

Table S28

male and female germline genes

identified as those having significantly higher expression ($P < .01$) in both adult wild type males and females as compared to adult male and female tudor progeny (one-tailed t-test).

+ qua actin_binding * qua * QUA1_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
+ DNA_binding * 3e-59 CAC2_YEAST CHROMATIN ASSEMBLY FACTOR P60 SUBUNIT (CAF-1 KD SUBUNIT) * 8e-33 HIRA *
4e-11 YZLL_CAEEL HYPOTHETICAL 43.1 KD TRP-ASP REPEATS CONTA [GPROTEINB // WD40_REGION // WD_REPEATS]
CG12892 CG12892 LD42270 47A9-47A9 ID:101D8
CG17129+ transcription_factor * [NLS_BP] CG17129 LD42420 61C9-61C9 dup:2/2 ID:101E10
CG5857 + unknown * CG5857 LD42327 95C-95C dup:2/2 ID:101E3
+ transcription_factor_binding * WD-repeat protein(aa) * 3e-05 YGA3_YEAST HYPOTHETICAL 62.8 KD TRP-ASP REPEATS
CONTAINING PROTEIN IN PMC1-TFG2 * 1e-07 Method: conceptual translation [WD40_REGION // WD40] CG11330 LD43270 26F5-
CG11330 26F6 ID:102B11
+ DNA_binding * TPR protein(aa) * 6e-74 PR06_YEAST PRE-MRNA SPLICING FACTOR PRP6 pre-mRNA splicing * 2e-12 62D9.a
CG6841 * 8e-08 contains similarity to multiple TPR domain [TPR_REGION // TPR_REPEAT // NLS_BP] CG6841 LD43276 75E2-75E3 ID:102B12
+ RplI215 enzyme * DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)(aa) * DMRPRIIA_2 RplI215 * DNA-
DIRECTED RNA POLYMERASE II LARGEST SUBUNIT(aa) * RNA poly [RNA_POL_II_REPEAT] CG1554 LD43558 10C4-10C5
CG1554 ID:102D12
+ 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
+ unknown * R07E5.1 protein (clone R07E5) - Caenorhabditis elegans(aa) * 7e-49 inserted at base Both 5' and 3' ends of P element
CG8833 Inverse PCR * cDNA EST comes fr [PRO_RICH // D111_DOMAIN // NLS_BP] CG8833 LD45361 74B1-74B1 ID:104C2
+ motor_protein * 9e-09 NUF1_YEAST NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110) * 6e-12 microtubule
CG4925 binding protein D-CLIP-190 * 2e-29 predicted using Genef CG4925 LD45682 72E5-72E5 dup:3/3 ID:104E9
+ unknown * Weak similarity to Yeast hypothetical protein * 1e-32 Weak similarity to Yeast hypothetical protein * * [D111_DOMAIN
CG10053// NLS_BP] CG10053 LD46678 84C7-84C7 dup:2/2 ID:105E12
CG5877 + unknown * CG5877 13B9-13B9 ID:105F1
+ motor_protein * KINESIN CENTRAL MOTOR (XKCM1)(aa) * kinesin heavy chain member 2(aa) * kinesin-like (mitotic centromere-
CG1453 associated kinesin)(aa) * kinesin heavy c[kinesin // KINESIN_MOTOR_DOMAIN1 // KIN] CG1453 LD47558 10A6-10A8 dup:2/2 ID:106F6
+ unknown * 9e-14 GCR protein - fruit fly (Drosophila melanogaster) * 1e-15 CMGCR1A_5 anon-Pen100DE * [PRION] CG2150
CG2150 LP02992 100E3-100E3 ID:108C10
+ Nhe1 transporter * 7e-65 hypothetical protein YDR456w - yeast (Saccharomyces cerevisiae) (U * sodium-hydrogen exchanger NHE1
