GENE	GO BIOLOGICAL PROCESS
CG30432	biological_process no biological data available
CG15234	-
CG9445	mesoderm development inferred from expression pattern
Tsp42Ee	-
CG11112	-
CG8712	-
<u>coilin</u>	-
CG30374	proteolysis inferred from electronic annotation with InterPro:IPR001254
CG14756	-
CG14759	-
CG34219	-
CG8237	-
CG8229	-
CG13742	-
CG30008	-
CG30017	biological_process no biological data available
Obp47a	sensory perception of chemical stimulus inferred from sequence or structural similarity with UniProtKB:P34174
000:55:	transport inferred from electronic annotation with InterPro:IPR006170
CG34224	
Cpr47Eg	transport inferred from electronic annotation with InterPro:IPR001588
CG13190 CG13159	biological_process no biological data available
CG33792	biological process no biological data available
CG33792 CG4616	<u>biologicai_process no biologicai data avaliable</u>
CG4716	
CG17048	<u>-</u>
CG17048	-
CG17030 CG17049	<u>-</u>
CG34236	- -
	- -
CG8589	- -
CG10102	-
CG12857	
Cyp6a21	
CG30472 CG30466	biological_process no biological data available biological_process no biological data available
CG30090	proteolysis inferred from electronic annotation with InterPro:IPR001254, InterPro:IPR001314, InterPro:IPR018114
CG33460	-
CG30099	_
CG15710	_
CG15711	_
CG33459	proteolysis inferred from electronic annotation with InterPro:IPR001254, InterPro:IPR001314, InterPro:IPR018114
CG4927	proteolysis non-traceable author statement
Acp53C14c	-
<u>tef</u>	male meiosis I inferred from mutant phenotype
	synapsis non-traceable author statement
	male meiosis chromosome segregation inferred from mutant phenotype
CG11400	<u> -</u>
CG15917	
CG10950	protein import into nucleus inferred from sequence or structural similarity with SGD_LOCUS:MTR10; SGD:S0005686
<u>Lhr</u>	-
CG34192	-
CG6520	DNA Starform of Control Control
Dcr-2	RNA interference inferred from direct assay
	RNA interference, production of siRNA inferred from direct assay RNA interference, siRNA loading onto RISC inferred from mutant phenotype
	RNA interference, sixting of mRNA for destruction inferred from mutant phenotype
	chromatin silencing inferred from mutant phenotype
	defense response to virus inferred from mutant phenotype

CG18186	chromatin assembly or disassembly inferred from electronic annotation with InterPro:IPR000953
CG10934	-
CG10931	_
PpY-55A	protein amino acid dephosphorylation inferred from sequence or structural similarity
CG14502	-
I(2)08717	wing disc dorsal/ventral pattern formation inferred from genetic interaction with Bx, ap
CG18605	-
CG7137	-
CG15124	-
CkIlbeta2	protein amino acid phosphorylation inferred from sequence or structural similarity
CG13871	-
CG15657	-
CG30391	-
CG30283	proteolysis inferred from electronic annotation with InterPro:IPR001254, InterPro:IPR001314, InterPro:IPR018114
comr	positive regulation of transcription from RNA polymerase II promoter inferred from mutant phenotype
	spermatogenesis inferred from mutant phenotype
CG11362	-
<u>CG4294</u>	phosphate metabolic process inferred from electronic annotation with InterPro:IPR008162
CG13512	biological process no biological data available
CG30270	-
CG30187	proteolysis inferred from electronic annotation with InterPro:IPR001254, InterPro:IPR001314, InterPro:IPR018114
CG32833	proteolysis inferred from electronic annotation with InterPro:IPR001254
<u>Gr59d</u>	sensory perception of taste inferred from sequence or structural similarity
Klp59C	mitotic sister chromatid segregation inferred from mutant phenotype
	microtubule-based movement inferred from sequence or structural similarity with EMBL:Y15894; protein_id:CAA75815
CG3162	nuclear mRNA splicing, via spliceosome inferred from sequence or structural similarity with UniProtKB:P26369
RpL22-like	translation inferred from sequence or structural similarity with HGNC_gene:RPL22; HGNC:10315; OMIM:180474
CG12782	poly(A)+ mRNA export from nucleus inferred from sequence or structural similarity with UniProtKB:P41838
CG13541	-
CG9863	-
CG30409	-
CG13557	-
CG13559	-
Gr59f	sensory perception of taste inferred from sequence or structural similarity
<u>IM18</u>	defense response inferred from direct assay
CG15800	ubiquitin-dependent protein catabolic process inferred from electronic annotation with InterPro:IPR001232, InterPro:IPR016072
CG30177	biological process no biological data available
CG13589	-
CG13590	-
CG33680	detection of hormone stimulus inferred from sequence or structural similarity with InterPro:IPR013053