GO analysis on WGCNA after resampling

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# Modules for the full dataset

# Full dataset  
  
# Load module names  
load("../../processed/DESEQ/Coexpression/modules.RData")  
  
# Read in multiple files by wildcard expansion on file paths  
getMods <- lapply(Sys.glob(  
 "../../processed/DESEQ/Coexpression/Mods/fbgn\_names/\*.txt",),read.table)  
  
# Rename column  
ss <- "FBgn"  
for (i in 1:length(getMods)) {  
 colnames(getMods[[i]]) <- ss   
}  
  
# Add column for module name to each module  
getMods <- mapply(cbind, getMods, "mod"=sort(modNames),   
 SIMPLIFY=FALSE)  
   
# Merge modules in list into one table (12569 + 45 grey)  
ll <- bind\_rows(getMods)

## Warning in bind\_rows\_(x, .id): Unequal factor levels: coercing to character

## Warning in bind\_rows\_(x, .id): binding character and factor vector,  
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# Resampled data  
  
# Genes uniquely assigned to module in less than half 50 of 100 datasets  
droppedGenes <- read.csv("../../processed/DESEQ/Coexpression/Resamp\_droppedGenes.csv")  
colnames(droppedGenes)[2] <- "mod"  
  
# Delete droppedGenes in ll  
dd <- ll[!(ll$FBgn %in% droppedGenes$FBgn),]  
#str(dd)  
#str(ll)  
  
# Move deleted genes to the grey module  
lld <- ll  
lld[ll$FBgn %in% droppedGenes$FBgn,"mod"] <- "grey"

# Compare module sizes

ll %>%   
 group\_by(mod) %>%  
 summarise(no\_rows = length(mod)) %>%  
 as.data.frame()

## mod no\_rows  
## 1 black 2956  
## 2 blue 1747  
## 3 brown 1084  
## 4 cyan 507  
## 5 darkgreen 199  
## 6 darkgrey 309  
## 7 darkred 84  
## 8 darkturquoise 79  
## 9 greenyellow 165  
## 10 grey 45  
## 11 lightcyan 117  
## 12 lightgreen 107  
## 13 lightyellow 107  
## 14 pink 382  
## 15 red 787  
## 16 royalblue 132  
## 17 salmon 157  
## 18 skyblue 52  
## 19 steelblue 44  
## 20 tan 163  
## 21 turquoise 3337  
## 22 white 54

ll$analysis <- "full"  
  
lld %>%  
 group\_by(mod) %>%  
 summarise(no\_rows = length(mod)) %>%  
 as.data.frame()

## mod no\_rows  
## 1 black 2886  
## 2 blue 1679  
## 3 brown 1042  
## 4 cyan 391  
## 5 darkgreen 68  
## 6 darkgrey 249  
## 7 darkred 60  
## 8 darkturquoise 65  
## 9 greenyellow 135  
## 10 grey 1049  
## 11 lightcyan 82  
## 12 lightgreen 102  
## 13 lightyellow 79  
## 14 pink 269  
## 15 red 759  
## 16 royalblue 85  
## 17 salmon 114  
## 18 skyblue 44  
## 19 steelblue 39  
## 20 tan 123  
## 21 turquoise 3240  
## 22 white 54

lld$analysis <- "resamp"  
  
# Check one module  
stlbl <- rbind(subset(ll, ll$mod=="steelblue"), subset(lld, lld$mod=="steelblue"))

# Gene Ontology on WGCNA modules

# Fbgn annotation file "Genes:fbgn\_annotation\_ID\_fb\_2018\_04.tsv"  
  
annot = read.csv("../../processed/DESEQ/Coexpression/FlyAnnotation.csv")  
dim(annot)

## [1] 12614 55

names(annot)

## [1] "X" "baseMean" "log2FoldChange" "lfcSE"   
## [5] "stat" "pvalue" "padj" "FC\_DR\_B"   
## [9] "FCse\_DR\_B" "stat\_DR\_B" "p\_DR\_B" "padj\_DR\_B"   
## [13] "FC\_HS\_B" "FCse\_HS\_B" "stat\_HS\_B" "p\_HS\_B"   
## [17] "padj\_HS\_B" "FC\_DRHS\_B" "FCse\_DRHS\_B" "stat\_DRHS\_B"   
## [21] "p\_DRHS\_B" "padj\_DRHS\_B" "FC\_DR\_H" "FCse\_DR\_H"   
## [25] "stat\_DR\_H" "p\_DR\_H" "padj\_DR\_H" "FC\_HS\_H"   
## [29] "FCse\_HS\_H" "stat\_HS\_H" "p\_HS\_H" "padj\_HS\_H"   
## [33] "FC\_DRHS\_H" "FCse\_DRHS\_H" "stat\_DRHS\_H" "p\_DRHS\_H"   
## [37] "padj\_DRHS\_H" "FC\_DR\_O" "FCse\_DR\_O" "stat\_DR\_O"   
## [41] "p\_DR\_O" "padj\_DR\_O" "FC\_HS\_O" "FCse\_HS\_O"   
## [45] "stat\_HS\_O" "p\_HS\_O" "padj\_HS\_O" "FC\_DRHS\_O"   
## [49] "FCse\_DRHS\_O" "stat\_DRHS\_O" "p\_DRHS\_O" "padj\_DRHS\_O"   
## [53] "symbol" "entrez" "name"

colnames(annot)[colnames(annot)=="X"] <- "FBgn"  
  
FBgenes <- lld$FBgn  
#FBgenes <- dd$FBgn  
  
FBgenes2annot = match(FBgenes, annot$FBgn)  
allIDs = annot$entrez[FBgenes2annot]  
  
  
# Module GO term enrichment  
  
# Enrichment table  
GOenr <- GOenrichmentAnalysis(lld$mod, allIDs,   
 organism = "fly",   
 #nBestP = 100,  
 pCut = 0.01)

## Warning in GOenrichmentAnalysis(lld$mod, allIDs, organism = "fly", pCut = 0.01): This function is deprecated and will be removed in the near future.   
## We suggest using the replacement function enrichmentAnalysis   
## in R package anRichment, available from the following URL:  
## https://labs.genetics.ucla.edu/horvath/htdocs/CoexpressionNetwork/GeneAnnotation/

## Loading required package: GO.db

## GOenrichmentAnalysis: loading annotation data...  
## ..of the 12614 Entrez identifiers submitted, 10334 are mapped in current GO categories.  
## ..will use 10334 background genes for enrichment calculations.  
## ..preparing term lists (this may take a while)..   
## ..working on label set 1 ..  
## ..calculating enrichments (this may also take a while)..  
## ..putting together terms with highest enrichment significance..

# GOenr1 <- GOenrichmentAnalysis(lld$mod, allIDs,   
# organism = "fly",   
# #nBestP = 100,  
# pCut = 0.01)  
  
tab <- GOenr$bestPTerms[[4]]$enrichment  
names(tab)

## [1] "module" "modSize" "bkgrModSize"   
## [4] "rank" "enrichmentP" "BonferoniP"   
## [7] "nModGenesInTerm" "fracOfBkgrModSize" "fracOfBkgrTermSize"  
## [10] "bkgrTermSize" "termID" "termOntology"   
## [13] "termName" "termDefinition"

write.csv(tab, file = "../../processed/DESEQ/Coexpression/resampMods/GOEnrichTab\_Resamp.csv",   
 row.names = FALSE)  
### Note message: GOenrichmentAnalysis: loading annotation data...  
### ..of the 12614 Entrez identifiers submitted, 10334 are mapped ###in current GO categories.  
### ..will use 10334 background genes for enrichment calculations.  
  
# View table on screen  
keepCols = c(1, 2, 5, 6, 7, 12, 13);  
screenTab = tab[, keepCols];  
  
# Round numeric columns to 2 decimal places:  
numCols = c(3, 4);  
screenTab[, numCols] = signif(apply(screenTab[, numCols], 2, as.numeric), 2)  
  
# Truncate the the term name to at most 40 characters  
screenTab[, 7] = substring(screenTab[, 7], 1, 40)  
  
# Shorten the column names:  
colnames(screenTab) = c("module", "size", "p-val", "Bonf", "nInTerm", "ont", "termName");  
rownames(screenTab) = NULL;  
  
