

Table S4

genes with three expression peaks

+ * 3e-25 predicted using Genefinder; cDNA EST comes from this * 4e-38 SPC1_HUMAN MICROSOMAL SIGNAL PEPTIDASE KD
CG1751 SUBUNIT (SPC25) * 3e-38 SPC1_CANFA MICR CG1751 10B17-10C1 dup:1/2 ID:101A12
CG17602+ unknown * CG17602 LD42024 20A1-20A1 ID:101B4
+ Dap160 signal_transduction * Dap160 * 0.000000000000000004* dynamin associated protein isoform Dap160-1 * 5e-08 hum-1 [EPS //
CG1099 EF_HAND // SH3DOMAIN // SH3 // N] CG1099 LD42142 39B1-39B1 ID:101C2
+ qua actin_binding * qua * QUAI_DROME VILLIN-LIKE PROTEIN QUAIL villin homolog qua * 9e-18 similar to gelsolin; cDNA EST
CG6433 comes from this gene * 3e-71 putative actin-bin [GELS // GELSOLIN] CG6433 LD42165 36C4-36C4 ID:101C8
+ enzyme * DMPEROX_5 Pxd * 7e-87 PERO_DROME PEROXIDASE PRECURSOR myeloperoxidase (EC 1.11. * similar to
peroxidase; cDNA EST comes from this gene; * 4e-93 PERM [MYB_2 // ANPEROXIDASE // peroxidase //] CG10211 LD42267 37A1-37A1
CG10211 ID:101D7
CG17129+ transcription_factor * [NLS_BP] CG17129 LD42420 61C9-61C9 dup:2/2 ID:101E10
+ 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
+ Aats-glupro enzyme * Aats-glupro * 1e-168 YH10_YEAST PUTATIVE PROLYL-TRNA SYNTHETASE YHR020W (PROLINE--TRNA
LIGASE) (PRORS * SYEP_DROME MULTIFUNCTIONAL AMINOACYL-TRNA S [WHEP-TRS // AA_TRNA_LIGASE_I // tRNA-sy] CG5394
CG5394 LD42739 95C13-95D1 ID:101F11
+ enzyme * 3e-76 alpha esterase * 1e-40 strong similarity to the type-B carboxylesterase/lipase family e * 3e-47 pdb|1MAH|A Chain A,
CG9858 Fasciculin2 - Mouse Acetyl [TONB_DEPENDENT_REC_1 // ESTERASE // COe] CG9858 LD42723 57F4-57F4 ID:101F9
CG15312+ transmembrane_receptor * [ig] CG15312 LD42756 9B1-9B1 ID:101G1
+ Cdic motor_protein * Cdic * cytoplasmic dynein intermediate chain isoform DIC5b(aa) * cytoplasmic dynein intermediate chain isoform
CG18000 DIC3a(aa) * 3e-83 cytoplasmic dynein CG18000 LD42953 19C1-19C1 dup:1/2 ID:101G10
+ unknown * 9e-56 cDNA EST comes from this gene; cDNA EST co * * [AROMATIC_AA_PERMEASE_2] CG5262 LD43196 77C1-
CG5262 77C1 ID:102B5
+ motor_protein * 7e-10 NUF1_YEAST NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110) * 2e-14 nonmuscle
CG5740 myosin-II heavy chain * 1e-10 Similarity to Human endosoma CG5740 LD43488 94A-96C1 dup:2/2 ID:102D1
CG4867 + unknown * 1e-21 BC10_HUMAN BLADDER CANCER KD PROTEIN 10kD protein * 1E-136* CG4867 LD43519 64E-64E ID:102D3
CG4702 + unknown * CG4702 LD43816 88A1-88A1 ID:102F9
+ unknown * protein kinase cAMP-dependent protein kinase) unlocalised cAMP-dependent protein kinase) map_position:77F * *
CG18677 CG18677 LD43873 77E8-77E8 ID:102G2
+ Prosbeta2 endopeptidase * Pros bgr;2 * 3e-71 PRCF_YEAST PROTEASOME COMPONENT PUP1 PRECURSOR (MACROPAIN
SUBUNIT PUP1) (PROTEIN * 1e-146 20S proteasome beta2 subunit * 4e-49 pr [PROTEASOME_B // PROTEASOME_PROTEASE //]
CG3329 CG3329 LD44234 71A3-71A3 ID:103A11
+ unknown * putative centromere protein(aa) * HYPOTHETICAL 75.7 KD PROTEIN T10F2.3 IN CHROMOSOME III(aa) * 6e-12
CG10107 SMT4_YEAST SMT4 PROTEIN SMT4 protein - yeast (CG10107 LD44235 65C3-65C3 dup:1/2 ID:103A12

CG1503 + unknown * CG1503 LD44327 19E7-19E7 ID:103B10
 + enzyme * isopeptidase T(aa) * 3e-68 UBPE_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (UBIQUITIN THIOLESTERASE 14) * 1e-125 Similar to ubiquitin carboxyl-term [UBA // UCH_2_1 // UCH_2_2 // UCH_2_3 //] CG12082 LD44295 63B10-
 CG12082 63B11 ID:103B7
 + chaperone * 5e-33 Similarity to Xenopus P58 protein cDNA EST * 3e-78 GP36b glycoprotein * 3e-83 coded for by C. elegans cDNA
 CG5510 yk74e11.5; coded for by C. elegans CG5510 95E3-95E3 dup:2/2 ID:103C4
 + Sb endopeptidase * trypsin-like serine protease(aa) * DMSTUBBLE_1 Sb * masquerade precursor - fruit fly (Drosophila melanogaster)(aa) * plasminogen activator, tiss[trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG4316 LD44584 89B9-89B9 dup:3/3
 CG4316 ID:103D10
 + unknown * 4e-14 YZG1_CAEEL HYPOTHETICAL 28.7 KD PROTEIN F13E6.1 IN CHROMOSOME X * 1e-13 D52 * 7e-20 tumor
 CG5174 protein D52-like hD54+ins2 isoform * 3e-14 CSPP28 CG5174 LD44733 55C11-55C11 dup:3/3 ID:103E10
 + DNA_binding * 4e-06 probable finger protein YOL054w - yeast (Saccharomyces cerevisiae) * 5e-22 contains similarity to C3HC4-
 CG13605 class zinc finger eleg * 1e-06 peroxis [zf-C3HC4] CG13605 LD44641 95D10-95D10 dup:2/2 ID:103E3
 + unknown * 5e-08 No definition line found * 5e-16 PSD-95/SAP90-associated protein-2 * 1e-16 PSD-95 binding protein * 1e-171
 CG8390 inserted at base Unknown 5' end of [NLS_BP] CG8390 LD44824 41E5-41E5 ID:103F11
 CG17260 + nucleic_acid_binding * [ZF_RING] CG17260 LD44813 23C5-23C5 ID:103F8
 + unknown * weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase * acyl-CoA thioesterase(aa) * contains weak
 CG1635 similarity to rat cytosolic acyl CG1635 LD44914 100D2-100D2 ID:103G3
 + cell_cycle_regulator * hypothetical protein(aa) * 8e-23 hypothetical protein YLR127c - yeast (Saccharomyces cerevisiae) * 3e-05
 CG3060 LI19_DROME LIN-19 HOMOLOG PROTEIN lin19 pro [CULLIN_2] CG3060 60A14-60A14 dup:2/3 ID:103H3
 + enzyme * protein(aa) * 3e-07 FMS1_YEAST FMS1 PROTEIN FMS1 protein - yeast (Saccharom * 6e-12 Cs protein [ADXRDTASE //
 CG17149 NAD_BINDING] CG17149 LD45081 77A4-77A4 ID:103H4
 + receptor * 1e-07 weak similarity with quinone oxidoreductase; cDNA EST * 2e-12 CGRP-receptor component protein; CGRP-RCP *
 CG4875 1e-13 CGRP-receptor component protei CG4875 LD45115 15B1-15B1 ID:103H8
 + unknown * fruit fly STS clone T7(dna) * PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT
 CG7217 71B)(aa) * PEROXISOMAL MEMBRANE PROTEIN PMP20(aa) * [AhpC-TSA] CG7217 LD45324 90E-90E dup:2/2 ID:104B9
 CG1780 + Idgf4 signal_transduction imaginal disc growth factor 4 Glyco_hydro_18 CG1780 ID:104D10
 CG4619 + unknown * CG4619 LD45607 30F1-30F1 dup:2/2 ID:104E4
 + unknown * partner of Ral-binding protein 1(aa) * 3e-09 PAN1_YEAST PAN1 PROTEIN poly(A)-specific ribonuclease (EC * 6e-06
 CG6192 PAST-1 * 3e-05 contain EF-hand-like c [EPS // PRO_RICH // EF_HAND_2] CG6192 LD45769 32D3-32D4 ID:104F7
 + unknown * forkhead (Drosophila) homolog (rhabdomyosarcoma)(aa) * forkhead protein FKHR(aa) * myeloid/lymphoid or mixed-
 CG3143 lineage leukemia (trithorax (Drosophila [Fork_head // FORKHEAD // FORK_HEAD_3] CG3143 LD45950 88A8-88A9 ID:104G8
 + enzyme * BLASTX 7.5E-52 FUM1[Fumarate hydratase (fumarase) (mitochondrial and cytoplasmic), converts L-malate to fumarate as
 CG4094 part of the TCA cycle(dna) * fum [DCRYSTALLIN // FUMRATELYASE // FUMARATE] CG4094 LD46083 6C7-6C7 ID:104H12
 + transporter * cystic fibrosis transmembrane conductance regulator(aa) * DMMDR49_2 Mdr49 * canalicular multispecific organic anion
 CG7627 transporter (ABC superfamily)(a[ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG7627 LD46040 29B2-29B2 dup:2/4 ID:104H4
 CG15081 + unknown * 5e-69 YG4W_YEAST HYPOTHETICAL 34.9 KD PROTEIN IN SMI1-PHO81 INTERGENIC REGION * 2e-29

L2CC_DROME L(2)37CC PROTEIN Cc protein - fruit fly (Drosop * 3 [PROHIBITIN // Band_7] CG15081 LD46344 55F2-55F2 ID:105C4
 + receptor * protein kinase C substrate 80K-H(aa) * similar to Human protein kinase C substrate, 80KD protein, heavy chain, SWISS-
 CG6453 PROT Accession Number * similar [LDLRA_2 // ER_TARGET // EF_HAND] CG6453 LD46533 36C4-36C4 ID:105D11
 + Cpr enzyme * NADPH-CYTOCHROME P450 REDUCTASE (CPR)(aa) * DMNCP450R_2 Cpr * NADPH--ferrihemoprotein
 reductase(aa) * 3e-92 NADPH-cytochrome P450 reductase precursor [oxidored_fad // FPNCR // FLAVODOXIN //] CG11567 LD46590
 CG11567 28C7-26C4 dup:4/4 ID:105E4
 + transcription_factor * 7e-06 MLP2_DROME MUSCLE LIM PROTEIN MLP84B muscle L * 2e-41 similar to LIM domain containing
 proteins (5 domains); cDNA EST yk * 1e-25 TES2_M[LIM_DOMAIN_1 // LIM // LIM_DOMAIN_2] CG11914 LD46723 73D1-73D3 dup:2/2
 CG11914 ID:105F4
 + Rpn7 endopeptidase * Subunit of the regulatory particle of the proteasome; Rpn7p(aa) * HYPOTHETICAL PROTEIN * 1e-66
 CG5378 hypothetical protein YPR108w - yeast (Saccharomyces c [PCI_DOMAIN // PCI] CG5378 LD47143 94B3-94B3 ID:106A8
 + enzyme * 3-hydroxyisobutyryl-coenzyme A hydrolase(aa) * 4e-37 YDAK_YEAST HYPOTHETICAL 56.3 KD PROTEIN IN ARO3-
 CG5044 KRS1 INTERGENIC REGION * 5e-89 similar to enoy [ECH] CG5044 LD47223 88F1-88F1 ID:106B5
 + endopeptidase * DMSTUBBLE_1 Sb * SERINE PROTEINASE STUBBLE (STUBBLE-STUBBLOID PROTEIN)(aa) * 2e-32 similar to
 plasminogen and to trypsin-like serine proteases elega [trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG4386 LD47230 58A2-58A2
 CG4386 ID:106B7
 + enzyme * VITELLOGENIN II PRECURSOR (YOLK PROTEIN 2)(aa) * lipoprotein lipase precursor(aa) * Chain A, Triacylglycerol
 CG5966 LipaseCOLIPASE COMPLEX(aa) * TRIACYLGL [TAGLIPASE // ESTERASE // lipase // LIPA] CG5966 LD47264 5C10-5D1 ID:106B8
 + enzyme * 3e-55 probable membrane protein YPR066w - yeast (Saccharomyces cerevisiae) * 3e-21 ubiquitin activating enzyme * 1e-
 CG13343 111 coded for by C. elegans cDNA [UBA_NAD // ThiF_family // NAD_BINDING /] CG13343 LD47462 50C14-50C14 ID:106D10
 + chaperone * FK506-binding protein FKBP51(aa) * 6e-20 FKBP_YEAST FK506-BINDING PROTEIN (FKBP) (PEPTIDYL-PROLYL
 CIS-TRANS ISOMERASE) (P * 6e-24 FKB2_DROME KD FK50 [TPR_REGION // FKBP // FKBP_PPIASE_1 //] CG4535 LD47530 30E1-
 CG4535 30E1 dup:2/2 ID:106E9
 CG11484 + transcription_factor_binding * [UBA] CG11484 LD47780 102D1-102D3 ID:106H12
 + unknown * 2e-09 YNY5_YEAST HYPOTHETICAL 20.4 KD PROTEIN IN RPA49-SUI1 INTERGENIC REGION * 2e-08 coded for by
 CG2843 C. elegans cDNA yk127b8.5; coded for by C. elegans [NLS_BP] CG2843 LD47748 23A7-23A7 ID:106H9
 + cin unknown * BACR37P7.g(aa) * MOLYBDENUM COFACTOR SYNTHESIS PROTEIN CINNAMON(aa) * DMCOFACTO_2 cin * 3e-
 05 hypothetical protein YMR244c-a - yeast (Saccharomyces [MOCF_BIOSYNTHESIS_1 // MOCF_BIOSYNTHESI] CG2945 LD47852 1A5-
 CG2945 1A5 dup:1/3 ID:107A8
 + transcription_factor * ZINC FINGER PROTEIN GLI1 (GLI-1)(aa) * PAIR-RULE PROTEIN ODD-PAIRED(aa) * hGLI2(aa) * cubitus
 CG4677 interruptus dominant protein(aa) [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG4677 LD47926 94D10-94D10 dup:2/3 ID:107B3
 CG9646 + unknown * No definition line found(aa) * protein(aa) * No definition line found * [NLS_BP] CG9646 LD47968 53F4-53F5 ID:107B7
 + unknown * Kelch-repeat protein, similar to Kel1 and Kel2; Kel3p(aa) * 2e-32 hypothetical protein YPL263c - yeast (Saccharomyces
 CG4069 cerevisiae) * 9e-06 host cell [NLS_BP] CG4069 LD47970 69C4-69C4 ID:107B8
 + transcription_factor * 4e-91 putative zinc finger protein * 8e-13 similar to Zinc finger, C2H2 type (4 domains); cDNA EST * 4e-27
 MFG2_MOUSE ZINC FINGER PROTEIN MFG-2 z[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG1602 LD48073 43D3-43D3
 CG1602 ID:107C11

CG13594 + unknown ANTIFREEZE1 CG13594 LP01106 ID:107D2
+ enzyme * ribulose-1,5-bisphosphate carboxylase/oxygenase N-methyltransferase(aa) * ribulose-1,5-bisphosphate

CG3042 carboxylase/oxygenase small subunit N-methyltra CG3042 LP01222 6E3-6E3 ID:107D9

CG1252 + Ccp84Ab structural_protein cuticle cluster 7 CUTICLE, insect_cuticle CG1252 LP01435 dup:2/2 ID:107E11
+ enzyme * cDNA EST comes from this gene; cDNA EST yk282d3.5 comes from this gene(aa) * 1e-06 CCA1_YEAST TRNA NUCLEOTIDYLTRANSFERASE PRECURSOR (TRNA ADENYLYLT [MET_TRANS // SAM_BIND] CG1239 LP01332 83C1-83C1 dup:2/2

CG1239 ID:107E5
+ unknown * PUTATIVE GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (GAMMA-BUTYROBETAINE

CG10814 HYDROXYLASE) (GAMMA-BBH)(aa) * gamma- butyrobetaine hydroxylase; gamma- CG10814 LP01339 50A6-50A6 dup:2/2 ID:107E6
+ unknown * ECDYSONE-INDUCED PROTEIN 74EFA (ETS-RELATED PROTEIN E74A)(aa) * 1e-62 ecdysone-induced protein E74A

CG6273 - fruit fly (Drosophila pseudoobscura) * 5e-91 e CG6273 LP01487 74E-74E ID:107F2
+ RNA_binding * RNA binding motif protein 7(aa) * predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or

CG11454 RNP domain); cDNA EST yk197f9.5 c [RBD // rrm] CG11454 LP01585 21B-21B dup:1/2 ID:107F7
+ peptidase * [pdb]1AYE Human Procarboxypeptidase A2(aa) * 4e-45 YHT2_YEAST HYPOTHETICAL 49.8 KD PROTEIN IN ACT3-YCK1 INTERGENIC REGION PRECURSOR * 0.0000000006* [CARBOXYPEPT_ZN_1 // CARBOXYPEPT_ZN_2 //] CG3097 LP01667

CG3097 5B6-5B6 ID:107G1
+ unknown * queuine trna-ribosyltransferase(aa) * 7e-98 TGT_CAEEL PUTATIVE QUEUINE TRNA-RIBOSYLTRANSFERASE

CG4947 (TRNA-GUANINE TRANSGLYCOSYL * TGT_BACSU QUEUINE TR CG4947 LP01967 21F1-21F1 ID:107H4
+ crol transcription_factor * crol * BLASTX 2.3E-25 Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds.(dna) * CROL

CG14938 GAMMA * 4e-14 HSN motor neurons m[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG14938 LP02106 33B1-33B1 dup:2/2 ID:107H9
+ P5cr enzyme * 6e-29 PROC_YEAST PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) * 1e-157 pyrroline 5-

CG6009 carboxylate reductase * 3e-52 similar to pyrroline-5- [P5CR] CG6009 LP02537 91E4-91E4 ID:108B2
+ serpin * ZG-21p protein - rat(aa) * protease inhibitor (ovalbumin type)(aa) * 9e-10 Similar to serine protease inhibitor * 2e-17

CG1342 PAI2_MOUSE PLASMINOGEN ACTIV [serpin] CG1342 LP03106 100A3-100A3 ID:108D8
+ Ptp4E protein_phosphatase * DMRPTP4E_2 Ptp4E * DMDPTP101_2 Ptp10D * protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type 4E, splice form A precursor - fruit fly (D[Y_phosphatase // TYR_PHOSPHATASE_PTP //] CG6899 LP03315 4D1-4D1 dup:2/2