CG12178 melanogast * 1e-117 similar to Sodium/hydr [Na_H_Exchange // NAHEXCHNGR] CG12178 LP02993 21B-21B ID:108C11
+ ligand_binding_or_carrier * Pen * 1e-107 IMA1_YEAST IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT)
CG4799 (SERINE-RICH RNA P * overgrown hematopoietic organs-31 tumor suppressor O [ARM_REPEAT // Armadillo_seg] CG4799 LP03126

31A1-31A1 ID:108D10

CG13330+ unknown * [NLS_BP] CG13330 50B2-50B2 dup:1/2 ID:108D11
CG4449 + unknown * CG4449 LP06117 97B1-94E9 ID:109G2
+ unknown * coded for by C. elegans cDNA yk61f1.3; coded for by C. elegans cDNA yk109h8.3; coded for by C. elegans cDNA
CG8576 CEESX42F; coded for by C. elegans cDNA CG8576 SD02002 65F5-65F5 ID:113D5
+ 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
+ unknown * UNKNOWN; PRC1(aa) * protein regulating cytokinesis 1; PRC1 * [G_PROTEIN_GAMMA] CG1655 SD02150 9F5-9F5
CG1655 ID:113F5
CG14619 endopeptidase SD04280 CG14619
CG17767+ transporter CG17767 SD05444 dup:2/2 ID:118G7.2
+ homology to voltage-sensitive calcium channel alpha 1 A and guanine nucleotide exchange factor DC3G CG7795 SD05570
CG7795 dup:1/2 ID:119A4
CG5290 + CG5290 SD05938 dup:2/2 ID:119F4.2
CG10716+ translation_factor CG10716 SD07020 dup:1/2 ID:120E3.2
CG1691 + RNA_binding CG1691 SD07045 dup:1/3 ID:120E7.2
CG12819+ CG12819 SD10401 dup:1/3 ID:125B6.2
+ unknown * Ykr081cp(aa) * 5e-49 YK61_YEAST HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION *
CG7993 ORF YKR401 * CG7993 GH01229 90F1-90F1 ID:30B8
+ motor_protein * protein(aa) * HYPOTHETICAL 123.7 KD PROTEIN C14C4.02 IN CHROMOSOME I(aa) * 2e-65 hypothetical
CG7783 protein YOL034w - yeast (Saccharomyces cerevisiae) * 3 [ATP_GTP_A2 // ATP_GTP_A] CG7783 GH01608 78E2-78E3 dup:2/2 ID:30E4
CG7183 + It has been mapped cytologically to 90F1 NLS_BP CG7183 GH02734 ID:31D10
CG13853+ unknown * CG13853 GH02671 96E1-96E1 ID:31D6
+ 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
CG8548 GH03057 76D2-76D3 ID:31G3
CG18178+ unknown * CG18178 GH03795 67C-67C ID:32C3
+ endopeptidase * PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP)(aa) * PUTATIVE ATP-DEPENDENT CLP
PROTEASE PROTEOLYTIC SUBUNIT, MITOCHONDRIAL PRECURSOR (ENDOPEPTIDAS [CLP_protease // CLP_PROTEASE_SER
CG5045 // CLP] CG5045 GH10833 31D10-31D10 ID:38D2
+ transcription_factor * 7e-08 zinc finger motif protein * 4e-07 similar to Zinc finger, C2H2 type (2 domains) eleg * 1e-08
ZFX1_MOUSE ZINC FINGER X-CHROMOSOMAL PRO[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG8092 GH12685 51E7-51E8
CG8092 dup:1/3 ID:40A8
+ structural_protein * nuclear pore protein; Nsp1p(aa) * nucleoporin p62(aa) * similar to nucleoporins(aa) * NUCLEAR PORE
CG6251 GLYCOPROTEIN P62 (NUCLEOPORIN P62)(aa) CG6251 GH12838 53B1-53B1 ID:40B9