# Set the width of R’s output  
options(width=95)  
  
# Enrichment table  
screenTab

## module size p-val Bonf nInTerm ont termName  
## 1 black 2886 3.9e-160 3.2e-156 1095 CC nucleus  
## 2 black 2886 6.9e-112 5.8e-108 1857 CC intracellular  
## 3 black 2886 2.7e-103 2.3e-99 1399 CC intracellular membrane-bounded organelle  
## 4 black 2886 9.6e-98 8.1e-94 1574 CC intracellular organelle  
## 5 black 2886 1.3e-94 1.1e-90 1009 CC protein-containing complex  
## 6 black 2886 2.1e-89 1.8e-85 936 BP nucleobase-containing compound metabolic  
## 7 black 2886 3.2e-82 2.6e-78 710 MF nucleic acid binding  
## 8 black 2886 6.6e-80 5.5e-76 882 BP gene expression  
## 9 black 2886 2.2e-79 1.9e-75 340 BP RNA processing  
## 10 black 2886 1.3e-77 1.1e-73 748 BP RNA metabolic process  
## 11 black 2886 1.6e-75 1.3e-71 348 BP chromosome organization  
## 12 black 2886 6.2e-59 5.2e-55 209 BP DNA metabolic process  
## 13 black 2886 2.3e-58 2.0e-54 308 CC chromosome  
## 14 black 2886 1.3e-54 1.1e-50 261 BP mitotic cell cycle  
## 15 black 2886 4.6e-52 3.8e-48 680 BP organelle organization  
## 16 black 2886 6.4e-52 5.3e-48 302 MF RNA binding  
## 17 black 2886 1.7e-47 1.4e-43 192 BP nuclear division  
## 18 black 2886 2.0e-46 1.7e-42 143 CC nucleolus  
## 19 black 2886 3.7e-46 3.1e-42 1401 BP nitrogen compound metabolic process  
## 20 black 2886 9.1e-43 7.6e-39 1429 BP cellular metabolic process  
## 21 black 2886 3.4e-42 2.9e-38 136 BP chromosome segregation  
## 22 black 2886 2.1e-40 1.7e-36 126 BP nuclear chromosome segregation  
## 23 black 2886 5.1e-40 4.3e-36 270 CC ribonucleoprotein complex  
## 24 black 2886 1.3e-39 1.1e-35 310 BP female gamete generation  
## 25 black 2886 2.0e-37 1.7e-33 1934 BP cellular process  
## 26 black 2886 9.6e-37 8.1e-33 228 CC nucleoplasm  
## 27 black 2886 7.0e-36 5.9e-32 175 BP mRNA processing  
## 28 black 2886 7.6e-35 6.3e-31 173 BP regulation of cell cycle  
## 29 black 2886 1.4e-34 1.2e-30 373 BP gamete generation  
## 30 black 2886 1.7e-33 1.4e-29 196 BP chromatin organization  
## 31 black 2886 2.0e-32 1.7e-28 890 BP cellular component organization  
## 32 black 2886 2.6e-32 2.2e-28 134 BP meiotic cell cycle  
## 33 black 2886 2.7e-32 2.2e-28 151 CC nuclear chromosome  
## 34 black 2886 3.9e-32 3.3e-28 86 BP DNA replication  
## 35 black 2886 2.3e-31 1.9e-27 131 BP cellular response to DNA damage stimulus  
## 36 black 2886 2.5e-30 2.1e-26 272 BP oogenesis  
## 37 black 2886 3.3e-30 2.7e-26 151 BP RNA splicing  
## 38 black 2886 7.4e-30 6.2e-26 154 CC chromatin  
## 39 black 2886 8.7e-30 7.3e-26 109 BP DNA repair  
## 40 black 2886 1.2e-29 1.0e-25 121 BP ribosome biogenesis  
## 41 black 2886 1.4e-29 1.2e-25 302 BP germ cell development  
## 42 black 2886 1.9e-29 1.6e-25 143 BP RNA splicing, via transesterification re  
## 43 black 2886 1.9e-29 1.6e-25 143 BP mRNA splicing, via spliceosome  
## 44 black 2886 1.2e-28 1.0e-24 94 BP sister chromatid segregation  
## 45 black 2886 2.9e-27 2.4e-23 116 BP regulation of mitotic cell cycle  
## 46 black 2886 3.6e-27 3.0e-23 71 BP DNA-dependent DNA replication  
## 47 black 2886 7.3e-27 6.1e-23 433 BP reproductive process  
## 48 black 2886 1.3e-25 1.1e-21 84 BP rRNA processing  
## 49 black 2886 6.7e-24 5.7e-20 438 BP reproduction  
## 50 black 2886 6.0e-23 5.0e-19 79 BP mitotic sister chromatid segregation  
## 51 black 2886 7.6e-23 6.3e-19 86 BP tRNA metabolic process  
## 52 black 2886 2.5e-22 2.1e-18 69 BP DNA recombination  
## 53 black 2886 1.1e-21 9.0e-18 64 MF helicase activity  
## 54 black 2886 2.7e-21 2.3e-17 324 MF DNA binding  
## 55 black 2886 3.9e-21 3.2e-17 82 BP cell cycle phase transition  
## 56 black 2886 8.0e-21 6.7e-17 638 BP regulation of metabolic process  
## 57 black 2886 1.5e-20 1.2e-16 76 BP nucleocytoplasmic transport  
## 58 black 2886 2.0e-20 1.7e-16 78 BP mitotic cell cycle phase transition  
## 59 black 2886 8.7e-20 7.3e-16 60 CC spliceosomal complex  
## 60 black 2886 2.3e-19 1.9e-15 384 BP multicellular organism reproduction  
## 61 black 2886 2.4e-19 2.0e-15 488 BP regulation of gene expression  
## 62 black 2886 3.6e-19 3.0e-15 72 CC nuclear envelope  
## 63 black 2886 5.5e-19 4.6e-15 70 BP regulation of cell cycle phase transitio  
## 64 black 2886 6.0e-19 5.0e-15 60 CC chromosome, centromeric region  
## 65 black 2886 6.2e-19 5.2e-15 98 BP RNA localization  
## 66 black 2886 7.6e-19 6.4e-15 45 BP female meiotic nuclear division  
## 67 black 2886 8.4e-19 7.1e-15 68 BP regulation of mitotic cell cycle phase t  
## 68 black 2886 3.7e-18 3.1e-14 48 BP meiotic chromosome segregation  
## 69 black 2886 1.1e-17 9.5e-14 32 CC small-subunit processome  
## 70 black 2886 1.9e-17 1.6e-13 55 BP RNA 3'-end processing  
## 71 black 2886 3.4e-17 2.9e-13 90 CC nuclear chromatin  
## 72 black 2886 3.4e-17 2.9e-13 71 BP eggshell formation  
## 73 black 2886 3.8e-17 3.2e-13 210 BP protein-containing complex assembly  
## 74 black 2886 4.4e-17 3.7e-13 31 CC replication fork  
## 75 black 2886 4.4e-17 3.7e-13 70 BP chorion-containing eggshell formation  
## 76 black 2886 8.7e-17 7.3e-13 35 CC chorion  
## 77 black 2886 2.3e-16 1.9e-12 400 BP cellular protein modification process  
## 78 black 2886 3.4e-16 2.8e-12 46 BP chromatin assembly or disassembly  
## 79 black 2886 1.0e-15 8.6e-12 45 CC RNA polymerase II, holoenzyme  
## 80 black 2886 2.0e-15 1.7e-11 48 BP nucleosome organization  
## 81 black 2886 2.3e-15 1.9e-11 94 BP histone modification  
## 82 black 2886 2.3e-15 1.9e-11 47 CC condensed chromosome  
## 83 black 2886 2.8e-15 2.4e-11 99 MF chromatin binding  
## 84 black 2886 3.0e-15 2.5e-11 719 BP biosynthetic process  
## 85 black 2886 3.3e-15 2.8e-11 43 MF ATP-dependent helicase activity  
## 86 black 2886 3.5e-15 2.9e-11 66 BP negative regulation of cell cycle  
## 87 black 2886 3.9e-15 3.3e-11 70 BP spindle organization  
## 88 black 2886 5.6e-15 4.7e-11 59 BP RNA catabolic process  
## 89 black 2886 8.6e-15 7.2e-11 54 BP protein-DNA complex assembly  
## 90 black 2886 1.6e-14 1.3e-10 683 MF protein binding  
## 91 black 2886 1.7e-14 1.4e-10 46 BP protein localization to nucleus  
## 92 black 2886 2.0e-14 1.7e-10 84 BP regulation of chromosome organization  
## 93 black 2886 2.2e-14 1.8e-10 59 BP RNA modification  
## 94 black 2886 2.8e-14 2.3e-10 42 BP chromosome separation  
## 95 black 2886 3.4e-14 2.8e-10 36 CC nuclear pore  
## 96 black 2886 4.0e-14 3.3e-10 66 MF methyltransferase activity  
## 97 black 2886 8.9e-14 7.5e-10 221 BP cellular macromolecule localization  
## 98 black 2886 9.1e-14 7.6e-10 40 BP RNA export from nucleus  
## 99 black 2886 9.8e-14 8.2e-10 139 BP microtubule cytoskeleton organization  
## 100 black 2886 9.8e-14 8.3e-10 39 BP mitotic cell cycle checkpoint  
## 101 black 2886 1.2e-13 9.6e-10 45 BP nuclear export  
## 102 black 2886 1.4e-13 1.2e-09 57 BP microtubule cytoskeleton organization in  
## 103 black 2886 2.0e-13 1.7e-09 50 BP regulation of mitotic nuclear division  
## 104 black 2886 2.4e-13 2.0e-09 40 BP chromosome condensation  
## 105 black 2886 2.5e-13 2.1e-09 49 BP negative regulation of mitotic cell cycl  
## 106 black 2886 3.0e-13 2.5e-09 84 CC transcription factor complex  
## 107 black 2886 3.2e-13 2.7e-09 48 BP mitotic spindle organization  
## 108 black 2886 3.2e-13 2.7e-09 37 CC kinetochore  
## 109 black 2886 3.4e-13 2.9e-09 34 BP mRNA transport  
## 110 black 2886 3.5e-13 2.9e-09 35 MF DNA-dependent ATPase activity  
## 111 black 2886 4.1e-13 3.4e-09 227 MF ATP binding  
## 112 black 2886 5.3e-13 4.5e-09 61 MF nuclease activity  
## 113 black 2886 5.3e-13 4.5e-09 41 BP protein export from nucleus  
## 114 black 2886 5.6e-13 4.7e-09 123 BP cell division  
## 115 black 2886 7.1e-13 5.9e-09 39 BP chromosome organization involved in meio  
## 116 black 2886 7.3e-13 6.1e-09 93 BP gene silencing  
## 117 black 2886 9.0e-13 7.5e-09 30 BP nucleosome assembly  
## 118 black 2886 9.0e-13 7.5e-09 30 CC catalytic step 2 spliceosome  
## 119 black 2886 9.4e-13 7.9e-09 548 BP regulation of cellular metabolic process  
## 120 black 2886 1.0e-12 8.5e-09 98 BP protein localization to organelle  
## 121 black 2886 1.3e-12 1.1e-08 41 BP import into nucleus  
## 122 black 2886 1.3e-12 1.1e-08 67 BP methylation  
## 123 black 2886 1.5e-12 1.3e-08 40 BP protein import into nucleus  
## 124 black 2886 2.1e-12 1.7e-08 38 BP chromatin assembly  
## 125 black 2886 2.2e-12 1.8e-08 49 MF nucleotidyltransferase activity  
## 126 black 2886 2.5e-12 2.1e-08 28 BP mRNA export from nucleus  
## 127 black 2886 2.8e-12 2.3e-08 45 BP positive regulation of cell cycle  
## 128 black 2886 2.9e-12 2.4e-08 35 BP ribonucleoprotein complex export from nu  
## 129 black 2886 3.4e-12 2.9e-08 24 BP nucleotide-excision repair  
## 130 black 2886 3.4e-12 2.9e-08 24 CC 90S preribosome  
## 131 black 2886 3.8e-12 3.1e-08 80 BP oocyte differentiation  
## 132 black 2886 4.6e-12 3.8e-08 46 BP transcription initiation from RNA polyme  
## 133 black 2886 4.7e-12 4.0e-08 228 MF adenyl ribonucleotide binding  
## 134 black 2886 4.8e-12 4.0e-08 51 BP double-strand break repair  
## 135 black 2886 5.2e-12 4.4e-08 220 BP negative regulation of gene expression  
## 136 black 2886 6.3e-12 5.3e-08 50 BP DNA-templated transcription, initiation  
## 137 black 2886 6.9e-12 5.8e-08 274 MF purine nucleotide binding  
## 138 black 2886 7.0e-12 5.9e-08 26 BP reciprocal meiotic recombination  
## 139 black 2886 8.6e-12 7.2e-08 34 CC pole plasm  
## 140 black 2886 9.0e-12 7.5e-08 51 BP protein acetylation  
## 141 black 2886 1.0e-11 8.5e-08 32 MF RNA methyltransferase activity  
## 142 black 2886 1.2e-11 9.7e-08 20 MF snoRNA binding  
## 143 black 2886 1.9e-11 1.6e-07 92 BP posttranscriptional regulation of gene e  
## 144 black 2886 1.9e-11 1.6e-07 158 BP translation  
## 145 black 2886 2.0e-11 1.7e-07 58 BP chromatin remodeling  
## 146 black 2886 2.3e-11 2.0e-07 45 CC cytoplasmic ribonucleoprotein granule  
## 147 black 2886 2.5e-11 2.1e-07 2262 CC cellular\_component  
## 148 black 2886 2.6e-11 2.2e-07 21 BP DNA replication initiation  
## 149 black 2886 2.8e-11 2.3e-07 68 BP ribonucleoprotein complex assembly  
## 150 black 2886 2.9e-11 2.4e-07 26 BP homologous recombination  
## 151 black 2886 2.9e-11 2.4e-07 49 BP tRNA processing  
## 152 black 2886 3.1e-11 2.6e-07 31 BP tRNA aminoacylation  
## 153 black 2886 3.1e-11 2.6e-07 31 BP DNA biosynthetic process  
## 154 black 2886 3.3e-11 2.7e-07 30 BP tRNA aminoacylation for protein translat  
## 155 black 2886 4.5e-11 3.7e-07 19 MF structural constituent of nuclear pore  
## 156 black 2886 4.6e-11 3.8e-07 45 CC ribonucleoprotein granule  
## 157 black 2886 5.0e-11 4.2e-07 42 BP nucleus organization  
## 158 black 2886 5.0e-11 4.2e-07 47 BP histone acetylation  
## 159 black 2886 5.6e-11 4.7e-07 58 CC nuclear transcription factor complex  
## 160 black 2886 6.1e-11 5.1e-07 38 BP ribosomal small subunit biogenesis  
## 161 black 2886 7.1e-11 6.0e-07 50 CC RNA polymerase II transcription factor c  
## 162 black 2886 8.7e-11 7.3e-07 45 CC small nuclear ribonucleoprotein complex  
## 163 black 2886 9.3e-11 7.8e-07 47 BP peptidyl-lysine acetylation  
## 164 black 2886 9.7e-11 8.1e-07 20 BP snRNA 3'-end processing  
## 165 black 2886 1.0e-10 8.4e-07 29 MF RNA helicase activity  
## 166 black 2886 1.1e-10 8.9e-07 27 MF ATP-dependent RNA helicase activity  
## 167 black 2886 1.1e-10 8.9e-07 27 MF RNA-dependent ATPase activity  
## 168 black 2886 1.2e-10 9.9e-07 162 BP microtubule-based process  
## 169 black 2886 1.2e-10 1.0e-06 46 BP mRNA catabolic process  
## 170 black 2886 1.5e-10 1.3e-06 53 BP establishment of RNA localization  
## 171 black 2886 1.6e-10 1.3e-06 21 BP snRNA processing  
## 172 black 2886 1.9e-10 1.6e-06 127 BP ovarian follicle cell development  
## 173 black 2886 1.9e-10 1.6e-06 32 BP RNA methylation  
## 174 black 2886 3.0e-10 2.6e-06 28 BP DNA damage checkpoint  
## 175 black 2886 3.1e-10 2.6e-06 54 CC spindle  
## 176 black 2886 3.3e-10 2.7e-06 40 BP nucleic acid phosphodiester bond hydroly  
## 177 black 2886 3.3e-10 2.8e-06 25 BP oocyte karyosome formation  
## 178 black 2886 3.6e-10 3.0e-06 19 CC nuclear replication fork  
## 179 black 2886 3.7e-10 3.1e-06 33 BP regulation of chromosome segregation  
## 180 black 2886 4.1e-10 3.4e-06 360 BP transcription, DNA-templated  
## 181 black 2886 6.2e-10 5.2e-06 86 BP axis specification  
## 182 black 2886 6.3e-10 5.3e-06 30 BP mitotic sister chromatid separation  
## 183 black 2886 7.0e-10 5.9e-06 37 BP nuclear-transcribed mRNA catabolic proce  
## 184 black 2886 7.1e-10 5.9e-06 46 BP eggshell chorion assembly  
## 185 black 2886 7.8e-10 6.5e-06 51 BP RNA transport  
## 186 black 2886 8.2e-10 6.9e-06 28 BP regulation of chromosome separation  
## 187 black 2886 8.4e-10 7.0e-06 33 BP double-strand break repair via homologou  
## 188 black 2886 8.4e-10 7.0e-06 33 BP recombinational repair  
## 189 black 2886 9.1e-10 7.6e-06 41 MF endonuclease activity  
## 190 black 2886 9.1e-10 7.6e-06 47 BP intracellular mRNA localization  
## 191 black 2886 9.2e-10 7.7e-06 27 MF aminoacyl-tRNA ligase activity  
## 192 black 2886 9.2e-10 7.7e-06 22 BP establishment of chromosome localization  
## 193 black 2886 9.9e-10 8.3e-06 26 CC condensed nuclear chromosome  
## 194 black 2886 1.1e-09 8.9e-06 67 BP oocyte development  
## 195 black 2886 1.1e-09 9.3e-06 83 BP regulation of gene expression, epigeneti  
## 196 black 2886 1.2e-09 1.0e-05 40 BP spindle assembly  
## 197 black 2886 1.8e-09 1.5e-05 29 BP G2/M transition of mitotic cell cycle  
## 198 black 2886 2.0e-09 1.7e-05 19 BP DNA amplification  
## 199 black 2886 2.0e-09 1.7e-05 19 BP regulation of transposition  
## 200 black 2886 2.0e-09 1.7e-05 391 MF transferase activity  
## 201 black 2886 2.2e-09 1.9e-05 297 MF nucleotide binding  
## 202 black 2886 2.4e-09 2.0e-05 27 BP metaphase/anaphase transition of mitotic  
## 203 black 2886 2.4e-09 2.0e-05 27 BP regulation of mitotic sister chromatid s  
## 204 black 2886 2.4e-09 2.0e-05 27 CC P granule  
## 205 black 2886 2.7e-09 2.3e-05 26 BP regulation of G2/M transition of mitotic  
## 206 black 2886 3.3e-09 2.8e-05 366 BP regulation of RNA metabolic process  
## 207 black 2886 4.8e-09 4.0e-05 17 BP spliceosomal snRNP assembly  
## 208 black 2886 5.2e-09 4.4e-05 81 MF mRNA binding  
## 209 black 2886 5.9e-09 5.0e-05 34 BP tRNA modification  
## 210 black 2886 6.0e-09 5.0e-05 27 BP maturation of SSU-rRNA  
## 211 black 2886 6.0e-09 5.0e-05 27 MF DNA helicase activity  
## 212 black 2886 8.0e-09 6.7e-05 25 BP telomere maintenance  
## 213 black 2886 8.9e-09 7.4e-05 19 CC condensed chromosome, centromeric region  
## 214 black 2886 9.0e-09 7.6e-05 24 BP regulation of mitotic metaphase/anaphase  
## 215 black 2886 9.0e-09 7.6e-05 24 MF DNA-directed 5'-3' RNA polymerase activi  
## 216 black 2886 1.2e-08 1.0e-04 183 BP cellular protein localization  
## 217 black 2886 1.3e-08 1.1e-04 59 BP oocyte axis specification  
## 218 black 2886 1.4e-08 1.2e-04 27 CC germ plasm  
## 219 black 2886 1.6e-08 1.4e-04 53 BP mitochondrial translation  
## 220 black 2886 2.3e-08 1.9e-04 36 MF histone binding  
## 221 black 2886 2.4e-08 2.0e-04 43 CC protein acetyltransferase complex  
## 222 black 2886 2.5e-08 2.1e-04 17 BP eggshell chorion gene amplification  
## 223 black 2886 2.5e-08 2.1e-04 17 BP negative regulation of transposition  
## 224 black 2886 3.0e-08 2.5e-04 22 BP RNA polyadenylation  
## 225 black 2886 3.2e-08 2.6e-04 27 MF single-stranded DNA binding  
## 226 black 2886 3.3e-08 2.7e-04 19 BP metaphase plate congression  
## 227 black 2886 3.4e-08 2.9e-04 131 BP epithelial cell development  
## 228 black 2886 3.7e-08 3.1e-04 14 BP female meiosis chromosome segregation  
## 229 black 2886 3.7e-08 3.1e-04 14 CC U5 snRNP  
## 230 black 2886 3.8e-08 3.2e-04 59 BP oocyte construction  
## 231 black 2886 4.9e-08 4.1e-04 31 MF chromatin DNA binding  
## 232 black 2886 5.2e-08 4.4e-04 37 BP pole plasm assembly  
## 233 black 2886 5.3e-08 4.5e-04 28 BP mRNA 3'-end processing  
## 234 black 2886 6.3e-08 5.3e-04 15 BP DNA replication