CG6899 ID:108E10

CG5904 + islet mitochondrial antigen CG5904 LP03542 ID:108F8
+ 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
+ brat transcription_factor * transcription factor(aa) * 1e-142 YOG2_CAEEL HYPOTHETICAL ZINC FINGER PROTEIN ZK112.2 IN CHROMOSOME III * 2e-38 protein * 9e-38 RING finger[ZF_BBOX // NHL // ZINC_FINGER_C2H2 // Z] CG10719 LP03649 37C4-37C

CG10719 dup:3/5 ID:108G1
+ transporter * renal organic cation transporter(aa) * solute carrier family (organic cation transporter), member 5(aa) * sodium-

CG17752 dependent carnitine transporter(aa) [sugar_tr] CG17752 LP04053 94D3-94D3 ID:108H10

CG16844 + CG16844 55C9-55C9 dup:1/2 ID:109A11

CG15013 + unknown * 3e-97 transmembrane protein * 3e-07 similar to cuticulin 1; cDNA EST comes from this gene; * 4e-99 DMDUSKY_1 dy *

5E-84 CG15013 LP05062 64B6-64B6 ID:109C3

+ Oscp enzyme * DMOSCPPRE_2 Oscp * ATP synthase, H⁺ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)(aa) * coded for b [ATPASEDELTA // OSCP] CG4307 90D1-90D1 dup:2/2 ID:109D2

+ Rrp1 DNA_repair_protein * DMRRP1_2 Rrp1 * RECOMBINATION REPAIR PROTEIN (DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE)(aa) * 7e-63 similar to AP endonucleases family 1; cDNA EST [AP_NUCLEASE_F1_3 // AP_endonucleas1 //] CG3178 LP05366

CG3178 23C2-23C2 ID:109D3

+ endopeptidase * Ser12 * Ser6 * mas * DMSNAKE_2 snk [trypsin // CHYMOTRYPSIN // TRYPSIN_CATA] CG9675 LP05929 15A1-15A1 ID:109F7

+ unknown * similar to S. cerevisiae hypothetical 240.3 kd protein in MSH3 3' * GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1(aa) * t7i23.15 protein.(a [LECTIN_LEGUME_BETA // FGGY_KINASES_2 //] CG1884 SD02024 45F3-45F4 dup:5/7 ID:113D9

+ aft unknown * 2e-05 YBR1_YEAST HYPOTHETICAL 34.7 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION * Adrift * 2e-22

CG5032 contains similarity to Methanococcus jannaschii cell d CG5032 SD02116 54E10-54E10 dup:3/3 ID:113E9

+ enzyme_inhibitor * protein(aa) * protein(aa) * protein(aa) * [ANK_REP // ank // ANK_REP_REGION] CG8465 SD02148 16B5-16B6 dup:2/4 ID:113F4

+ ligand_binding_or_carrier * ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TTP)(aa) * retinaldehyde-binding protein, CRALBP Peptide, * retinaldehyde-binding protein 1(aa) * tocophero [CRETINALDHBP // CRAL_TRIO] CG10026 SD02235 37E3-37E3 ID:113G7

+ enzyme * type II membrane protein(aa) * Similarity with yeast hypothetical protein (PIR accession number * brn * beta-1,3-N-acetylglucosaminyltransferase(a [ALDOKETO_REDUCTASE_3] CG8668 SD02482 28E-28E ID:114B11

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

+ unknown * BLASTX 1.9E-12 Dictyostelium discoideum AAC-rich mRNA (AAC11).(dna) * 5e-87 inserted at base Both 5' and 3' ends

CG7502 of P element Inverse PCR * [PRO_RICH // NLS_BP] CG7502 SD02606 18B1-18B1 ID:114D5

+ DNA_binding * 2e-33 inserted at base 5' end of P element Inverse PCR * * [MYB_1 // NLS_BP] CG15610 SD02691 53E-53E5 dup:2/2 ID:114E11

+ nbA ion_channel * nbA * DMCA1_2 Ca- agr;1D * CCA1_DROME CALCIUM CHANNEL ALPHA-1 SUBUNIT (CACOPHONY PROTEIN) (NIGHTBLIND A PR * unc-2 gene product [NACHANNEL // ion_trans // CACHANNEL //] CG1522 10F10-11A1 dup:2/2 ID:114F12

+ enzyme * dihydrosphingosine phosphate lyase (also known as sphingosine phosphate lyase); Dpl1p(aa) * Similar to glutamate decarboxylase(aa) * sphingosine-1-p CG8946 SD02978 53F10-53F10 dup:3/3 ID:114H12

CG13868+ unknown * 0.000000000000008* * CG13868 SD03066 56F17-57A dup:4/4 ID:115B4

+ unknown * contains a single LIM domain at the N-terminus.; cDNA EST comes from this gene; cDNA EST comes from this gene;

CG10439 cDNA EST yk357g9.5 comes from this ge [LIM_DOMAIN_1 // LIM_DOMAIN_2] CG10439 SD03168 57B1-57B1 ID:115C12

CG5444 + transcription_factor CG5444 dup:3/3 ID:115D3

+ unknown * pre-mRNA cleavage factor Im (25kD)(aa) * putative protein(aa) * predicted using Genefinder; cDNA EST yk236h6.3

CG3689 comes from this gene; cDNA EST yk23 CG3689 SD03330 67B2-67B2 dup:2/2 ID:115E9

+ signal_transduction * 5e-15 VPS9 protein - yeast (*Saccharomyces cerevisiae*) (Z46 * 7e-28 cDNA EST yk210c11.3 comes from this
 CG9139 gene; cDNA EST yk210c11.5 co * 3e-09 Ras inhi CG9139 SD03358 61F5-62B4 dup:3/4 ID:115F1
 + RNA_binding * 2e-05 SUWA_DROME SUPPRESSOR OF WHITE APRICOT PROTEIN * 0.0000003* 4e-10 predicted protein * 2e-
 CG6615 07 DMSUWA_6 su(w<up>a</up>) [SURP // PRO_RICH] CG6615 SD03435 73E4-73E4 dup:2/2 ID:115F12
 CG18278+ unknown * CG18278 SD03412 50A9-50A9 ID:115F5
 + enzyme * ripening-induced protein(aa) * 4e-20 putative protein * Strong similarity to auxin-induced protein from *Vigna radiata* and a *
 CG17221 ripening-induced pro [adh_zinc] CG17221 SD03451 23C5-23C5 ID:115G6
 + Fas3 cell_adhesion * FASCICLIN III PRECURSOR (FAS III)(aa) * DMFCNIII_4 Fas3 * 0.00001* fasciclin III precursor - fruit fly
 CG5803 (*Drosophila melanogaster*) CG5803 36F6-36F6 ID:115H8
 + Xpd DNA_repair_protein Xeroderma pigmentosum D nucleotide-excision repair DEAH_ATP_HELICASE, XRODRMPGMNTD CG9433
 CG9433 SD04012 dup:3/3 ID:116E7
 CG17556+ unknown CG17556 SD04068 dup:2/2 ID:116F7.2
 CG8593 + unknown CG8593 dup:2/2 ID:116H4
 + transcription_factor * 1e-10 YJF6_YEAST HYPOTHETICAL 98.9 KD ZINC FINGER PROTEIN IN BTN1-PEP8 INTERGENIC REG *
 7e-12 Kr-h * 1e-05 similar to Zinc finger, C2H2 type[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG13620 96A13-96A14 dup:3/3
 CG13620 ID:116H5.2
 CG5530 + expressed in the embryo (head , mesectoderm , mesoderm , mesoderm anlagen CG5530 SD04373 dup:1/2 ID:117B10
 CG5953 + It has been mapped cytologically to 36A2--3 PRO_RICH CG5953 SD04335 dup:1/3 ID:117B7
 CG2818 + unknown PHO85 protein PIPLC_X_DOMAIN CG2818 SD04355 dup:1/2 ID:117B8
 CG1707 + CG1707 SD04870 dup:2/2 ID:118A2.2
 CG15618+ CG15618 SD04871 dup:1/4 ID:118A3
 + unknown * 1e-149 inserted at base Both 5' and 3' ends of P element Inverse PCR * BLASTX 4.2E-08 Carrot gene for extensin.(dna)
 CG8929 * 2e-61 inserted at base Both 5 [PRO_RICH // NLS_BP] CG8929 SD04973 57A-57A dup:2/3 ID:118B9
 CG2385 + CG2385 SD05054 dup:1/2 ID:118C5
 CG2971 + CG2971 ID:118D1
 CG7143 + DNA_repair_protein CG7143 SD05329 dup:2/2 ID:118F3
 + enzyme * alpha-1,6-fucosyltransferase(aa) * No definition line found(aa) * fucosyltransferase (alpha (1,6) fucosyltransferase)(aa) *
 CG2448 1e-100 No definition lin CG2448 SD05335 10D4-10D4 dup:2/2 ID:118F5
 + transporter * Ydr205wp(aa) * 5e-09 Zn/Cd resistance gene * 1e-06 cDNA EST yk447c2.5 comes from this gene; cDNA EST co * 1e-
 CG6672 06 zinc transporter ZnT-1 - mouse ZnT-1 [KININOGEN] CG6672 86D7-86D7 dup:1/2 ID:118G3
 CG8368 + enzyme CG8368 SD05518 ID:118H9
 CG7161 + CG7161 SD05642 dup:1/2 ID:119B4
 + transcription_factor * requiem, apoptosis response zinc finger gene; neuroD4; ubi-d4(aa) * All-1 related protein(aa) * probable
 CG12238 transcription factor requiem - mouse(aa) * [PHD] CG12238 SD05644 18D9-18D10 dup:2/3 ID:119B5
 CG18019+ CG18019 SD06401 dup:2/2 ID:119G12.2

CG3075 + transcription_factor CG3075 SD06336 dup:2/2 ID:119G4.2
 + 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
 CG3608 + chaperone CG3608 SD09850 dup:1/2 ID:124C12.2
 CG15009+ CG15009 SD10052 dup:1/2 ID:124F9.2
 CG3973 + CG3973 dup:1/2 ID:124H12.2
 CG2604 + unknown CG2604 SD10384 dup:1/2 ID:125B2.2
 + emb transporter * CRM1_YEAST CHROMOSOME REGION MAINTENANCE PROTEIN CRM1 * strong similarity to CRM1
 CG13387 chromosome maintenance protein from y * exportin (CRM1, yeast, ho [LIPOYL // IBN_NT] CG13387 GH01059 29C1-29C1 dup:1/2 ID:30A3
 CG18466+ Nmdmc NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE CG18466 GH01066 85C5-85C5 ID:30A5
 CG8979 + enzyme_inhibitor * 7e-15 proteasome inhibitor hPI31 subunit * * CG8979 GH01278 48D7-48D7 ID:30B10
 + DNA_binding * ISWI PROTEIN (IMITATION SWI PROTEIN) (NUCLEOSOME REMODELING FACTOR KD SUBUNIT) (NURF-140)
 CG5899 (CHRAK KD SUBUNIT)(aa) * DMISWI_6 lswi * 8e-94 YAB9_YEAST [helicase_C // SNF2_N] CG5899 GH01406 33A1-33A1 ID:30C10
 + dim-7 unknown * RanBP7(aa) * 1e-73 NMD5_YEAST NONSENSE-MEDIATED MRNA DECAY PROTEIN NMD5 * 8E-26*
 CG7935 RanBP7/importin [IBN_NT] CG7935 GH01576 66B9-67E3 dup:3/3 ID:30E1
 + unknown * nucleolar protein(aa) * 1e-108 nucleolar protein * 1e-109 cell cycle-regulated factor p78 * 8e-06 Hypothetical protein
 CG1135 [FHA_DOMAIN // FHA] CG1135 GH01794 64A4-64A4 ID:30F12
 + enzyme * coded for by C. elegans cDNA yk108f3.3; coded for by C. elegans cDNA yk104h5.3; coded for by C. elegans cDNA
 CG5590 yk117a1.3; coded for by C. elegans cDN [GDHRDH // adh_short] CG5590 GH01709 98A6-98A6 ID:30F4
 + unknown * 5e-09 SHP1_YEAST SHP1 PROTEIN hypothetical protein YBL058w - ye * 1e-34 p47 * 2e-33 p47 XY40 * undulin -
 CG11139 human (fragment) undulin CG11139 GH01724 43C4-43C5 dup:3/3 ID:30F6
 + transcription_factor * regulatory protein LBP1d - human (fragment)(aa) * NF2d9 - mouse(aa) * transcription factor LBP1a -
 CG3459 human(aa) * 4e-19 alpha-globin transcription fact CG3459 GH01967 46E6-46E8 ID:30H1
 + enzyme * glycerate kinase, putative(aa) * HYPOTHETICAL 40.0 KD PROTEIN C13B9.2 IN CHROMOSOME III(aa) * 2e-40 440aa
 CG9886 long hypothetical protein * TUD4_AGRVI PU CG9886 GH02560 23F1-23F1 ID:31C10
 + arginaseenzyme * putative * 1e-11 ARG1_YEAST ARGINASE (EC 3.5.3.1) - yeast (Saccharo * 1e-107 /motif=(desc;; /ma * 1e-08 similar
 CG18104 to CG18104 GH02581 1B5-1B5 ID:31C12
 + BcDNA:GH02536 unknown * Contains similarity to from C. elegans.(aa) * unknown(aa) * 2e-88 predicted using Genefinder; cDNA EST
 CG8230 comes from this g * 2e-49 Contains similarity CG8230 GH02536 44F12-44F12 ID:31C8
 + unknown * 1e-25 kraken * 3e-13 dJ222E13.1 (N-terminal part of novel protein with some similarit * 7e-05 TPES_PSEPU
 CG5707 TROPINESTERASE (ATROPINESTERASE) (ATROPINE [ESTERASE // abhydrolase] CG5707 GH02816 62D2-62D2 dup:2/2 ID:31E3
 CG11073+ unknown * BLASTX 8.6E-13 Macaca mulatta mucin (MUC2) mRNA, partial cds.(dna) * * CG11073 GH02992 58C1-58C2 ID:31F8
 CG1408 + BcDNA:GH03163 unknown * * * CG1408 GH03163 100B-100B dup:1/2 ID:31G10
 + unknown * GLUTAMATE--CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE)
 CG4919 (GAMMA-ECS) (GCS LIGHT CHAIN)(aa) * glutamate-cysteine ligase regu CG4919 GH03051 94C3-94C3 ID:31G2
 CG8548 + karyopherin-alpha1 ligand_binding_or_carrier * karyopherin- agr;1 * karyopherin alpha 1(aa) * 1e-129 IMA1_YEAST IMPORTIN ALPHA

SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (SERINE-RICH RNA[ARM_REPEAT // Armadillo_seg // NLS_BP] CG8548 GH03057 76D2-76D3 ID:31G3

CG12167+ unknown * [PRO_RICH // ATP_GTP_A] CG12167 GH03350 83B1-83B1 ID:31H6

CG10658+ Os9 unknown * Os9 * * CG10658 GH03980 38B1-38B1 ID:32D2

+ Sptr enzyme * sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)(aa) * ORF 7(aa) * similar to glucose 1-dehydrogenase(aa) * sepiapterin reductase; [GDHRDH // adh_short] CG12117 GH04031 7E7-7E7 ID:32D8

+ ion_channel * 6e-15 similar to PDZ domain (Also known as DHR or GLGF).; cDNA EST EMBL: * 3e-17 protein co-factor * 1e-18

CG10939 E3KARP Na+/H+ exchanger regulatory facto [PDZ // NLS_BP] CG10939 GH04176 54B18-54C1 dup:2/2 ID:32E6

+ Motor-protein motor_protein * 1e-152 motor protein * 2e-40 coded for by C. elegans cDNA yk119d2.3; coded for by C. elegans cDNA

CG6455 yk86f8.3; c * 6e-50 motor protein * 1e-154 DMMOTPR [WD_REPEATS] CG6455 GH04666 93F14-93F14 ID:33A1

+ transporter * 4e-41 similar to matrin F/G containing C4-type zinc-fingers * 4e-79 PGT_HUMAN PROSTAGLANDIN TRANSPORTER

CG3811 (PGT) prostaglandin tr * 2e-76 PGT_RAT PROST CG3811 GH04717 30B10-30B10 ID:33A7

+ enzyme * weakly similar to furin-like proteases; 35% Similarity to * weakly similar to furin-like proteases in 3' exon(aa) * 2e-17

CG8481 weakly similar to furin-I [Acetyltransf // NLS_BP] CG8481 GH04732 85E8-85E8 ID:33A9

+ unknown * 1e-87 cDNA EST yk500f6.3 comes from this gene; cDNA EST come * 1e-119 unknown * 1e-88 hypothetical protein *

CG14997 CGI-44 protein [FADPNR] CG14997 GH04863 64E2-64B4 ID:33B10

+ alphaCopsignal_transduction * agr;Cop * coatomer alpha subunit(aa) * alpha-COP (Z466 * 5e-67 Similarity to Human Coatomer beta' subunit (SW:COPP_HUMAN); cDNA E [GPROTEINBRPT // WD40_REGION // WD_REPEATS] CG7961 GH04856 62A10-62A10 dup:2/3

CG7961 ID:33B8

CG18616+ CG18616 GH04932 ID:33C5

+ 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 GH04978

CG7028 61A6-61A6 ID:33D1

+ chaperone * KD HEAT SHOCK PROTEIN, MITOCHONDRIAL (HSP10) (10 KD CHAPERONIN)(aa) * 1e-17 CH10_YEAST KD HEAT SHOCK PROTEIN, MITOCHONDRIAL (HSP10) (10 KD CHAPERONI [LUM_BINDING // CHAPERONIN10 // cpn10] CG11267 GH05109

CG11267 69F2-69F2 ID:33D12

+ enzyme * phosphatidylserine-specific phospholipase A1 deltaC(aa) * PS-PLA1(aa) * DMYOLK_4 Yp1 * VITELLOGENIN I

CG4979 PRECURSOR (YOLK PROTEIN 1)(aa) [TAGLIPASE // ESTERASE // lipase] CG4979 GH05003 89B7-89B7 dup:2/2 ID:33D4

+ 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 dup:2/2

CG12189 ID:33E10

+ EG:22E5.3 enzyme * RNA 3'-terminal phosphate cyclase(aa) * 1e-10 RTC1_YEAST RNA 3'-TERMINAL PHOSPHATE CYCLASE (RNA-3'-PHOSPHATE CYCLASE) (RNA CY * /match=(desc;; /ma * [RCT] CG4061 GH05410 2C7-2C7 ID:33F4

CG4061 + Mlc1 * DMMYLALK_2 Mlc1 * indirect flight muscle isoform; putative(aa) * 1e-07 YGK6_YEAST HYPOTHETICAL CALCIUM-BINDING