CG1071 + E2f2 transcription_factor * E2f2 * 1e-174 E2F-like transcription factor (E2F2) * 7e-14 predicted using Genefinder; cDNA EST comes

from this * 3e-18 E2F5_MOUSE TRANSCRIPTION FAC CG1071 GH13089 39B3-39B3 ID:40D1
 + glutathione_transferase * predicted using Genefinder; similar to Glutathione S-transferases.(aa) * 2e-11 YKJ3_CAEEEL
 CG6662 HYPOTHETICAL 42.8 KD PROTEIN C02D5.3 IN CHROMOSOME III * 7 [GST] CG6662 66D5-66D5 dup:2/2 ID:40H2
 + noi RNA_binding * noi * noisette(aa) * 1e-30 PR09_YEAST PRE-MRNA SPLICING FACTOR PRP9 PRP9 protein - ye * noisette
 CG2925 [ZF_MATRIN] CG2925 LD22754 83B4-83B4 ID:43C11
 CG3167 + unknown * CG3167 LD24895 60B1-60B1 ID:43G9
 + motor_protein * 1e-155 inserted at base 5' end of P element Inverse PCR * * [bZIP] CG3183 LD25484 42B3-42B3 dup:1/2
 CG3183 ID:44A3
 + enzyme homology to NADPH--ferrihemoprotein reductase and NADPH-cytochrome P450 reductase FAD_binding, FLAVODOXIN,
 CG13667 FPNCR, PHEHYDRX] CG13667 LD25514 dup:2/2 ID:44A6
 + unknown * Putative homolog of subunit of bovine prefoldin, a chaperone comprised of six subunits; Gim5p(aa) * c-myc binding
 CG7048 protein MM-1(aa) * 4e-21 YMJ4_YEAS CG7048 LD25740 94B4-94B4 ID:44B4
 CG11329+ unknown * 1e-16 inserted at base 5' end of P element Inverse PCR * * CG11329 LD26217 26F6-26F6 ID:44C11
 CG13322+ unknown CG13322 LD26432 dup:2/3 ID:44D11
 + aret RNA_binding * aret * 8e-06 polyadenylate-binding protein * 1e-148 testis-specific RNP-type RNA binding protein * 2e-29 elav-
 CG6319 type ribonucleoprotein coded [RBD // HUDSXL RNA // rrm] CG6319 33D-33D4 dup:3/3 ID:44D5
 + EG:66A1.2 transcription_factor_binding * map_position:4C6 * map_position:4C6 * map_position:4C6 * by match; 1-mat CG12179
 CG12179 LD28429 4C6-4C7 ID:45F3
 + unknown * 7e-10 /match=(desc: * 9e-10 K10D2.3 gene product * 1e-10 The gene is expressed ubiquitously.; The protein * 1e-09
 CG1091 caffeine-induced death protein >g [PAP_ASSOCIATED // PAP_CORE // PAP // AA] CG1091 84C1-84C1 dup:3/3 ID:45F7
 + chaperone * 1e-07 STI1_YEAST HEAT SHOCK PROTEIN STI1 stress-induced protein * 1e-08 Hsp70/Hsp90 organizing protein
 CG2947 homolog * 1e-54 similar to TPR Domain (2 doma [RNP_1 // TPR_REGION // TPR_REPEAT // TP] CG2947 3F6-3F6 dup:3/4 ID:45F9
 CG9107 + CG9107 LD29822 dup:3/3 ID:46E8
 CG14459+ none none CG14459 LD29969 ID:46F11
 + motor_protein * 4e-28 KIP1_YEAST KINESIN-LIKE PROTEIN KIP1 kinesin-related prot * 6e-33 PAV-KLP protein * 4e-33 Similar
 CG12298 to kinesin-like protein; coded for by C. ele [kinesin // KINESIN_MOTOR_DOMAIN2 // KIN] CG12298 LD30305 54E7-54E7 ID:46H7
 CG2682 + transcription_factor CG2682 ID:47A11
 CG8617 + CG8617 LD30408 dup:1/2 ID:47A4
 + snRNP70KRNA_binding * U1 SMALL NUCLEAR RIBONUCLEOPROTEIN KD (U1 SNRNP KD) (SNRNP70)(aa) * DMRNP70K_6