checkpoint  
## 235 black 2886 6.9e-08 5.8e-04 640 BP protein metabolic process  
## 236 black 2886 7.2e-08 6.1e-04 44 BP oocyte anterior/posterior axis specifica  
## 237 black 2886 7.9e-08 6.6e-04 22 BP sister chromatid cohesion  
## 238 black 2886 8.3e-08 6.9e-04 45 BP maternal determination of anterior/poste  
## 239 black 2886 8.5e-08 7.1e-04 16 BP mitotic G2/M transition checkpoint  
## 240 black 2886 8.5e-08 7.1e-04 16 CC small nucleolar ribonucleoprotein comple  
## 241 black 2886 8.5e-08 7.1e-04 16 CC preribosome, large subunit precursor  
## 242 black 2886 8.5e-08 7.1e-04 16 CC U4/U6 x U5 tri-snRNP complex  
## 243 black 2886 8.5e-08 7.1e-04 16 MF cyclin-dependent protein serine/threonin  
## 244 black 2886 9.8e-08 8.2e-04 20 CC chromosome, telomeric region  
## 245 black 2886 1.0e-07 8.5e-04 51 BP asymmetric cell division  
## 246 black 2886 1.1e-07 8.8e-04 18 BP negative regulation of G2/M transition o  
## 247 black 2886 1.1e-07 8.8e-04 18 CC nucleosome  
## 248 black 2886 1.1e-07 8.8e-04 18 MF endoribonuclease activity, producing 5'-  
## 249 black 2886 1.3e-07 1.1e-03 24 BP fertilization  
## 250 black 2886 1.5e-07 1.2e-03 177 MF pyrophosphatase activity  
## 251 black 2886 1.5e-07 1.3e-03 43 MF S-adenosylmethionine-dependent methyltra  
## 252 black 2886 1.6e-07 1.3e-03 112 CC microtubule cytoskeleton  
## 253 black 2886 1.7e-07 1.4e-03 53 BP chromatin silencing  
## 254 black 2886 1.7e-07 1.5e-03 179 MF hydrolase activity, acting on acid anhyd  
## 255 black 2886 1.9e-07 1.6e-03 22 CC spindle microtubule  
## 256 black 2886 2.1e-07 1.7e-03 332 BP regulation of transcription, DNA-templat  
## 257 black 2886 2.1e-07 1.8e-03 11 BP mitotic DNA replication checkpoint  
## 258 black 2886 2.1e-07 1.8e-03 11 MF DNA replication origin binding  
## 259 black 2886 2.6e-07 2.2e-03 170 MF nucleoside-triphosphatase activity  
## 260 black 2886 2.6e-07 2.2e-03 20 BP mRNA polyadenylation  
## 261 black 2886 2.7e-07 2.2e-03 177 MF hydrolase activity, acting on acid anhyd  
## 262 black 2886 3.1e-07 2.6e-03 31 BP pole plasm RNA localization  
## 263 black 2886 3.1e-07 2.6e-03 62 MF transcription coregulator activity  
## 264 black 2886 3.5e-07 2.9e-03 47 BP germarium-derived egg chamber formation  
## 265 black 2886 3.6e-07 3.0e-03 23 BP regulation of DNA replication  
## 266 black 2886 3.9e-07 3.3e-03 40 BP centrosome cycle  
## 267 black 2886 4.4e-07 3.7e-03 220 BP protein localization  
## 268 black 2886 4.4e-07 3.7e-03 22 BP single fertilization  
## 269 black 2886 4.5e-07 3.8e-03 80 CC polytene chromosome  
## 270 black 2886 4.7e-07 3.9e-03 128 BP intracellular protein transport  
## 271 black 2886 5.2e-07 4.4e-03 27 BP positive regulation of cell cycle proces  
## 272 black 2886 5.3e-07 4.4e-03 12 BP vitelline membrane formation involved in  
## 273 black 2886 5.5e-07 4.6e-03 58 BP anterior/posterior axis specification  
## 274 black 2886 5.6e-07 4.7e-03 81 BP protein modification by small protein co  
## 275 black 2886 5.9e-07 5.0e-03 24 CC nuclear periphery  
## 276 black 2886 7.2e-07 6.0e-03 30 BP pole plasm mRNA localization  
## 277 black 2886 7.3e-07 6.1e-03 28 CC protein kinase complex  
## 278 black 2886 7.3e-07 6.1e-03 28 MF histone acetyltransferase activity  
## 279 black 2886 7.7e-07 6.5e-03 19 CC U2 snRNP  
## 280 black 2886 7.7e-07 6.5e-03 19 MF damaged DNA binding  
## 281 black 2886 8.0e-07 6.7e-03 178 BP peptide metabolic process  
## 282 black 2886 8.1e-07 6.8e-03 13 BP rRNA methylation  
## 283 black 2886 8.2e-07 6.9e-03 39 BP gene silencing by RNA  
## 284 black 2886 8.9e-07 7.4e-03 18 CC spindle midzone  
## 285 black 2886 9.0e-07 7.6e-03 25 BP mitotic cell cycle, embryonic  
## 286 black 2886 9.0e-07 7.6e-03 25 BP positive regulation of mitotic cell cycl  
## 287 black 2886 9.2e-07 7.7e-03 31 BP ribosomal large subunit biogenesis  
## 288 black 2886 9.9e-07 8.3e-03 17 CC chromocenter  
## 289 black 2886 9.9e-07 8.3e-03 14 BP regulation of meiotic cell cycle  
## 290 black 2886 1.1e-06 9.0e-03 15 BP negative regulation of mitotic metaphase  
## 291 black 2886 1.2e-06 9.9e-03 24 CC serine/threonine protein kinase complex  
## 292 black 2886 1.3e-06 1.1e-02 44 BP microtubule organizing center organizati  
## 293 black 2886 1.3e-06 1.1e-02 197 BP cytoskeleton organization  
## 294 black 2886 1.4e-06 1.1e-02 36 MF N-acetyltransferase activity  
## 295 black 2886 1.4e-06 1.1e-02 33 BP intracellular mRNA localization involved  
## 296 black 2886 1.5e-06 1.3e-02 20 BP maturation of SSU-rRNA from tricistronic  
## 297 black 2886 1.6e-06 1.3e-02 34 BP intracellular mRNA localization involved  
## 298 black 2886 1.6e-06 1.3e-02 34 MF ribonuclease activity  
## 299 black 2886 1.8e-06 1.5e-02 55 BP embryonic axis specification  
## 300 black 2886 2.0e-06 1.7e-02 11 CC mRNA cleavage and polyadenylation specif  
## 301 black 2886 2.0e-06 1.7e-02 127 BP cell proliferation  
## 302 black 2886 2.1e-06 1.7e-02 40 MF acetyltransferase activity  
## 303 black 2886 2.3e-06 1.9e-02 28 CC heterochromatin  
## 304 black 2886 2.3e-06 2.0e-02 37 MF N-acyltransferase activity  
## 305 black 2886 2.5e-06 2.1e-02 53 BP anterior/posterior axis specification, e  
## 306 black 2886 2.5e-06 2.1e-02 34 BP asymmetric stem cell division  
## 307 black 2886 2.8e-06 2.4e-02 12 BP spindle assembly involved in female meio  
## 308 black 2886 2.8e-06 2.4e-02 12 BP regulation of mitotic cell cycle, embryo  
## 309 black 2886 2.8e-06 2.4e-02 12 BP N-terminal protein amino acid modificati  
## 310 black 2886 2.8e-06 2.4e-02 12 BP RNA surveillance  
## 311 black 2886 2.8e-06 2.4e-02 12 CC condensed chromosome kinetochore  
## 312 black 2886 2.8e-06 2.4e-02 12 CC integrator complex  
## 313 black 2886 3.0e-06 2.5e-02 23 BP ATP-dependent chromatin remodeling  
## 314 black 2886 3.0e-06 2.5e-02 16 BP mitotic chromosome condensation  
## 315 black 2886 3.0e-06 2.5e-02 16 BP negative regulation of sister chromatid   
## 316 black 2886 3.1e-06 2.6e-02 48 BP stem cell division  
## 317 black 2886 3.2e-06 2.7e-02 20 CC mitotic spindle  
## 318 black 2886 3.3e-06 2.8e-02 13 BP DNA strand elongation involved in DNA re  
## 319 black 2886 3.3e-06 2.8e-02 13 BP anaphase-promoting complex-dependent cat  
## 320 black 2886 3.3e-06 2.8e-02 13 MF DNA-directed DNA polymerase activity  
## 321 black 2886 3.3e-06 2.8e-02 56 BP regulation of translation  
## 322 black 2886 3.4e-06 2.9e-02 14 BP transcription by RNA polymerase I  
## 323 black 2886 3.4e-06 2.9e-02 14 BP mitotic metaphase plate congression  
## 324 black 2886 3.4e-06 2.9e-02 14 BP mitotic spindle assembly checkpoint  
## 325 black 2886 3.4e-06 2.9e-02 33 BP posttranscriptional gene silencing  
## 326 black 2886 3.5e-06 2.9e-02 9 CC chaperone complex  
## 327 black 2886 4.3e-06 3.6e-02 48 BP regulation of chromatin organization  
## 328 black 2886 5.2e-06 4.4e-02 27 BP pole plasm oskar mRNA localization  
## 329 black 2886 5.2e-06 4.4e-02 27 MF endoribonuclease activity  
## 330 black 2886 5.2e-06 4.4e-02 37 BP dorsal/ventral axis specification  
## 331 black 2886 5.6e-06 4.7e-02 23 BP meiotic spindle organization  
## 332 black 2886 6.3e-06 5.3e-02 17 CC U2-type spliceosomal complex  
## 333 black 2886 6.7e-06 5.6e-02 314 MF anion binding  
## 334 black 2886 6.8e-06 5.7e-02 112 MF ATPase activity  
## 335 black 2886 6.9e-06 5.8e-02 240 MF drug binding  
## 336 black 2886 7.3e-06 6.1e-02 10 CC nuclear exosome (RNase complex)  
## 337 black 2886 7.3e-06 6.1e-02 10 CC transcription factor TFIIH holo complex  
## 338 black 2886 8.9e-06 7.4e-02 15 BP mitotic DNA damage checkpoint  
## 339 black 2886 8.9e-06 7.4e-02 15 MF 3'-5' DNA helicase activity  
## 340 black 2886 9.8e-06 8.2e-02 35 CC histone acetyltransferase complex  
## 341 black 2886 9.9e-06 8.3e-02 11 BP nuclear RNA surveillance  
## 342 black 2886 9.9e-06 8.3e-02 11 CC kinetochore microtubule  
## 343 black 2886 1.0e-05 8.4e-02 31 BP posttranscriptional gene silencing by RN  
## 344 black 2886 1.0e-05 8.4e-02 14 BP tRNA methylation  
## 345 black 2886 1.1e-05 8.9e-02 287 MF carbohydrate derivative binding  
## 346 black 2886 1.1e-05 9.1e-02 13 BP maturation of 5.8S rRNA  
## 347 black 2886 1.1e-05 9.1e-02 13 BP negative regulation of DNA recombination  
## 348 black 2886 1.1e-05 9.1e-02 13 CC mRNA cleavage factor complex  
## 349 black 2886 1.1e-05 9.1e-02 13 MF snRNA binding  
## 350 black 2886 1.1e-05 9.2e-02 12 BP piRNA metabolic process  
## 351 black 2886 1.1e-05 9.2e-02 12 CC anaphase-promoting complex  
## 352 black 2886 1.1e-05 9.2e-02 12 CC carboxy-terminal domain protein kinase c  
## 353 black 2886 1.3e-05 1.1e-01 22 MF deoxyribonuclease activity  
## 354 black 2886 1.4e-05 1.1e-01 30 MF kinase regulator activity  
## 355 black 2886 1.4e-05 1.1e-01 42 CC cullin-RING ubiquitin ligase complex  
## 356 black 2886 1.4e-05 1.2e-01 8 BP promoter clearance from RNA polymerase I  
## 357 black 2886 1.4e-05 1.2e-01 8 BP transcriptional open complex formation a  
## 358 black 2886 1.4e-05 1.2e-01 8 BP female meiosis I  
## 359 black 2886 1.4e-05 1.2e-01 8 CC chaperonin-containing T-complex  
## 360 black 2886 1.5e-05 1.3e-01 165 BP positive regulation of gene expression  
## 361 black 2886 1.6e-05 1.4e-01 28 MF protein kinase regulator activity  
## 362 black 2886 1.7e-05 1.4e-01 19 BP mitotic spindle assembly  
## 363 black 2886 1.7e-05 1.5e-01 145 MF transferase activity, transferring phosp  
## 364 black 2886 1.7e-05 1.5e-01 16 BP DNA endoreduplication  
## 365 black 2886 1.7e-05 1.5e-01 16 CC transcription factor TFIID complex  
## 366 black 2886 1.7e-05 1.5e-01 16 MF ATP-dependent DNA helicase activity  
## 367 black 2886 2.1e-05 1.8e-01 15 BP negative regulation of mitotic nuclear d  
## 368 black 2886 2.1e-05 1.8e-01 15 BP spindle assembly involved in meiosis  
## 369 black 2886 2.2e-05 1.9e-01 18 BP nuclear-transcribed mRNA catabolic proce  
## 370 black 2886 2.4e-05 2.0e-01 20 MF 3'-5' exonuclease activity  
## 371 black 2886 2.6e-05 2.2e-01 153 MF zinc ion binding  
## 372 black 2886 2.6e-05 2.2e-01 25 BP heterochromatin organization  
## 373 black 2886 2.7e-05 2.2e-01 33 BP mitotic cytokinesis  
## 374 black 2886 2.7e-05 2.3e-01 113 MF double-stranded DNA binding  
## 375 black 2886 2.7e-05 2.3e-01 9 BP nuclear pore organization  
## 376 black 2886 2.7e-05 2.3e-01 9 BP histone mRNA metabolic process  
## 377 black 2886 2.7e-05 2.3e-01 9 BP rRNA catabolic process  
## 378 black 2886 2.7e-05 2.3e-01 9 BP snoRNA 3'-end processing  
## 379 black 2886 2.7e-05 2.3e-01 9 CC condensed chromosome outer kinetochore  
## 380 black 2886 2.8e-05 2.4e-01 56 CC microtubule organizing center  
## 381 black 2886 2.9e-05 2.4e-01 17 BP histone exchange  
## 382 black 2886 3.0e-05 2.5e-01 35 BP male meiotic nuclear division  
## 383 black 2886 3.0e-05 2.5e-01 54 CC ubiquitin ligase complex  
## 384 black 2886 3.2e-05 2.7e-01 21 MF RNA polymerase II transcription factor b  
## 385 black 2886 3.4e-05 2.8e-01 12 BP extracellular matrix assembly  
## 386 black 2886 3.4e-05 2.9e-01 10 BP meiotic chromosome separation  
## 387 black 2886 3.4e-05 2.9e-01 10 CC condensed nuclear chromosome, centromeri  
## 388 black 2886 3.4e-05 2.9e-01 10 CC Prp19 complex  
## 389 black 2886 3.4e-05 2.9e-01 10 CC U12-type spliceosomal complex  
## 390 black 2886 3.4e-05 2.9e-01 10 MF rRNA methyltransferase activity  
## 391 black 2886 3.6e-05 3.0e-01 11 BP mismatch repair  
## 392 black 2886 3.6e-05 3.0e-01 11 BP nuclear DNA replication  
## 393 black 2886 3.6e-05 3.0e-01 11 CC exosome (RNase complex)  
## 394 black 2886 3.7e-05 3.1e-01 401 BP cell development  
## 395 black 2886 3.9e-05 3.3e-01 28 BP protein lipidation  
## 396 black 2886 4.0e-05 3.4e-01 22 BP centrosome duplication  
## 397 black 2886 4.3e-05 3.6e-01 18 BP GPI anchor biosynthetic process  
## 398 black 2886 4.3e-05 3.6e-01 18 BP response to UV  
## 399 black 2886 4.6e-05 3.8e-01 46 BP protein folding  
## 400 black 2886 4.8e-05 4.0e-01 15 BP production of small RNA involved in gene  
## 401 black 2886 5.2e-05 4.3e-01 148 BP establishment of protein localization  
## 402 black 2886 5.5e-05 4.6e-01 88 BP male gamete generation  
## 403 black 2886 5.7e-05 4.8e-01 7 BP peptidyl-arginine methylation  
## 404 black 2886 5.7e-05 4.8e-01 7 BP histone arginine methylation  
## 405 black 2886 5.7e-05 4.8e-01 7 BP peptidyl-arginine N-methylation  
## 406 black 2886 5.7e-05 4.8e-01 7 BP rRNA base methylation  
## 407 black 2886 5.7e-05 4.8e-01 7 CC transcription factor TFIIH core complex  
## 408 black 2886 5.7e-05 4.8e-01 7 CC MCM complex  
## 409 black 2886 5.7e-05 4.8e-01 7 CC Yb body  
## 410 black 2886 5.7e-05 4.8e-01 7 CC cytoplasmic U snRNP body  
## 411 black 2886 5.7e-05 4.8e-01 7 MF DNA clamp loader activity  
## 412 black 2886 5.7e-05 4.8e-01 7 MF histone-arginine N-methyltransferase act  
## 413 black 2886 5.7e-05 4.8e-01 24 BP germ-line stem cell division  
## 414 black 2886 5.8e-05 4.9e-01 19 BP G1/S transition of mitotic cell cycle  
## 415 black 2886 5.9e-05 4.9e-01 70 BP protein ubiquitination  
## 416 black 2886 6.0e-05 5.0e-01 14 BP regulation of cyclin-dependent protein s  
## 417 black 2886 6.0e-05 5.0e-01 14 MF peptidyl-prolyl cis-trans isomerase acti  
## 418 black 2886 6.2e-05 5.2e-01 44 CC centrosome  
## 419 black 2886 7.4e-05 6.2e-01 13 MF transcription factor activity, RNA polym  
## 420 black 2886 7.4e-05 6.2e-01 13 MF nucleosome binding  
## 421 black 2886 8.3e-05 7.0e-01 36 CC mitochondrial ribosome  
## 422 black 2886 8.9e-05 7.5e-01 12 BP protein peptidyl-prolyl isomerization  
## 423 black 2886 8.9e-05 7.5e-01 12 BP production of miRNAs involved in gene si  
## 424 black 2886 9.1e-05 7.7e-01 21 MF rRNA binding  
## 425 black 2886 9.9e-05 8.3e-01 8 BP mRNA cleavage  
## 426 black 2886 9.9e-05 8.3e-01 8 BP N-terminal protein amino acid acetylatio  
## 427 black 2886 9.9e-05 8.3e-01 8 BP intra-S DNA damage checkpoint  
## 428 black 2886 9.9e-05 8.3e-01 8 BP nuclear mRNA surveillance  
## 429 black 2886 9.9e-05 8.3e-01 8 CC nuclear pore outer ring  
## 430 black 2886 9.9e-05 8.3e-01 8 CC site of double-strand break  
## 431 black 2886 9.9e-05 8.3e-01 8 MF peptide alpha-N-acetyltransferase activi  
## 432 black 2886 1.0e-04 8.4e-01 25 BP regulation of chromatin silencing  
## 433 black 2886 1.0e-04 8.7e-01 11 BP homologous chromosome segregation  
## 434 black 2886 1.1e-04 8.8e-01 17 BP centriole assembly  
## 435 black 2886 1.1e-04 9.1e-01 33 BP protein methylation  
## 436 black 2886 1.1e-04 9.2e-01 142 BP protein transport  
## 437 black 2886 1.1e-04 9.5e-01 36 BP regulation of gene silencing  
## 438 black 2886 1.1e-04 9.5e-01 38 CC microtubule  
## 439 black 2886 1.1e-04 9.6e-01 10 BP base-excision repair  
## 440 black 2886 1.1e-04 9.6e-01 10 BP poly(A)+ mRNA export from nucleus  
## 441 black 2886 1.1e-04 9.6e-01 10 CC RNA polymerase I complex  
## 442 black 2886 1.2e-04 9.7e-01 9 BP endomitotic cell cycle  
## 443 black 2886 1.2e-04 9.7e-01 9 MF 3'-5'-exodeoxyribonuclease activity  
## 444 black 2886 1.2e-04 9.7e-01 9 MF RNA polymerase II CTD heptapeptide repea  
## 445 black 2886 1.2e-04 1.0e+00 27 BP translational initiation  
## 446 black 2886 1.2e-04 1.0e+00 20 BP protein targeting to mitochondrion  
## 447 black 2886 1.2e-04 1.0e+00 20 BP response to ionizing radiation  
## 448 black 2886 1.2e-04 1.0e+00 20 BP positive regulation of translation  
## 449 black 2886 1.3e-04 1.0e+00 14 CC SAGA complex  
## 450 black 2886 1.3e-04 1.0e+00 14 CC SAGA-type complex  
## 451 black 2886 1.3e-04 1.0e+00 29 BP histone methylation  
## 452 black 2886 1.3e-04 1.0e+00 29 CC nuclear body  
## 453 black 2886 1.4e-04 1.0e+00 18 BP GPI anchor metabolic process  
## 454 black 2886 1.4e-04 1.0e+00 18 CC P-body  
## 455 black 2886 1.4e-04 1.0e+00 94 MF ATPase activity, coupled  
## 456 black 2886 1.4e-04 1.0e+00 16 BP regulation of response to DNA damage sti  
## 457 black 2886 1.4e-04 1.0e+00 16 CC euchromatin  
## 458 black 2886 1.7e-04 1.0e+00 123 BP negative regulation of transcription, DN  
## 459 black 2886 1.9e-04 1.0e+00 17 CC mediator complex  
## 460 black 2886 2.1e-04 