CG5596 PROTEIN IN TAF60-G4P1 INTERGENIC REGI [THIOL_PROTEASE_HIS // EF_HAND_2] CG5596 98A6-98A6 dup:2/4 ID:33F5

+ enzyme_inhibitor * COMPLEMENT C3 PRECURSOR (CONTAINS: C3A ANAPHYLATOXIN)(aa) * alpha-2-macroglobulin(aa) *

CG7068 alpha-2-macroglobulin(aa) * 1e-121 similar to Alpha-2-macrog [A2M // ALPHA_2_MACROGLOBULIN] CG7068 GH05679 28C-28C

ID:33G11

CG18238+ unknown * CG18238 GH05783 84F-84F ID:33H10
+ enzyme * 5e-32 GAA1_YEAST GAA1 PROTEIN membrane protein END2 - yeast (Sa * 4e-26 No definition line found * 3e-67
CG3033 UNKNOWN hGAA1 * CG3033 GH05723 5C2-5C3 ID:33H2
+ l(2)gl tumor_suppressor (lethal (2) giant larvae) L2GL_DROME LETHAL(2) GIANT LARVAE PROTEIN (P127 LETHAL2GIANT, NLS_BP,
CG2671 RCC1_2, WD_REPEATS] CG2671 GH05740 dup:2/2 ID:33H6
+ transporter * solute carrier family (organic anion transporter), member 7(aa) * BLASTX 4.2E-24 Rattus organic cation transporter
CG9317 OCT1A mRNA, complete cds.(dna) * [sugar_tr] CG9317 GH05908 38E3-38E3 dup:1/2 ID:34A5
+ cytoskeletal_structural_protein * 7e-12 YIL2_YEAST HYPOTHETICAL 123.6 KD PROTEIN IN POR2-COX5B INTERGENIC
REGION * 3e-11 ankyrin ankyrin m * 1e-10 contains similarity to[ANK_REP // ank // ANK_REP_REGION] CG5822 GH05978 25C1-25C1
CG5822 dup:3/4 ID:34B3
+ VhaSFD transporter * kDa vacuolar H(+)-ATPase subunit(aa) * coded for by C. elegans cDNA yk89e9.5; coded for by C. elegans cDNA
CG17332 cm7g5; coded for by C. elegans cDNA cm14 CG17332 GH05981 36A7-36A7 ID:34B4
+ angel enzyme * DMANGEL_3 angel * GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL EFFECTOR
CG12273 (CARBON CATABOLITE REPRESSOR PROTEIN 4)(aa) * NOCTURNIN (RHYTHM CG12273 GH06351 59F4-59F4 dup:2/2 ID:34E2
+ enzyme * 3e-40 4-nitrophenylphosphatase (EC 3.1.3.41) - yeast (Saccharomyces cerevisiae) * 6e-26 by content; 1-meth * 4e-52
CG5567 contains similarity to 4-nitrophe CG5567 GH06744 75A4-75A4 ID:34G7
CG3752 + enzyme CG3752 dup:1/2 ID:34H5
+ unknown * 2e-22 YJJ7_YEAST HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION * 4e-40 No definition
CG6746 line found * 2e-68 inserted at base Both 5' and CG6746 GH07085 33B9-33B9 ID:35A11
CG5059 + unknown * CG5059 GH07036 77C4-77C4 ID:35A4
CG13850+ unknown * CG13850 GH07286 96E1-96E1 ID:35C4
+ Rab-RP1 enzyme * rab-related protein 3(aa) * Rab-RP3 * 4e-28 YPT7_YEAST GTP-BINDING PROTEIN YPT7 GTP-binding protein Y *
CG8024 2e-25 strong similarity to the YPT1 sub-fami [ras // NLS_BP // PROTEIN_KINASE_ATP //] CG8024 GH07310 45B3-45B4 ID:35C8
+ structural_protein * MICROFIBRILLAR-ASSOCIATED PROTEIN (ASSOCIATED MICROFIBRIL PROTEIN) (AMF)(aa) * predicted
CG1017 using Genefinder; similar to MICROFIBRILLAR-ASSOCIATED PRO CG1017 GH07619 62B10-62B11 dup:2/2 ID:35E3
+ cell_adhesion * DMSLIT_2 sli * DMNOTCH3_2 N * 2e-05 NOTC_DROME NEUROGENIC LOCUS NOTCH PROTEIN PRECURSOR
CG9572 growth * 7e-07 GLP1_CAEEL GLP-1 PROTEIN PRECURSOR glp1 prote [EGF_2] CG9572 GH07746 19C1-19C1 ID:35F1
+ Hr78 transcription_factor * DMSVP1_2 svp * Hr78 * nuclear receptor XR78E/F(aa) * HR78_DROME NUCLEAR HORMONE
RECEPTOR HR78 (DHR78) (NUCLEAR RECEPTOR XR78E/F) [STROIDFINGER // hormone_rec // zf-C4 //] CG7199 GH08073 78D7-
CG7199 78D7 ID:35H10
+ 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
+ unknown * 4e-24 MANB_CAEEL PROBABLE BETA-MANNOSIDASE PRECURSOR (MANNANASE) (MANNASE) * 2e-39
CG12582 mannosidase, beta A, lysosomal BETA-MANNOSIDASE PRECURSO * 1e-40 CG12582 GH09594 82A-82A ID:37B4
CG1469 + Fer2LCH ligand_binding_or_carrier FERRITIN PRECURSOR CG1469 ID:37H10

+ structural_protein * U4/U6-associated RNA splicing factor(aa) * 9e-24 hypothetical protein YDR473c - yeast (Saccharomyces cerevisiae) (U * 1e-101 cDNA EST comes from thi [NLS_BP] CG7757 GH10477 76D7-76D7 ID:38A4
 CG7757 + BcDNA:GH10614 enzyme * 2e-49 GCY_YEAST GCY PROTEIN GCY1 protein - yeast (Saccharomyces * 3e-58 Similarity to Human aldose reductase (SW:ALDR_HUMAN) * 1e-77 ALDR_MOUSE ALDO [ALDKETRDASE // ALDOKETO_REDUCTASE_1 //] CG10863
 CG10863 GH10614 64A1-64A1 ID:38B5
 CG1623 + unknown * CG1623 GH10642 46B12-46B13 ID:38B9
 + endopeptidase * 5e-32 Similarity to human placental protein * 2e-42 glucocorticoid-sensitive T cell-specific protein - mouse * 5e-41
 CG2145 placental protein (serine protease) CG2145 GH10845 10A1-10A1 dup:2/2 ID:38D4
 + receptor * glutamyl cyclase(aa) * 3e-32 YFI8_YEAST HYPOTHETICAL 41.0 KD PROTEIN IN UGS1-FAB1 INTERGENIC REGION
 CG10487 * 3e-62 similar to guanylate cyclase; cDNA EST CG10487 GH11174 64F4-64F4 ID:38F11
 + unknown * similar to GABA and glycine receptors(aa) * 6e-75 similar to GABA and glycine receptors * [TPR_REPEAT] CG4525
 CG4525 GH11140 89A6-89A6 ID:38F8
 + TFIIEalpha transcription_factor * 6e-23 T2EA_YEAST TRANSCRIPTION INITIATION FACTOR IIE, ALPHA SUBUNIT (TFIIE-ALPHA)
 CG10415 (TRA * TFIIE large subunit * 7e-35 cDNA EST yk210d12.5 comes from CG10415 GH11150 68C13-68C13 ID:38F9
 + Nmd3 unknown * 1e-115 NMD3_YEAST NONSENSE-MEDIATED MRNA DECAY PROTEIN Nmd3p * 1e-125 Similarity to Yeast
 CG3460 nonsense-mediated mRNA decay protein (SW:NMD3_Y * 1e-143 CG [CYTOCHROME_C] CG3460 GH11261 2E1-2E1 ID:38G5
 + unknown * unknown(aa) * 4e-12 putative Bop-like zinc finger protein * 1e-19 DMC103B4 [IPNS_1 // CYTOCHROME_C] CG8503
 CG8503 GH11294 50E8-50E8 ID:38G9
 + Rpn5 endopeptidase * proteasome (prosome, macropain) 26S subunit, non-ATPase, 12(aa) * 5e-42 hypothetical protein YDL147w - yeast (Saccharomyces cerevisiae) * 2e-81 No d [PCI_DOMAIN // PCI // NLS_BP] CG1100 GH11341 83C-83C ID:38H3
 CG1100 + NaCP60E ion_channel * DMSODCHA_6 para * DMCA1_2 Ca- agr;1D * sodium channel protein - fruit fly (Drosophila melanogaster) (fragments) * 4e-76 similar to dihydropyridine- [NACHANNEL // ion_trans // CATION_CHANNE] CG9071 GH11402 60E4-60E5 dup:2/2
 CG9071 ID:38H6
 + signal_transduction * 3e-48 cdc4, incomplete, len: 579, CAI, 0.15, CC4_YEAST CELL DIVISI * 2e-61 Slimb * 5e-32 YKY4_CAEEL HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CO[GPROTEINBRPT // F-box // WD_REPEATS //] CG15010 GH11648 64B4-64B4
 CG15010 dup:2/3 ID:39B6
 CG3825 + unknown * CG3825 GH11727 60A14-60A14 dup:1/3 ID:39C1
 + transporter * 40-kDa V-ATPase subunit(aa) * 3e-85 VATX_YEAST VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE
 CG2934 AC39 SUBUNIT) (V-ATPASE * 1e-172 Ac39/physophilin * 1e- CG2934 GH11776 4A1-4A1 ID:39C4
 + enzyme * FLAVONOL 3-SULFOTRANSFERASE (F3-ST)(aa) * steroid sulfotransferase 3(aa) * sulfotransferase family 2B, member
 CG5428 1(aa) * sulfotransferase, estrogen-pre [Sulfotransfer] CG5428 GH11818 59F4-59F4 ID:39C6
 + unknown * HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III(aa) * IMPLANTATION-ASSOCIATED PROTEIN(aa)
 CG7830 * N33 PROTEIN(aa) * 9e-99 kDa encoded by N33 [THIOREDOXIN_2] CG7830 29A4-29A4 dup:2/2 ID:39D4
 + Pfk enzyme * DMPFK_5 Pfk * DMPFK_5 Pfk * 1e-151 phosphofructokinase, beta subunit * K6PF_DROME 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) [PFK // PHFRCTKINASE] CG4001 GH12192
 CG4001 46E4-46E4 dup:4/5 ID:39E11
 CG3174 + enzyme * 1e-30 YHX6_YEAST HYPOTHETICAL 42.4 KD PROTEIN IN ENO2-STB5 INTERGENIC REGION * 9e-53 similar to flavin-

containing monooxygenases * 2e-29 FMO3_MOUSE [ADXRDTASE // FADPNR // FMO-like // PNDR] CG3174 GH12207 42B3-42B3
dup:2/2 ID:39E12

+ enzyme * Ynr027wp(aa) * 8e-44 YEC9_YEAST HYPOTHETICAL 35.6 KD PROTEIN IN MCM3-VMA3 INTERGENIC REGION * 2e-
CG4446 57 PDXK_CAEEL PUTATIVE PYRIDOXINE KINASE (PYRIDOXAL [pfkB] CG4446 GH12231 67B1-67B1 ID:39F3

+ I(2)37Ccunknown * HYPOTHETICAL 31.8 KD PROTEIN IN CHROMOSOME II(aa) * DMCCR_5 I(2)37Cc * mitochondrial protein,
CG10691 prohibitin homolog; similar to S. cerevisiae Phb2p; Ph [PROHIBITIN // Band_7] CG10691 GH12454 37C1-37C1 ID:39G6

+ ken transcription_factor * ken * ken(aa) * 8e-09 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * 9e-10 zinc
CG5575 finger protein PAG-3 [BTB // zf-C2H2 // ZINC_FINGER_C2H2 // Z] CG5575 GH12495 60A6-60A7 ID:39G8

+ Idgf2 enzyme * IDGF2 * 5e-09 probable membrane protein YDR371w - yeast (Saccharomyces cerevisiae) * disc growth factor * 3e-24
CG4475 CHIT_CAEEL PUTATIVE ENDOCHITINASE co [2SGLOBULIN // Glyco_hydro_18] CG4475 GH12581 36A1-36A1 ID:39H4

+ chaperone * embryonal lethal (2)13-1 (el(2)13-1) - fruit fly (Drosophila melanogaster)(aa) * 4e-16 HS27_DROME HEAT SHOCK
CG4461 PROTEIN heat shock protein - f * 9e-10 [HSP20] CG4461 GH12586 67B1-67B1 ID:39H6

+ cell_adhesion * DMSCA_3 sca * 2e-21 sca protein * 1e-09 coded for by C. elegans cDNA yk9a2.5; coded for by C. elegans cDNA
CG1889 yk9a2.3; simi * 5e-30 ficolin-A [fibrinogen_C] CG1889 GH12692 9A3-9A3 ID:40A10

+ unknown * ABC transporter, ATP-binding protein, putative(aa) * 2e-18 conserved protein * daunorubicin resistance membrane
CG6166 protein (drrB) * CG6166 GH12746 97A9-97A9 dup:1/2 ID:40B5

+ TppII peptidase * tripeptidyl peptidase II; dTPP II; subtilisin-like serine protease * 1e-135 YQS6_CAEEL HYPOTHETICAL SUBTILASE-
CG3991 TYPE PROTEINASE F21H12.6 IN CHROMOSOME [Peptidase_S8 // SUBTILASE_SER // SUBTIL] CG3991 GH12811 49F7-49F7 ID:40B7

+ unknown * Similar to Plasmodium falciparum glutamic acid-rich protein precursor * cDNA EST comes from this gene; cDNA EST
CG10955 comes from this gene; cDNA EST come [PRO_RICH] CG10955 GH12904 58D6-58D6 dup:1/3 ID:40C2

+ protein_kinase * v-akt murine thymoma viral oncogene homolog 2(aa) * protein kinase C(aa) * PROTEIN KINASE C, THETA TYPE
(NPKC-THETA)(aa) * PROTEIN KINASE C-LIKE (P[PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG2049 GH12918 45C-45C
CG2049 dup:2/2 ID:40C5

+ transporter * VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) (V-ATPASE KD ACCESSORY PROTEIN)(aa) *
CG8186 1e-58 VATD_YEAST VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPAS CG8186 GH12958 52A10-52A10 ID:40C8

+ Mipp2 protein_phosphatase * Mipp2 * multiple inositol polyphosphate phosphatase 2; MIPP2 * 1e-27 multiple inositol polyphosphate
CG4317 phosphatase * 1e-25 multiple inositol polyphosp [CYTOCHROME_B_QO] CG4317 GH13296 5D2-5D2 dup:4/4 ID:40E4

+ Pgym78 enzyme * phosphoglyceromutase - fruit fly (Drosophila melanogaster)(aa) * DMPGLY_4 Pgym78 * 7e-48 pdb|4PGM|A Chain A,
CG1721 Saccharomyces Cerevisiae Phosphoglycer [PGAM // PG_MUTASE] CG1721 GH13304 99A1-99A1 dup:2/2 ID:40E5

+ enzyme * phosphoglucomutase(aa) * 1e-152 PGM2_YEAST PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE 2) (PGM
2) * coded for by C. elegans cDNA cm17h1; coded for by [PGM_PMM // PGMPMM // ATP_GTP_A] CG5165 GH13311 72D7-72D7 dup:2/2
CG5165 ID:40E6

+ transporter * 5e-75 Na(+)-dependent inorganic phosphate cotransporter mela * 7e-67 YLD2_CAEEL HYPOTHETICAL 52.7 KD
CG3036 PROTEIN C38C10.2 IN CHROMOSOME III * 4e-46 NPT1 [NLS_BP] CG3036 GH13494 26D1-26D1 dup:3/4 ID:40F10

+ OstStt3 enzyme * STT3_YEAST OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT STT3 * STT3_CAEEL OLIGOSACCHARYL
TRANSFERASE STT3 SUBUNIT HOMOLOG * STT3_MOUSE OLIGOSACCHARYL [ATPASE_ALPHA_BETA] CG7748 GH13452 98F6-
CG7748 98F6 ID:40F6