 snRNP27D * ribonucleoprotein antigen(aa) * small nuclear ribonucleopr [RNP_1 // RBD // rrm // NLS_BP] CG8749 LD30455 27C7-27C7
 CG8749 dup:1/2 ID:47A8
 + fzy cell_cycle_regulator * fzy * 2e-76 YGA3_YEAST HYPOTHETICAL 62.8 KD TRP-ASP REPEATS CONTAINING PROTEIN IN
 PMC1-TFG2 * Method: conceptual translation supplied by au[WD40_REGION // FIZZY_DOMAIN // WD_REPEA] CG4274 LD30572
 CG4274 35F8-35F8 dup:1/2 ID:47B7
 CG6962 + CG6962 ID:47C2
 CG11982+ transcription_factor * putative ring zinc finger protein NY-REN-43 antigen(aa) * putative protein(aa) * hypothetical protein, similar

to PRAJA1 * DMGOLTHA_3 gol [zf-C3HC4 // ZF_RING] CG11982 LD30985 85C4-85C4 dup:3/3 ID:47D12
 + unknown * 3e-05 No definition line found * 1e-32 topoisomerase I-binding RS protein * 8e-11 ring finger protein * tumor protein
 CG15104 p53-binding protein p53 bindin [zf-C3HC4 // ZINC_FINGER_C3HC4 // NLS_BP] CG15104 56A-56A dup:3/3 ID:47D3
 CG7730 + unknown * CG7730 LD31138 73E4-73E4 dup:2/2 ID:47E12
 + enzyme * 1e-109 RSP5_YEAST UBIQUITIN--PROTEIN LIGASE RSP5 hypothetical pr * 2e-48 similar to hypothetical proteins from
 CG4943 yeast (YKL162) and rat (PIR: * 3e-90 [HECT_DOMAIN // HECT // WW_rsp5_WWP // C] CG4943 LD31242 54D3-54D3 dup:2/3 ID:47F12
 + RNA_binding * putative protein(aa) * homologous to mouse gene PC326:GenBank Accession Number * putative protein(aa) * 5e-
 CG8001 08 Cdc40p [WD40_REGION // WD40] CG8001 LD31538 62B1-62B2 dup:1/2 ID:47G10
 CG18592+ * CG18592 25C3-25C3 dup:1/2 ID:47H11
 CG14318+ It has been mapped cytologically to 90C2--4 CG14318 LD31673 ID:47H5
 CG10364+ msb1l unknown * CG10364 LD32040 37F2-37F2 ID:48A8
 CG18398+ unknown * CG18398 LD32306 37B8-37B8 ID:48B8
 CG3883 + unknown * clot.500(dna)** CG3883 LD32410 21D2-21D2 ID:48C2
 + transporter * MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM20 HOMOLOG (MITOCHONDRIAL KD OUTER
 MEMBRANE PROTEIN) (OUTER MITOCHONDRIAL MEMBRANE RECEPTOR TOM20)(aa) * 2e [NLS_BP] CG7654 LD34461 76E2-
 CG7654 76E2 ID:49D10
 + enzyme * nuclear protein methyltransferase (mono- and asymmetrically dimethylating enzyme); Hmt1p(aa) * protein N-
 CG6563 methyltransferase 3(aa) * protein N-methy [SAM_BIND] CG6563 LD34544 88E8-88E8 dup:2/2 ID:49E3
 CG11446+ unknown * CG11446 GH01717 2A3-2A3 ID:54G6
 + und peptidase * 1e-107 AMP2_YEAST METHIONINE AMINOPEPTIDASE (METAP 2) (PEPTIDASE M 2) (U * methionine
 CG4008 aminopeptidase * 1e-38 Similarity to Rat initiation factor ass [Peptidase_M24 // MAPEPTIDASE] CG4008 GH03119 30D1-30D1 ID:55G6
 + motor_protein * 8e-08 /motif=(desc: * 7e-11 contains similarity to a C3HC4-class zinc finger * 1e-20 mTRIP * 3e-20 hTRIP [zf-
 CG5140 C3HC4 // NLS_BP // ZF_RING] CG5140 GH03577 55B9-55B9 ID:56A7
 CG18004+ unknown * CG18004 GH04870 47C6-47C6 dup:2/2 ID:57D2