1.0e+00 24 MF ribonucleoprotein complex binding  
## 461 black 2886 2.1e-04 1.0e+00 12 BP female germ-line stem cell asymmetric di  
## 462 black 2886 2.3e-04 1.0e+00 6 BP regulation of syncytial blastoderm mitot  
## 463 black 2886 2.3e-04 1.0e+00 6 BP protein sumoylation  
## 464 black 2886 2.3e-04 1.0e+00 6 BP peptidyl-arginine methylation, to asymme  
## 465 black 2886 2.3e-04 1.0e+00 6 BP replication fork processing  
## 466 black 2886 2.3e-04 1.0e+00 6 BP distributive segregation  
## 467 black 2886 2.3e-04 1.0e+00 6 BP nucleotide-excision repair, DNA incision  
## 468 black 2886 2.3e-04 1.0e+00 6 CC origin recognition complex  
## 469 black 2886 2.3e-04 1.0e+00 6 CC nuclear origin of replication recognitio  
## 470 black 2886 2.3e-04 1.0e+00 6 CC Pwp2p-containing subcomplex of 90S preri  
## 471 black 2886 2.3e-04 1.0e+00 6 CC egg coat  
## 472 black 2886 2.3e-04 1.0e+00 6 MF protein-arginine omega-N asymmetric meth  
## 473 black 2886 2.3e-04 1.0e+00 21 CC polytene chromosome interband  
## 474 black 2886 2.3e-04 1.0e+00 18 BP transcription elongation from RNA polyme  
## 475 black 2886 2.5e-04 1.0e+00 16 BP centriole replication  
## 476 black 2886 2.5e-04 1.0e+00 16 CC centriole  
## 477 black 2886 2.5e-04 1.0e+00 16 CC transcriptional repressor complex  
## 478 black 2886 2.5e-04 1.0e+00 16 MF basal RNA polymerase II transcription ma  
## 479 black 2886 2.6e-04 1.0e+00 28 BP lipoprotein metabolic process  
## 480 black 2886 2.6e-04 1.0e+00 11 BP cleavage involved in rRNA processing  
## 481 black 2886 2.7e-04 1.0e+00 29 MF transcription coactivator activity  
## 482 black 2886 2.8e-04 1.0e+00 19 CC transcription elongation factor complex  
## 483 black 2886 2.9e-04 1.0e+00 74 MF protein-containing complex binding  
## 484 black 2886 3.1e-04 1.0e+00 10 BP maturation of 5.8S rRNA from tricistroni  
## 485 black 2886 3.1e-04 1.0e+00 10 BP mitotic recombination  
## 486 black 2886 3.1e-04 1.0e+00 10 BP NLS-bearing protein import into nucleus  
## 487 black 2886 3.1e-04 1.0e+00 10 MF ATP-dependent 3'-5' RNA helicase activit  
## 488 black 2886 3.3e-04 1.0e+00 13 MF transcription factor activity, RNA polym  
## 489 black 2886 3.6e-04 1.0e+00 7 BP mRNA 3'-end processing by stem-loop bind  
## 490 black 2886 3.6e-04 1.0e+00 7 BP septin cytoskeleton organization  
## 491 black 2886 3.6e-04 1.0e+00 7 BP nuclear-transcribed mRNA catabolic proce  
## 492 black 2886 3.6e-04 1.0e+00 7 CC prefoldin complex  
## 493 black 2886 3.6e-04 1.0e+00 7 CC Ndc80 complex  
## 494 black 2886 3.6e-04 1.0e+00 7 CC nuclear pore central transport channel  
## 495 black 2886 3.6e-04 1.0e+00 7 CC outer mitochondrial membrane protein com  
## 496 black 2886 3.6e-04 1.0e+00 7 MF ubiquitin-like modifier activating enzym  
## 497 black 2886 3.6e-04 1.0e+00 7 MF protein-arginine N-methyltransferase act  
## 498 black 2886 3.6e-04 1.0e+00 7 MF DNA polymerase binding  
## 499 black 2886 3.6e-04 1.0e+00 9 BP interstrand cross-link repair  
## 500 black 2886 3.6e-04 1.0e+00 9 CC Myb complex  
## 501 black 2886 3.6e-04 1.0e+00 9 CC brahma complex  
## 502 black 2886 3.6e-04 1.0e+00 9 CC Cul4-RING E3 ubiquitin ligase complex  
## 503 black 2886 3.6e-04 1.0e+00 9 CC DNA repair complex  
## 504 black 2886 3.6e-04 1.0e+00 9 MF RNA polymerase I activity  
## 505 black 2886 3.7e-04 1.0e+00 29 MF protein transporter activity  
## 506 black 2886 3.9e-04 1.0e+00 8 BP double-strand break repair via nonhomolo  
## 507 black 2886 3.9e-04 1.0e+00 8 BP egg activation  
## 508 black 2886 3.9e-04 1.0e+00 8 BP double-strand break repair via synthesis  
## 509 black 2886 3.9e-04 1.0e+00 8 BP positive regulation of transcription by   
## 510 black 2886 3.9e-04 1.0e+00 8 CC preribosome, small subunit precursor  
## 511 black 2886 3.9e-04 1.0e+00 8 MF aminoacyl-tRNA editing activity  
## 512 black 2886 4.4e-04 1.0e+00 12 BP maturation of LSU-rRNA  
## 513 black 2886 4.4e-04 1.0e+00 12 CC RNA polymerase III complex  
## 514 black 2886 5.2e-04 1.0e+00 17 BP gene silencing by miRNA  
## 515 black 2886 5.2e-04 1.0e+00 17 BP germ-line cyst formation  
## 516 black 2886 5.2e-04 1.0e+00 17 CC mitochondrial small ribosomal subunit  
## 517 black 2886 5.7e-04 1.0e+00 11 BP regulation of chromatin assembly or disa  
## 518 black 2886 5.7e-04 1.0e+00 11 BP pyrimidine nucleotide biosynthetic proce  
## 519 black 2886 5.7e-04 1.0e+00 11 BP negative regulation of DNA replication  
## 520 black 2886 5.7e-04 1.0e+00 11 CC NuA4 histone acetyltransferase complex  
## 521 black 2886 6.1e-04 1.0e+00 18 BP oocyte fate determination  
## 522 black 2886 6.5e-04 1.0e+00 33 MF ubiquitin protein ligase activity  
## 523 black 2886 7.2e-04 1.0e+00 16 BP histone H3 acetylation  
## 524 black 2886 7.3e-04 1.0e+00 10 BP regulation of oskar mRNA translation  
## 525 black 2886 7.3e-04 1.0e+00 10 CC cyclin-dependent protein kinase holoenzy  
## 526 black 2886 7.3e-04 1.0e+00 10 CC nuclear euchromatin  
## 527 black 2886 7.3e-04 1.0e+00 10 MF cyclin-dependent protein serine/threonin  
## 528 black 2886 7.5e-04 1.0e+00 460 BP cell differentiation  
## 529 black 2886 7.7e-04 1.0e+00 957 CC cytoplasm  
## 530 black 2886 7.8e-04 1.0e+00 201 BP transcription by RNA polymerase II  
## 531 black 2886 8.3e-04 1.0e+00 17 BP germarium-derived oocyte differentiation  
## 532 black 2886 8.8e-04 1.0e+00 31 BP regulation of RNA splicing  
## 533 black 2886 9.1e-04 1.0e+00 9 CC nuclear chromosome, telomeric region  
## 534 black 2886 9.1e-04 1.0e+00 9 CC RNA polymerase II, core complex  
## 535 black 2886 9.1e-04 1.0e+00 9 CC Ino80 complex  
## 536 black 2886 9.1e-04 1.0e+00 9 MF endodeoxyribonuclease activity, producin  
## 537 black 2886 9.3e-04 1.0e+00 5 BP transcription-dependent tethering of RNA  
## 538 black 2886 9.3e-04 1.0e+00 5 BP spindle assembly involved in female meio  
## 539 black 2886 9.3e-04 1.0e+00 5 BP polarity specification of anterior/poste  
## 540 black 2886 9.3e-04 1.0e+00 5 BP attachment of GPI anchor to protein  
## 541 black 2886 9.3e-04 1.0e+00 5 BP DNA replication, Okazaki fragment proces  
## 542 black 2886 9.3e-04 1.0e+00 5 BP CENP-A containing nucleosome assembly  
## 543 black 2886 9.3e-04 1.0e+00 5 BP kinetochore assembly  
## 544 black 2886 9.3e-04 1.0e+00 5 BP maintenance of protein location in nucle  
## 545 black 2886 9.3e-04 1.0e+00 5 BP nuclear polyadenylation-dependent ncRNA   
## 546 black 2886 9.3e-04 1.0e+00 5 BP protein localization to nuclear envelope  
## 547 black 2886 9.3e-04 1.0e+00 5 BP pre-mRNA cleavage required for polyadeny  
## 548 black 2886 9.3e-04 1.0e+00 5 CC DNA replication factor A complex  
## 549 black 2886 9.3e-04 1.0e+00 5 CC DNA replication factor C complex  
## 550 black 2886 9.3e-04 1.0e+00 5 CC Elg1 RFC-like complex  
## 551 black 2886 9.3e-04 1.0e+00 5 CC box C/D snoRNP complex  
## 552 black 2886 9.3e-04 1.0e+00 5 CC SMN complex  
## 553 black 2886 9.3e-04 1.0e+00 5 CC SMN-Sm protein complex  
## 554 black 2886 9.3e-04 1.0e+00 5 CC Rb-E2F complex  
## 555 black 2886 9.3e-04 1.0e+00 5 CC GPI-anchor transamidase complex  
## 556 black 2886 9.3e-04 1.0e+00 5 CC vitelline envelope  
## 557 black 2886 9.3e-04 1.0e+00 5 CC Lsm1-7-Pat1 complex  
## 558 black 2886 9.3e-04 1.0e+00 5 MF RNA polymerase II core promoter sequence  
## 559 black 2886 9.3e-04 1.0e+00 5 MF DNA topoisomerase activity  
## 560 black 2886 9.3e-04 1.0e+00 5 MF U2 snRNA binding  
## 561 black 2886 9.3e-04 1.0e+00 5 MF 5'-3' DNA helicase activity  
## 562 black 2886 9.4e-04 1.0e+00 136 CC cytoskeleton  
## 563 black 2886 9.8e-04 1.0e+00 62 BP anterior/posterior pattern specification  
## 564 black 2886 9.9e-04 1.0e+00 15 BP pole cell development  
## 565 black 2886 9.9e-04 1.0e+00 15 BP germarium-derived oocyte fate determinat  
## 566 black 2886 9.9e-04 1.0e+00 15 MF endodeoxyribonuclease activity  
## 567 black 2886 1.0e-03 1.0e+00 19 BP phosphatidylinositol biosynthetic proces  
## 568 black 2886 1.1e-03 1.0e+00 129 BP positive regulation of transcription, DN  
## 569 black 2886 1.1e-03 1.0e+00 34 BP regulation of embryonic development  
## 570 black 2886 1.1e-03 1.0e+00 20 BP glycolipid biosynthetic process  
## 571 black 2886 1.1e-03 1.0e+00 8 BP nuclear-transcribed mRNA catabolic proce  
## 572 black 2886 1.1e-03 1.0e+00 8 BP cytoplasmic translational initiation  
## 573 black 2886 1.1e-03 1.0e+00 8 BP attachment of spindle microtubules to ki  
## 574 black 2886 1.1e-03 1.0e+00 8 CC nuclear lamina  
## 575 black 2886 1.1e-03 1.0e+00 8 CC ribonuclease P complex  
## 576 black 2886 1.1e-03 1.0e+00 8 CC meiotic spindle  
## 577 black 2886 1.1e-03 1.0e+00 8 MF ribonuclease P activity  
## 578 black 2886 1.1e-03 1.0e+00 13 BP syncytial blastoderm mitotic cell cycle  
## 579 black 2886 1.1e-03 1.0e+00 32 BP germ-line stem cell population maintenan  
## 580 black 2886 1.1e-03 1.0e+00 11 BP DNA duplex unwinding  
## 581 black 2886 1.2e-03 1.0e+00 64 MF transcription factor binding  
## 582 black 2886 1.2e-03 1.0e+00 28 MF translation factor activity, RNA binding  
## 583 black 2886 1.2e-03 1.0e+00 58 CC cell cortex  
## 584 black 2886 1.3e-03 1.0e+00 7 BP protein deneddylation  
## 585 black 2886 1.3e-03 1.0e+00 7 BP resolution of meiotic recombination inte  
## 586 black 2886 1.3e-03 1.0e+00 7 BP tRNA 5'-leader removal  
## 587 black 2886 1.3e-03 1.0e+00 7 BP pyrimidine ribonucleotide biosynthetic p  
## 588 black 2886 1.3e-03 1.0e+00 7 BP positive regulation of mitotic metaphase  
## 589 black 2886 1.3e-03 1.0e+00 7 BP kinetochore organization  
## 590 black 2886 1.3e-03 1.0e+00 7 CC cytoplasmic exosome (RNase complex)  
## 591 black 2886 1.3e-03 1.0e+00 7 CC transcription export complex  
## 592 black 2886 1.3e-03 1.0e+00 7 CC synaptonemal complex  
## 593 black 2886 1.3e-03 1.0e+00 7 CC COP9 signalosome  
## 594 black 2886 1.3e-03 1.0e+00 7 CC replication fork protection complex  
## 595 black 2886 1.3e-03 1.0e+00 7 CC polytene chromosome, telomeric region  
## 596 black 2886 1.3e-03 1.0e+00 6 BP leading strand elongation  
## 597 black 2886 1.3e-03 1.0e+00 6 BP lagging strand elongation  
## 598 black 2886 1.3e-03 1.0e+00 6 BP transposition, DNA-mediated  
## 599 black 2886 1.3e-03 1.0e+00 6 BP deoxyribonucleotide biosynthetic process  
## 600 black 2886 1.3e-03 1.0e+00 6 BP primary miRNA processing  
## 601 black 2886 1.3e-03 1.0e+00 6 BP septin ring organization  
## 602 black 2886 1.3e-03 1.0e+00 6 BP U4 snRNA 3'-end processing  
## 603 black 2886 1.3e-03 1.0e+00 6 BP positive regulation of methylation-depen  
## 604 black 2886 1.3e-03 1.0e+00 6 CC U4 snRNP  
## 605 black 2886 1.3e-03 1.0e+00 6 CC post-mRNA release spliceosomal complex  
## 606 black 2886 1.3e-03 1.0e+00 6 MF four-way junction DNA binding  
## 607 black 2886 1.3e-03 1.0e+00 17 CC nuclear membrane  
## 608 black 2886 1.3e-03 1.0e+00 17 MF histone methyltransferase activity  
## 609 black 2886 1.4e-03 1.0e+00 136 MF enzyme binding  
## 610 black 2886 1.5e-03 1.0e+00 10 CC polytene chromosome chromocenter  
## 611 black 2886 1.5e-03 1.0e+00 10 MF RNA polymerase III activity  
## 612 black 2886 1.5e-03 1.0e+00 12 BP positive regulation of chromatin silenci  
## 613 black 2886 1.5e-03 1.0e+00 12 BP regulation of DNA-dependent DNA replicat  
## 614 black 2886 1.5e-03 1.0e+00 12 MF Ran GTPase binding  
## 615 black 2886 1.6e-03 1.0e+00 20 MF translation initiation factor activity  
## 616 black 2886 1.6e-03 1.0e+00 67 BP blastoderm segmentation  
## 617 black 2886 1.6e-03 1.0e+00 15 BP regulation of DNA-templated transcriptio  
## 618 black 2886 1.6e-03 1.0e+00 191 BP intracellular transport  
## 619 black 2886 1.7e-03 1.0e+00 73 MF ubiquitin-like protein transferase activ  
## 620 black 2886 1.7e-03 1.0e+00 25 BP regulation of protein serine/threonine k  
## 621 black 2886 1.8e-03 1.0e+00 72 BP embryonic pattern specification  
## 622 black 2886 1.8e-03 1.0e+00 33 MF unfolded protein binding  
## 623 black 2886 1.8e-03 1.0e+00 16 CC spindle pole  
## 624 black 2886 1.8e-03 1.0e+00 38 BP stem cell population maintenance  
## 625 black 2886 1.8e-03 1.0e+00 69 BP spermatogenesis  
## 626 black 2886 2.0e-03 1.0e+00 30 BP protein polyubiquitination  
## 627 black 2886 2.0e-03 1.0e+00 9 MF nuclear localization sequence binding  
## 628 black 2886 2.1e-03 1.0e+00 18 BP nucleus localization  
## 629 black 2886 2.1e-03 1.0e+00 11 MF tRNA methyltransferase activity  
## 630 black 2886 2.1e-03 1.0e+00 27 BP regulation of mRNA splicing, via spliceo  
## 631 black 2886 2.5e-03 1.0e+00 30 BP regulation of mRNA processing  
## 632 black 2886 2.6e-03 1.0e+00 8 BP rRNA transcription  
## 633 black 2886 2.6e-03 1.0e+00 8 CC U2-type prespliceosome  
## 634 black 2886 2.6e-03 1.0e+00 12 BP positive regulation of DNA-templated tra  
## 635 black 2886 2.6e-03 1.0e+00 12 BP female germ-line cyst formation  
## 636 black 2886 2.6e-03 1.0e+00 12 MF exodeoxyribonuclease activity  
## 637 black 2886 2.7e-03 1.0e+00 61 BP mitochondrion organization  
## 638 black 2886 2.7e-03 1.0e+00 16 BP RNA interference  
## 639 black 2886 2.9e-03 1.0e+00 10 CC mitochondrial intermembrane space  
## 640 black 2886 3.1e-03 1.0e+00 20 BP neuroblast division  
## 641 black 2886 3.1e-03 1.0e+00 13 BP regulation of pole plasm oskar mRNA loca  
## 642 black 2886 3.1e-03 1.0e+00 13 BP regulation of G1/S transition of mitotic  
## 643 black 2886 3.3e-03 1.0e+00 7 BP DNA-templated transcription, termination  
## 644 black 2886 3.3e-03 1.0e+00 7 BP DNA replication-independent nucleosome o  
## 645 black 2886 3.3e-03 1.0e+00 7 CC U6 snRNP  
## 646 black 2886 3.3e-03 1.0e+00 7 CC RSC-type complex  
## 647 black 2886 3.3e-03 1.0e+00 7 CC aminoacyl-tRNA synthetase multienzyme co  
## 648 black 2886 3.3e-03 1.0e+00 7 CC histone locus body  
## 649 black 2886 3.4e-03 1.0e+00 68 MF ubiquitin-protein transferase activity  
## 650 black 2886 3.6e-03 1.0e+00 11 BP regulation of translational initiation  
## 651 black 2886 3.6e-03 1.0e+00 11 MF tRNA binding  
## 652 black 2886 3.7e-03 1.0e+00 15 BP nuclear migration  
## 653 black 2886 3.8e-03 1.0e+00 4 BP exonucleolytic trimming to generate matu  
## 654 black 2886 3.8e-03 1.0e+00 4 BP oocyte maturation  
## 655 black 2886 3.8e-03 1.0e+00 4 BP astral microtubule organization  
## 656 black 2886 3.8e-03 1.0e+00 4 BP sperm aster formation  
## 657 black 2886 3.8e-03 1.0e+00 4 BP meiotic DNA double-strand break formatio  
## 658 black 2886 3.8e-03 1.0e+00 4 BP establishment of meiotic spindle localiz  
## 659 black 2886 3.8e-03 1.0e+00 4 BP protein K11-linked ubiquitination  
## 660 black 2886 3.8e-03 1.0e+00 4 BP nuclear retention of pre-mRNA at the sit  
## 661 black 2886 3.8e-03 1.0e+00 4 BP nuclear polyadenylation-dependent rRNA c  
## 662 black 2886 3.8e-03 1.0e+00 4 BP nuclear polyadenylation-dependent tRNA c  
## 663 black 2886 3.8e-03 1.0e+00 4 BP positive regulation of oxidative phospho  
## 664 black 2886 3.8e-03 1.0e+00 4 CC alpha DNA polymerase:primase complex  
## 665 black 2886 3.8e-03 1.0e+00 4 CC epsilon DNA polymerase complex  
## 666 black 2886 3.8e-03 1.0e+00 4 CC cortical microtubule cytoskeleton  
## 667 black 2886 3.8e-03 1.0e+00 4 CC mismatch repair complex  
## 668 black 2886 3.8e-03 1.0e+00 4 CC male germline ring canal  
## 669 black 2886 3.8e-03 1.0e+00 4 CC nuclear pore inner ring  
## 670 black 2886 3.8e-03 1.0e+00 4 MF GPI-anchor transamidase activity  
## 671 black 2886 3.8e-03 1.0e+00 4 MF RNA-DNA hybrid ribonuclease activity  
## 672 black 2886 3.8e-03 1.0e+00 4 MF structural constituent of chorion  
## 673 black 2886 3.8e-03 1.0e+00 4 MF U6 snRNA binding  
## 674 black 2886 3.8e-03 1.0e+00 4 MF U3 snoRNA binding  
## 675 black 2886 3.8e-03 1.0e+00 4 MF ATP-dependent 5'-3' DNA helicase activit  
## 676 black 2886 3.9e-03 1.0e+00 9 BP regulation of DNA repair  
## 677 black 2886 3.9e-03 1.0e+00 9 MF chromatin insulator sequence binding  
## 678 black 2886 4.0e-03 1.0e+00 6 BP meiotic DNA double-strand break processi  
## 679 black 2886 4.0e-03 1.0e+00 6 BP formation of translation preinitiation c  
## 680 black 2886 4.0e-03 1.0e+00 6 BP DNA topological change  
## 681 black 2886 4.0e-03 