+ Pgd enzyme * 6-phosphogluconate dehydrogenase(aa) * DMPGD_1 Pgd * 1e-177 6PG1_YEAST 6-PHOSPHOGLUCONATE
 DEHYDROGENASE, DECARBOXYLATING * 6PGD_DROME 6-PHOSPHOGLU [6PGD // 6PGDHDRGNASE] CG3724 GH13486 2D6-2D6
 CG3724 ID:40F9
 CG2046 + unknown * CG2046 GH13924 83C-83C ID:41A10
 + structural_protein * E25 protein(aa) * integral membrane protein 2(aa) * 2e-07 putative integral membrane pro * 1e-08 dJ696H22.1
 CG3662 (mouse E25 like protein) [NLS_BP] CG3662 GH14111 21D2-21D2 ID:41C3
 none + none GH14214 ID:41C7
 + unknown * Ylr193cp(aa) * bromodeoxyuridine-sensitive transcript protein - chicken(aa) * hypothetical protein(aa) * CGI-107
 CG9131 protein(aa) CG9131 GH14384 26B2-26B3 ID:41D12
 + endopeptidase * VESICULAR-FUSION PROTEIN NSF1 (N-ETHYLMALIMIDE-SENSITIVE FUSION PROTEIN 1) (NEM-
 SENSITIVE FUSION PROTEIN 1) (COMATOSE PROTEIN)(aa) * 8e-67 CC48_YEA [AAA // ATP_GTP_A] CG11919 GH14288 47C6-47C6
 CG11919 dup:2/2 ID:41D2
 + defense/immunity_protein * UNKNOWN(aa) * 3e-07 peptidoglycan recognition protein precursor * TNF superfamily, member (LTB)-
 CG5523 like (peptidoglycan recognition * hypothetical prote CG5523 GH14535 66A5-66A5 dup:2/2 ID:41E10
 + electron_transfer * 3e-39 ETFB_YEAST PROBABLE ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF) * 7e-
 CG7834 61 contains similarity to electron transfer flavoprotein beta [ETF_beta] CG7834 GH14462 99C4-99C4 dup:2/2 ID:41E7
 + enzyme * DMGST_3 Gsd1 * 2e-10 probable membrane protein YLL060c - yeast (Saccharomyces cerevisiae) * 3e-37
 CG5164 GTT1_DROME GLUTATHIONE S-TRANSFERASE 1-1 (CLASS-T [GST] CG5164 GH14654 55C9-55C9 ID:41F10
 + enzyme * NADH-ubiquinone oxidoreductase B22 subunit homolog(aa) * 6e-22 similar to NADH-ubiquinone oxidoreductase B22 (B.
 CG9306 taurus, SP:NI2M * 1e-26 NI2M_BOVIN CG9306 GH14794 34B6-34B6 ID:41G11
 + EG:86E4.2 enzyme * 6e-67 YH04_YEAST HYPOTHETICAL 91.2 KD PROTEIN IN RPS7A-SCH9 INTERGENIC REGION *
 CG3810 /match=(desc;; /ma * 1e-157 similar to mannosyl-oligosaccharide alph [GLYHDLASE47] CG3810 GH14693 2B15-2B16 dup:1/2 ID:41G2
 + motor_protein * Cdic * cytoplasmic dynein intermediate chain isoform DIC2c(aa) * DYNEIN INTERMEDIATE CHAIN 3, CILIARY(aa)
 CG10859 * 3e-07 cytoplasmic dynein intermediate ch [NLS_BP] CG10859 GH14707 34B7-34B7 ID:41G3
 + enzyme * 1e-103 IDH2_YEAST ISOCITRATE DEHYDROGENASE MITOCHONDRIAL SUBUNIT PRECURSOR (IS * 1e-139
 IDHA_CAEEL PROBABLE ISOCITRATE DEHYDROGENASE (NAD), MITOCHON [IDH_IMDH // isodh] CG12233 GH14729 18D3-18D3
 CG12233 ID:41G6
 + EG:63B12.8 unknown * 1e-50 PEP8_YEAST VACUOLAR PROTEIN SORTING/TARGETING PROTEIN PEP8 * /match=(desc;; /ma * 1e-
 CG14804 111 YLNO_CAEEL HYPOTHETICAL 37.4 KD PROTEIN T20D3.7 IN CH [NLS_BP] CG14804 GH15034 2B13-2B13 ID:42A6
 + cell_cycle_regulator * 6e-16 YG13_YEAST CULLIN B hypothetical protein YGR003w - yeas * 2e-71 LI19_DROME LIN-19
 HOMOLOG PROTEIN lin19 protein * 1e-173 CUL5_CAEEL CUL-5 P[CULLIN_2 // NLS_BP // ANTIFREEZEI // Cu] CG1401 GH15159
 CG1401 98F10-98F10 ID:42B5
 CG18522 + unknown * CG18522 GH15266 88F-88F8 dup:1/2 ID:42C1
 + transcription_factor * HYPOTHETICAL 46.7 KD PROTEIN C50C3.8 IN CHROMOSOME III(aa) * hypothetical protein(aa) *
 CG11275 intracisternal A particle-promoted polypeptide(aa) * 2e-08 [BTB] CG11275 GH15267 58C5-58C5 ID:42C2
 + scf ligand_binding_or_carrier * scf * 1e-110 supercoiling factor * 1e-72 coded for by C. elegans cDNA yk67a3.5; coded for by C.
 CG9148 elegans cDNA yk90a3.5; co * 7e-90 calumenin [EF_HAND // EF_HAND_2] CG9148 GH15277 62B4-62B4 ID:42C4

+ ligand_binding_or_carrier * DMC30B8 * ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TTP)(aa) * alpha tocopherol
 CG2663 transfer protein(aa) * 62D9.a(aa) [CRETINALDHBP // CRAL_TRIO] CG2663 GH15295 83A6-83A6 ID:42C7
 CG8954 + unknown * [NLS_BP] CG8954 LD22235 34D6-34D6 dup:2/2 ID:43B8
 + not endopeptidase * PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C (UBIQUITIN THIOLESTERASE)
 (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN[UCH_2_1 // UCH_2_3 // UCH-1 // NLS_BP /] CG4166
 CG4166 LD22730 75D1-75D1 dup:1/2 ID:43C10
 + enzyme * 1e-34 GLO2_YEAST HYDROXYACYLGLUTATHIONE HYDROLASE ISOZYME (GLYOXALASE II) (GLX II) * 8e-60 similar
 CG4365 to Metallo-beta-lactamase superfamily el * 3e-85 [lactamase_B] CG4365 77E-77E dup:1/3 ID:43C6
 + Mpcp transporter * 2e-71 YEO3_YEAST PUTATIVE MITOCHONDRIAL CARRIER YER053C hypoth * phosphate transporter precursor
 melanogas * 1e-132 MPCP_CAEEL MITOCHONDRIAL PHOSPHA [mito_carr // RCC1_2 // MITOCH_CARRIER] CG4994 LD23031 70E-
 CG4994 70E dup:3/4 ID:43D12
 CG7614 + Mat1 transcription_factor CDK7/cyclin H assembly factor NLS_BP, ZF_RING, ZINC_FINGER_C3HC4, zf-C] CG7614 LD23429 ID:43F4
 + Cyt-c2 electron_transfer * DMCYCDC4_4 Cyt-c2 * 9e-36 pdb|2YCC| Cytochrome c (Isozyme 1) (Oxidized) (Mutant With Cys Replaced
 CG17903 By Thr) (C102T * 1e-59 CYC2_DROME CYTOCHROME C-2 c [CYTCHRMCIAB // cytochrome_c] CG17903 LD23501 36A7-36A7 ID:43F5
 + 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
 CG3167 + unknown * CG3167 LD24895 60B1-60B1 ID:43G9
 CG9666 + enzyme possible protein methyltransferase N12N6MTFRASE, N6_MTASE, SAM_BIND CG9666 LD25448 dup:1/3 ID:43H12
 + peroxidase MITOCHONDRIAL THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE AhpC-TSA CG5826 LD25877 dup:2/3
 CG5826 ID:44B9
 + motor_protein * PLECTIN(aa) * plectin 1, intermediate filament binding protein, 500kD(aa) * 4e-07 integrin homolog - yeast
 (Saccharomyces cerevisiae) * 9e-05 myo[GRAM_POS_ANCHORING // PRO_RICH // NLS_B] CG11098 LD26265 26F3-26F3 dup:4/9
 CG11098 ID:44D2
 + endopeptidase * Saccharolysin (oligopeptidase yscD); Prd1p(aa) * NEUROLYSIN PRECURSOR (NEUROTENSIN
 ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOP [Peptidase_M3] CG11771 LD26931 98F1-98F1
 CG11771 dup:4/5 ID:44F10
 + protein_phosphatase * 4e-56 P2C2_YEAST PROTEIN PHOSPHATASE 2C HOMOLOG (PP2C-2) hyp * 9e-20 unknown * 1e-108
 P2C2_CAEEL PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (PP2C) * 4 [PP2C // PP2C_1 // PP2C_2] CG17746 64A3-64A3
 CG17746 dup:4/4 ID:44F12
 CG6564 + unknown CG6564 LD27203 ID:44H2
 + Gdh enzyme * 7e-28 glutamate dehydrogenase dehyd * glutamate dehydrogenase (NAD(P)+) * 1e-180 Similarity to Drosophila
 Glutamate dehydrogenase cDNA * DHE3_MOUSE [GLFV_DEHYDROGENASE // GLFDHDRGNASE // G] CG5320 95C-95C13 dup:2/2
 CG5320 ID:45F11
 + sgg protein_kinase * DMSGG46_2 sgg * 5e-98 MDS1_YEAST SERINE/THREONINE-PROTEIN KINASE MDS1/RIM11 pr * zeste-white
 3-A - fruit fly (Drosophila melanogaster) * 1e-141 pred [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG2621 3B2-3B3 dup:1/2
 CG2621 ID:45G9

CG11207+ unknown CG11207 dup:2/2 ID:45H2
 CG8309 + CG8309 dup:2/3 ID:46A12
 CG16944+ sesB transporter ADP/ATP translocase ADPTRNSLCASE, MITOCARRIER CG16944 ID:46A4
 + ncd motor_protein * DMCLARET_4 ncd * 3e-75 KAR3_YEAST KINESIN-LIKE PROTEIN KAR3 (NUCLEAR FUSION PROTEIN) *
 NCD_DROME CLARET SEGREGATIONAL PROTEIN * 4e-61 YNZ2_CAEEL PU [kinesin // KINESIN_MOTOR_DOMAIN1 // KIN] CG7831
 CG7831 99C5-99C5 ID:46A9
 + protein_kinase * DMTKABL3_2 Abl * TAK1 (TGF-beta-activated kinase)(aa) * TGF-beta activated kinase 1b(aa) * TGF-beta activated
 CG1388 kinase 1c(aa) [PROTEIN_KINASE_ST // EGF_1 // TYRKINASE] CG1388 19E1-19E1 dup:1/4 ID:46B1
 + ND42 enzyme * NADH-ubiquinone oxidoreductase kDa subunit(aa) * DMNUBO42K ND42 * NADH-UBIQUINONE OXIDOREDUCTASE
 CG6343 KD SUBUNIT PRECURSOR (COMPLEX I-42KD) (CI-42KD)(aa [ATP_GTP_A] CG6343 93F14-94A1 ID:46B3
 CG10928+ CG10928 LD29844 dup:3/3 ID:46E11
 CG6224 + dbo actin_binding CG6224 LD29988 dup:1/3 ID:46G1
 + enzyme * 1e-29 GTT1_DROME GLUTATHIONE S-TRANSFERASE 1-1 (CLASS-THETA) glu * 6e-12 GTT1_MOUSE
 CG10065 GLUTATHIONE S-TRANSFERASE THETA (CLASS-THETA) * 3e-11 glutathion [GST] CG10065 LD30165 84C-84C dup:1/3 ID:46G12
 CG9949 + SEVEN IN ABSENTIA DNA binding ubiquitin-dependent protein degradation ZF_RING CG9949 LD30265 ID:46H3
 + chaperone It encodes a chaperone involved in proteolysis and peptidolysis which is a component of the mitochondrion
 CG4164 DNAJPROTEIN, DNAJ_1, DNAJ_2, DnaJ CG4164 LD30318 ID:46H8
 CG12306+ protein_kinase CG12306 ID:47A2
 + transcription_factor * general transcription factor IIH, polypeptide (52kD subunit)(aa) * TFIIH subunit Tfb2; has homology to CAK and
 CG7764 human IIH subunits; Tfb2p(aa) * 9e-71 CG7764 LD30622 71D3-71D4 ID:47B11
 + transporter * 8e-72 contains similarity to xanthine/uracil permeases family elegans * 1e-136 yolk sac permease-like molecule * 1e-136
 CG6293 sodium-dependent vitamin C tr [xan_ur_permease // XANTH_URACIL_PERMASE] CG6293 LD30822 86A2-86A2 ID:47C11
 + unknown * 4e-09 predicted using Genefinder; similar to emp24/gp25L/p24 family; cDN * 1e-08 putative T1/ST2 receptor binding
 CG10733 protein precursor * 2e-07 putative [EMP24_GP25L] CG10733 LD30746 65A3-65A3 ID:47C7
 CG11490+ unknown CG11490 dup:1/3 ID:47C9
 CG5100 + unknown * [PRO_RICH // NLS_BP] CG5100 LD31243 77C4-77C4 dup:1/4 ID:47G1
 CG10632+ enzyme * 2e-05 DMANKY_5 Ank * * [ANK_REP // ank // ANK_REP_REGION // NLS] CG10632 LD31582 69C4-69C6 ID:47H1
 + translation_factor * translation repressor NAT1(aa) * eukaryotic protein synthesis initiation factor(aa) * 2e-19 IF41_YEAST
 CG3845 EUKARYOTIC INITIATION FACTOR 4F SUBUNIT P150 CG3845 LD32057 49E1-49E1 dup:1/2 ID:48A10
 + transcription_factor * 1e-11 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * 4e-20 CROL BETA * 2e-08
 similar to Zinc finger, C2H2 type (4 domains); cDNA EST *[ZF_MATRIN // zf-C2H2 // ZINC_FINGER_C2H] CG17806 LD32088 93B1-93B1
 CG17806 ID:48A11
 CG5995 + unknown * CG5995 LD31910 97F3-97F4 dup:1/2 ID:48A2
 + ligand_binding_or_carrier * 2e-13 62D9.a * 2e-25 retinaldehyde-binding protein C * 2e-15 DMC30B8 * /match=(desc;; /ma
 CG10657 [CRETINALDHBP // CRAL_TRIO] CG10657 LD32330 69C2-69C2 dup:2/2 ID:48B10
 CG2899 + ksr protein_kinase * KSR(aa) * KSR(aa) * ksr * 6e-19 hypothetical protein YPL141c - yeast (Saccharomyces cerevisiae) (

[PROTEIN_KINASE_TYR // DAG_PE_BINDING_DO] CG2899 83B1-83B1 dup:2/2 ID:48C6
+ enzyme * similar to Transketolase; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this
CG8199 gene; cDNA EST comes from this gene [E1_dehydrog // NLS_BP] CG8199 LD32808 85D25-85D25 dup:2/2 ID:48D12
+ motor_protein * ARX(aa) * 1e-58 UBA2_YEAST UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING
PROTEIN * 2e-28 ubiquitin activating enzyme * 1e-67 simila[UBA_NAD // ThiF_family // NAD_BINDING /] CG7528 LD33023 67E3-67E3
CG7528 dup:5/5 ID:48E10
CG18551+ unknown * CG18551 LD33058 88E1-88E1 ID:48F3
+ unknown * protein(aa) * SSXT PROTEIN (SYNOVIAL SARCOMA, TRANSLOCATED TO X CHROMOSOME) (SYT PROTEIN)(aa) *
CG10555 synovial sarcoma, translocated to X chromosome(aa) * [PRO_RICH] CG10555 LD33241 7E2-7E3 dup:2/2 ID:48G6
+ RNA_binding * DMRM62RH_2 Rm62 * RNA helicase(aa) * mitochondrial DEAD box protein(aa) * VASA PROTEIN(aa) [helicase_C
CG7878 // KH-domain // KH_DOMAIN //] CG7878 LD33749 84F1-84F1 ID:49A7
+ I(3)03670 unknown * DMC507_2 anon-I * 5e-93 head-elevated expression in 0.9 kb * 8e-92 inserted at base Unknown 5' end of P element
CG1715 Plasmid rescue * CG1715 LD33960 100B-100B ID:49B8
+ EG:84H4.1 chaperone * by content; by match; 2-match_description=TORSINA.; 2-match_species=HOMO SAP...(aa) * 7e-55 similarity to
CG3024 35.1KD hypothetical yeast protein (Swiss [CLPPROTEASEA] CG3024 LD34179 4C7-4C7 ID:49C9
+ pelo unknown * pelo * 9e-61 DOM34 protein - yeast (Saccharomyces cerevisiae) (X77 * PELO_DROME PELOTA PROTEIN pelota *
CG3959 1e-120 YNU6_CAEEL HYPOTHETICAL 42.9 KD PROT CG3959 LD34262 30C6-30C7 ID:49D2
+ peptidase * 1e-62 S2P * 2e-62 S2P * SP2 metalloprotease * S2P metalloprotease [ZINC_PROTEASE // SREBPS2PTASE] CG8988
CG8988 LD34294 48C-48C ID:49D4
+ unknown * P38IP(aa) * Lola-like protein(aa) * GAGA-581 Adf-2 isoform(aa) * 0.000002 [NLS_BP] CG17689 LD34837 70B2-70B2
CG17689 ID:49F7
+ unknown * 1e-146 inserted at base Unknown 5' end of P element Plasmid rescue * * [ZINC_FINGER_C2H2 //
CG5580 ZINC_FINGER_C2H2_2] CG5580 LD35038 55C4-55C4 ID:49G3
+ enzyme * 5e-19 VIT1_DROME VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1) vitell * 6e-23 pancreatic lipase related protein *
CG17292 3e-25 pancreatic lipase-related protei [TAGLIPASE // ESTERASE // lipase] CG17292 GH01208 29B3-29B3 ID:54B11
+ ion_channel * Glu-RIIB * glutamate receptor precursor - human (fragment)(aa) * 9e-14 glutamate receptor DGLuRIIB * 4e-17
CG17274 ionotropic glutamate receptor - Caenorhab [lig_chan // ATP_GTP_A] CG17274 GH01149 93A1-93A1 ID:54B6
+ Dph5 enzyme * similar to diphthine synthase(aa) * 7e-73 DPH5_YEAST DIPHTHINE SYNTHASE (DIPHTAMIDE BIOSYNTHESIS
CG5275 METHYLTRANSFERASE) * 1e-84 CGI-30 protein * 3e-74 [TP_methylase] CG5275 GH01248 94B8-94B9 ID:54C3
+ Diacyl glycerol kinase enzyme æDgk gene product is expressed predominantly in the embryonic CNS and adult nervous system and
CG1535 muscle DAGK, DAGKa, DAGKc, NLS_BP CG1535 GH01459 dup:2/2 ID:54D12
CG5532 + unknown * CG5532 GH01442 59F7-59F7 ID:54D9
+ enzyme * long-chain-fatty-acid--CoA ligase (fadD-8)(aa) * similar to 4-coumarate-coA ligase; cDNA EST yk455e10.3 comes from
CG4563 this gene; cDNA EST yk455e10.5 c [AMP-binding] CG4563 GH01595 60D2-60D2 ID:54F5
CG18212+ unknown * [NLS_BP] CG18212 GH01770 90C-90C ID:54G11
CG8605 + unknown * 3e-08 pi034 * * CG8605 GH01880 65F2-65F2 ID:54H8

