE RAS-RELATED PRO [ALDEHYDE_DEHYDR_CYS // ras // ATP_GTP_A] CG17515 GH27649
 CG17515 cyto_unknown ID:81F2
 + enzyme * G4 nucleic acid binding protein, involved in tRNA aminoacylation; Arc1p(aa) * PROBABLE METHIONYL-TRNA
 CG8235 SYNTHETASE (METHIONINE--TRNA LIGASE) (METRS)(a CG8235 GH27932 44F9-44F9 ID:82A6
 CG6050 + translation_factor CG6050 GM14682 ID:83C4
 + chaperone * HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR(aa) * DNAJ PROTEIN
 HOMOLOG (DROJ1)(aa) * 1e-06 SCJ1_YEAST SCJ1 PROTEIN SCJ1 protein [DnaJ // DNAJ_2] CG9089 LD21896 15B4-15B4
 CG9089 dup:2/2 ID:83E11
 + unknown * BRcore-Q1-Z1 protein - fruit fly (*Drosophila melanogaster*)(aa) * BROAD-COMPLEX CORE-TNT1-Q1-Z1 PROTEIN
 CG5166 (BRCORE-TNT1-Q1-Z1) (CONTAINS: BROAD-COMPLEX CG5166 LD22183 88F-88F dup:3/3 ID:83F9
 + nucleic_acid_binding * 3e-09 GOLI_DROME GOLIATH PROTEIN (G1 PROTEIN) regulatory protei * 1e-10 contains similarity
 to C3HC4-type zinc fingers (Pfam; zf-C3HC4.hmm, score; [zf-C3HC4 // PRO_RICH // NLS_BP // ZF_RI] CG6923 LD22771 86F6-
 CG6923 86F6 ID:83G8
 + * Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST comes from this gene; cDNA EST
 CG2221 comes from this gene; cDNA EST CG2221 9B14-9B14 dup:3/3 ID:84B2
 + peptidase * insulin-regulated membrane aminopeptidase IRAP(aa) * LEUKOTRIENE A-4 HYDROLASE (LTA-4 HYDROLASE)
 (LEUKOTRIENE A(4) HYDROLASE)(aa) * LEUKOTRIENE A-4 [ALADIPTASE // Peptidase_M1 // ZINC_PROT] CG10602 LD27070
 CG10602 37B4-37B5 ID:86B9
 + toc motor_protein * map_position:23D4 * 6e-30 Toucan protein * 8e-32 DMTOC toc * map_position:23D4 CG9660 LD27161
 CG9660 23D-23D3 dup:1/2 ID:86C6
 CG9028 + unknown * 2e-15 inserted at base 5' end of P element Inverse PCR * CG9028 LD27194 70C8-70C9 dup:2/2 ID:86D1
 CG7396 + unknown * [PPASE // NLS_BP] CG7396 LD27215 71E1-71E1 dup:2/2 ID:86D3
 CG8237 + Autosomal Highly Conserved Protein CG8237 LD27256 dup:2/2 ID:86D5
 + unknown * 8e-15 YKK3_CAEEL HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III >g *
 CG10795 YJ05_CAEEL HYPOTHETICAL 85.1 KD NUCLEASE C41D11.5 simila * CG10795 LD27358 57D11-57D11 dup:2/2 ID:86E3
 CG5466 + unknown CG5466 LD27620 dup:2/2 ID:86F11
 + NTPase enzyme * NTPase * 3e-37 GDA1_YEAST GUANOSINE-DIPHOSPHATASE (GDPASE) guanosine-dip * NTPase * 2e-56
 CG3059 similar to GDA1/CD39 (nucleoside phosphatase) family; cDNA [NLS_BP // GDA1_CD39] CG3059 LD27725 23B5-23B6 ID:86G12
 + transmembrane_receptor * contains similarity to M. musculus patched * 1e-21 No definition line found * [PEROXIDASE_1 //
 CG2019 5TM_BOX // NLS_BP] CG2019 LD27661 83C4-83C4 dup:3/4 ID:86G4