1.0e+00 6 BP negative regulation of oskar mRNA transl  
## 682 black 2886 4.0e-03 1.0e+00 6 BP male germ-line cyst encapsulation  
## 683 black 2886 4.0e-03 1.0e+00 6 BP positive regulation of cell division  
## 684 black 2886 4.0e-03 1.0e+00 6 BP phosphorylation of RNA polymerase II C-t  
## 685 black 2886 4.0e-03 1.0e+00 6 BP positive regulation of protein localizat  
## 686 black 2886 4.0e-03 1.0e+00 6 CC multimeric ribonuclease P complex  
## 687 black 2886 4.0e-03 1.0e+00 6 MF flap endonuclease activity  
## 688 black 2886 4.1e-03 1.0e+00 18 BP regulation of cell division  
## 689 black 2886 4.2e-03 1.0e+00 19 BP asymmetric neuroblast division  
## 690 black 2886 4.4e-03 1.0e+00 5 BP negative regulation of transposition, DN  
## 691 black 2886 4.4e-03 1.0e+00 5 BP female meiosis II  
## 692 black 2886 4.4e-03 1.0e+00 5 BP positive regulation of transcription of   
## 693 black 2886 4.4e-03 1.0e+00 5 BP polarity specification of dorsal/ventral  
## 694 black 2886 4.4e-03 1.0e+00 5 BP regulation of transposition, RNA-mediate  
## 695 black 2886 4.4e-03 1.0e+00 5 BP tRNA catabolic process  
## 696 black 2886 4.4e-03 1.0e+00 5 BP nucleosome positioning  
## 697 black 2886 4.4e-03 1.0e+00 5 BP snRNA transcription by RNA polymerase II  
## 698 black 2886 4.4e-03 1.0e+00 5 BP exonucleolytic nuclear-transcribed mRNA   
## 699 black 2886 4.4e-03 1.0e+00 5 BP negative regulation of meiotic nuclear d  
## 700 black 2886 4.4e-03 1.0e+00 5 BP positive regulation of translational ini  
## 701 black 2886 4.4e-03 1.0e+00 5 BP replication fork protection  
## 702 black 2886 4.4e-03 1.0e+00 5 BP RNA phosphodiester bond hydrolysis, exon  
## 703 black 2886 4.4e-03 1.0e+00 5 CC ribonuclease MRP complex  
## 704 black 2886 4.4e-03 1.0e+00 5 CC chromosome passenger complex  
## 705 black 2886 4.4e-03 1.0e+00 5 CC septin cytoskeleton  
## 706 black 2886 4.4e-03 1.0e+00 5 CC nuclear pore nuclear basket  
## 707 black 2886 4.4e-03 1.0e+00 5 MF nucleosomal DNA binding  
## 708 black 2886 4.7e-03 1.0e+00 13 BP heterochromatin organization involved in  
## 709 black 2886 4.7e-03 1.0e+00 13 BP regulation of embryonic pattern specific  
## 710 black 2886 5.0e-03 1.0e+00 10 BP pole cell formation  
## 711 black 2886 5.0e-03 1.0e+00 10 BP heterochromatin assembly  
## 712 black 2886 5.0e-03 1.0e+00 10 BP regulation of cytokinesis  
## 713 black 2886 5.0e-03 1.0e+00 10 MF protein transmembrane transporter activi  
## 714 black 2886 5.3e-03 1.0e+00 91 MF sequence-specific double-stranded DNA bi  
## 715 black 2886 5.3e-03 1.0e+00 8 BP exit from mitosis  
## 716 black 2886 5.3e-03 1.0e+00 8 BP regulation of mRNA stability  
## 717 black 2886 5.3e-03 1.0e+00 8 MF aspartic-type endopeptidase activity  
## 718 black 2886 5.4e-03 1.0e+00 36 BP neuroblast proliferation  
## 719 black 2886 5.5e-03 1.0e+00 21 BP negative regulation of translation  
## 720 black 2886 5.5e-03 1.0e+00 21 CC mitochondrial large ribosomal subunit  
## 721 black 2886 5.9e-03 1.0e+00 11 BP germarium-derived female germ-line cyst   
## 722 black 2886 5.9e-03 1.0e+00 11 MF peptide transmembrane transporter activi  
## 723 black 2886 6.0e-03 1.0e+00 55 CC mitochondrial matrix  
## 724 black 2886 6.3e-03 1.0e+00 25 BP regulation of protein catabolic process  
## 725 black 2886 6.6e-03 1.0e+00 12 MF signal sequence binding  
## 726 black 2886 7.0e-03 1.0e+00 9 BP nuclear-transcribed mRNA catabolic proce  
## 727 black 2886 7.0e-03 1.0e+00 9 BP regulation of RNA stability  
## 728 black 2886 7.0e-03 1.0e+00 9 BP positive regulation of mitotic nuclear d  
## 729 black 2886 7.0e-03 1.0e+00 9 MF translation initiation factor binding  
## 730 black 2886 7.0e-03 1.0e+00 9 MF RNA polymerase binding  
## 731 black 2886 7.0e-03 1.0e+00 22 BP somatic stem cell division  
## 732 black 2886 7.1e-03 1.0e+00 13 BP transcription preinitiation complex asse  
## 733 black 2886 7.1e-03 1.0e+00 13 BP regulation of intracellular mRNA localiz  
## 734 black 2886 7.1e-03 1.0e+00 7 BP mitochondrial RNA processing  
## 735 black 2886 7.1e-03 1.0e+00 7 BP postreplication repair  
## 736 black 2886 7.1e-03 1.0e+00 7 BP mitotic sister chromatid cohesion  
## 737 black 2886 7.1e-03 1.0e+00 7 BP regulation of exit from mitosis  
## 738 black 2886 7.1e-03 1.0e+00 7 BP sperm chromatin decondensation  
## 739 black 2886 7.1e-03 1.0e+00 7 BP nucleosome mobilization  
## 740 black 2886 7.1e-03 1.0e+00 7 MF 5'-3' exonuclease activity  
## 741 black 2886 7.2e-03 1.0e+00 21 BP morphogenesis of follicular epithelium  
## 742 black 2886 7.6e-03 1.0e+00 42 MF tubulin binding  
## 743 black 2886 7.7e-03 1.0e+00 16 MF mRNA 3'-UTR binding  
## 744 black 2886 7.8e-03 1.0e+00 33 BP regulation of protein kinase activity  
## 745 black 2886 8.3e-03 1.0e+00 10 BP oocyte microtubule cytoskeleton polariza  
## 746 black 2886 8.3e-03 1.0e+00 10 BP sterol biosynthetic process  
## 747 black 2886 8.8e-03 1.0e+00 81 BP positive regulation of cellular protein   
## 748 black 2886 9.2e-03 1.0e+00 11 BP centrosome separation  
## 749 black 2886 9.2e-03 1.0e+00 11 MF methylated histone binding  
## 750 black 2886 9.3e-03 1.0e+00 21 BP regulation of protein stability  
## 751 black 2886 9.3e-03 1.0e+00 21 BP glycerophospholipid biosynthetic process  
## 752 black 2886 9.5e-03 1.0e+00 6 BP DNA replication-independent nucleosome a  
## 753 black 2886 9.5e-03 1.0e+00 6 BP mitotic G2 DNA damage checkpoint  
## 754 black 2886 9.5e-03 1.0e+00 6 BP synapsis  
## 755 black 2886 9.5e-03 1.0e+00 6 BP regulation of meiotic nuclear division  
## 756 black 2886 9.5e-03 1.0e+00 6 BP nucleolar large rRNA transcription by RN  
## 757 black 2886 9.5e-03 1.0e+00 6 BP positive regulation of nuclear-transcrib  
## 758 black 2886 9.5e-03 1.0e+00 6 CC exocyst  
## 759 black 2886 9.5e-03 1.0e+00 6 MF core promoter sequence-specific DNA bind  
## 760 black 2886 9.7e-03 1.0e+00 8 BP response to X-ray  
## 761 black 2886 9.7e-03 1.0e+00 8 BP regulation of chromatin assembly  
## 762 black 2886 9.7e-03 1.0e+00 8 BP female sex determination  
## 763 black 2886 9.7e-03 1.0e+00 8 BP production of siRNA involved in RNA inte  
## 764 black 2886 9.7e-03 1.0e+00 8 BP oocyte localization involved in germariu  
## 765 black 2886 9.7e-03 1.0e+00 8 BP germline ring canal formation  
## 766 black 2886 9.7e-03 1.0e+00 8 BP negative regulation of chromatin silenci  
## 767 black 2886 9.7e-03 1.0e+00 8 BP regulation of histone acetylation  
## 768 black 2886 9.7e-03 1.0e+00 8 MF P-P-bond-hydrolysis-driven protein trans  
## 769 black 2886 9.9e-03 1.0e+00 12 BP transcription by RNA polymerase III  
## 770 black 2886 9.9e-03 1.0e+00 12 BP microtubule polymerization  
## 771 black 2886 9.9e-03 1.0e+00 25 BP negative regulation of phosphorylation  
## 772 blue 1679 4.1e-32 3.4e-28 261 CC plasma membrane  
## 773 blue 1679 6.2e-32 5.2e-28 161 CC cell projection  
## 774 blue 1679 1.5e-28 1.3e-24 136 CC integral component of plasma membrane  
## 775 blue 1679 3.4e-28 2.9e-24 138 CC intrinsic component of plasma membrane  
## 776 blue 1679 1.9e-27 1.6e-23 122 CC neuron projection  
## 777 blue 1679 4.9e-27 4.1e-23 271 CC cell periphery  
## 778 blue 1679 7.9e-25 6.7e-21 149 BP nervous system process  
## 779 blue 1679 4.1e-24 3.4e-20 265 CC intrinsic component of membrane  
## 780 blue 1679 9.4e-24 7.9e-20 261 CC integral component of membrane  
## 781 blue 1679 3.7e-23 3.1e-19 98 MF transmembrane signaling receptor activit  
## 782 blue 1679 8.9e-23 7.5e-19 111 MF signaling receptor activity  
## 783 blue 1679 1.2e-19 9.8e-16 409 CC membrane  
## 784 blue 1679 7.8e-18 6.6e-14 38 MF neurotransmitter receptor activity  
## 785 blue 1679 1.4e-15 1.2e-11 83 BP chemical synaptic transmission  
## 786 blue 1679 2.2e-15 1.9e-11 83 BP synaptic signaling  
## 787 blue 1679 2.3e-14 2.0e-10 45 MF G protein-coupled receptor activity  
## 788 blue 1679 3.8e-14 3.2e-10 296 BP signaling  
## 789 blue 1679 4.8e-14 4.1e-10 61 MF ion channel activity  
## 790 blue 1679 5.1e-14 4.3e-10 51 MF cation channel activity  
## 791 blue 1679 5.4e-14 4.5e-10 63 MF channel activity  
## 792 blue 1679 7.5e-14 6.3e-10 65 BP G protein-coupled receptor signaling pat  
## 793 blue 1679 9.6e-14 8.0e-10 40 CC transmembrane transporter complex  
## 794 blue 1679 1.2e-13 1.0e-09 77 CC synapse  
## 795 blue 1679 2.2e-13 1.8e-09 298 BP cell communication  
## 796 blue 1679 6.5e-13 5.4e-09 59 BP sensory perception of chemical stimulus  
## 797 blue 1679 6.9e-13 5.8e-09 33 BP regulation of membrane potential  
## 798 blue 1679 2.1e-12 1.8e-08 41 CC cilium  
## 799 blue 1679 3.0e-12 2.5e-08 61 CC axon  
## 800 blue 1679 3.4e-12 2.8e-08 40 CC neuronal cell body  
## 801 blue 1679 5.4e-12 4.5e-08 42 CC cell body  
## 802 blue 1679 7.1e-12 5.9e-08 103 BP ion transport  
## 803 blue 1679 7.1e-11 6.0e-07 16 MF G protein-coupled amine receptor activit  
## 804 blue 1679 7.3e-11 6.2e-07 73 BP cation transport  
## 805 blue 1679 4.9e-10 4.1e-06 73 MF inorganic cation transmembrane transport  
## 806 blue 1679 7.6e-10 6.3e-06 75 MF cation transmembrane transporter activit  
## 807 blue 1679 9.2e-10 7.7e-06 103 BP cell-cell signaling  
## 808 blue 1679 1.3e-09 1.1e-05 63 BP ion transmembrane transport  
## 809 blue 1679 2.7e-09 2.3e-05 28 CC neuron projection membrane  
## 810 blue 1679 4.2e-09 3.5e-05 44 CC dendrite  
## 811 blue 1679 5.9e-09 4.9e-05 241 BP signal transduction  
## 812 blue 1679 1.0e-08 8.4e-05 69 BP synapse organization  
## 813 blue 1679 1.4e-08 1.2e-04 41 BP mating  
## 814 blue 1679 1.9e-08 1.6e-04 92 MF ion transmembrane transporter activity  
## 815 blue 1679 2.7e-08 2.2e-04 22 MF extracellular ligand-gated ion channel a  
## 816 blue 1679 2.8e-08 2.3e-04 49 MF metal ion transmembrane transporter acti  
## 817 blue 1679 2.8e-08 2.4e-04 16 MF voltage-gated cation channel activity  
## 818 blue 1679 2.9e-08 2.4e-04 39 BP mating behavior  
## 819 blue 1679 3.9e-08 3.3e-04 32 BP courtship behavior  
## 820 blue 1679 4.0e-08 3.3e-04 23 CC cation channel complex  
## 821 blue 1679 4.5e-08 3.8e-04 28 BP sensory perception of mechanical stimulu  
## 822 blue 1679 4.9e-08 4.1e-04 9 BP monoamine transport  
## 823 blue 1679 5.2e-08 4.4e-04 42 CC presynapse  
## 824 blue 1679 6.4e-08 5.3e-04 21 BP potassium ion transport  
## 825 blue 1679 7.8e-08 6.6e-04 30 BP male mating behavior  
## 826 blue 1679 1.0e-07 8.6e-04 41 BP reproductive behavior  
## 827 blue 1679 1.4e-07 1.2e-03 77 BP taxis  
## 828 blue 1679 1.5e-07 1.3e-03 28 BP male courtship behavior  
## 829 blue 1679 1.6e-07 1.3e-03 24 BP sensory perception of sound  
## 830 blue 1679 2.3e-07 1.9e-03 18 BP potassium ion transmembrane transport  
## 831 blue 1679 2.5e-07 2.1e-03 27 CC secretory vesicle  
## 832 blue 1679 3.4e-07 2.8e-03 27 MF ligand-gated ion channel activity  
## 833 blue 1679 3.6e-07 3.0e-03 8 BP dopamine transport  
## 834 blue 1679 4.0e-07 3.3e-03 34 BP modulation of chemical synaptic transmis  
## 835 blue 1679 4.7e-07 3.9e-03 21 BP G protein-coupled receptor signaling pat  
## 836 blue 1679 5.5e-07 4.6e-03 17 MF potassium channel activity  
## 837 blue 1679 7.5e-07 6.3e-03 20 BP adenylate cyclase-modulating G protein-c  
## 838 blue 1679 8.2e-07 6.9e-03 22 BP cyclic-nucleotide-mediated signaling  
## 839 blue 1679 1.1e-06 8.8e-03 41 BP learning or memory  
## 840 blue 1679 1.1e-06 9.4e-03 35 BP cell-cell adhesion  
## 841 blue 1679 1.4e-06 1.1e-02 28 BP cilium assembly  
## 842 blue 1679 1.6e-06 1.4e-02 8 CC acetylcholine-gated channel complex  
## 843 blue 1679 1.6e-06 1.4e-02 8 MF acetylcholine-gated cation-selective cha  
## 844 blue 1679 1.7e-06 1.4e-02 29 CC cell leading edge  
## 845 blue 1679 1.9e-06 1.6e-02 42 BP cation transmembrane transport  
## 846 blue 1679 2.1e-06 1.8e-02 30 BP chemosensory behavior  
## 847 blue 1679 2.1e-06 1.8e-02 22 CC synaptic membrane  
## 848 blue 1679 2.6e-06 2.1e-02 24 BP motor neuron axon guidance  
## 849 blue 1679 2.6e-06 2.2e-02 10 BP synaptic transmission, cholinergic  
## 850 blue 1679 3.2e-06 2.7e-02 16 BP drug transport  
## 851 blue 1679 3.3e-06 2.8e-02 43 BP metal ion transport  
## 852 blue 1679 3.6e-06 3.0e-02 45 BP locomotory behavior  
## 853 blue 1679 3.9e-06 3.3e-02 48 BP response to drug  
## 854 blue 1679 4.1e-06 3.4e-02 103 MF transmembrane transporter activity  
## 855 blue 1679 4.4e-06 3.7e-02 13 CC presynaptic active zone  
## 856 blue 1679 5.1e-06 4.2e-02 59 BP axon guidance  
## 857 blue 1679 5.7e-06 4.8e-02 10 BP inter-male aggressive behavior  
## 858 blue 1679 5.8e-06 4.9e-02 114 BP locomotion  
## 859 blue 1679 6.2e-06 5.2e-02 9 CC synaptic vesicle membrane  
## 860 blue 1679 6.4e-06 5.3e-02 35 BP neurotransmitter transport  
## 861 blue 1679 6.4e-06 5.4e-02 17 MF neuropeptide receptor activity  
## 862 blue 1679 6.7e-06 5.7e-02 32 BP synaptic vesicle cycle  
## 863 blue 1679 7.1e-06 6.0e-02 39 BP adult behavior  
## 864 blue 1679 8.4e-06 7.1e-02 21 CC exocytic vesicle  
## 865 blue 1679 8.6e-06 7.2e-02 85 BP cell morphogenesis involved in neuron di  
## 866 blue 1679 8.6e-06 7.2e-02 28 BP cilium organization  
## 867 blue 1679 1.1e-05 9.1e-02 7 MF G protein-coupled serotonin receptor act  
## 868 blue 1679 1.3e-05 1.1e-01 17 BP circadian sleep/wake cycle  
## 869 blue 1679 1.3e-05 1.1e-01 17 MF G protein-coupled peptide receptor activ  
## 870 blue 1679 1.3e-05 1.1e-01 128 BP neuron differentiation  
## 871 blue 1679 1.4e-05 1.2e-01 9 CC exocytic vesicle membrane  
## 872 blue 1679 1.4e-05 1.2e-01 8 CC voltage-gated potassium channel complex  
## 873 blue 1679 1.4e-05 1.2e-01 8 MF calcium-dependent phospholipid binding  
## 874 blue 1679 1.5e-05 1.3e-01 18 MF peptide receptor activity  
## 875 blue 1679 1.5e-05 1.3e-01 46 BP cell adhesion  
## 876 blue 1679 1.6e-05 1.3e-01 85 BP neuron projection morphogenesis  
## 877 blue 1679 1.8e-05 1.5e-01 14 BP adenylate cyclase-activating G protein-c  
## 878 blue 1679 1.8e-05 1.5e-01 35 BP monovalent inorganic cation transport  
## 879 blue 1679 2.0e-05 1.6e-01 6 BP regulation of dopamine secretion  
## 880 blue 1679 2.1e-05 1.8e-01 109 BP neuron development  
## 881 blue 1679 2.2e-05 1.9e-01 36 BP inorganic cation transmembrane transport  
## 882 blue 1679 2.6e-05 2.2e-01 5 MF monoamine transmembrane transporter acti  
## 883 blue 1679 2.6e-05 2.2e-01 5 MF sodium channel regulator activity  
## 884 blue 1679 2.6e-05 2.2e-01 36 BP circadian rhythm  
## 885 blue 1679 2.8e-05 2.4e-01 12 BP heterophilic cell-cell adhesion via plas  
## 886 blue 1679 3.1e-05 2.6e-01 88 BP neuron projection development  
## 887 blue 1679 3.3e-05 2.8e-01 8 CC potassium channel complex  
## 888 blue 1679 3.8e-05 3.2e-01 10 BP aggressive behavior  
## 889 blue 1679 3.9e-05 3.3e-01 19 CC synaptic vesicle  
## 890 blue 1679 4.0e-05 3.4e-01 89 BP cell morphogenesis involved in different  
## 891 blue 1679 4.1e-05 3.4e-01 172 BP nervous system development  
## 892 blue 1679 4.6e-05 3.8e-01 24 CC transport vesicle  
## 893 blue 1679 5.1e-05 4.3e-01 20 BP calcium ion regulated exocytosis  
## 894 blue 1679 5.3e-05 4.5e-01 9 MF voltage-gated potassium channel activity  
## 895 blue 1679 5.3e-05 4.5e-01 67 BP axon development  
## 896 blue 1679 5.4e-05 4.5e-01 65 BP axonogenesis  
## 897 blue 1679 5.5e-05 4.6e-01 29 BP neuron recognition  
## 898 blue 1679 5.5e-05 4.6e-01 27 BP sensory perception of smell  
## 899 blue 1679 5.6e-05 4.7e-01 24 BP adult locomotory behavior  
## 900 blue 1679 5.6e-05 4.7e-01 24 MF sodium ion transmembrane transporter act  
## 901 blue 1679 6.1e-05 5.1e-01 92 BP transmembrane transport  
## 902 blue 1679 6.5e-05 5.5e-01 10 MF channel regulator activity  
## 903 blue 1679 7.3e-05 6.2e-01 23 BP regulation of secretion  
## 904 blue 1679 8.3e-05 6.9e-01 20 BP regulated exocytosis  
## 905 blue 1679 8.3e-05 7.0e-01 110 MF transporter activity  
## 906 blue 1679 9.0e-05 7.5e-01 13 MF chloride transmembrane transporter activ  
## 907 blue 1679 9.0e-05 7.5e-01 15 BP cAMP-mediated signaling  
## 908 blue 1679 9.0e-05 7.6e-01 23 BP regulation of circadian rhythm  
## 909 blue 1679 9.5e-05 7.9e-01 27 BP circadian behavior  
## 910 blue 1679 