CG8401 + unknown * CG8401 GH01937 52E3-52E4 ID:55A1
 CG11293+ unknown * CG11293 GH02327 59F4-59F4 ID:55B11
 CG4716 + unknown * CG4716 GH02313 50A1-50A1 dup:2/3 ID:55B9
 + enzyme * 1e-47 CACP_YEAST CARNITINE O-ACETYLTRANSFERASE PRECURSOR (CARNITINE ACETYLASE) * 4e-37 choline
 CG12428 acetyltransferase * 3e-66 similar to Carnitate acyltr [Carn_acyltransf] CG12428 GH02484 98A8-98A9 dup:1/4 ID:55C12
 + 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
 + actin_binding * filamin(aa) * 1e-103 similar to endothelial actin-binding protein repeats; cDNA EST EMB * 7e-11 actin binding protein
 CG11605 ABP-280 * 3e-90 gamma filamin [Filamin // FILAMIN_REPEAT] CG11605 GH03013 58F7-58F7 dup:1/3 ID:55F5
 CG9005 + cell_adhesion * 0.000000000000000003 * CG9005 GH03037 48B1-48B2 dup:2/5 ID:55F7
 + unknown * 2e-17 FMR2 protein * 1e-17 X mental retardation X ment * lymphoid nuclear protein related to AF4 * [HMGI_Y //
 CG8817 NLS_BP] CG8817 GH03237 23C1-23C1 dup:1/2 ID:55G11
 CG6272 + transcription_factor C/EBP CCAAT/enhancer-binding protein B_ZIP, NLS_BP CG6272 GH03576 ID:56A6
 + unknown * ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9)(aa) * ATP-
 CG5172 DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (N CG5172 GH03633 15E5-15E5 ID:56B2
 + Cyt-b5 electron_transfer * CYBR_DROME PROTEIN TU-36B (CYTOCHROME B5-RELATED PROTEIN) * 9e-66 CYBR_DROVI
 CYTOCHROME B5 RELATED PROTEIN cytochrome b5 * DMTU36B_4 Cyt-b5 * delta [CYTOCHROME_B5_2 // heme_1] CG13279
 CG13279 GH03691 36A9-36A9 ID:56B5
 CG2767 + enzyme aldose reductase ALDOKETO_REDUCTASE_1, ALDOKETO_REDUCTASE] CG2767 ID:56C2
 CG15608+ unknown * 2e-06 CGI-62 protein * [NLS_BP] CG15608 GH03957 53F6-53F7 dup:1/3 ID:56D12
 + Pkg21D protein_kinase * Pkg21D * 1e-64 cAMP-dependent protein kinase subunit (put.); putative * protein kinase (EC 2.7.1.37), cGMP-
 CG3324 dependent - fruit fly (Drosophila melanog [PROTEIN_KINASE_ST // CGMPKINASE // cNMP] CG3324 GH03852 21E1-21E1 ID:56D3
 CG5433 + Klc motor_protein KINESIN LIGHT CHAIN (KLC) ATP_GTP_A, KINESINLIGHT,KINESIN_LIGHT, T] CG5433 ID:56D9
 + Bc larval_serum_protein * pro-phenol oxidase A1 * pro-phenol oxidase subunit 1; proPO-p1 * DMORA_2 Bc * prophenoloxidase
 CG5779 [TYROSINASE_2 // hemocyanin // HEMOCYANIN] 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 * 5e-42
 CG5725 putative protein * coded for by C. CG5725 GH04001 77B6-77B6 dup:3/3 ID:56E4
 + peptidase * 5e-10 carboxypeptidase s * 3e-90 Similarity to Human aminoacylase-1 (SW:ACY1_HUMAN) * 1e-109 aminoacylase
 AMINOACYLASE-1 (N-A * 1e-103 ACY1_PIG AMIN [ARGE_DAPE_CPG2_1 // ARGE_DAPE_CPG2_2] CG6465 GH04054 86C2-86C2
 CG6465 dup:2/2 ID:56E8
 + unknown * antigen 5-related 2(aa) * antigen 5-related protein(aa) * Ag5r2 * 7e-12 predicted using Genefinder; Similarity to Human
 CG9400 testis-specific pr [SCP // GATASE_TYPE_II] CG9400 GH04057 12E2-12E2 dup:2/2 ID:56E9
 + unknown * secretory carrier membrane protein 2(aa) * 1e-43 partial CDS * 4e-54 SCA3_MOUSE SECRETORY CARRIER-
 ASSOCIATED MEMBRANE PROTEIN * 7e-64 SCA1_HUMAN SEC [PHOSPHOPANTETHEINE] CG9195 GH04264 13D1-13D1 dup:2/2
 CG9195 ID:56G2
 CG10199+ I(3)82Fdunknown * L82A(aa) * map_position:82F5-6 * [NLS_BP // ATP_GTP_A] CG10199 GH04293 83A2-83A3 dup:2/3 ID:56G9

CG5348 + Sodium/calcium exchanger protein Na⁺/Ca²⁺,K⁺-exchanging protein homolog Na_Ca_Ex CG5348 GH04570 ID:57A12
+ transporter * 3e-23 YNK1_YEAST HYPOTHETICAL 80.0 KD PROTEIN IN POL1-RAS2 INTERGENIC REGION * 4e-58 cDNA EST

CG8785 comes from this gene; cDNA EST * 7e-21 putative amino [AROMATIC_AA_PERMEASE_2] CG8785 GH04538 49B7-49B7 ID:57A5

CG4524 + unknown * CG4524 GH04692 14F5-14F5 ID:57B12

CG4962 + unknown * CG4962 GH04593 72E2-72E2 ID:57B2

CG18455+ Optix unknown * transcription factor RNA polymerase II transcription factor) cell nucleus) * * CG18455 GH04859 44A2-44A2 ID:57C11
+ enzyme * ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (PROTEIN 9) (SUBUNIT C)(aa) * 5e-12 ATP synthase (EC

CG1746 3.6.1.-) c chain - Caenorhabditis elegans * 3e- [ATPASE_C // ATPASEC // ATP-synt_C] CG1746 GH04827 100B9-100B9 ID:57C6
+ enzyme * 4e-16 LIPB_YEAST PROBABLE LIPOATE-PROTEIN LIGASE B PRECURSOR (LIPOATE BIOSYNTHESIS PR * 6e-09

CG9804 lipoate-protein ligase B * 8e-36 LIPB_ARATH PUTATIVE L [LIPB] CG9804 GH04831 82C1-82C1 ID:57C7

CG9896 + unknown * [NLS_BP] CG9896 GH05301 59C1-59C1 ID:57G12

CG5073 + CG5073 ID:57H3
+ Cyp6a8 cytochrome_P450 * DMCYP6A2A_5 Cyp6a2 * cytochrome p450 monooxygenase * 3e-37 predicted using Genefinder; similar to

CG10248 cytochrome P450 * 5e-49 cytochrome P450 3A11 - mou [EP450II // p450 // P450 // MITP450 // C] CG10248 GH05558 51D2-51D2 ID:58A6

CG11477+ unknown * CG11477 GH05565 12E2-12E2 ID:58A7
+ Hrb87F RNA_binding * Rbm(aa) * similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST yk474h4.3 comes

CG12749 from this gene; cDNA EST yk505c10.3 comes from [RNP_1 // RBD // rrm] CG12749 GH05625 87F7-87F7 ID:58B2

CG1980 + don juan unknown It encodes a product which is expressed in the adult (testis) NLS_BP CG1980 GH05702 ID:58B6
+ Rbf cell_cycle_regulator * DMRBFPRTN_2 Rbf * EST comes from the 3' UTR m * 3e-24 similar to retinoblastoma proteins * 1e-84

CG7413 RBL1_MOUSE RETINOBLASTOMA-LIKE PROTEIN (107 KD RETI CG7413 GH05946 1C2-1C2 ID:58D10

CG3920 + unknown * CG3920 GH05923 24C-24C dup:1/2 ID:58D7
+ Rab-RP3 signal_transduction * Rab1 * Rab-RP3 * 3e-47 coding sequence YP2 gene * 1e-121 rab-related protein [ras // ATP_GTP_A //

CG7062 RASTRNSFRMNG] CG7062 GH06528 66C5-66C5 ID:59A1
+ enzyme * UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP)

CG4347 (UGPASE)(aa) * similar to UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRA CG4347 GH06691 67A9-67B1 dup:1/3 ID:59B7

CG17035+ unknown * [PA2_HIS] CG17035 GH07145 72C1-72C1 ID:59D4

CG18512+ CG18512 GH07187 ID:59D7
+ transcription_factor * putative PHD-type zinc finger(aa) * Atu(aa) * myeloid/lymphoid or mixed-lineage leukemia 2(aa) * ATP-

CG2926 dependent chromatin assembly factor la[zf-C3HC4 // ZINC_FINGER_C3HC4 // PHD //] CG2926 GH07267 83B4-83B4 dup:4/4 ID:59E6
+ enzyme * similar to Gila monster phospholipase A2; similar to * PHOSPHOLIPASE A2 ISOZYMES PA2/PA4

CG3009 (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE)(aa) * 2e-21 PA2_APIME [PA2_HIS] CG3009 GH07387 4C7-4C7 ID:59F5
+ BG:DS00180.8 cell_adhesion * DMTENA_3 Ten-a * DMC901PRT C901 * DMDDELTA_4 DI * 3e-20 C901 protein [EGF_2] CG16882

CG16882 GH07717 34E1-34E1 dup:3/4 ID:59H10
+ motor_protein * dynein light chain-A(aa) * DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN LIGHT

CG1938 CHAIN A) (DLC-A)(aa) * 1e-38 cDNA EST comes from th [ATP_GTP_A] CG1938 GH07739 10A10-10A10 dup:2/3 ID:60A3

CG11303+ 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 dup:2/3 ID:60B10
+ Mgstl enzyme (Microsomal glutathione S-transferase-like) microsomal glutathione S-transferase-like protein [Drosophila melanogaster]
CG1742 >g MAPEG CG1742 GH08455 dup:1/2 ID:60F10
+ enzyme * spermidine synthase(aa) * SPERMIDINE SYNTHASE (PUTRESCINE AMINOPROPYLTRANSFERASE) (SPDSY)(aa) * 1e-77 SPEE_YEAST SPERMIDINE SYNTHASE (PUTRESCINE AMI [SAM_BIND // ATP_GTP_A] CG8327 GH08387 85E2-85E2 dup:2/3 CG8327 ID:60F4
+ peptidase * carboxypeptidase D(aa) * CARBOXYPEPTIDASE PRECURSOR(aa) * * CpepE [CARBOXYPEPT_ZN_1 // CG4678 CARBOXYPEPT_ZN_2 //] CG4678 GH08425 15A2-15A3 dup:2/3 ID:60F8
none + none GH08762 ID:60H10
+ bgcn unknown * EUKARYOTIC TRANSLATION INITIATION FACTOR (EIF-6)(aa) * map_position:60A2+ * EUKARYOTIC CG17611 TRANSLATION INITIATION FACTOR (EIF-6)(aa) * integrin beta bin CG17611 GH08760 60A4-60A4 dup:1/2 ID:60H9
+ translation_factor * hypothetical translation initiation factor(aa) * HYPOTHETICAL 40.9 KD PROTEIN C01G10.9 IN CHROMOSOME CG11334 V(aa) * 3e-66 YP18_YEAST HYPOTHETICAL 45.0 KD P [IF-2B] CG11334 GH08894 100C-100C dup:1/2 ID:61B5
CG3987 + unknown * CG3987 GH09123 88E4-88E5 dup:2/3 ID:61D3
+ endopeptidase * prolyl endopeptidase(aa) * 3e-06 PPCE_PIG PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE) * prolyl oligopeptidase (EC 3.4.21.26) - human [PROLIGOPTASE // Peptidase_S9 // ESTERAS] CG2528 GH09342 40A6-40A6 CG2528 dup:2/2 ID:61F2
CG10508 + unknown * [WW_DOMAIN_2] CG10508 GH09378 78C4-78C4 dup:3/6 ID:61F6
+ unknown * 2e-13 YJT6_YEAST HYPOTHETICAL 36.2 KD PROTEIN IN UBP12-CDC6 INTERGENIC REGION * 8e-18
CG9798 YLF4_CAEEL HYPOTHETICAL 34.1 KD PROTEIN C40H1.4 IN CHROMOSOME CG9798 GH09808 82C1-82C2 dup:3/4 ID:61H12
+ enzyme * similar to pig tubulin-tyrosine ligase.(aa) * 4e-06 YBU4_YEAST HYPOTHETICAL 86.4 KD PROTEIN IN PHO5-VPS15 CG16833 INTERGENIC REGION * 1e-76 similar to tubul CG16833 GH09663 32C5-34A5 dup:1/3 ID:61H3
CG1822 + CG1822 dup:2/2 ID:62B10
+ enzyme * 5e-18 4-nitrophenylphosphatase (EC 3.1.3.41) - yeast (Saccharomyces cerevisiae) * 1e-10 by content; 1-meth * 1e-24 CG5577 YMQ1_CAEEL HYPOTHETICAL 88.1 KD P CG5577 GH10306 75A4-75A4 ID:62D3
CG18069 + CaMKII protein_kinase proline rich calmodulin-dependent protein kinase PROTEIN_KINASE_DOM, pkinase CG18069 ID:62D9
+ DNA_binding * 2e-05 ROX1_YEAST ROX1 REPRESSOR (HYPOXIC FUNCTION REPRESSOR) (HEME-DEPENDENT REPRESSIO * 7e-14 bobby sox * 4e-30 similar to HMG box transcription fa [LIPOCALIN // HMG // HMG_box // PRO_RICH] CG5067 CG5067 GH10633 95A4-92D9 ID:62F8
+ enzyme * similar to plant chloroplast and prokaryotic carbonic anhydrases(aa) * 2e-63 similar to plant chloroplast and prokaryotic CG11967 carbonic anhydrases * 2e-1 [Pro_CA] CG11967 GH10821 85C3-85C3 ID:62H4
+ transporter * 3e-29 ITR2_YEAST MYO-INOSITOL TRANSPORTER myo-inositol transp * 1e-24 glucose transporter 1; CeGT1 * 9e-22 Contains similarity to Pfam domain: (suga [SUGRTRANSPORT // SUGAR_TRANSPORT_1 // SU] CG1213 GH10929 83C4-83C4 dup:1/3 CG1213 ID:63A7
+ enzyme * similarity to enoyl CoA hydratase. Amino terminus shows similarity to acyl-CoA binding domains; cDNA EST comes from CG13890 this gene; cDNA EST comes from [ECH // NLS_BP] CG13890 GH11143 61D4-61D4 ID:63B12

+ endopeptidase * serine protease 18D(aa) * 1e-34 SNAK_DROME SERINE PROTEASE SNAKE PRECURSOR serine proteina * 1e-15 kallikrein * 1e-22 coagulation factor XI [trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG11841 GH11046 98F9-98F10 dup:2/2
 CG11841 ID:63B4
 + enzyme * gamma-aminobutyric acid transaminase(aa) * PROBABLE 4-AMINOBUTYRATE AMINOTRANSFERASE,
 CG7433 MITOCHONDRIAL PRECURSOR (GAMMA-AMINO-N-BUTYRATE TRANSAMINASE) CG7433 GH11161 76E2-76E2 dup:1/4 ID:63C3
 + unknown * 1e-37 Contains similarity to Pfam domain: (zf-C3HC4), Score=13.0 * 9e-33 nicotinic acetylcholine receptor-associated
 CG1909 46K protein - mouse (J03 * 5e-3 [TPR_REPEAT // ZF_RING] CG1909 GH11191 102C5-102C5 dup:1/3 ID:63C6
 + Dynein heavy chain at 93AB motor_protein DYNEIN BETA CHAIN, CILIARY ATP_GTP_A, MITOCH_CARRIER, NLS_BP, THIOL]
 CG3723 CG3723 GH11420 ID:63D9
 + EG:25E8.1 chaperone * Similarity to HSP70's.; cDNA EST CEESD26F comes from this gene; cDNA EST CEMSB16F comes from this gene; cDNA EST CEMSB16FB comes from this gene; cDN [HEATSHOCK70 // HSP70 // HSP70_3] CG2918 GH11566 2F1-2F2 dup:2/2
 CG2918 ID:63E12
 + unknown * cold inducible glycoprotein 30(aa) * 5e-15 SUR4 * 8e-53 YYS3_CAEEL HYPOTHETICAL 51.5 KD PROTEIN IN
 CG3971 CHROMOSOME IV (U * 2e-49 membrane glycoprotein Cl CG3971 GH11554 73B1-77B1 dup:2/2 ID:63E9
 + unknown * 1e-06 ectodermal (ect) - fruit fly (Drosophila melanogaster) (strain Oregon-R) * * [NLS_BP] CG6611 GH11838 67D2-
 CG6611 67D2 ID:63H3
 + enzyme * DNA-DIRECTED RNA POLYMERASE II KD POLYPEPTIDE (RNA POLYMERASE II SUBUNIT 5)(aa) * polymerase (RNA)
 CG6572 II (DNA directed) polypeptide G(aa) * 7e-33 RPB7_ [S1] CG6572 GH11867 88E8-88E8 ID:63H5
 + Hel89B DNA_binding * TBP-associated factor 172(aa) * Hel89B * 89B helicase(aa) * MOT1_YEAST PROBABLE HELICASE MOT1
 CG4261 MOT1 protein - yeast (S [helicase_C // SNF2_N] CG4261 GH12153 89B3-89B3 dup:1/2 ID:64C3
 + cytoskeletal_structural_protein * putative protein transport protein sec7 homolog(aa) * DmCDS(aa) * pleckstrin and Sec7 domain
 CG6941 protein(aa) * PROTEIN TRANSPORT [SPECTRINPH // PH // SEC7 // Sec7 // MIT] CG6941 GH12441 94B10-94B10 dup:2/2 ID:64E4
 + * membane-type metalloproteinase precursor(aa) * MATRIX METALLOPROTEINASE-14 PRECURSOR (MMP-14) (MEMBRANE-
 TYPE MATRIX METALLOPROTEINASE 1) (MT-MMP 1) [Peptidase_M10 // hemopexin // ZINC_PROT] CG1794 45F6-46A1 dup:4/5
 CG1794 ID:64E7
 + signal_transduction * 5e-23 VP27_YEAST VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27 * 3e-10
 /match=(desc:; /ma * 9e-65 coded for by C. elegans cDNA yk21d11.3; coded [FYVE_DOMAIN // FYVE // HRS_DOMAIN] CG2903
 CG2903 GH12653 23A6-23A7 ID:64F12
 + unknown * hypothetical protein * 1E-162* hypothetical protein * hypothetical protein, 5' partial [S5A_REDUCTASE] CG6282
 CG6282 GH12549 68C1-68C1 dup:3/4 ID:64F4
 + transporter * cellutagmin I sytVI - rat(aa) * DMPKC53E_2 inaC * DMSYT_2 syt * 4e-40 SY65_DROME SYNAPTOTAGMIN (P65)
 CG3020 synaptotagmin - fruit fly ([SYNAPTOTAGMN // C2 // C2_DOMAIN_2 // PR] CG3020 GH12656 71A3-71A4 ID:64G1
 + RNA_binding * BLASTX 2.0E-34 Arabidopsis thaliana Col-O putative RNA helicase A mRNA, complete cds.(dna) * DMMLE_2 mle *
 CG9323 1e-79 hypothetical protein YLR419w - yeas [PROTEIN_SPLICING // G_PROTEIN_RECEPTOR] CG9323 GH12763 38E5-38E5 ID:64G12
 + unknown * 3e-08 probable membrane protein YLR251w - yeast (Saccharomyces cerevisiae) * 1e-08 /match=(desc: * 3e-15
 CG10854 PMP2_MOUSE KD PEROXISOMAL MEMBRANE PROTEIN CG10854 GH12661 64C4-64C4 ID:64G2
 CG1970 + enzyme * NADH-UBIQUINONE OXIDOREDUCTASE KD SUBUNIT PRECURSOR (COMPLEX I-49KD) (CI-49KD)(aa) * BLASTX

2.1E-17 Bovine mRNA fragment for kDa subunit of mitochon [COMPLEX1_49K // complex1_49Kd] CG1970 GH13128 102C5-102C5
dup:2/3 ID:65B10

CG7549 + unknown * [HTH_LACI_FAMILY] CG7549 GH13023 84F-84F ID:65B2
+ unknown * No definition line found(aa) * 4e-06 probable membrane protein YPR091c - yeast (*Saccharomyces cerevisiae*) * 6e-43 No