 CG3312 + CG3312 ID:57H12
 CG8592 + stil unknown * 1e-171 STAND STILL (Y * 1e-173 stil * * [NLS_BP] CG8592 GH06596 49B2-49B2 ID:59A10
 + unknown * cDNA EST yk429e10.5 comes from this gene; cDNA EST yk431d3.5 comes * gene e1 protein - mouse * is a human
 CG14967 counterpart of mouse e1 gene. * 7e-20 hypo CG14967 GH07785 63C1-64A3 dup:1/3 ID:60A7
 CG3528 + unknown * CG3528 GH08765 22F-22F dup:1/2 ID:60H11
 + 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
 + RNA_binding * 6e-21 predicted using Genefinder; cDNA EST comes from this g * 5e-39 suppressor of white apricot homolog * 5e-
 CG6695 39 suppressor of white apricot homolog [NLS_BP] CG6695 GH08943 96A17-96A17 dup:1/3 ID:61C1
 + 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
 CG6230 + BcDNA:GH06032 transporter * DSERCA_2 Ca-P60A * 1e-158 ATC6_YEAST PROBABLE CALCIUM-TRANSPORTING ATPASE

hypoth * Similarity to Yeast E1-E2 ATPase YEL031W (SW:YED1_YEAST); cDNA E[COF_2 // CATATPASE // E1-E2_ATPase] CG6230
 GH13756 32D4-32D4 dup:2/2 ID:65F6
 + * 2e-09 SUR4_YEAST SUR4 PROTEIN (SRE1 PROTEIN) SUR4 protein - yea * 2e-13 predicted using Genefinder; similar to
 CG12138 GNS1/SUR4 family; cDNA EST * 3e-12 MU [NLS_BP] CG12138 46C-46C dup:3/4 ID:70C10
 + unknown * predicted using hexExon; MAL3P6.28 Hypothetical protein, len: aa; Similarity to model organism hypothetical proteins
 CG18042 (C.elegans, D.melanogaster, S. CG18042 GH20177 31B1-31B1 ID:72D3
 + enzyme * putative exonuclease(aa) * 2e-41 hypothetical protein YOL080c - yeast (Saccharomyces cerevisiae) * 2e-15
 CG6833 /match=(desc;; /ma * 8e-39 predicted using [Exonuclease] CG6833 GH21710 70C12-70C12 dup:1/2 ID:74A8
 + 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 // rrm] CG10377 27C-
 CG10377 27C dup:6/8 ID:76B1
 + 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
 + enzyme * 1e-43 CCR4_YEAST GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL EFFECTOR (C
 CG5534 * 2e-07 ANGEL * 3e-86 predicted using Genefinder; Similarity CG5534 GH27503 95E6-95E6 dup:2/2 ID:81E4
 CG5048 + unknown * CG5048 GH27783 70F1-70F1 ID:81H2
 + 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-
 CG4466 67B2 ID:83A12
 + nucleic_acid_binding * 3e-09 GOLI_DROME GOLIATH PROTEIN (G1 PROTEIN) regulatory protei * 1e-10 contains similarity to
 C3HC4-type zinc fingers (Pfam; zf-C3HC4.hmm, score; [zf-C3HC4 // PRO_RICH // NLS_BP // ZF_RI] CG6923 LD22771 86F6-86F6
 CG6923 ID:83G8
 CG14030 + protein_kinase mitotic checkpoint control protein kinase B-like PROTEIN_KINASE_ATP CG14030 LD22858 dup:1/2 ID:83H1
 + exu RNA_binding * Exuperantia (exu) protein - fruit fly (Drosophila melanogaster)(aa) * exu * 1e-158 exuperantia protein - fruit fly
 CG8994 (Drosophila virilis) * exu [LECTIN_LEGUME_BETA] CG8994 LD26657 57B2-57B2 ID:85G4