9.9e-05 8.3e-01 16 BP synaptic target recognition  
## 911 blue 1679 1.1e-04 8.9e-01 10 BP cilium movement  
## 912 blue 1679 1.3e-04 1.0e+00 27 BP rhythmic behavior  
## 913 blue 1679 1.4e-04 1.0e+00 5 BP cellular response to calcium ion  
## 914 blue 1679 1.4e-04 1.0e+00 5 MF octopamine receptor activity  
## 915 blue 1679 1.4e-04 1.0e+00 5 MF sodium:chloride symporter activity  
## 916 blue 1679 1.6e-04 1.0e+00 15 CC postsynaptic membrane  
## 917 blue 1679 1.6e-04 1.0e+00 25 BP exocytosis  
## 918 blue 1679 1.7e-04 1.0e+00 98 BP cell morphogenesis  
## 919 blue 1679 1.7e-04 1.0e+00 16 BP calcium ion homeostasis  
## 920 blue 1679 1.7e-04 1.0e+00 7 BP phospholipase C-activating G protein-cou  
## 921 blue 1679 1.8e-04 1.0e+00 13 BP response to mechanical stimulus  
## 922 blue 1679 1.8e-04 1.0e+00 13 MF neurotransmitter transporter activity  
## 923 blue 1679 1.9e-04 1.0e+00 21 BP sleep  
## 924 blue 1679 1.9e-04 1.0e+00 6 MF phosphatidylserine binding  
## 925 blue 1679 2.0e-04 1.0e+00 23 BP regulation of behavior  
## 926 blue 1679 2.0e-04 1.0e+00 14 BP regulation of circadian sleep/wake cycle  
## 927 blue 1679 2.1e-04 1.0e+00 22 BP synaptic vesicle transport  
## 928 blue 1679 2.1e-04 1.0e+00 4 MF dopamine neurotransmitter receptor activ  
## 929 blue 1679 2.1e-04 1.0e+00 15 BP homophilic cell adhesion via plasma memb  
## 930 blue 1679 2.2e-04 1.0e+00 141 BP neurogenesis  
## 931 blue 1679 2.3e-04 1.0e+00 21 BP neuromuscular synaptic transmission  
## 932 blue 1679 2.4e-04 1.0e+00 11 CC axoneme  
## 933 blue 1679 2.4e-04 1.0e+00 13 BP circadian sleep/wake cycle, sleep  
## 934 blue 1679 2.6e-04 1.0e+00 19 BP learning  
## 935 blue 1679 2.6e-04 1.0e+00 9 BP response to carbon dioxide  
## 936 blue 1679 2.7e-04 1.0e+00 18 BP synaptic vesicle exocytosis  
## 937 blue 1679 3.0e-04 1.0e+00 20 BP cell-cell junction organization  
## 938 blue 1679 3.1e-04 1.0e+00 22 BP synaptic vesicle localization  
## 939 blue 1679 3.1e-04 1.0e+00 37 MF calcium ion binding  
## 940 blue 1679 3.7e-04 1.0e+00 34 BP cell projection assembly  
## 941 blue 1679 3.7e-04 1.0e+00 32 BP response to light stimulus  
## 942 blue 1679 4.0e-04 1.0e+00 12 BP regulation of circadian sleep/wake cycle  
## 943 blue 1679 4.1e-04 1.0e+00 9 CC ciliary basal body  
## 944 blue 1679 4.4e-04 1.0e+00 5 BP neurotransmitter loading into synaptic v  
## 945 blue 1679 4.4e-04 1.0e+00 5 MF acetylcholine receptor activity  
## 946 blue 1679 4.6e-04 1.0e+00 16 BP neuropeptide signaling pathway  
## 947 blue 1679 4.7e-04 1.0e+00 27 BP memory  
## 948 blue 1679 4.9e-04 1.0e+00 30 BP ion homeostasis  
## 949 blue 1679 5.0e-04 1.0e+00 24 BP neurotransmitter secretion  
## 950 blue 1679 5.5e-04 1.0e+00 133 BP generation of neurons  
## 951 blue 1679 5.9e-04 1.0e+00 14 BP olfactory learning  
## 952 blue 1679 5.9e-04 1.0e+00 14 CC septate junction  
## 953 blue 1679 5.9e-04 1.0e+00 7 MF ATP-dependent microtubule motor activity  
## 954 blue 1679 6.4e-04 1.0e+00 20 BP cellular metal ion homeostasis  
## 955 blue 1679 6.6e-04 1.0e+00 11 BP calcium ion transmembrane transport  
## 956 blue 1679 7.1e-04 1.0e+00 16 BP phototransduction  
## 957 blue 1679 7.1e-04 1.0e+00 16 BP associative learning  
## 958 blue 1679 8.4e-04 1.0e+00 6 MF ammonium transmembrane transporter activ  
## 959 blue 1679 9.1e-04 1.0e+00 9 BP male courtship behavior, veined wing vib  
## 960 blue 1679 9.1e-04 1.0e+00 9 BP response to insecticide  
## 961 blue 1679 9.2e-04 1.0e+00 24 BP detection of stimulus involved in sensor  
## 962 blue 1679 9.2e-04 1.0e+00 18 CC postsynapse  
## 963 blue 1679 9.5e-04 1.0e+00 28 BP cation homeostasis  
## 964 blue 1679 9.7e-04 1.0e+00 4 BP cellular sodium ion homeostasis  
## 965 blue 1679 9.7e-04 1.0e+00 4 BP serotonin receptor signaling pathway  
## 966 blue 1679 9.7e-04 1.0e+00 4 BP cellular potassium ion homeostasis  
## 967 blue 1679 9.7e-04 1.0e+00 4 BP sodium ion export across plasma membrane  
## 968 blue 1679 9.7e-04 1.0e+00 4 BP cellular response to glucose starvation  
## 969 blue 1679 9.7e-04 1.0e+00 4 BP regulation of presynaptic cytosolic calc  
## 970 blue 1679 9.7e-04 1.0e+00 4 CC sodium:potassium-exchanging ATPase compl  
## 971 blue 1679 9.7e-04 1.0e+00 4 MF delayed rectifier potassium channel acti  
## 972 blue 1679 9.7e-04 1.0e+00 4 MF sodium:potassium-exchanging ATPase activ  
## 973 blue 1679 9.7e-04 1.0e+00 13 BP response to anesthetic  
## 974 blue 1679 9.9e-04 1.0e+00 8 BP negative regulation of synaptic transmis  
## 975 blue 1679 9.9e-04 1.0e+00 8 CC secretory granule  
## 976 blue 1679 1.0e-03 1.0e+00 7 BP sodium ion transmembrane transport  
## 977 blue 1679 1.1e-03 1.0e+00 5 CC cytoskeleton of presynaptic active zone  
## 978 blue 1679 1.1e-03 1.0e+00 5 MF adrenergic receptor activity  
## 979 blue 1679 1.1e-03 1.0e+00 24 BP metal ion homeostasis  
## 980 blue 1679 1.1e-03 1.0e+00 18 BP cell-cell junction assembly  
## 981 blue 1679 1.2e-03 1.0e+00 15 BP sodium ion transport  
## 982 blue 1679 1.2e-03 1.0e+00 14 BP cellular calcium ion homeostasis  
## 983 blue 1679 1.3e-03 1.0e+00 20 CC receptor complex  
## 984 blue 1679 1.3e-03 1.0e+00 9 BP male courtship behavior, veined wing ext  
## 985 blue 1679 1.5e-03 1.0e+00 8 BP sensory perception of bitter taste  
## 986 blue 1679 1.5e-03 1.0e+00 10 BP neuron cellular homeostasis  
## 987 blue 1679 1.5e-03 1.0e+00 10 CC dynein complex  
## 988 blue 1679 1.6e-03 1.0e+00 45 BP regulation of transport  
## 989 blue 1679 1.6e-03 1.0e+00 11 CC plasma membrane bounded cell projection   
## 990 blue 1679 1.6e-03 1.0e+00 7 BP presynaptic active zone organization  
## 991 blue 1679 1.6e-03 1.0e+00 12 BP sensory perception of taste  
## 992 blue 1679 1.8e-03 1.0e+00 3 BP peptide amidation  
## 993 blue 1679 1.8e-03 1.0e+00 3 BP cellular response to dopamine  
## 994 blue 1679 1.8e-03 1.0e+00 3 MF dopamine neurotransmitter receptor activ  
## 995 blue 1679 1.8e-03 1.0e+00 3 MF peptidylamidoglycolate lyase activity  
## 996 blue 1679 1.8e-03 1.0e+00 3 MF serotonin:sodium symporter activity  
## 997 blue 1679 1.8e-03 1.0e+00 9 BP cyclic nucleotide metabolic process  
## 998 blue 1679 1.8e-03 1.0e+00 9 BP regulation of cytosolic calcium ion conc  
## 999 blue 1679 1.9e-03 1.0e+00 23 BP cellular ion homeostasis  
## 1000 blue 1679 2.0e-03 1.0e+00 19 BP olfactory behavior  
## 1001 blue 1679 2.0e-03 1.0e+00 12 BP amino acid transmembrane transport  
## 1002 blue 1679 2.1e-03 1.0e+00 11 BP larval locomotory behavior  
## 1003 blue 1679 2.1e-03 1.0e+00 17 BP eye-antennal disc development  
## 1004 blue 1679 2.1e-03 1.0e+00 5 BP regulation of sodium ion transport  
## 1005 blue 1679 2.1e-03 1.0e+00 5 BP potassium ion homeostasis  
## 1006 blue 1679 2.1e-03 1.0e+00 5 CC presynaptic active zone cytoplasmic comp  
## 1007 blue 1679 2.1e-03 1.0e+00 5 MF voltage-gated calcium channel activity  
## 1008 blue 1679 2.2e-03 1.0e+00 28 BP microtubule-based movement  
## 1009 blue 1679 2.2e-03 1.0e+00 28 BP signal release  
## 1010 blue 1679 2.3e-03 1.0e+00 14 BP larval behavior  
## 1011 blue 1679 2.5e-03 1.0e+00 9 BP antennal development  
## 1012 blue 1679 2.5e-03 1.0e+00 9 CC growth cone  
## 1013 blue 1679 2.5e-03 1.0e+00 9 MF taste receptor activity  
## 1014 blue 1679 2.5e-03 1.0e+00 6 BP anesthesia-resistant memory  
## 1015 blue 1679 2.5e-03 1.0e+00 6 BP mechanosensory behavior  
## 1016 blue 1679 2.5e-03 1.0e+00 6 BP regulation of response to drug  
## 1017 blue 1679 2.5e-03 1.0e+00 6 CC axonemal dynein complex  
## 1018 blue 1679 2.6e-03 1.0e+00 4 CC nucleotide-activated protein kinase comp  
## 1019 blue 1679 2.6e-03 1.0e+00 4 CC BBSome  
## 1020 blue 1679 2.6e-03 1.0e+00 4 MF oxidoreductase activity, acting on paire  
## 1021 blue 1679 2.6e-03 1.0e+00 10 MF glutamate receptor activity  
## 1022 blue 1679 2.8e-03 1.0e+00 14 MF microtubule motor activity  
## 1023 blue 1679 2.9e-03 1.0e+00 17 MF motor activity  
## 1024 blue 1679 3.0e-03 1.0e+00 8 BP male courtship behavior, veined wing gen  
## 1025 blue 1679 3.1e-03 1.0e+00 18 CC neuron projection terminus  
## 1026 blue 1679 3.2e-03 1.0e+00 40 BP secretion by cell  
## 1027 blue 1679 3.2e-03 1.0e+00 12 MF calcium channel activity  
## 1028 blue 1679 3.6e-03 1.0e+00 18 MF odorant binding  
## 1029 blue 1679 3.7e-03 1.0e+00 13 BP amino acid transport  
## 1030 blue 1679 3.8e-03 1.0e+00 5 BP calcium ion import  
## 1031 blue 1679 3.8e-03 1.0e+00 5 BP potassium ion import across plasma membr  
## 1032 blue 1679 3.8e-03 1.0e+00 5 MF cell-cell adhesion mediator activity  
## 1033 blue 1679 3.9e-03 1.0e+00 6 CC ciliary transition zone  
## 1034 blue 1679 4.1e-03 1.0e+00 8 BP synaptic transmission, glutamatergic  
## 1035 blue 1679 4.4e-03 1.0e+00 15 BP apical junction assembly  
## 1036 blue 1679 4.4e-03 1.0e+00 10 MF drug transmembrane transporter activity  
## 1037 blue 1679 4.4e-03 1.0e+00 9 MF ionotropic glutamate receptor activity  
## 1038 blue 1679 4.5e-03 1.0e+00 13 BP septate junction assembly  
## 1039 blue 1679 4.7e-03 1.0e+00 17 BP detection of chemical stimulus involved   
## 1040 blue 1679 4.9e-03 1.0e+00 12 MF SNARE binding  
## 1041 blue 1679 5.0e-03 1.0e+00 7 BP dendrite self-avoidance  
## 1042 blue 1679 5.1e-03 1.0e+00 15 CC cytoplasmic vesicle membrane  
## 1043 blue 1679 5.1e-03 1.0e+00 23 CC cell-cell junction  
## 1044 blue 1679 5.3e-03 1.0e+00 11 BP detection of visible light  
## 1045 blue 1679 5.3e-03 1.0e+00 22 CC microtubule associated complex  
## 1046 blue 1679 5.3e-03 1.0e+00 16 CC vesicle membrane  
## 1047 blue 1679 5.4e-03 1.0e+00 13 BP detection of chemical stimulus involved   
## 1048 blue 1679 5.5e-03 1.0e+00 4 BP camera-type eye development  
## 1049 blue 1679 5.5e-03 1.0e+00 4 BP adenylate cyclase-activating adrenergic   
## 1050 blue 1679 5.5e-03 1.0e+00 4 BP postsynaptic membrane assembly  
## 1051 blue 1679 5.5e-03 1.0e+00 4 CC voltage-gated calcium channel complex  
## 1052 blue 1679 5.5e-03 1.0e+00 4 CC integral component of synaptic vesicle m  
## 1053 blue 1679 5.5e-03 1.0e+00 4 CC outer dynein arm  
## 1054 blue 1679 5.6e-03 1.0e+00 8 BP visual behavior  
## 1055 blue 1679 5.8e-03 1.0e+00 37 BP cellular homeostasis  
## 1056 blue 1679 5.8e-03 1.0e+00 14 BP calcium ion transport  
## 1057 blue 1679 5.9e-03 1.0e+00 6 BP adult walking behavior  
## 1058 blue 1679 5.9e-03 1.0e+00 6 BP positive regulation of circadian sleep/w  
## 1059 blue 1679 6.3e-03 1.0e+00 34 BP response to radiation  
## 1060 blue 1679 6.3e-03 1.0e+00 17 CC axon terminus  
## 1061 blue 1679 6.4e-03 1.0e+00 5 BP adenylate cyclase-inhibiting G protein-c  
## 1062 blue 1679 6.4e-03 1.0e+00 5 BP adult feeding behavior  
## 1063 blue 1679 6.4e-03 1.0e+00 5 BP presynaptic membrane organization  
## 1064 blue 1679 6.4e-03 1.0e+00 5 BP response to odorant  
## 1065 blue 1679 6.4e-03 1.0e+00 32 CC extracellular matrix  
## 1066 blue 1679 6.4e-03 1.0e+00 3 BP glial cell apoptotic process  
## 1067 blue 1679 6.4e-03 1.0e+00 3 CC intracellular cyclic nucleotide activate  
## 1068 blue 1679 6.4e-03 1.0e+00 3 CC neuronal cell body membrane  
## 1069 blue 1679 6.4e-03 1.0e+00 3 MF intracellular cyclic nucleotide activate  
## 1070 blue 1679 6.5e-03 1.0e+00 13 MF amino acid transmembrane transporter act  
## 1071 blue 1679 7.0e-03 1.0e+00 7 BP cyclic nucleotide biosynthetic process  
## 1072 blue 1679 7.0e-03 1.0e+00 7 BP neurotransmitter biosynthetic process  
## 1073 blue 1679 7.0e-03 1.0e+00 7 BP positive regulation of circadian rhythm  
## 1074 blue 1679 7.3e-03 1.0e+00 9 BP photoreceptor cell axon guidance  
## 1075 blue 1679 7.3e-03 1.0e+00 8 MF neurotransmitter:sodium symporter activi  
## 1076 blue 1679 7.7e-03 1.0e+00 32 BP regulation of synapse structure or activ  
## 1077 blue 1679 8.3e-03 1.0e+00 16 CC apical junction complex  
## 1078 blue 1679 8.5e-03 1.0e+00 6 MF dynein light chain binding  
## 1079 blue 1679 8.6e-03 1.0e+00 12 BP protein complex oligomerization  
## 1080 blue 1679 8.9e-03 1.0e+00 97 BP intracellular signal transduction  
## 1081 blue 1679 9.8e-03 1.0e+00 5 CC calcium channel complex  
## 1082 blue 1679 9.8e-03 1.0e+00 5 MF guanylate cyclase activity  
## 1083 brown 1042 8.8e-39 7.4e-35 85 MF serine-type peptidase activity  
## 1084 brown 1042 1.3e-38 1.1e-34 85 MF serine hydrolase activity  
## 1085 brown 1042 1.5e-34 1.2e-30 76 MF serine-type endopeptidase activity  
## 1086 brown 1042 3.7e-32 3.1e-28 119 MF peptidase activity  
## 1087 brown 1042 3.5e-24 3.0e-20 86 MF endopeptidase activity  
## 1088 brown 1042 1.3e-21 1.1e-17 228 MF hydrolase activity  
## 1089 brown 1042 9.4e-19 7.9e-15 133 BP proteolysis  
## 1090 brown 1042 1.3e-14 1.1e-10 32 MF exopeptidase activity  
## 1091 brown 1042 2.3e-14 2.0e-10 34 BP chitin metabolic process  
## 1092 brown 1042 1.3e-13 1.1e-09 34 MF chitin binding  
## 1093 brown 1042 1.1e-10 9.3e-07 370 MF catalytic activity  
## 1094 brown 1042 1.8e-10 1.5e-06 15 MF carboxypeptidase activity  
## 1095 brown 1042 5.2e-09 4.4e-05 22 BP fatty acid biosynthetic process  
## 1096 brown 1042 6.2e-09 5.2e-05 18 MF metalloexopeptidase activity  
## 1097 brown 1042 6.8e-09 5.7e-05 10 MF alkaline phosphatase activity  
## 1098 brown 1042 1.9e-08 1.6e-04 7 MF phospholipase A1 activity  
## 1099 brown 1042 2.0e-08 1.7e-04 113 CC extracellular region  
## 1100 brown 1042 1.2e-07 9.8e-04 75 BP transmembrane transport  
## 1101 brown 1042 4.2e-07 3.5e-03 27 BP fatty acid metabolic process  
## 1102 brown 1042 4.5e-07 3.8e-03 22 MF proton transmembrane transporter activit  
## 1103 brown 1042 1.3e-06 1.1e-02 15 MF aminopeptidase activity  
## 1104 brown 1042 1.4e-06 1.2e-02 10 MF metallocarboxypeptidase activity  
## 1105 brown 1042 2.4e-06 2.0e-02 10 MF fatty acid synthase activity  
## 1106 brown 1042 2.4e-06 2.0e-02 10 MF solute:proton symporter activity  
## 1107 brown 1042 3.1e-06 2.6e-02 5 MF serine-type carboxypeptidase activity  
## 1108 brown 1042 5.7e-06 4.8e-02 8 CC plasma membrane proton-transporting V-ty  
## 1109 brown 1042 6.4e-06 5.3e-02 10 CC proton-transporting V-type ATPase comple  
## 1110 brown 1042 6.4e-06 5.3e-02 10 MF proton-transporting ATPase activity, rot  
## 1111 brown 1042 8.7e-06 7.3e-02 9 BP very long-chain fatty acid biosynthetic   
## 1112 brown 1042 9.2e-06 7.7e-02 25 MF metallopeptidase activity  
## 1113 brown 1042 1.4e-05 1.2e-01 9 BP fatty acid elongation  
## 1114 brown 1042 1.5e-05 1.2e-01 35 MF active transmembrane transporter activit  
## 1115 brown 1042 1.5e-05 1.2e-01 10 BP ATP hydrolysis coupled proton transport  
## 1116 brown 1042 1.7e-05 1.4e-01 5 MF serine-type exopeptidase activity  
## 1117 brown 1042 1.9e-05 1.6e-01 8 BP fatty acid elongation, saturated fatty a  
## 1118 brown 1042 1.9e-05 1.6e-01 8 BP fatty acid elongation, unsaturated fatty  
## 1119 brown 1042 1.9e-05 1.6e-01 8 BP fatty acid elongation, monounsaturated f  
## 1120 brown 1042 1.9e-05 1.6e-01 8 BP fatty acid elongation, polyunsaturated f  
## 1121 brown 1042 1.9e-05 1.6e-01 8 MF carbohydrate:proton symporter activity  
## 1122 brown 1042 1.9e-05 1.6e-01 22 MF carbohydrate binding  
## 1123 brown 1042 2.9e-05 2.4e-01 71 MF transmembrane transporter activity  
## 1124 brown 1042 2.9e-05 2.4e-01 12 BP sphingolipid biosynthetic process  
## 1125 brown 1042 3.2e-05 2.6e-01 8 MF fatty acid elongase activity  
## 1126 brown 1042 3.4e-05 2.9e-01 9 BP peptide catabolic process  
## 1127 brown 1042 3.4e-05 2.9e-01 14 CC vacuolar membrane  
## 1128 brown 1042 3.8e-05 3.2e-01 6 BP somitogenesis  
## 1129 brown 1042 3.8e-05 3.2e-01 6 MF maltose alpha-glucosidase activity  
## 1130 brown 1042 3.8e-05 3.2e-01 33 MF transferase activity, transferring acyl   
## 1131 brown 1042 4.8e-05 4.0e-01 61 BP lipid metabolic process  
## 1132 brown 1042 4.9e-05 4.1e-01 34 BP lipid biosynthetic process  
## 1133 brown 1042 5.1e-05 4.3e-01 8 MF metalloaminopeptidase activity  
## 1134 brown 1042 5.1e-05 4.3e-01 9 MF fatty acid ligase activity  
## 1135 brown 1042 5.1e-05 4.3e-01 9 MF CoA-ligase activity  
## 1136 brown 1042 5.4e-05 4.6e-01 14 BP sphingolipid metabolic process  
## 1137 brown 1042 6.9e-05 