CG5741 definition line found * 3e-05 h CG5741 GH13177 66E4-66E4 ID:65C6
+ enzyme * 4e-09 YGX7_YEAST HYPOTHETICAL 108.2 KD PROTEIN IN SAP4-OST5 INTERGENIC REGION * 3e-06 DEAD-box
protein * 8e-43 predicted using Genefinder; similar t [SPRY_DOMAIN // PHOSPHOPANTETHEINE // SP] CG11763 GH13409 47A7-47A7
CG11763 dup:3/3 ID:65D6

+ cell_adhesion * bt * 3e-17 projectin * 6e-18 twitchin - *Caenorhabditis elegans* twitchin * 1e-14 protein-tyrosine-phosphatase (EC
CG4668 3.1.3.48), receptor type sigma pr[FNTYPEIII // RIBOSOMAL_S2_1 // PRO_RICH] CG4668 GH13550 36A6-36A6 dup:3/3 ID:65E2
+ Pka-C3 protein_kinase * PROTEIN KINASE DC2(aa) * DMDC2_2 Pka-C3 * 5e-88 cAMP-dependent protein kinase subunit (put.);

CG6117 putative * 2e-99 KAPC_CAEEL CAMP-DEPENDENT PROTEIN KIN CG6117 GH13608 72B1-72B2 dup:3/3 ID:65E5
+ Cyp4e1 cytochrome_P450 * cytochrome P450, Cyp4e2 - fruit fly (*Drosophila melanogaster*) (U5 * 6e-79 predicted using Genefinder;

CG2062 similar to cytochrome P450 * 3e-50 CYP4B1 [EP450II // p450 // P450 // MITP450 // C] CG2062 GH13635 44C1-44C2 dup:2/2 ID:65E8
+ transporter * furosemide-sensitive K-Cl cotransporter(aa) * BLASTX 7.2E-55 *Rattus furosemide-sensitive K-Cl cotransporter (KCC2)*

CG5594 mRNA, complete cds.(dna) * 6e-49 [AMINO_ACID_PERMEASE_2 // KCLTRANSPORT] CG5594 GH13642 60A9-60A10 dup:4/5 ID:65E9
+ endopeptidase * INSULIN-DEGRADING ENZYME (INSULYSIN) (INSULINASE) (INSULIN PROTEASE)(aa) * DMD1DE_2 Ide * 2e-

CG2025 63 STE23 protein - yeast (*Saccharomyces cerevisiae*) Ste [Peptidase_M16 // INSULINASE] CG2025 GH13968 10F2-10F2 ID:65G10

CG15390 + unknown * CG15390 GH14074 22E-22E ID:65H11
+ peptidase * AMINOPEPTIDASE N (MICROSOMAL AMINOPEPTIDASE) (MEMBRANE GLYCOPROTEIN H11)(aa) *
aminopeptidase N homolog(aa) * 5e-88 aminopeptidase yscII * 5e-97 Sim [ALADIPTASE // Peptidase_M1] CG5845 GH14075 93F6-93F6
CG5845 dup:2/2 ID:65H12

+ structural_protein * nuclear pore protein; Seh1p(aa) * similar to WD domain, G-beta repeat (2 domains); cDNA EST yk258d4.3

CG8722 comes from this gene; cDNA EST yk338d5.3 comes [GPROTEINBRPT // WD40] CG8722 GH14024 43F9-43F9 ID:65H2

CG9264 + transporter * CG9264 GH14216 39A6-39A7 ID:66B5
+ 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
+ unknown * predicted trithorax protein(aa) * INTEGRAL MEMBRANE PROTEIN DGCR2/IDD PRECURSOR (SEIZURE-RELATED

CG4285 MEMBRANE-BOUND ADHESION PROTEIN)(aa) * BLASTX 7.0E [RCC1_2] CG4285 GH14388 90D1-90D1 ID:66C9
+ enzyme * GCSP_YEAST GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXY * similar

CG3999 to glycine dehydrogenase * GCSP_HUMAN GLYCINE DEHYDROGEN CG3999 GH14537 85F16-85F16 dup:2/2 ID:66E3
+ * cDNA EST yk335d8.5 comes from this gene; cDNA EST yk335d8.3 comes from this gene(aa) * 2e-23 cDNA EST yk335d8.5

CG4972 comes from this gene; cDNA EST yk335 CG4972 31D7-31D8 dup:2/2 ID:67A10
+ electron_transfer * CYTOCHROME B5 (CYTB5)(aa) * 3e-17 cytochrome b5 * 1e-25 Similarity to Human cytochrome b5
(SW:CYB5_HUMAN); cDNA EST EMBL:D * 2e-30 CYB5_MOUSE CY[Cytochrome_B5 // CYTOCHROME B5 // CYTOCH] CG2140

CG2140 GH15091 43D-43D dup:3/3 ID:67B9

+ pn signal_transduction * PRUNE protein(aa) * DMPRUNEG_2 pn * 1e-16 PPX1_YEAST EXOPOLYPHOSPHATASE
 CG3461 (METAPHOSPHATASE) exopolyph * PRUNE protein CG3461 GH15456 2E1-2E1 dup:2/2 ID:67E10
 + cytoskeletal_structural_protein * 8e-19 protein * sorting nexin * Y254_HUMAN HYPOTHETICAL PROTEIN KIA * [BEM_DOMAIN //
 CG1514 GRK] CG1514 GH16154 7C8-7C8 ID:68C11
 + unknown * 1e-109 weak similarity to Bacillus and Pseudomonas probable glucarate transporters (G * 2e-06 conserved hypothetical
 CG1358 protein * 2E-46* C05G5.1 CG1358 GH16188 43E3-43E4 dup:2/2 ID:68D3
 + drongo signal_transduction * drongo * 9e-25 Drongo * 4e-12 HIV-1 Rev binding protein NUCLEOPO * 1E-151 [ArfGap // ZF_GCS //
 CG3365 REVINTRACTNG] CG3365 GH16240 21D2-21E3 dup:2/2 ID:68D8
 + motor_protein * receptor-associated protein(aa) * 9e-14 predicted using Genefinder; Similarity to Human alpha-2-macroglobu * 2e-
 CG8507 16 heparin binding protein * 5e-18 CG8507 GH16343 86D1-86D1 dup:3/3 ID:68E5
 + unknown * 9e-36 by content; 1-meth * 1e-43 YS15_CAEEL HYPOTHETICAL 41.1 KD PROTEIN IN CHROMOSOME II * 1e-42 Sqv-
 CG3881 8-like protein * 7e-47 UDP-glucuronyltransfera CG3881 GH16433 30C2-30C2 ID:68F5
 + RfaBp unknown * retinoid- and fatty acid-binding glycoprotein * 1e-15 C. elegans vitellogenin precursor, vit-5 (Spieth et al., NAR * 4e-07
 CG11064 prepro-vWF (aa -22 to 137 [vwd // Vitellogenin_N // NLS_BP] CG11064 GH18004 102F4-102F4 ID:70A10
 + tko ribosomal_protein * 2e-21 YN8K_YEAST PUTATIVE 40S MITOCHONDRIAL RIBOSOMAL PROTEIN YNR036C * 2e-76
 RT12_DROME MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S12 PRECURSOR (TECHNICA [RIBOSOMAL_S12 // Ribosomal_S12 //
 CG7925 RIBOS] CG7925 GH17961 3A2-3A2 ID:70A6
 CG3835 + EG:87B1.3 actin_binding * * alkylglycerone phosphate synthase precursor(aa) * DMC87B1 CG3835 GH18028 2D4-2D6 ID:70B4
 + 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
 + ine neurotransmitter_transporter * ine * DMROSA_2 rosa * neurotransmitter transporter * 1e-119 Similarity to Human Na(+)/Cl(-)-
 CG15444 dependent GABA transporter (SW:NTG [NANEUSMPORT // SNF] CG15444 GH18083 24F6-24F6 ID:70C4
 + enzyme_inhibitor * RNase L inhibitor (clone 8) - human(aa) * probable membrane protein YDR091c - yeast (Saccharomyces
 CG5651 cerevisiae) * 3e-07 P-glycoprotein/multidrug resi [fer4 // ATP_GTP_A2 // ABC_TRANSPORTER /] CG5651 GH18088 66E5-66E5 ID:70C5
 + peptidase * 5e-60 putative metalloprotease; Method: conceptual translation supplied by author * 1e-23 coded for by C. elegans cDNA
 CG8196 yk27b10.3; coded for by C. el [PEPDITASEA // Peptidase_M2] CG8196 GH18145 45A6-45A6 ID:70D1
 + * NADP-dependent isocitrate dehydrogenase(aa) * 1e-148 IDHP_YEAST ISOCITRATE DEHYDROGENASE (NADP),
 CG7176 MITOCHONDRIAL PRECURSOR (OXALOSUCCIN * 1e-180 simil [IDH_IMDH // isodh] CG7176 66C8-66C8 dup:3/4 ID:70D6
 CG18539 + unknown * CG18539 GH18493 55C4-55C4 ID:70F10
 + serpin * 2e-30 Similar to serine protease inhibitor * 1e-33 serine proteinase inhibitor * 5e-42 SCC2_HUMAN SQUAMOUS CELL
 CG7722 CARCINOMA ANTIGEN (SCCA-2) (LEUPIN) [serpin // SERPIN] CG7722 GH18514 47C7-47C7 dup:2/4 ID:70F12
 CG4975 + unknown * 4e-05 BE46_MOUSE BRAIN PROTEIN E46 gene E46 protein - mouse * * CG4975 GH18454 54E5-54E5 ID:70F8
 + RNA_binding * mus308 * Ygr271wp(aa) * similar to Helicases conserved C-terminal domain; cDNA EST comes from this gene;
 CG5205 cDNA EST yk430a5.5 comes from this gene; cD [HELICASE // DEAD // ATP_GTP_A] CG5205 GH18520 88F6-88F6 ID:70G1
 + enzyme * ubiquitin fusion degradation protein; Ufd1p(aa) * UBIQUITIN FUSION DEGRADATION PROTEIN HOMOLOG (UB
 CG6233 FUSION PROTEIN 1)(aa) * 2e-47 UFD1_YEAST UBIQUITI CG6233 GH18603 70E3-70E3 ID:70G10
 CG7995 + glycerol_kinase * 1e-83 GLPK_YEAST GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE) (GLYCEROKINASE)

(* 1e-116 similar to glycerol kinase * 1e-147 GLPK_MOUSE G[FGGY_KINASES_1 // FGGY_KINASES_2 // FGG] CG7995 GH18690 62B1-62B1 dup:2/3 ID:70H9

CG4951 + unknown * CG4951 GH18902 98B2-98B3 ID:71A8

+ unknown * 4e-29 YO87_CAEEL HYPOTHETICAL 28.5 KD PROTEIN IN CHROMOSOME III * 6e-18 putative protein *

CG5862 [PCI_DOMAIN // NLS_BP] CG5862 GH18921 95F5-95F5 dup:1/2 ID:71A9

+ signal_transduction * rab11 binding protein(aa) * 5e-41 YM22_YEAST HYPOTHETICAL 94.3 KD TRP-ASP REPEATS CONTAINING PROTEIN IN SNZ1-YPK2 * 1e-07 transcription initiati[GPROTEINBRPT // WD40_REGION // WD40] CG7814 GH19431

CG7814 99C7-99C7 dup:2/2 ID:71E8

+ eIF-4a translation_factor * DMEIF4A_3 Eif4a * EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)(aa) * EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) (STIMULATOR FACTOR I KD COMPONENT) [helicase_C // HELICASE // DEAD // DEAD_] CG9075 GH19518

CG9075 26B1-26B1 dup:3/5 ID:71F5

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

+ transporter * DMC171D11 * DMMDR65_2 Mdr65 * 8e-46 STE6_YEAST MATING FACTOR A SECRETION PROTEIN STE6 (MULTIPLE DRUG RESISTANCE PROT * 4e-86 MDR4_DROME MULTIDRUG RE [ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr]

CG1824 CG1824 GH19726 11B12-11B12 ID:71H4

+ enzyme * 1e-133 SYLM_YEAST LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (LEUCINE--TRNA LIGASE * 1e-08 predicted using Genefinder; Similarity to Yeast isol [tRNA-synt_1 // TRNASYNTHLEU // AA_TRNA_] CG7479 64C-64C ID:71H7

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

CG8205 + enzyme * aldehyde oxidase(aa) * DMXDH_4 ry * xanthine dehydrogenase(aa) * XANTHINE DEHYDROGENASE (XD) (ROSY LOCUS PROTEIN)(aa) [dehydrog_molyb // Ald_Xan_dh_C // fer2] CG6045 GH20168 88F8-88F8 ID:72D2

CG6045 + 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

+ electron_transfer * unknown(aa) * NITRATE REDUCTASE (NAD(P)H) (NR)(aa) * nitrate reductase NR1 (393 AA)(aa) * 2e-86 PP11_YEAST SERINE/THREONINE PROTEIN PHOSPHATA[oxidored_fad // FPNCR // PHEHYDRXLASE /] CG5946 GH20485 68D3-68D3 dup:1/2 ID:72G4

CG5946 + transporter * DMORCT2_2 Orct * organic cationic transporter-like 1(aa) * 9e-08 ITR2_YEAST MYO-INOSITOL TRANSPORTER

CG3790 myo-inositol transp * 6e-75 putative organic ca [SERPIN // sugar_tr] CG3790 GH20501 49D-49D ID:72G6

CG15892+ CG15892 ID:72H4

+ unknown * density regulated protein drp1(aa) * 2e-08 YJY4_YEAST HYPOTHETICAL 22.5 KD PROTEIN IN SPC1-ILV3

CG9099 INTERGENIC REGION * 4e-13 hypothetical protein * 8e- [SUI1_2 // NLS_BP] CG9099 GH20858 15B1-15B1 ID:73B7

+ transporter * pot. w(+) polypeptide(aa) * WHITE PROTEIN HOMOLOG(aa) * Active transport ATPase; Adp1p(aa) * BROWN

CG3327 PROTEIN(aa) [ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG3327 GH20863 25A1-25A1 ID:73B9

+ peptidase * 1e-24 YBY9_YEAST PUTATIVE SERINE CARBOXYPEPTIDASE IN ESR1-IRA1 INTERGENIC REGION * 2e-83 similar to BPTI/KUNITZ inhibitor domain; cDNA EST come * 8e [ESTERASE // serine_carbpept // CRBOXYPT] CG3344 GH21114 61C9-61C9

CG3344 ID:73D10

CG1944 + Cyp4p2 cytochrome_P450 * DMC152A3 * DMCYP4D2_12 Cyp4d2 * 6e-09 CP56_YEAST CYTOCHROME P450-DIT2 (CYTOCHROME

P450 56) cyt * 3e-53 cytochrome P450 cytochrome P4 [EP450II // p450 // P450 // MITP450 // C] CG1944 GH21174 45C-45C dup:2/2 ID:73E8
 + transporter * 5e-27 HXT0_YEAST HEXOSE TRANSPORTER HXT10 hexose transport pro * 9e-42 GTRL_DROME GLUCOSE TRANSPORTER-LIKE PROTEIN glucose transpo * 4e-22 predicted [SUGRTRNSPORT // SUGAR_TRANSPORT_1 // SU] CG6484
 CG6484 GH21490 54D2-54D2 ID:73G7
 + transporter * 8e-32 YG5F_YEAST PUTATIVE MITOCHONDRIAL CARRIER YGR257C hypot * 2e-06 phosphate transporter precursor melanogas * 2e-53 YQ51_CAEEL PUTATIVE MITOCHON [mito_carr // MITOCH_CARRIER] CG14209 GH21653 18D8-18D8 ID:73H12
 CG14209 ID:73H12
 + Rpt4 endopeptidase * 26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED ATPASE DOMAIN PROTEIN 44)(aa) * CG3455 Pros45 proteosome subunit homolog(aa) * 1e-134 SUG2_YEAST PROB CG3455 GH21618 5E1-5E1 dup:2/2 ID:73H8
 + corto nucleic_acid_binding * corto * CENTROSOMAL AND CHROMOSOMAL FACTOR (CCF) (CHROMOCENTROSOMIN)(aa) * CP- CG2530 1(aa) * inserted at base Both 5' and 3' ends of P element Inverse PCR CG2530 GH21787 82F5-82F5 ID:74B1
 CG2530 ID:74B1
 + rux unknown * CELL CYCLE NEGATIVE REGULATOR ROUGHX(aa) * rux * 1e-170 rux * [NLS_BP] CG4336 GH22074 5D1-5D1 ID:74D12
 CG4336 ID:74D12
 + enzyme * carnitine racemase - Escherichia coli(aa) * ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (SHORT CHAIN ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATA [GRAM_POS_ANCHORING // ECH] CG6984 GH22096 53F10-53F10 dup:2/2 ID:74E5
 CG6984 dup:2/2 ID:74E5
 + jdp chaperone * 1e-11 SCJ1_YEAST SCJ1 PROTEIN SCJ1 protein - yeast (Saccharomyce * 1e-09 DNJ1_DROME DNAJ PROTEIN HOMOLOG (DROJ1) droj1 * 1e-10 YRY1_CAEEL HYPOTHETIC [GRAM_POS_ANCHORING // DnaJ // DNAJPROTE] CG2239 GH22106 99F8-99F10 dup:3/3 ID:74E7
 CG2239 99F8-99F10 dup:3/3 ID:74E7
 + transporter * MITOCHONDRIAL FAD CARRIER PROTEIN FLX1(aa) * UCP2(aa) * 5e-26 YIA6_YEAST PUTATIVE MITOCHONDRIAL CARRIER YIL006W probabl * 4e-09 ADT_DROME ADP,ATP CA [mito_carr] CG8026 GH22139 45B4-45B5 dup:2/2 ID:74E9
 CG8026 ID:74E9
 + enzyme * 3-hydroxy-3-methylglutaryl-CoA-synthase(aa) * Similar to hydroxymethylglutaryl-CoA synthase; coded for by C. elegans CG4311 cDNA cm01e7(aa) * 3-hydroxy-3- [HMG_CoA_synt // HMG_COA_SYNTHASE] CG4311 GH22436 53A5-53B1 dup:2/4 ID:74G8
 CG4311 ID:74G8
 + prd transcription_factor * SEGMENTATION PROTEIN PAIRED(aa) * DMPRD_5 prd * 3e-58 similar to 'Paired box' domain, homeobox protein (paired subfamily * 2e-87 PAX3_MOUSE PAIRE[PAX // HOMEBOX_1 // homeobox // HOMEBOX] CG6716 GH22686 33B14-33B14 ID:75B4
 CG6716 ID:75B4
 + enzyme * 6e-06 YD40_YEAST HYPOTHETICAL 42.3 KD PROTEIN IN YTA2-DIT1 INTERGENIC REGION * 4e-33 predicted using CG12177 Genefinder; similar to Inosine-uridine preferri [IU_nuc_hydro] CG12177 GH22706 12B1-12B1 ID:75B7
 CG12177 ID:75B7
 + unknown * 1e-35 probable membrane protein YOR245c - yeast (Saccharomyces cerevisiae) * 3e-58 K07B1.4 gene product * 9e-21 CG1942 hypothetical protein * predicted usi CG1942 GH22719 43E11-43E11 ID:75B9
 CG1942 ID:75B9
 + Flo-2 unknown * 1e-176 flotillin-2 * 1e-114 epidermal surface antigen * 1e-114 flotillin epidermal surface antigen - human * 1e-114 CG11547 growth-associated protein [NLS_BP] CG11547 GH22754 13A3-13A4 ID:75C4
 CG11547 ID:75C4
 + Fragile-X-related RNA_binding * FRAGILE X MENTAL RETARDATION SYNDROME RELATED PROTEIN 1(aa) * Fxr2h(aa) * protein isoform d(aa) * 6e-81 FMR1_MOUSE FRAGILE X MENTAL RETARDATION [KH-domain // TONB_DEPENDENT_REC_1 // KH] CG6203 GH22839 85F10-85F11 ID:75D2
 CG6203 ID:75D2