 + Dhod enzyme * DMDHORO_3 Dhod * 2e-10 PYRD_YEAST DIHYDROOROTATE DEHYDROGENASE (DIHYDROOROTATE
 OXIDASE) (DHODEHASE) * dihydroorotate oxidase (EC 1.3.3.1), mitochond [FMN_ENZYMES // DHODEHASE_1 // DHodehase]
 CG9741 CG9741 LD28427 85A10-85A10 dup:2/2 ID:87E10
 + RNA_binding * dJ22E13.3.2 (PUTATIVE partial isoform 2)(aa) * DMBNBR_2 bnb * CG6961 LD28479 17D5-17D5 dup:3/4
 CG6961 ID:87F6
 CG10346 + chaperone * CG10346 37A4-37A4 dup:1/3 ID:87G7
 + unknown * histone acetyltransferase 1(aa) * histone acetyltransferase; Hat1p(aa) * weak similarity with SINR protein (Swiss Prot
 CG2051 accession number cDNA EST co [NLS_BP] CG2051 83C-83C dup:2/3 ID:88F12
 + RNA_binding * pre-mRNA cleavage factor Im (68kD)(aa) * 2e-16 Similarity to Brassica glycine-rich RNA-binding protein
 CG7185 (SW:GR10_B * 2e-29 HPBR17-7 protein - human H [RBD // rrm // PRO_RICH // NLS_BP] CG7185 66C6-66C7 dup:3/5 ID:88H10
 CG15435 + nucleic_acid_binding * [ZINC_FINGER_C2H2 // ZINC_FINGER_C2H2_2] CG15435 LD35850 24F5-24F5 ID:95D9

+ protein_kinase * DMRNASTK_2 mnb * protein kinase Dyrk1B(aa) * MNB(aa) * SRPK1(aa) [PROTEIN_KINASE_ST //
 CG8174 PROTEIN_KINASE_DOM] CG8174 LD35909 51F11-51F11 dup:3/3 ID:95E3
 + Noa36 nucleic_acid_binding * nucleolar protein, putative(aa) * 1e-111 cysteine-rich protein * 1e-110 Zn finger factor * [NLS_BP]
 CG10009 CG10009 LD37139 98D3-98D3 dup:2/2 ID:96E5
 CG13601 + unknown * 7e-08 No definition line found * * CG13601 LD37258 95C-95C ID:96F10
 CG10076 + unknown * PEM-5(aa) * * CG10076 38C6-38C7 dup:3/5 ID:96H9
 CG6425 + unknown * CG6425 LD39291 97C3-97C3 dup:2/2 ID:98E3
 CG5194 + unknown * CG5194 LD39537 66F1-66F1 ID:98F8
 + enzyme * protein(aa) * 3e-83 predicted using Genefinder; Similarity in 3' end to Human * 5e-16 TTL_BOVIN TUBULIN--
 CG10057 TYROSINE LIGASE (TTL) * similar to tubulin [ZF_MATRIN // NLS_BP] CG10057 LD39904 96B19-96B20 dup:2/2 ID:99A1
 + BcDNA:GH02220 enzyme * OXA1 homolog - human(aa) * 3e-25 OXA1_YEAST CYTOCHROME OXIDASE BIOGENESIS PROTEIN
 CG6404 OXA1 PRECURSOR * 2e-29 Similarity to Human OXA1HS protein (cytochr CG6404 LD40470 67F4-67F4 dup:3/3 ID:99E10
 + DNA_repair_protein * DMDNAPOLD_2 DNAPol- dgr; * DNA polymerase zeta subunit; Rev3p(aa) * 1e-152 DPOZ_YEAST DNA
 POLYMERASE ZETA CATALYTIC SUBUNIT DNA-dire * 2e-69 DPOD_D[DNAPOLB // DNA_POLYMERASE_B // DNA_pol_] CG1925
 CG1925 LD40801 43E16-43E17 ID:99H4
 CG1404 + enzyme CG1404 ID:99H5
 + motor_protein * * similar to S. pombe phosphoprotein * BLASTX 2.1E-09 P.falciparum merozoite surface antigen (MSA-2) gene,
 CG8176 complete cds.(dna) * BLASTX 5.7E-22 Homo [ZINC_PROTEASE] CG8176 LD40806 86C1-85D23 dup:3/3 ID:99H6
 CG8175 + CG8175 metchinikonin dup:3/3 ID:Path + Ctrl1 + kras54