+ BG:DS01219.1 unknown * 1e-20 YKQ3_CAEEL HYPOTHETICAL 42.1 KD PROTEIN C06E1.3 IN CHROMOSOME III (L1 * *
 CG4482 CG4482 LD27791 35B9-35B9 ID:86H4
 + unknown * 5e-29 candidate adaptor protein CED-6 * 8e-05 m-Numb * 2e-07 E2a-Pbx1-associated protein * 3e-05 JIP-1 related
 CG11804 protein [PTB_DOMAIN // PID] CG11804 LD28347 45D7-45D8 ID:87D10
 CG6988 + CG6988 dup:1/3 ID:87F2
 + trio cytoskeletal_structural_protein huntingtin-associated protein interacting protein CRAL_TRIO, GRF_DBL, PH_DOMAIN,
 CG9208 RhoGEF, S] CG9208 LD28463 dup:2/3 ID:87F3
 + structural_protein * 0.000000000006 * 2e-06 nonmuscle myosin-II heavy chain * 2e-07 Identity to myosin heavy chain C
 CG12702 (SW:MYSC_CAEEL); cDNA EST EMBL:M8 * 0.0000001 CG12702 18F1-18F2 dup:1/3 ID:88G4
 + 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 dup:2/2
 CG5345 ID:95F11
 CG5541 + unknown * [C_TYPE_LLECTIN_1] CG5541 LD37145 13A8-13A8 dup:3/3 ID:96E6
 CG13601 + unknown * 7e-08 No definition line found * * CG13601 LD37258 95C-95C ID:96F10
 + transporter * cationic amino acid transporter-1(aa) * solute carrier family (cationic amino acid transporter, y+ system), member
 1(aa) * LOW-AFFINITY CATIONIC AMI [aa_permeases // AMINO_ACID_PERMEASE_2] CG11128 LD37241 79F5-79F6 dup:2/2
 CG11128 ID:96F8
 + cell_cycle_regulator * non-p53 regulated PA26-T1 nuclear protein(aa) * 2e-72 p53 regulated PA26-T3 nuclear protein * p53
 CG11299 regulated PA26-T2 nuclear protein * CG11299 LD39604 59F5-59F6 ID:98G2
 + Abl protein_kinase * DMTKABL3_2 Abl * Dsrc41(aa) * TYROSINE-PROTEIN KINASE DASH/ABL(aa) * 2e-16 SPK1_YEAST
 PROTEIN KINASE SPK1 (SERINE-PROTEIN KINASE 1) [SH2DOMAIN // SH3DOMAIN // PRO_RICH // P] CG4032 LD39618 77A3-
 CG4032 73B1 ID:98G4
 + protein_kinase * 9e-52 SSK2_YEAST SERINE/THREONINE PROTEIN KINASE SSK2 (SUPPRESSOR OF SENSOR KINASE
 2) * 5e-34 protein kinase (EC 2.7.1.37) 2B - fruit fly (Drosop[PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG7717 LD39970
 CG7717 93F9-93F9 dup:3/5 ID:99B2
 + unknown * DIMETHYLADENOSINE TRANSFERASE (S-ADENOSYLMETHIONINE-6-N', N'-ADENOSYL(RRNA)
 DIMETHYLTRANSFERASE) (16S RRNA DIMETHYLASE) (HIGH LEVEL KASUGAMYCIN RESI [RrnaAD] CG7319 LD40326 71C2-
 CG7319 71C2 dup:2/2 ID:99D9
 + BcDNA:GH02220 enzyme * OXA1 homolog - human(aa) * 3e-25 OXA1_YEAST CYTOCHROME OXIDASE BIOGENESIS
 PROTEIN OXA1 PRECURSOR * 2e-29 Similarity to Human OXA1HS protein (cytochr CG6404 LD40470 67F4-67F4 dup:3/3
 CG6404 ID:99E10
 + for unknown * CGMP-DEPENDENT PROTEIN KINASE, ISOZYME FORMS T1/T3 (CGK) (PROTEIN FORAGING)(aa) * *
 CG10033 CG10033 LD40611 25B1-25B1 dup:3/4 ID:99F10
 + transcription_factor_binding * Fas-binding protein(aa) * ETS1 associated protein EAP1/Daxx(aa) * 2e-13 Fas-binding protein *
 CG9537 9e-09 Fas-binding protein Daxx [NLS_BP] CG9537 LD30183 26D6-26D7 dup:3/5 ID:Farhad's BB9
 + enzyme * 2e-25 pancreatic lipase related protein * 1e-26 pancreatic lipase-related protein * 1e-31 phospholipase, GPL -
 CG4267 guinea pig * LIP1_HUMAN PANCREAT[DOLALLERGEN // TAGLIPASE // ESTERASE //] CG4267 ck01198 22D3-22D3 dup:2/2

ID:Farhad's BD12

CG13800 + unknown * [PRO_RICH // NLS_BP] CG13800 ck01201 62E-62E dup:2/2 ID:Farhad's BE1

CG10130 + CG10130 sec61b ID:Farhad's BF2