5.8e-01 7 CC vacuolar proton-transporting V-type ATPa  
## 1138 brown 1042 1.1e-04 9.5e-01 59 CC extracellular space  
## 1139 brown 1042 1.3e-04 1.0e+00 14 MF hydrolase activity, acting on carbon-nit  
## 1140 brown 1042 1.5e-04 1.0e+00 9 MF phospholipase activity  
## 1141 brown 1042 1.5e-04 1.0e+00 19 CC peroxisome  
## 1142 brown 1042 1.8e-04 1.0e+00 7 MF dipeptidyl-peptidase activity  
## 1143 brown 1042 1.9e-04 1.0e+00 14 MF lipase activity  
## 1144 brown 1042 2.0e-04 1.0e+00 23 CC vacuole  
## 1145 brown 1042 2.2e-04 1.0e+00 17 MF hydrolase activity, hydrolyzing O-glycos  
## 1146 brown 1042 3.0e-04 1.0e+00 17 MF hydrolase activity, acting on carbon-nit  
## 1147 brown 1042 3.0e-04 1.0e+00 29 MF transferase activity, transferring acyl   
## 1148 brown 1042 3.6e-04 1.0e+00 15 CC cell surface  
## 1149 brown 1042 4.6e-04 1.0e+00 18 BP cell fate specification  
## 1150 brown 1042 5.1e-04 1.0e+00 4 MF aminoacylase activity  
## 1151 brown 1042 5.5e-04 1.0e+00 5 CC vacuolar proton-transporting V-type ATPa  
## 1152 brown 1042 5.9e-04 1.0e+00 11 MF ATPase coupled ion transmembrane transpo  
## 1153 brown 1042 5.9e-04 1.0e+00 74 MF transporter activity  
## 1154 brown 1042 6.0e-04 1.0e+00 17 MF hydrolase activity, acting on glycosyl b  
## 1155 brown 1042 7.4e-04 1.0e+00 53 MF ion transmembrane transporter activity  
## 1156 brown 1042 9.4e-04 1.0e+00 5 CC proton-transporting V-type ATPase, V0 do  
## 1157 brown 1042 9.6e-04 1.0e+00 6 BP wax biosynthetic process  
## 1158 brown 1042 9.6e-04 1.0e+00 6 MF fatty-acyl-CoA reductase (alcohol-formin  
## 1159 brown 1042 1.2e-03 1.0e+00 18 BP lipid catabolic process  
## 1160 brown 1042 1.4e-03 1.0e+00 6 BP long-chain fatty-acyl-CoA metabolic proc  
## 1161 brown 1042 1.5e-03 1.0e+00 5 MF galactose binding  
## 1162 brown 1042 1.7e-03 1.0e+00 14 BP membrane lipid biosynthetic process  
## 1163 brown 1042 1.9e-03 1.0e+00 10 BP neuroblast differentiation  
## 1164 brown 1042 1.9e-03 1.0e+00 12 MF symporter activity  
## 1165 brown 1042 2.1e-03 1.0e+00 4 CC vacuolar proton-transporting V-type ATPa  
## 1166 brown 1042 2.1e-03 1.0e+00 16 BP membrane lipid metabolic process  
## 1167 brown 1042 2.3e-03 1.0e+00 8 BP stem cell fate determination  
## 1168 brown 1042 2.8e-03 1.0e+00 9 BP acyl-CoA metabolic process  
## 1169 brown 1042 3.3e-03 1.0e+00 7 BP neuroblast fate determination  
## 1170 brown 1042 3.3e-03 1.0e+00 5 MF alpha-mannosidase activity  
## 1171 brown 1042 3.5e-03 1.0e+00 4 BP mannose metabolic process  
## 1172 brown 1042 3.5e-03 1.0e+00 4 BP Malpighian tubule tip cell differentiati  
## 1173 brown 1042 3.5e-03 1.0e+00 4 MF secondary active sulfate transmembrane t  
## 1174 brown 1042 3.6e-03 1.0e+00 44 BP cellular lipid metabolic process  
## 1175 brown 1042 4.2e-03 1.0e+00 14 MF carboxylic ester hydrolase activity  
## 1176 brown 1042 4.4e-03 1.0e+00 3 BP cuticle hydrocarbon biosynthetic process  
## 1177 brown 1042 4.4e-03 1.0e+00 3 BP sex determination, establishment of X:A   
## 1178 brown 1042 4.7e-03 1.0e+00 5 MF mannosidase activity  
## 1179 brown 1042 5.5e-03 1.0e+00 4 CC proton-transporting V-type ATPase, V1 do  
## 1180 brown 1042 5.5e-03 1.0e+00 4 MF single-stranded DNA endodeoxyribonucleas  
## 1181 brown 1042 5.8e-03 1.0e+00 37 MF cation transmembrane transporter activit  
## 1182 brown 1042 6.0e-03 1.0e+00 6 BP regulation of intracellular pH  
## 1183 brown 1042 6.1e-03 1.0e+00 8 BP cell fate commitment involved in pattern  
## 1184 brown 1042 6.2e-03 1.0e+00 2 BP sphingomyelin catabolic process  
## 1185 brown 1042 6.2e-03 1.0e+00 2 BP mitochondrial proton-transporting ATP sy  
## 1186 brown 1042 6.2e-03 1.0e+00 2 BP induction of bacterial agglutination  
## 1187 brown 1042 6.2e-03 1.0e+00 2 BP smooth septate junction assembly  
## 1188 brown 1042 6.2e-03 1.0e+00 2 MF strictosidine synthase activity  
## 1189 brown 1042 6.2e-03 1.0e+00 2 MF acid sphingomyelin phosphodiesterase act  
## 1190 brown 1042 6.8e-03 1.0e+00 10 BP proton transmembrane transport  
## 1191 brown 1042 7.5e-03 1.0e+00 6 BP sensory organ precursor cell fate determ  
## 1192 brown 1042 7.5e-03 1.0e+00 6 BP regulation of cellular pH  
## 1193 brown 1042 7.6e-03 1.0e+00 7 BP neuroblast fate commitment  
## 1194 brown 1042 7.7e-03 1.0e+00 21 BP sulfur compound metabolic process  
## 1195 brown 1042 8.1e-03 1.0e+00 35 MF inorganic cation transmembrane transport  
## 1196 brown 1042 8.2e-03 1.0e+00 4 BP sulfate transport  
## 1197 brown 1042 8.2e-03 1.0e+00 4 BP sphingolipid catabolic process  
## 1198 brown 1042 8.2e-03 1.0e+00 4 MF sulfate transmembrane transporter activi  
## 1199 cyan 391 1.0e-08 8.6e-05 9 MF proton-transporting ATPase activity, rot  
## 1200 cyan 391 7.8e-08 6.5e-04 7 CC plasma membrane proton-transporting V-ty  
## 1201 cyan 391 2.0e-07 1.7e-03 8 CC proton-transporting V-type ATPase comple  
## 1202 cyan 391 4.1e-07 3.4e-03 8 BP ATP hydrolysis coupled proton transport  
## 1203 cyan 391 4.2e-07 3.5e-03 10 MF ATPase coupled ion transmembrane transpo  
## 1204 cyan 391 5.8e-07 4.8e-03 36 BP transmembrane transport  
## 1205 cyan 391 9.7e-07 8.1e-03 17 BP inorganic cation transmembrane transport  
## 1206 cyan 391 1.1e-06 9.5e-03 14 MF chitin binding  
## 1207 cyan 391 1.7e-06 1.5e-02 10 BP proton transmembrane transport  
## 1208 cyan 391 3.6e-06 3.0e-02 13 BP chitin metabolic process  
## 1209 cyan 391 5.3e-06 4.4e-02 17 BP cation transmembrane transport  
## 1210 cyan 391 9.5e-06 7.9e-02 4 BP response to copper ion  
## 1211 cyan 391 1.0e-05 8.5e-02 12 MF ATPase activity, coupled to transmembran  
## 1212 cyan 391 1.7e-05 1.5e-01 22 BP cation transport  
## 1213 cyan 391 1.9e-05 1.6e-01 20 BP ion transmembrane transport  
## 1214 cyan 391 3.7e-05 3.1e-01 37 MF transporter activity  
## 1215 cyan 391 4.2e-05 3.5e-01 8 BP response to metal ion  
## 1216 cyan 391 4.4e-05 3.7e-01 5 CC vacuolar proton-transporting V-type ATPa  
## 1217 cyan 391 5.2e-05 4.3e-01 33 MF transmembrane transporter activity  
## 1218 cyan 391 5.5e-05 4.6e-01 28 BP ion transport  
## 1219 cyan 391 8.6e-05 7.2e-01 14 BP response to toxic substance  
## 1220 cyan 391 9.8e-05 8.2e-01 17 MF active transmembrane transporter activit  
## 1221 cyan 391 1.0e-04 8.5e-01 9 BP Malpighian tubule development  
## 1222 cyan 391 1.0e-04 8.7e-01 8 CC vacuolar membrane  
## 1223 cyan 391 1.2e-04 1.0e+00 4 CC proton-transporting V-type ATPase, V1 do  
## 1224 cyan 391 1.3e-04 1.0e+00 9 BP digestive tract morphogenesis  
## 1225 cyan 391 1.5e-04 1.0e+00 10 MF proton transmembrane transporter activit  
## 1226 cyan 391 1.9e-04 1.0e+00 13 BP monovalent inorganic cation transport  
## 1227 cyan 391 1.9e-04 1.0e+00 4 CC proton-transporting V-type ATPase, V0 do  
## 1228 cyan 391 2.2e-04 1.0e+00 11 BP digestive tract development  
## 1229 cyan 391 2.4e-04 1.0e+00 12 MF heme binding  
## 1230 cyan 391 2.5e-04 1.0e+00 13 MF iron ion binding  
## 1231 cyan 391 2.6e-04 1.0e+00 20 MF inorganic cation transmembrane transport  
## 1232 cyan 391 2.7e-04 1.0e+00 4 BP anterior Malpighian tubule development  
## 1233 cyan 391 2.8e-04 1.0e+00 13 MF lipid binding  
## 1234 cyan 391 4.6e-04 1.0e+00 22 MF cofactor binding  
## 1235 cyan 391 4.8e-04 1.0e+00 20 MF cation transmembrane transporter activit  
## 1236 cyan 391 5.8e-04 1.0e+00 7 BP glutathione metabolic process  
## 1237 cyan 391 6.0e-04 1.0e+00 11 BP fatty acid metabolic process  
## 1238 cyan 391 6.1e-04 1.0e+00 25 MF ion transmembrane transporter activity  
## 1239 cyan 391 6.1e-04 1.0e+00 10 BP cellular ion homeostasis  
## 1240 cyan 391 7.0e-04 1.0e+00 4 BP response to zinc ion  
## 1241 cyan 391 7.7e-04 1.0e+00 10 BP heart development  
## 1242 cyan 391 8.2e-04 1.0e+00 2 BP iron ion import across plasma membrane  
## 1243 cyan 391 8.2e-04 1.0e+00 2 BP detoxification of iron ion  
## 1244 cyan 391 8.2e-04 1.0e+00 2 CC collagen type IV trimer  
## 1245 cyan 391 8.2e-04 1.0e+00 2 CC intracellular ferritin complex  
## 1246 cyan 391 8.2e-04 1.0e+00 2 MF alpha-amylase activity  
## 1247 cyan 391 8.2e-04 1.0e+00 2 MF phosphatidylinositol-5-phosphate binding  
## 1248 cyan 391 8.2e-04 1.0e+00 2 MF pristanoyl-CoA oxidase activity  
## 1249 cyan 391 9.7e-04 1.0e+00 11 BP cation homeostasis  
## 1250 cyan 391 1.1e-03 1.0e+00 5 BP striated muscle tissue development  
## 1251 cyan 391 1.1e-03 1.0e+00 5 BP cardiocyte differentiation  
## 1252 cyan 391 1.2e-03 1.0e+00 3 BP cellular iron ion homeostasis  
## 1253 cyan 391 1.2e-03 1.0e+00 3 CC vacuolar proton-transporting V-type ATPa  
## 1254 cyan 391 1.2e-03 1.0e+00 11 CC vacuole  
## 1255 cyan 391 1.5e-03 1.0e+00 11 BP ion homeostasis  
## 1256 cyan 391 1.6e-03 1.0e+00 8 BP cellular metal ion homeostasis  
## 1257 cyan 391 1.7e-03 1.0e+00 5 BP muscle tissue development  
## 1258 cyan 391 2.4e-03 1.0e+00 3 BP cardiac muscle tissue development  
## 1259 cyan 391 2.4e-03 1.0e+00 3 CC vacuolar proton-transporting V-type ATPa  
## 1260 cyan 391 2.4e-03 1.0e+00 2 BP ectoderm and mesoderm interaction  
## 1261 cyan 391 2.4e-03 1.0e+00 2 BP response to iron ion  
## 1262 cyan 391 2.4e-03 1.0e+00 2 MF amylase activity  
## 1263 cyan 391 2.7e-03 1.0e+00 9 BP metal ion homeostasis  
## 1264 cyan 391 3.0e-03 1.0e+00 5 BP midgut development  
## 1265 cyan 391 3.2e-03 1.0e+00 3 BP vacuolar acidification  
## 1266 cyan 391 3.4e-03 1.0e+00 5 MF antioxidant activity  
## 1267 cyan 391 3.7e-03 1.0e+00 23 BP homeostatic process  
## 1268 cyan 391 4.2e-03 1.0e+00 3 BP iron ion homeostasis  
## 1269 cyan 391 4.3e-03 1.0e+00 5 BP transition metal ion homeostasis  
## 1270 cyan 391 4.5e-03 1.0e+00 12 BP metal ion transport  
## 1271 cyan 391 4.7e-03 1.0e+00 2 BP positive regulation of axon extension in  
## 1272 cyan 391 4.7e-03 1.0e+00 2 CC collagen trimer  
## 1273 cyan 391 4.7e-03 1.0e+00 2 MF gamma-glutamylcyclotransferase activity  
## 1274 cyan 391 4.7e-03 1.0e+00 2 MF glutathione peroxidase activity  
## 1275 cyan 391 4.7e-03 1.0e+00 2 MF proton-exporting ATPase activity, phosph  
## 1276 cyan 391 4.8e-03 1.0e+00 5 MF glutathione transferase activity  
## 1277 cyan 391 5.1e-03 1.0e+00 7 BP divalent metal ion transport  
## 1278 cyan 391 5.2e-03 1.0e+00 4 MF peroxidase activity  
## 1279 cyan 391 5.4e-03 1.0e+00 3 MF ATPase activity, coupled to transmembran  
## 1280 cyan 391 6.0e-03 1.0e+00 4 MF oxidoreductase activity, acting on perox  
## 1281 cyan 391 7.7e-03 1.0e+00 37 CC extracellular region  
## 1282 cyan 391 7.7e-03 1.0e+00 2 BP nucleoside transport  
## 1283 cyan 391 7.7e-03 1.0e+00 2 BP cardiac muscle cell differentiation  
## 1284 cyan 391 7.7e-03 1.0e+00 2 BP nucleoside transmembrane transport  
## 1285 cyan 391 7.7e-03 1.0e+00 2 MF nucleoside transmembrane transporter act  
## 1286 cyan 391 7.7e-03 1.0e+00 2 MF ferrous iron binding  
## 1287 cyan 391 7.7e-03 1.0e+00 2 MF acyl-CoA hydrolase activity  
## 1288 cyan 391 7.7e-03 1.0e+00 2 MF phosphatidylinositol-3,5-bisphosphate bi  
## 1289 cyan 391 7.8e-03 1.0e+00 6 MF transferase activity, transferring alkyl  
## 1290 cyan 391 8.2e-03 1.0e+00 3 CC lysosomal membrane  
## 1291 cyan 391 8.9e-03 1.0e+00 4 BP transition metal ion transport  
## 1292 cyan 391 8.9e-03 1.0e+00 4 BP cell-substrate adhesion  
## 1293 cyan 391 8.9e-03 1.0e+00 5 BP Malpighian tubule morphogenesis  
## 1294 cyan 391 9.3e-03 1.0e+00 49 CC intrinsic component of membrane  
## 1295 cyan 391 9.6e-03 1.0e+00 7 MF hydrolase activity, hydrolyzing O-glycos  
## 1296 cyan 391 9.9e-03 1.0e+00 3 BP intracellular pH reduction  
## 1297 darkgreen 68 8.4e-11 7.1e-07 37 BP multicellular organism development  
## 1298 darkgreen 68 4.0e-09 3.3e-05 37 BP anatomical structure development  
## 1299 darkgreen 68 4.1e-09 3.5e-05 28 BP anatomical structure morphogenesis  
## 1300 darkgreen 68 7.7e-09 6.4e-05 29 BP signaling  
## 1301 darkgreen 68 1.3e-08 1.1e-04 29 BP cell communication  
## 1302 darkgreen 68 1.4e-08 1.2e-04 37 BP developmental process  
## 1303 darkgreen 68 1.7e-08 1.4e-04 19 BP regulation of signal transduction  
## 1304 darkgreen 68 2.7e-08 2.3e-04 17 BP morphogenesis of an epithelium  
## 1305 darkgreen 68 3.2e-08 2.7e-04 26 BP signal transduction  
## 1306 darkgreen 68 3.3e-08 2.8e-04 20 BP generation of neurons  
## 1307 darkgreen 68 7.2e-08 6.1e-04 20 BP neurogenesis  
## 1308 darkgreen 68 7.4e-08 6.2e-04 32 MF protein binding  
## 1309 darkgreen 68 8.1e-08 6.8e-04 22 BP nervous system development  
## 1310 darkgreen 68 1.4e-07 1.2e-03 18 BP animal organ morphogenesis  
## 1311 darkgreen 68 1.5e-07 1.2e-03 27 BP cell differentiation  
## 1312 darkgreen 68 1.9e-07 1.6e-03 14 BP regulation of localization  
## 1313 darkgreen 68 2.1e-07 1.8e-03 16 BP cytoskeleton organization  
## 1314 darkgreen 68 3.2e-07 2.7e-03 20 BP epithelium development  
## 1315 darkgreen 68 4.8e-07 4.0e-03 22 BP animal organ development  
## 1316 darkgreen 68 5.4e-07 4.5e-03 11 BP actin cytoskeleton organization  
## 1317 darkgreen 68 5.4e-07 4.5e-03 16 BP intracellular signal transduction  
## 1318 darkgreen 68 5.6e-07 4.7e-03 15 BP imaginal disc development  
## 1319 darkgreen 68 8.0e-07 6.7e-03 17 BP neuron differentiation  
## 1320 darkgreen 68 9.0e-07 7.6e-03 11 BP actin filament-based process  
## 1321 darkgreen 68 1.2e-06 1.0e-02 20 BP tissue development  
## 1322 darkgreen 68 1.8e-06 1.5e-02 13 BP epithelial tube morphogenesis  
## 1323 darkgreen 68 1.9e-06 1.6e-02 16 BP tube development  
## 1324 darkgreen 68 2.0e-06 1.7e-02 15 BP neuron development  
## 1325 darkgreen 68 3.3e-06 2.8e-02 13 BP neuron projection development  
## 1326 darkgreen 68 3.7e-06 3.1e-02 16 BP regulation of developmental process  
## 1327 darkgreen 68 4.0e-06 3.4e-02 9 BP establishment or maintenance of cell pol  
## 1328 darkgreen 68 4.1e-06 3.5e-02 13 BP tube morphogenesis  
## 1329 darkgreen 68 4.3e-06 3.6e-02 14 BP cell morphogenesis  
## 1330 darkgreen 68 4.8e-06 4.0e-02 6 BP mushroom body development  
## 1331 darkgreen 68 5.0e-06 4.1e-02 7 BP brain development  
## 1332 darkgreen 68 5.6e-06 4.7e-02 22 BP cell development  
## 1333 darkgreen 68 1.0e-05 8.4e-02 7 BP regulation of cellular localization  
## 1334 darkgreen 68 1.1e-05 9.6e-02 20 CC cell periphery  
## 1335 darkgreen 68 1.1e-05 9.6e-02 13 BP instar larval or pupal development  
## 1336 darkgreen 68 1.6e-05 1.3e-01 7 BP head development  
## 1337 darkgreen 68 1.8e-05 1.5e-01 10 BP negative regulation of signal transducti  
## 1338 darkgreen 68 2.1e-05 1.8e-01 11 BP protein phosphorylation  
## 1339 darkgreen 68 2.2e-05 1.9e-01 31 BP cellular component organization  
## 1340 darkgreen 68 3.0e-05 2.5e-01 18 CC plasma membrane  
## 1341 darkgreen 68 3.6e-05 3.0e-01 6 BP dorsal closure  
## 1342 darkgreen 68 3.8e-05 3.2e-01 14 BP cell surface receptor signaling pathway  
## 1343 darkgreen 68 4.1e-05 3.4e-01 5 BP pole plasm assembly  
## 1344 darkgreen 68 4.3e-05 3.6e-01 13 BP post-embryonic development  
## 1345 darkgreen 68 5.3e-05 4.5e-01 8 BP central nervous system development  
## 1346 darkgreen 68 5.4e-05 4.5e-01 10 BP wing disc development  
## 1347 darkgreen 68 6.3e-05 5.3e-01 11 BP metamorphosis  
## 1348 darkgreen 68 6.5e-05 5.4e-01 6 BP synaptic vesicle cycle  
## 1349 darkgreen 68 7.9e-05 6.6e-01 10 BP imaginal disc morphogenesis  
## 1350 darkgreen 68 8.2e-05 6.9e-01 6 BP morphogenesis of embryonic epithelium  
## 1351 darkgreen 68 1.3e-04 1.0e+00 4 BP hippo signaling  
## 1352 darkgreen 68 1.3e-04 1.0e+00 3 BP negative regulation of cell adhesion  
## 1353 darkgreen 68 1.3e-04 1.0e+00 9 MF kinase activity  
## 1354 darkgreen 68 1.3e-04 1.0e+00 5 BP regulation of embryonic development  
## 1355 darkgreen 68 1.4e-04 1.0e+00 5 BP oocyte anterior/posterior axis specifica  
## 1356 darkgreen 68 1.6e-04 1.0e+00 5 BP maternal determination of anterior/poste  
## 1357 darkgreen 68 1.7e-04 1.0e+00 7 CC axon  
## 1358 darkgreen 68 1.8e-04 1.0e+00 4 BP regulation of cell adhesion  
## 1359 darkgreen 68 1.8e-04 1.0e+00 3 BP adherens junction assembly  
## 1360 darkgreen 68 1.8e-04 1.0e+00 9 BP axon development  
## 1361 darkgreen 68 1.9e-04 1.0e+00 4 BP pole plasm oskar mRNA