+ enzyme * probable membrane protein YPR184w - yeast (*Saccharomyces cerevisiae*) * similar to Alpha amylase; cDNA EST
 CG9485 yk217a9.5 comes from this gene; * amylo-1, [ISOCITRATE_LYASE] CG9485 GH22856 57D4-57D5 dup:3/4 ID:75D8
 + cell_adhesion * 2e-11 CHAO_DROME CHAOPTIN PRECURSOR (PHOTORECEPTOR CELL-SPECIFIC MEMBRANE PROTEIN) *
 3e-06 Similarity to Rat insulin-like growth factor binding prote [LRR // LEURICHRPT // NLS_BP] CG15658 GH22922 57C7-57C7 dup:2/2
 CG15658 ID:75E6
 + neurotransmitter_transporter * SerT * glycine transporter type-2(aa) * SODIUM- AND CHLORIDE-DEPENDENT GABA
 TRANSPORTER 3(aa) * hypothetical protein T23G5.5 - Caenor[NA_NEUROTRAN_SYMP_1 // NANEUSMPORT // N] CG8380 GH22929
 CG8380 53C-53C dup:2/2 ID:75E8
 + transporter * retinal rod Na/Ca+K exchanger(aa) * Na/Ca,K-exchanger(aa) * 2e-06 probable membrane protein YDL206w - yeast
 CG1090 (*Saccharomyces cerevisiae*) * 1e-05 Na/C CG1090 GH23040 82B1-82B1 ID:75G4
 + agt DNA_repair_protein * O-6-alkylguanine-DNA alkyltransferase(aa) * agt * 3e-16 MGMT_YEAST METHYLATED-DNA--PROTEIN-
 CYSTEINE METHYLTRANSFERASE (6-O-METHYLGUANINE * 2e-10 MGM [Methyltransf_1 // MGMT] CG1303 GH23047 84C4-84C4
 CG1303 ID:75G5
 + shi enzyme * dynamin(aa) * DMDDYN4_2 shi * dynamin II - human(aa) * dynamin-like protein - fruit fly (*Drosophila melanogaster*)(aa)
 CG18102 CG18102 GH23121 13F9-13F10 dup:1/2 ID:75H1
 + defense/immunity_protein * similar to rat autoimmune target protein p69 * 1e-39 similar to rat autoimmune target protein p69 * 5e-67
 CG10566 ICAp69 * 1e-64 diabetes mellitus type I au CG10566 GH23156 78B4-78C1 ID:75H6
 CG13787 + It has been mapped cytologically to 28A1 CG13787 GH23165 ID:75H7
 CG7962 + CG7962 GH23282 ID:76A8
 + Hrb27C RNA_binding * DMHRP481_2 Hrb27C * HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48)
 (HRP48.1)(aa) * 2e-36 NAB4_YEAST NUCLEAR POLYADENYLATED RNA-BINDING PROTE [RNP_1 // RBD // rm] CG10377 27C-27C
 CG10377 dup:6/8 ID:76B1
 + structural_protein * Ran/TC4-binding nucleopore protein(aa) * RanBP2 protein - mouse (fragment)(aa) * RAN binding protein 2;
 CG11856 nucleoporin 358(aa) * HTF9-A protein[GRAM_POS_ANCHORING // zf-RanBP // ZF_RA] CG11856 GH23370 96C4-96C5 dup:2/4 ID:76B5
 CG3348 + unknown * CG3348 GH23384 97F6-97F6 ID:76B8
 + Atpalphatransporter * 3e-78 ATC1_YEAST CALCIUM-TRANSPORTING ATPASE (GOLGI CA2+-ATPASE) * ATNA_DROME
 SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA CHAIN (SODIUM PUMP) (NA+/ [NAKATPASE // Na_K_ATPase_C //
 CG5670 ATPASE_E1] CG5670 GH23483 93B-93B dup:2/3 ID:76C12
 CG13551 + GH20780 CG13551 GH23524 ID:76D4
 + unknown * 0-44 PROTEIN(aa) * HYPOTHETICAL 14.6 KD PROTEIN IN REC104-SOL3 INTERGENIC REGION(aa) *
 CG9396 HYPOTHETICAL 16.3 KD PROTEIN F53F10.3 IN CHROMOSOME I(aa) * h CG9396 GH23618 86C3-86C3 dup:2/2 ID:76E7
 + endopeptidase * DMSTUBBLE_1 Sb * zgr;Try * 2e-22 TRYI_DROME TRYPSIN IOTA PRECURSOR iota trypsin * 2e-15 kallikrein
 CG9898 [trypsin // CHYMOTRYPSIN // TRYPSIN_CATA] CG9898 GH23641 59B8-59B8 ID:76F1
 + pyd enzyme * DMD477 pyd * TamA(aa) * 1e-16 coded for by *C. elegans* cDNA yk25e5.3; coded for by *C. elegans* cDNA yk25e5.5; si *
 CG9763 1e-138 ZO1_MOUSE TIGHT JUNCTION PRO [Guanylate_kin // GUANYLATE_KINASE_2 //] CG9763 GH23642 85B4-85B5 ID:76F2
 + enzyme * hexaprenyl pyrophosphate synthetase; Coq1p(aa) * 9e-26 COQ1_YEAST HEXAPRENYL PYROPHOSPHATE
 CG10585 SYNTHETASE PRECURSOR (HPS) * 9e-13 trans-prenyltransferas [ATP_GTP_A] CG10585 GH23839 78A6-78A6 ID:76H7

CG6043 + unknown * [PRO_RICH] CG6043 GH24071 34A11-34B1 ID:77B11
+ enzyme * DMGST_3 GstD1 * 2e-44 unknown * 1e-13 GTT1_MOUSE GLUTATHIONE S-TRANSFERASE THETA (CLASS-THETA) *

CG17534 6e-16 glutathione S-transferase theta GLUTATHIONE S [GST] CG17534 55C9-55C9 dup:4/4 ID:77B3
+ enzyme * phosphatidylinositol synthase; Pis1p(aa) * phosphatidylinositol synthase(aa) * phosphatidylinositol synthase(aa) * 2e-31

CG9245 PIS_YEAST CDP-DIACYLGLYCERO [CDP_ALCOHOL_P_TRANSF // CDP_ALCOHOL_P_T] CG9245 GH24502 13E14-13E14 ID:77F7
+ Uba1 enzyme * ubiquitin-activating enzyme * ubiquitin activating enzyme * predicted using Genefinder; Similarity to Mouse ubiquitin-

CG1782 activati * UBA1_MOUSE UBIQUIT [UBA_NAD // ThiF_family // UBIQUITIN_ACT] CG1782 GH24511 46A1-46A1 dup:3/3 ID:77F8
+ transporter * 3e-11 aquaporin * 4e-15 BIB_DROME NEUROGENIC PROTEIN BIG BRAIN bib protein - frui * 6e-15 similar to MIP

CG4019 protein * 1e-28 MIP_MOUSE LENS FIBER MAJOR [MINTRINSICP // MIP] CG4019 GH25142 59F1-59F2 ID:78C12
+ transporter * peroxisomal Ca-dependent solute carrier(aa) * Similarity to N.crassa ADP/ATP carrier protein (SW:ADT_NEUCR)(aa)

CG4392 * 1e-38 probable membrane protein [mito_carr // MITOCARRIER // ADPTRNSLCAS] CG4392 GH25190 69B3-69B3 dup:2/2 ID:78D7
+ Pk92B protein_kinase * coded for by C. elegans cDNA CEESN53F; similar to protein kinases including CDC15 in yeast(aa) *

DMPK92B_4 Pk92B * 8e-43 protein kinase * protei[PROTEIN_KINASE_ST // TYRKINASE // PROTE] CG4720 GH25453 92B8-92B8
CG4720 dup:2/3 ID:78F7

CG5677 + CG5677 dup:2/2 ID:78H3
+ signal_transduction * actin-filament binding protein Frabin(aa) * DMD547_2 still-life * 2e-14 still life type * 1e-34 guanine nucleotide

CG7511 exchange factor UNC-73A [GRF_DBL // RhoGEF // PH_DOMAIN] CG7511 GH25579 66A7-66A7 ID:78H4
+ motor_protein * homeotic most like HMPB_DROME: homeotic proboscipedia protein(aa) * 1e-05 neurofilament triplet H1 protein -

CG12105 rabbit (fragment) neuro * * [GRAM_POS_ANCHORING // NLS_BP] CG12105 GH26183 62A-62A dup:2/2 ID:79F12
+ BG:DS01068.2 unknown * hypothetical protein(aa) * 1e-98 R08F11.1 gene product * 7e-50 putative protein * unknown

CG7469 [HMG_COA_REDUCTASE_2] CG7469 GH26380 34F5-34F5 dup:2/2 ID:79H12
+ unknown * 5e-07 hypothetical protein YOL114c - yeast (Saccharomyces cerevisiae) * 2e-17 R02F2.2 gene product * 3e-23 immature

CG6094 colon carcinoma transcript prote [NLS_BP] CG6094 GH26345 31E5-31E5 ID:79H6

CG16724+ tra CG16724 tra dup:2/2 ID:8-31 cntrlBA5

CG11387+ cut CG11387 cut dup:2/2 ID:8-31 cntrlBB6
+ spdo actin_binding * sanpodo protein(aa) * 1e-179 sanpodo protein * 8e-47 Similar to tropomodulin; coded for by C. elegans cDNA

CG1539 yk88e7.5; coded for by C. * 6e-47 TMOD_MO CG1539 sanpodo 100A-100A dup:3/3 ID:8-31 cntrlBC5
+ inv transcription_factor * SEGMENTATION POLARITY PROTEIN ENGRAILED(aa) * DMINVR_2 inv * INVECTED PROTEIN(aa) * 2e-

CG17835 29 HM16_CAEEL HOMEBOX PROTEIN ENGRAILED-LIKE CEH-16 homology CG17835 inv 47F17-48A dup:3/4 ID:8-31 cntrlBD4
+ fu12 enzyme * 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE(aa) * PUTATIVE 1-ACYL-SN-GLYCEROL-3-

PHOSPHATE ACYLTRANSFERASE T06E8.1 (1- AGP ACYLTRANSFERASE) (1-AG [GLYCEROL_ACYLTRANS] CG17608 GH26888
CG17608 29C4-29C4 ID:80F12

+ cell_adhesion * yl * 9e-73 YL_DROME PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL) puta * 1e-96 contains similarity
to EGF-like domains * 1e-132 AM2 receptor [LDLRA_2 // LDLRECEPTOR // EGF_2 // EGF_] CG4823 GH26833 96F1-96F1 dup:2/2

CG4823 ID:80F6
+ endopeptidase * SORCIN(aa) * 8e-12 YG25_YEAST HYPOTHETICAL 38.4 KD PROTEIN IN MUP1-SPR3 INTERGENIC REGION *

CG17765 1e-15 CAN_DROME CALPAIN (CALCIUM-ACTIVATED NEUTRAL PROTE [EF_HAND // ehand // EF_HAND_2] CG17765 47A9-47A9

dup:3/3 ID:81A2
 + Vha55 enzyme * ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2(aa) * H+-ATPase
 CG17369 beta subunit(aa) * PROBABLE VACUOLAR [ATP-synt_ab] CG17369 GH27148 87C5-87C5 dup:3/3 ID:81A7
 + yin transporter * opt1 long(aa) * 8e-17 PTR2_YEAST PEPTIDE TRANSPORTER PTR2 (PEPTIDE PERMEASE PTR2) * 8e-74 high-
 CG2913 affinity peptide transporter * 2e-06 cAMP inducible p [PTR2 // PTR2_1 // PTR2_2] CG2913 GH27264 4A1-4A1 dup:2/2 ID:81B12
 CG8861 + unknown * CG8861 GH27383 85D7-85D7 ID:81C12
 CG11625 + unknown * CG11625 GH27289 92A4-92A4 dup:2/2 ID:81C4
 + unknown * 2e-11 cDNA EST CEMSB78F comes from this gene; cDNA EST yk293d9.3 comes * 2e-10 Unknown * CG12118
 CG12118 GH27430 8D2-8D2 dup:3/4 ID:81D8
 + 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
 + ligand_binding_or_carrier * verprolin(aa) * mucin (clone PGM-2A) - pig(aa) * Sec23-interacting protein p125(aa) * DMCLPTN_6 Cpn
 CG8552 [GRAM_POS_ANCHORING] CG8552 GH27701 28E-28E9 dup:3/3 ID:81F10
 + enzyme * threonyl-tRNA synthetase(aa) * threonyl-tRNA synthetase (aa 1-734) * SYTC_CAEEL PROBABLE THREONYL-TRNA
 SYNTHETASE, CYTOPLASMIC (THREONINE--TRNA LIG [TRNASYNTHTHR // tRNA-synt_2b // AA_TRNA] CG5353 GH27773 33C1-
 CG5353 33C1 ID:81G11
 + 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 62E5-62E5
 CG16761 ID:81G8
 CG2865
 + Galpha49B signal_transduction * 7e-50 GBA2_YEAST GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-2 SUBUNIT (GP2-ALPHA)
 * 1e-169 GBQ3_DROME GUANINE NUCLEOTIDE-BINDING PROTEIN G(Q), ALPH[GPROTEINA // G-alpha // GPROTEINAQ // G]
 CG17759 CG17759 GH28437 49B3-49B5 ID:82D7
 + transporter * similar to C. elegans protein and to rat synaptic vesicle protein * putative integral membrane transport protein(aa) *
 CG8654 HYPOTHETICAL 84.8 KD PROTEIN [sugar_tr] CG8654 GH28654 56F-56F dup:2/2 ID:82E12
 + cytoskeletal_structural_protein * erythroid ankyrin(aa) * DMCACTUSB_8 cact * 1e-07 probable membrane protein YOR034c - yeast
 CG17492 (Saccharomyces cerevisiae) [ANK_REP // ank // ANK_REP_REGION // ZF_] CG17492 GH28686 37B10-37B11 dup:5/6 ID:82F5
 CG12040 + unknown similar to GTPase-activating (rhoGAP) like protein CRAL_TRIO CG12040 GH28696 dup:2/2 ID:82F6
 + Lk6 protein_kinase * 7e-51 LK6 protein kinase * 2e-06 similar to serine/threonine kinase; cDNA EST comes fro * 2e-11 map kinase
 CG17342 interacting kinase * 3e-12 Putative map k [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG17342 GH28825 86F7-86F7 ID:82G11
 CG13316 + * 0.000000002 * * CG13316 3F2-3F2 ID:82G7
 + Hsp27 chaperone * DMHSP27G_3 Hsp27 * 1e-118 HS27_DROME HEAT SHOCK PROTEIN heat shock protein - f * 3e-13 Contains
 similarity to Pfam domain: (HSP20), Score=130.7, * 2 [TONB_DEPENDENT_REC_1 // HSP20 // ACRYST] CG4466 GM13686 67B2-67B2
 CG4466 ID:83A12
 + enzyme * NADH:ubiquinone dehydrogenase kDa subunit(aa) * similar to NADH-ubiquinone oxidoreductase; cDNA EST comes from
 CG9140 this gene; cDNA EST comes from this [COMPLEX1_51K_1 // COMPLEX1_51K_2] CG9140 GM14163 26B3-26B3 ID:83B12

+ * similar to Gila monster phospholipase A2; similar to * 2e-22 phospholipase A2 (EC 3.1.1.4) Pa5 - Gila monster phosph * 8e-89
 CG1583 inserted at base Both 5' [PA2_HIS] CG1583 7D14-7D15 dup:2/2 ID:83B8
 + Ank cytoskeletal_structural_protein * DMANKY_5 Ank * 8e-16 YIL2_YEAST HYPOTHETICAL 123.6 KD PROTEIN IN POR2-COX5B
 CG1651 INTERGENIC REGION * ankyrin ankyrin m * AO13 ankyrin [ank // ZU5] CG1651 LD21682 101F1-101F1 dup:3/4 ID:83E5
 CG3416 + translation_factor CG3416 LD22193 dup:2/2 ID:83F10
 CG18282 + unknown * CG18282 LD22270 5E1-5E1 ID:83F11
 + transporter * 1e-28 ZRC1_YEAST ZINC/CADMIUM RESISTANCE PROTEIN heavy metal * 2e-10 cDNA EST comes from this gene
 CG17723 elegans * 3e-31 zinc transporter ZnT-1 - mouse ZnT CG17723 LD22804 63C4-63C5 ID:83G10
 CG7590 + unknown * CG7590 LD22812 68B1-68B1 ID:83G11
 CG1800 + RNA_binding double-stranded binding protein DSRBD CG1800 LD23072 dup:3/4 ID:83H11
 + zf30C transcription_factor * leukemia/lymphoma related factor cLRF(aa) * zf30C * 4e-17 YJF6_YEAST HYPOTHETICAL 98.9 KD ZINC
 FINGER PROTEIN IN BTN1-PEP8 INTERGENIC REG * zinc f[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG3998 LD23102 30D1-
 CG3998 30D1 ID:83H12
 + B4 unknown * No definition line found(aa) * No definition line found * 1e-16 inserted at base 5' end of P element Inverse PCR *
 CG9239 [NLS_BP] CG9239 LD22933 36D1-36D1 dup:4/5 ID:83H6
 CG6712 + unknown NLS_BP CG6712 LD23405 dup:2/2 ID:84B8
 + unknown * NY-REN-18 antigen(aa) * BS4 PROTEIN(aa) * 3e-35 hypothetical protein * BS4 [UBA] CG15445 19E7-19E7 dup:2/3
 CG15445 ID:84E5
 + Paps enzyme * 3-prime-phosphoadenosine 5-prime-phosphosulfate synthase 1(aa) * DMPAPSSYN_2 Paps * 7e-54 KAPS_YEAST
 CG8363 ADENYLISULFATE KINASE (APS KINASE) (ATP ADENOS [ATP_GTP_A] CG8363 LD25351 76D4-76D5 ID:84F7
 + transcription_factor * C43H6.7 gene product(aa) * HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II(aa) *
 CG5880 hypothetical protein(aa) * 5e-15 probable membrane protei [ZF_DHHC] CG5880 LD25420 97E8-97E8 ID:84F9
 + enzyme * 1e-82 Similar to NADH-ubiquinone oxidoreductase kd subunit; coded for by C. elegans * 4e-88 NADH dehydrogenase
 CG12079 (ubiquinone) Fe-S protein (30kD) (NAD [complex1_30Kd] CG12079 63B11-63B11 dup:2/2 ID:84H8
 + numb unknown * NUMB PROTEIN(aa) * DMNUMB_2 numb * 3e-42 similar to Phosphotyrosine interaction domain (PTB/PID).; cDNA
 CG3779 EST * 8e-67 m-Numb [PTB_DOMAIN // PID // NLS_BP // ATP_GTP_] CG3779 LD25907 30B5-30B6 dup:1/3 ID:85A11
 + Pros45 endopeptidase * Ug * 1e-157 PRS8_YEAST 26S PROTEASE REGULATORY SUBUNIT HOMOLOG (SUG1 PROTEIN) (CIM3
 CG1489 PROTE * Pros45 proteosome subunit homolog * 1e-176 similar to AT [AAA // ATP_GTP_A] CG1489 LD26005 19F2-19F2 ID:85B12
 CG9591 + unknown * 2e-12 inserted at base 5' end of P element Inverse PCR * * CG9591 LD26057 87F8-87F8 dup:2/2 ID:85C4
 + unknown * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST
 CG8312 yk266f8.5 comes from this gene; cDNA EST yk28 [NLS_BP] CG8312 LD26277 85E-85E dup:2/2 ID:85D8
 + CRAG ligand_binding_or_carrier * CRAG protein * 1e-145 contains similarity to human MAP kinase-activating death domain * 1e-120
 CG12737 protein * 3e-16 Rab3 GDP/GTP exchange protein [DENN_DOMAIN // CYTOCHROME_C] CG12737 LD26363 7F4-7F4 dup:6/6 ID:85E3
 + enzyme * ACONITATE HYDRATASE, MITOCHONDRIAL PRECURSOR (CITRATE HYDRO-LYASE) (ACONITASE)(aa) *
 ACON_YEAST ACONITATE HYDRATASE, MITOCHONDRIAL PRECURSOR (CITRA [ACONITASE_2 // Aconitase_C // THIOLASE_]
 CG9244 CG9244 LD26837 39B3-39B3 dup:3/3 ID:85H6

CG9201 + unknown * [THIOREDOXIN] CG9201 LD26971 13D2-13D2 ID:86A3
 + unknown * 1e-29 predicted using Genefinder * 1e-33 unknown * 1e-29 predicted using Genefinder * 1e-33 unknown [ESTERASE]
 CG10038 CG10038 LD26985 87B11-87B11 ID:86A6
 CG9304 + unknown * 8e-42 cDNA EST comes from this gene * 2e-20 antigen * C15A7.2 * CG9304 LD26991 58B5-58B5 ID:86A7
 + cell_cycle_regulator * protein(aa) * HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III(aa) * 5e-05
 USF2_MOUSE UPSTREAM STIMULATORY FACTOR (UPSTREAM TRANSCRIPT[HLH // HELIX_LOOP_HELIX_2 // NLS_BP] CG18362
 CG18362 LD27073 39D1-39D2 dup:3/4 ID:86B10
 CG7843 + arsenate resistance protein ARS2 CG7843 LD27090 dup:2/2 ID:86B12
 CG10171 + unknown * CG10171 LD27069 70A5-70A5 ID:86B8
 + glutathione_transferase * 1e-24 contains similarity to glutathione S transferases * 2e-26 glutathione-S-transferase homolog * 2e-30
 CG6673 glutathione-S-transferase like glutathion [GST] CG6673 LD27185 66D4-66D5 ID:86C12
 + dco protein_kinase * serin/threonin-kinase(aa) * dbt * Ckl agr; * DMDG2CD5_3 for [PROTEIN_KINASE_ST //
 CG2048 PROTEIN_KINASE_DOM] CG2048 LD27173 100B-100B ID:86C9
 + transporter * 2e-14 aquaporin * 5e-22 BIB_DROME NEUROGENIC PROTEIN BIG BRAIN bib protein - frui * 6e-22 similar to MIP
 CG7777 transmembrane protein; cDNA EST yk459g7.3 c [MINTRINSICP // MIP] CG7777 LD27313 47F13-47F13 ID:86D9
 CG1444 + enzyme PUTATIVE STEROID DEHYDROGENASE ADH_SHORT, GDHRDH, adh_short CG1444 LD27387 dup:3/3 ID:86E5
 + 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 51E9-51E9
 CG8079 dup:2/2 ID:86E8
 CG1716 + transcription_factor ATP_GTP_A, DEAD_ATP_HELICASE, NLS_BP, PR] CG1716 LD27627 ID:86F12
 + enzyme (L76944) calmodulin-dependent cyclic nucleotide phosphodiesterase [Mus musculus] HELIX_LOOP_HELIX, PDEASE_I,
 CG14940 PDEase, PDIE] CG14940 LD27504 dup:2/2 ID:86F3
 + Cdk8 protein_kinase * Cdk8(aa) * 3e-67 cyclin-dependent kinase chain SRB10 - yeast (Saccharomyces cerevisiae) * Cdk8 * 1e-127
 CG10572 Similarity to Human cell division protein ki [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG10572 LD27520 69D3-69D3 ID:86F4
 + unknown * predicted using Genefinder; Similarity in 3' end to Human protein cDNA EST comes from this gene; cDNA EST comes
 CG9986 from this gene; cDNA EST comes from CG9986 LD27564 98D4-98D4 ID:86F8
 CG8229 + unknown * CG8229 LD27667 44F12-45A1 dup:2/2 ID:86G5
 CG4710 + unknown * CG4710 21E-21E dup:2/2 ID:86H5
 CG9680 + RNA_binding CG9680 ID:86H8
 + DNA_repair_protein * 5e-20 predicted using Genefinder; similar to MUTT protein like; cDNA EST * 9e-05 YZGD_BACSU
 HYPOTHETICAL 45.4 KD PROTEIN IN THIAMINASE I 5'REGION * [MUTT // mutT // MUTTDOMAIN] CG10898 LD28119 86E13-86E13
 CG10898 ID:87C5
 + 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
 CG1065 + Scsalphaenzyme * succinyl-CoA synthetase alpha subunit(aa) * 7e-75 SUCA_YEAST PROBABLE SUCCINYL-COA LIGASE (GDP-

FORMING), ALPHA-CHAIN PRECURSOR (S * 8e-41 succinyl c CG1065 64C4-64C4 dup:2/4 ID:87F1

CG10627+ CG10627 ID:87F7

CG1542 + CG1542 ID:88A10

+ wal electron_transfer * 2e-61 ETFA_YEAST PROBABLE ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT PRECURSOR (ALP * 1e-106 ETFA_CAEEL PROBABLE ELECTRON TRANSFER FLAVOPROTEIN AL [ETF_alpha // ETF_ALPHA] CG8996 48B6-48B6

CG8996 dup:1/3 ID:88A12

CG3661

+ * 2e-47 precursor TRG1 protein * D-ERp60=protein disulphide isomerase isoform/multifunctional endoplasmic retic * 1e-136

CG8983 predicted using Genefinder; S [THIOREDOXIN // THIOREDOXIN_2 // thioered] CG8983 48D1-48D1 dup:3/4 ID:88D12

+ apoptosis_inhibitor * DIHA(aa) * lap2 * 3e-07 inhibitor of apoptosis protein * 8e-06 coded for by C. elegans cDNA yk27g3.5; coded

CG17019 for by C. elegans cDNA yk27g3.3; Si [NLS_BP // ZF_RING] CG17019 49E1-49E1 dup:6/6 ID:88E10

CG18858+ CG18858 ID:88F6

+ ion_channel * NY-REN-45 antigen(aa) * contains similarity to the A-type potassium current class of channel proteins(aa) *

CG9467 /match=(desc;; /match=(desc;; /match=(d [BTB // GAPDH // WD_REPEATS] CG9467 85E10-85E10 dup:3/5 ID:88F9

CG9172 + enzyme CG9172 ID:89A10

+ BcDNA:LD29885 unknown * coatomer protein complex, subunit epsilon(aa) * PROBABLE COATOMER EPSILON SUBUNIT (EPSILON-

CG9543 COAT PROTEIN) (EPSILON-COP)(aa) * COATOMER EPSILON SUBUNI CG9543 LD29885 26D7-26D7 dup:1/2 ID:89D2

CG4488 + protein_kinase CG4488 ID:89H8

+ unknown * hypothetical protein(aa) * 2e-19 probable membrane protein YPR105c - yeast (Saccharomyces cerevisiae) * 2e-40

CG7456 contains similarity to Arabidopsis me CG7456 LD35507 31E4-31E4 dup:2/2 ID:95B1

+ * Anchor protein. Mediates attachment of autophagosomes to microtubules.; Aut2p(aa) * similar to Histidine acid phosphatases;

CG4428 cDNA EST yk432a1.3 come CG4428 21E2-21E2 dup:4/4 ID:95B10

+ unknown * 1e-52 NUC1_YEAST MITOCHONDRIAL NUCLEASE nuclease NUC1 (EC 3.1.30 * 5e-77 YJ05_CAEEL HYPOTHETICAL

85.1 KD NUCLEASE C41D11.5 simila * 2e-68 NUCG_MOUSE [NUCLEASE_NON_SPEC // Endonuclease] CG8862 LD35517 48F1-48F1

CG8862 ID:95B2

+ * canalicular multispecific organic anion transporter (ABC superfamily)(aa) * cadmium resistance protein YCF1 - yeast

CG10441 (Saccharomyces cerevisiae) * 1e- [ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG10441 37B9-37B9 dup:1/2 ID:95C1

+ defense/immunity_protein * 1e-101 inserted at base Both 5' and 3' ends of P element Inverse PCR * * CG8187 LD35843 52A10-

CG8187 52A10 ID:95D8

+ lace enzyme * 1e-107 LCB2_YEAST SERINE PALMITOYLTRANSFERASE (LONG CHAIN BASE BIOSYNTHESIS PROTEIN * 2e-24

delta-aminolevulinate synthase * 1e-128 Similar to serin [aminotran_2 // AA_TRANSFER_CLASS_2 // N] CG4162 LD36009 35D3-35D3

CG4162 dup:2/2 ID:95E11

+ 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

CG6398 + unknown * 8e-16 coded for by C. elegans cDNA yk81c2.5 * * CG6398 LD36024 16D4-16D4 dup:2/2 ID:95F3

CG7802 + unknown * 2e-10 transmembrane protein * 6e-12 weak similarity to plasminogens * 2e-12 DMDUSKY_1 dy * similar to cuticlin

[NLS_BP] CG7802 LD36439 99C5-99C5 ID:96A7

+ enzyme * bgr;ggt-l * protein farnesyl transferase beta subunit(aa) * farnesyl protein transferase subunit B(aa) * predicted using CG17565 Genefinder; Similarity t [prenyltrans] CG17565 LD36454 89C3-89C3 dup:1/2 ID:96A8

+ Sap47 unknown * synapse associated protein sap47-2 - fruit fly (Drosophila melanogaster)(aa) * DMSAP472_2 Sap47 * 1e-99 synapse- CG8884 associated protein sap47-1 - fruit f CG8884 LD36546 89B1-89B2 ID:96B2

+ unknown * HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III(aa) * CGI-150 protein(aa) * 3e-21 Similar to CG1532 protein from Brassica oleracea which is simila [Glyoxalase] CG1532 LD36566 19E6-19E6 ID:96B4

+ electron_transfer * 2e-36 C561_CAEEL PUTATIVE CYTOCHROME B561 (CYTOCHROME B-561) hy * 6e-37 cytochrome B561 * CG1275 4e-39 C561_HUMAN CYTOCHROME B561 (CYTOCHROME B-561) cytoch CG1275 LD36721 62D4-62D5 dup:1/2 ID:96C1

+ Ndr protein_kinase * DMPROKINX_2 Ndr * Ndr protein kinase(aa) * 1e-128 KNQ1_YEAST PROBABLE SERINE/THREONINE- PROTEIN KINASE YNL161W * 1e-175 coded for by C. elegans [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG8637 LD37189

CG8637 76D3-76D3 dup:2/2 ID:96E10

+ pnut cytoskeletal_structural_protein * pnut * PEANUT PROTEIN(aa) * 3e-82 cell division cycle protein * 1e-134 CDC10 [GTP_CDC // CG8705 NLS_BP // ATP_GTP_A] CG8705 LD37170 44B3-44B4 dup:2/2 ID:96E9

+ enzyme * BLASTX 2.5E-12 FMS1|Protein with similarity to Candida albicans corticosteroid-binding protein CBP1(dna) * I(2)37Cs * CG8032 Fms1p(aa) * 1e-12 FMS1_YEAST F [NAD_BINDING] CG8032 LD37279 85A11-85A11 dup:1/2 ID:96G1

+ ion_channel * outer membrane protein(aa) * The gene product is related to adenylyl cyclase.(aa) * 1e-18 DLG1_DROME CG5462 LETHAL(1)DISCS LARGE-1 TUMOR SUPPRESSOR PROTEIN [PDZ] CG5462 LD37377 100B1-97B9 dup:1/3 ID:96G9

+ enzyme * coded for by C. elegans cDNA yk16b2.3; coded for by C. elegans cDNA yk16b2.5; Similar to amidase.(aa) * 1e-23 putative CG5112 yeast amidase * 3e-21 coded f [Amidase // AMIDAS] CG5112 LD38433 99B4-99B4 ID:97F10

CG8180 + unknown * 1E-178** [ANTIFREEZEI] CG8180 LD38554 52A4-52A4 dup:1/2 ID:97G8

+ * 2e-45 sulfate permease * 1e-27 Similar to sulfate transporter. * 9e-33 DTD_MOUSE SULFATE TRANSPORTER (DIASTROPHIC CG5002 DYSPLASIA PROTEIN HOMOLOG) (ST-OB) [Sulfate_transp // SUGAR_TRANSPORT_2] CG5002 54E7-54E7 ID:97G9

+ BcDNA:LD03471 transcription_factor_binding * SEC13-RELATED PROTEIN(aa) * cytoplasmic protein involved in release of transport vesicles from the ER; Sec13p(aa) * PROTEIN TRANSPORT PROTEIN SEC13([WD40_REGION // WD40] CG6773 LD38669 94F1-94F1

CG6773 ID:97H2

+ DNA_binding * 7e-32 NAM7_YEAST NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT * 1e-27 nonsense-mediated mRNA decay trans-acting factor * 2[ZINC_FINGER_C2H2 // PRO_RICH // ATP_GTP] CG6701 LD38709 50C21-

CG6701 50C22 dup:2/2 ID:97H8

+ RasGAP signal_transduction * RasGap protein(aa) * 2e-16 BUD2_YEAST INHIBITORY REGULATOR PROTEIN BUD2/CLA2 GTPase- * RasGap protein * 1e-40 similar to GTPase-activating p[RAS_GTPASE_ACTIV_2 // SH2DOMAIN // C2 /] CG9209 LD38909 14A1-14A1

CG9209 dup:1/2 ID:98B8

CG18011 + nucleic_acid_binding * CG18011 LD39136 46E8-46E8 ID:98C11

+ enzyme * 9e-41 /match=(desc;; /ma * 5e-35 cDNA EST comes from this gene; cDNA EST co * 9e-06 Ubc84D * contains similarity to CG4502 ubiquitin-conjugatin enzymes (Pf [UQ_con // UBIQUITIN_CONJUGAT_2] CG4502 LD39243 27E4-27E4 ID:98D9

CG4501 + enzyme CG4501 ID:98H6

CG4586 + enzyme * 2e-45 acyl-coenzyme A oxidase * 1e-100 Similarity to Rat Acyl-CoA oxidase I (SW:CAO1_RAT); cDNA EST EMBL: * 1e-

116 peroxisomal acyl-CoA oxidase * 1e CG4586 LD40103 6E4-6E4 ID:99B12
 + Rab10 cell_cycle_regulator * Rab1 * 4e-56 SEC4_YEAST RAS-RELATED PROTEIN SEC4 GTP-binding protein SE * 1e-111 Rab10 *
 9e-80 strong similarity to the YPT1 sub-family of RAS pro[SIGMA54_INTERACT_1 // ras // ATP_GTP_A] CG17060 LD39986 19C1-19C2
 CG17060 ID:99B3
 + EG:52C10.2 signal_transduction * 1e-100 by content; 1-meth * 3e-43 YUE1_CAEEL HYPOTHETICAL 19.6 KD PROTEIN F16H9.1 IN
 CHROMOSOME X * 2e-31 RGS5_MOUSE REGULATOR OF G-PROTEIN SIGNALIN [GRK // RGS] CG5036 LD40005 54F1-54F1 dup:2/3
 CG5036 ID:99B4
 + * similar to S. cerevisiae nitrogen permease regulator * G21 protein(aa) * homologous to yeast nitrogen permease (candidate tumor
 CG9104 suppressor)(aa) * 3e CG9104 15A11-15B1 dup:1/2 ID:99C3
 + unknown * ilvB (bacterial acetolactate synthase)-like(aa) * BLASTX 4.8E-22 YEL020C|Protein with similarity to oxalyl-CoA
 CG11208 decarboxylase from Oxalobacter formig [TPP_enzymes // TPP_ENZYMES] CG11208 LD40177 56F14-56F14 ID:99C5
 CG13840 + CG13840 LD40283 ID:99D4
 + unknown * 2e-49 kraken * 1e-19 dJ222E13.1 (N-terminal part of novel protein with some similarit * 6e-12 TPES_PSEPU
 TROPINESTERASE (ATROPINESTERASE) (ATROPINE [ESTERASE // EF_HAND // abhydrolase] CG11309 LD40450 78C8-78C9
 CG11309 dup:4/4 ID:99E7
 + unknown * 5e-70 weak similarity to HSP90 * 1e-05 YXAQ_BACSU HYPOTHETICAL 37.5 KD PROTEIN IN GNTR-HTPG
 CG2982 INTERGENIC REGION * CG2982 LD40453 4B5-4B5 dup:2/2 ID:99E8
 CG8633 + unknown CG8633 GJB.Hx4 dup:1/2 ID:Farhad's BA5
 CG4376 + Actn alpha-actinin (Flightless A) CG4376 GH06025 ID:Farhad's BB6
 CG9432 + CG9432 G041 dup:1/4 ID:Farhad's BC7
 CG5772 + transporter CG5772 ck00325 ID:Farhad's BD8
 CG15288 + CG15288 ck01592 ID:Farhad's BE4
 CG10816 + CG10816 drosocin dup:1/3 ID:Path + Ctrl1 + kras62