localization  
## 1362 darkgreen 68 2.0e-04 1.0e+00 2 BP heparin metabolic process  
## 1363 darkgreen 68 2.0e-04 1.0e+00 2 BP ephrin receptor signaling pathway  
## 1364 darkgreen 68 2.0e-04 1.0e+00 2 MF guanylate kinase activity  
## 1365 darkgreen 68 2.1e-04 1.0e+00 3 BP establishment of mitotic spindle orienta  
## 1366 darkgreen 68 2.1e-04 1.0e+00 9 BP taxis  
## 1367 darkgreen 68 2.2e-04 1.0e+00 8 BP wing disc morphogenesis  
## 1368 darkgreen 68 2.2e-04 1.0e+00 5 BP microtubule cytoskeleton organization in  
## 1369 darkgreen 68 2.4e-04 1.0e+00 7 BP regulation of protein phosphorylation  
## 1370 darkgreen 68 2.4e-04 1.0e+00 6 CC apical part of cell  
## 1371 darkgreen 68 2.5e-04 1.0e+00 9 BP developmental growth  
## 1372 darkgreen 68 2.6e-04 1.0e+00 4 BP pole plasm mRNA localization  
## 1373 darkgreen 68 2.8e-04 1.0e+00 9 CC neuron projection  
## 1374 darkgreen 68 2.8e-04 1.0e+00 10 BP neuron projection morphogenesis  
## 1375 darkgreen 68 2.8e-04 1.0e+00 12 BP locomotion  
## 1376 darkgreen 68 2.8e-04 1.0e+00 4 BP pole plasm RNA localization  
## 1377 darkgreen 68 3.0e-04 1.0e+00 4 BP regulation of intracellular transport  
## 1378 darkgreen 68 3.0e-04 1.0e+00 9 BP compound eye development  
## 1379 darkgreen 68 3.5e-04 1.0e+00 8 BP compound eye morphogenesis  
## 1380 darkgreen 68 3.6e-04 1.0e+00 3 BP negative regulation of organ growth  
## 1381 darkgreen 68 3.8e-04 1.0e+00 6 CC cell cortex  
## 1382 darkgreen 68 3.8e-04 1.0e+00 11 BP phosphorylation  
## 1383 darkgreen 68 4.0e-04 1.0e+00 10 BP cell-cell signaling  
## 1384 darkgreen 68 4.1e-04 1.0e+00 3 BP regulation of pole plasm oskar mRNA loca  
## 1385 darkgreen 68 4.6e-04 1.0e+00 8 BP eye morphogenesis  
## 1386 darkgreen 68 4.6e-04 1.0e+00 3 BP response to gravity  
## 1387 darkgreen 68 4.6e-04 1.0e+00 3 BP gravitaxis  
## 1388 darkgreen 68 4.6e-04 1.0e+00 3 BP establishment of spindle orientation  
## 1389 darkgreen 68 4.6e-04 1.0e+00 3 BP regulation of embryonic pattern specific  
## 1390 darkgreen 68 4.6e-04 1.0e+00 7 BP regulation of phosphorylation  
## 1391 darkgreen 68 4.7e-04 1.0e+00 9 BP eye development  
## 1392 darkgreen 68 4.7e-04 1.0e+00 4 BP establishment of cell polarity  
## 1393 darkgreen 68 4.7e-04 1.0e+00 4 BP intracellular mRNA localization involved  
## 1394 darkgreen 68 4.8e-04 1.0e+00 6 BP embryonic development via the syncytial   
## 1395 darkgreen 68 4.8e-04 1.0e+00 10 BP sensory organ development  
## 1396 darkgreen 68 4.9e-04 1.0e+00 11 BP cellular macromolecule localization  
## 1397 darkgreen 68 4.9e-04 1.0e+00 7 BP regulation of transport  
## 1398 darkgreen 68 5.0e-04 1.0e+00 8 BP post-embryonic appendage morphogenesis  
## 1399 darkgreen 68 5.0e-04 1.0e+00 4 BP regulation of organ growth  
## 1400 darkgreen 68 5.1e-04 1.0e+00 2 BP heparan sulfate proteoglycan biosyntheti  
## 1401 darkgreen 68 5.1e-04 1.0e+00 2 BP border follicle cell delamination  
## 1402 darkgreen 68 5.1e-04 1.0e+00 2 MF spectrin binding  
## 1403 darkgreen 68 5.1e-04 1.0e+00 6 MF protein serine/threonine kinase activity  
## 1404 darkgreen 68 5.1e-04 1.0e+00 7 MF protein kinase activity  
## 1405 darkgreen 68 5.2e-04 1.0e+00 3 BP regulation of intracellular mRNA localiz  
## 1406 darkgreen 68 5.2e-04 1.0e+00 3 CC type I terminal bouton  
## 1407 darkgreen 68 5.3e-04 1.0e+00 10 BP cell morphogenesis involved in different  
## 1408 darkgreen 68 5.5e-04 1.0e+00 8 BP microtubule cytoskeleton organization  
## 1409 darkgreen 68 5.7e-04 1.0e+00 4 BP intracellular mRNA localization involved  
## 1410 darkgreen 68 5.8e-04 1.0e+00 3 BP establishment of mitotic spindle localiz  
## 1411 darkgreen 68 6.0e-04 1.0e+00 8 BP imaginal disc-derived appendage morphoge  
## 1412 darkgreen 68 6.1e-04 1.0e+00 5 BP morphogenesis of a polarized epithelium  
## 1413 darkgreen 68 6.4e-04 1.0e+00 8 BP appendage morphogenesis  
## 1414 darkgreen 68 6.4e-04 1.0e+00 6 BP transmembrane receptor protein tyrosine   
## 1415 darkgreen 68 6.9e-04 1.0e+00 9 BP regulation of cell differentiation  
## 1416 darkgreen 68 6.9e-04 1.0e+00 5 BP anterior/posterior axis specification, e  
## 1417 darkgreen 68 7.0e-04 1.0e+00 8 BP imaginal disc-derived appendage developm  
## 1418 darkgreen 68 7.1e-04 1.0e+00 2 BP negative regulation of response to wound  
## 1419 darkgreen 68 7.1e-04 1.0e+00 3 BP melanotic encapsulation of foreign targe  
## 1420 darkgreen 68 7.1e-04 1.0e+00 4 BP cell-cell junction assembly  
## 1421 darkgreen 68 7.2e-04 1.0e+00 8 BP cell fate commitment  
## 1422 darkgreen 68 7.4e-04 1.0e+00 5 BP oocyte axis specification  
## 1423 darkgreen 68 7.5e-04 1.0e+00 4 BP regulation of oogenesis  
## 1424 darkgreen 68 8.2e-04 1.0e+00 25 CC membrane  
## 1425 darkgreen 68 8.3e-04 1.0e+00 5 BP embryonic axis specification  
## 1426 darkgreen 68 8.3e-04 1.0e+00 5 BP oocyte construction  
## 1427 darkgreen 68 8.6e-04 1.0e+00 5 BP response to wounding  
## 1428 darkgreen 68 8.6e-04 1.0e+00 10 CC cell projection  
## 1429 darkgreen 68 8.8e-04 1.0e+00 4 BP cell-cell junction organization  
## 1430 darkgreen 68 9.0e-04 1.0e+00 9 MF transferase activity, transferring phosp  
## 1431 darkgreen 68 9.3e-04 1.0e+00 6 BP embryo development ending in birth or eg  
## 1432 darkgreen 68 9.4e-04 1.0e+00 2 CC type Ib terminal bouton  
## 1433 darkgreen 68 9.6e-04 1.0e+00 9 BP growth  
## 1434 darkgreen 68 9.8e-04 1.0e+00 6 BP blastoderm segmentation  
## 1435 darkgreen 68 9.9e-04 1.0e+00 5 BP anterior/posterior axis specification  
## 1436 darkgreen 68 1.0e-03 1.0e+00 7 BP imaginal disc-derived wing morphogenesis  
## 1437 darkgreen 68 1.0e-03 1.0e+00 3 BP spindle localization  
## 1438 darkgreen 68 1.1e-03 1.0e+00 4 BP organ growth  
## 1439 darkgreen 68 1.1e-03 1.0e+00 9 BP cell morphogenesis involved in neuron di  
## 1440 darkgreen 68 1.2e-03 1.0e+00 7 BP cell division  
## 1441 darkgreen 68 1.2e-03 1.0e+00 6 BP cell adhesion  
## 1442 darkgreen 68 1.3e-03 1.0e+00 51 BP cellular process  
## 1443 darkgreen 68 1.3e-03 1.0e+00 5 BP oocyte development  
## 1444 darkgreen 68 1.3e-03 1.0e+00 20 BP organelle organization  
## 1445 darkgreen 68 1.5e-03 1.0e+00 4 BP intracellular mRNA localization  
## 1446 darkgreen 68 1.5e-03 1.0e+00 4 BP negative regulation of developmental gro  
## 1447 darkgreen 68 1.5e-03 1.0e+00 2 BP negative regulation of microtubule depol  
## 1448 darkgreen 68 1.5e-03 1.0e+00 3 BP adherens junction organization  
## 1449 darkgreen 68 1.5e-03 1.0e+00 3 BP encapsulation of foreign target  
## 1450 darkgreen 68 1.5e-03 1.0e+00 6 BP embryonic pattern specification  
## 1451 darkgreen 68 1.6e-03 1.0e+00 11 BP protein localization  
## 1452 darkgreen 68 1.7e-03 1.0e+00 3 BP establishment or maintenance of microtub  
## 1453 darkgreen 68 1.8e-03 1.0e+00 3 BP regulation of smoothened signaling pathw  
## 1454 darkgreen 68 1.9e-03 1.0e+00 3 BP regulation of imaginal disc growth  
## 1455 darkgreen 68 2.0e-03 1.0e+00 7 MF phosphotransferase activity, alcohol gro  
## 1456 darkgreen 68 2.2e-03 1.0e+00 2 BP pole plasm protein localization  
## 1457 darkgreen 68 2.2e-03 1.0e+00 2 BP regulation of ATPase activity  
## 1458 darkgreen 68 2.2e-03 1.0e+00 2 BP basal protein localization  
## 1459 darkgreen 68 2.2e-03 1.0e+00 2 BP delamination  
## 1460 darkgreen 68 2.2e-03 1.0e+00 2 MF nucleoside monophosphate kinase activity  
## 1461 darkgreen 68 2.2e-03 1.0e+00 6 BP regulation of developmental growth  
## 1462 darkgreen 68 2.2e-03 1.0e+00 15 BP cellular protein modification process  
## 1463 darkgreen 68 2.3e-03 1.0e+00 4 BP eye photoreceptor cell development  
## 1464 darkgreen 68 2.5e-03 1.0e+00 5 BP oocyte differentiation  
## 1465 darkgreen 68 2.6e-03 1.0e+00 4 BP neurotransmitter secretion  
## 1466 darkgreen 68 2.6e-03 1.0e+00 4 BP neuroblast proliferation  
## 1467 darkgreen 68 2.6e-03 1.0e+00 3 BP melanization defense response  
## 1468 darkgreen 68 2.6e-03 1.0e+00 3 MF Rho GTPase binding  
## 1469 darkgreen 68 2.7e-03 1.0e+00 9 BP pattern specification process  
## 1470 darkgreen 68 2.7e-03 1.0e+00 6 BP embryonic morphogenesis  
## 1471 darkgreen 68 2.8e-03 1.0e+00 5 CC cell junction  
## 1472 darkgreen 68 2.9e-03 1.0e+00 6 BP segmentation  
## 1473 darkgreen 68 3.0e-03 1.0e+00 3 BP synaptic vesicle recycling  
## 1474 darkgreen 68 3.0e-03 1.0e+00 3 CC basolateral plasma membrane  
## 1475 darkgreen 68 3.0e-03 1.0e+00 2 BP regulation of microtubule depolymerizati  
## 1476 darkgreen 68 3.0e-03 1.0e+00 2 BP negative regulation of ion transport  
## 1477 darkgreen 68 3.1e-03 1.0e+00 8 BP microtubule-based process  
## 1478 darkgreen 68 3.1e-03 1.0e+00 5 MF Ras GTPase binding  
## 1479 darkgreen 68 3.3e-03 1.0e+00 7 BP axonogenesis  
## 1480 darkgreen 68 3.4e-03 1.0e+00 4 BP asymmetric cell division  
## 1481 darkgreen 68 3.4e-03 1.0e+00 5 MF small GTPase binding  
## 1482 darkgreen 68 3.4e-03 1.0e+00 2 BP heparan sulfate proteoglycan biosyntheti  
## 1483 darkgreen 68 3.4e-03 1.0e+00 2 BP axon regeneration  
## 1484 darkgreen 68 3.5e-03 1.0e+00 4 BP establishment of planar polarity  
## 1485 darkgreen 68 3.5e-03 1.0e+00 4 BP establishment of tissue polarity  
## 1486 darkgreen 68 3.6e-03 1.0e+00 5 BP RNA localization  
## 1487 darkgreen 68 3.6e-03 1.0e+00 5 BP anterior/posterior pattern specification  
## 1488 darkgreen 68 3.9e-03 1.0e+00 4 BP negative regulation of growth  
## 1489 darkgreen 68 3.9e-03 1.0e+00 2 BP heparan sulfate proteoglycan metabolic p  
## 1490 darkgreen 68 4.1e-03 1.0e+00 19 BP regulation of cellular metabolic process  
## 1491 darkgreen 68 4.1e-03 1.0e+00 4 BP photoreceptor cell development  
## 1492 darkgreen 68 4.1e-03 1.0e+00 3 BP imaginal disc growth  
## 1493 darkgreen 68 4.1e-03 1.0e+00 3 BP behavioral response to ethanol  
## 1494 darkgreen 68 4.2e-03 1.0e+00 7 BP epithelial cell development  
## 1495 darkgreen 68 4.2e-03 1.0e+00 4 BP Wnt signaling pathway  
## 1496 darkgreen 68 4.3e-03 1.0e+00 61 BP biological\_process  
## 1497 darkgreen 68 4.4e-03 1.0e+00 8 BP mitotic cell cycle  
## 1498 darkgreen 68 4.4e-03 1.0e+00 2 BP negative regulation of imaginal disc gro  
## 1499 darkgreen 68 4.4e-03 1.0e+00 2 BP positive regulation of smoothened signal  
## 1500 darkgreen 68 4.7e-03 1.0e+00 4 BP stem cell proliferation  
## 1501 darkgreen 68 4.8e-03 1.0e+00 7 BP cell proliferation  
## 1502 darkgreen 68 4.9e-03 1.0e+00 2 BP positive regulation of hippo signaling  
## 1503 darkgreen 68 4.9e-03 1.0e+00 2 BP apical protein localization  
## 1504 darkgreen 68 5.0e-03 1.0e+00 3 BP smoothened signaling pathway  
## 1505 darkgreen 68 5.0e-03 1.0e+00 5 MF GTPase binding  
## 1506 darkgreen 68 5.3e-03 1.0e+00 5 BP axis specification  
## 1507 darkgreen 68 5.3e-03 1.0e+00 3 BP apical junction assembly  
## 1508 darkgreen 68 5.3e-03 1.0e+00 6 BP axon guidance  
## 1509 darkgreen 68 5.5e-03 1.0e+00 22 BP protein metabolic process  
## 1510 darkgreen 68 5.5e-03 1.0e+00 2 BP microtubule depolymerization  
## 1511 darkgreen 68 5.5e-03 1.0e+00 2 BP asymmetric protein localization involved  
## 1512 darkgreen 68 5.5e-03 1.0e+00 2 MF protein tyrosine/serine/threonine phosph  
## 1513 darkgreen 68 5.5e-03 1.0e+00 20 BP regulation of metabolic process  
## 1514 darkgreen 68 5.5e-03 1.0e+00 3 BP cortical actin cytoskeleton organization  
## 1515 darkgreen 68 5.6e-03 1.0e+00 4 BP positive regulation of protein phosphory  
## 1516 darkgreen 68 5.8e-03 1.0e+00 3 BP regulation of cell shape  
## 1517 darkgreen 68 5.8e-03 1.0e+00 3 BP synaptic vesicle exocytosis  
## 1518 darkgreen 68 5.8e-03 1.0e+00 3 CC cell cortex region  
## 1519 darkgreen 68 5.9e-03 1.0e+00 1 BP ultradian rhythm  
## 1520 darkgreen 68 5.9e-03 1.0e+00 1 BP positive regulation of peptidyl-threonin  
## 1521 darkgreen 68 5.9e-03 1.0e+00 1 BP regulation of border follicle cell delam  
## 1522 darkgreen 68 5.9e-03 1.0e+00 1 BP 5S class rRNA transcription by RNA polym  
## 1523 darkgreen 68 5.9e-03 1.0e+00 1 BP zonula adherens maintenance  
## 1524 darkgreen 68 5.9e-03 1.0e+00 1 BP negative regulation of focal adhesion as  
## 1525 darkgreen 68 5.9e-03 1.0e+00 1 BP cell morphogenesis involved in Malpighia  
## 1526 darkgreen 68 5.9e-03 1.0e+00 1 BP negative regulation of ecdysone receptor  
## 1527 darkgreen 68 5.9e-03 1.0e+00 1 BP regulation of axo-dendritic protein tran  
## 1528 darkgreen 68 5.9e-03 1.0e+00 1 BP protein localization to presynapse  
## 1529 darkgreen 68 5.9e-03 1.0e+00 1 CC interphase microtubule organizing center  
## 1530 darkgreen 68 5.9e-03 1.0e+00 1 CC microtubule minus-end  
## 1531 darkgreen 68 5.9e-03 1.0e+00 1 MF phosphatidylinositol-3,4,5-trisphosphate  
## 1532 darkgreen 68 5.9e-03 1.0e+00 1 MF activin receptor activity, type I  
## 1533 darkgreen 68 5.9e-03 1.0e+00 1 MF ephrin receptor binding  
## 1534 darkgreen 68 5.9e-03 1.0e+00 1 MF protein N-terminus binding  
## 1535 darkgreen 68 5.9e-03 1.0e+00 1 MF PTB domain binding  
## 1536 darkgreen 68 5.9e-03 1.0e+00 1 MF inositol-1,3,4,5-tetrakisphosphate 3-pho  
## 1537 darkgreen 68 5.9e-03 1.0e+00 1 MF phosphatidylinositol-3,4-bisphosphate 3-  
## 1538 darkgreen 68 6.0e-03 1.0e+00 6 BP chemical synaptic transmission  
## 1539 darkgreen 68 6.0e-03 1.0e+00 3 BP regulation of protein catabolic process  
## 1540 darkgreen 68 6.1e-03 1.0e+00 2 BP cell-matrix adhesion  
## 1541 darkgreen 68 6.1e-03 1.0e+00 2 BP proteoglycan biosynthetic process  
## 1542 darkgreen 68 6.1e-03 1.0e+00 2 BP negative regulation of hippo signaling  
## 1543 darkgreen 68 6.1e-03 1.0e+00 2 BP response to axon injury  
## 1544 darkgreen 68 6.2e-03 1.0e+00 6 BP synaptic signaling  
## 1545 darkgreen 68 6.3e-03 1.0e+00 4 MF actin binding  
## 1546 darkgreen 68 6.4e-03 1.0e+00 4 BP pigment metabolic process  
## 1547 darkgreen 68 6.6e-03 1.0e+00 3 BP calcium ion regulated exocytosis  
## 1548 darkgreen 68 6.6e-03 1.0e+00 4 BP response to alcohol  
## 1549 darkgreen 68 6.7e-03 1.0e+00 2 CC apicolateral plasma membrane  
## 1550 darkgreen 68 6.8e-03 1.0e+00 4 BP positive regulation of phosphorylation  
## 1551 darkgreen 68 7.2e-03 1.0e+00 3 BP instar larval development  
## 1552 darkgreen 68 7.2e-03 1.0e+00 3 BP regulated exocytosis  
## 1553 darkgreen 68 7.2e-03 1.0e+00 3 CC terminal bouton  
## 1554 darkgreen 68 7.3e-03 1.0e+00 2 BP negative regulation of smoothened signal  
## 1555 darkgreen 68 7.8e-03 1.0e+00 4 BP signal release  
## 1556 darkgreen 68 7.8e-03 1.0e+00 6 MF cytoskeletal protein binding  
## 1557 darkgreen 68 7.8e-03 1.0e+00 3 BP cortical cytoskeleton organization  
## 1558 darkgreen 68 8.0e-03 1.0e+00 4 BP neurotransmitter transport  
## 1559 darkgreen 68 8.0e-03 1.0e+00 2 BP regulation of microtubule polymerization  
## 1560 darkgreen 68 8.3e-03 1.0e+00 6 BP regulation of cell cycle  
## 1561 darkgreen 68 8.5e-03 1.0e+00 12 BP phosphate-containing compound metabolic   
## 1562 darkgreen 68 8.7e-03 1.0e+00 2 BP apical constriction  
## 1563 darkgreen 68 8.7e-03 1.0e+00 3 BP regulation of canonical Wnt signaling pa  
## 1564 darkgreen 68 9.4e-03 1.0e+00 6 BP regulation of growth  
## 1565 darkgreen 68 9.4e-03 1.0e+00 2 BP establishment of imaginal disc-derived w  
## 1566 darkgreen 68 9.4e-03 1.0e+00 2 BP clathrin-dependent endocytosis  
## 1567 darkgreen 68 9.4e-03 1.0e+00 3 BP mitotic spindle organization  
## 1568 darkgreen 68 9.4e-03 1.0e+00 3 CC axon terminus  
## 1569 darkgreen 68 9.8e-03 1.0e+00 3 CC neuron projection terminus  
## 1570 darkgrey 249 1.2e-08 9.9e-05 18 MF Ras GTPase binding  
## 1571 darkgrey 249 1.2e-08 1.0e-04 19 MF GTPase binding  
## 1572 darkgrey 249 1.6e-08 1.3e-04 18 MF small GTPase binding  
## 1573 darkgrey 249 2.5e-07 2.1e-03 37 BP regulation of signal transduction  
## 1574 darkgrey 249 6.1e-07 5.1e-03 11 BP regulation of Ras protein signal transdu  
## 1575 darkgrey 249 1.6e-06 1.4e-02 11 BP regulation of small GTPase mediated sign  
## 1576 darkgrey 249 3.5e-06 2.9e-02 9 MF Ras guanyl-nucleotide exchange factor ac  
## 1577 darkgrey 249 3.8e-06 3.2e-02 10 MF guanyl-nucleotide exchange factor activi  
## 1578 darkgrey 249 8.6e-06 7.2e-02 13 BP Ras protein signal transduction  
## 1579 darkgrey 249 1.0e-05 8.7e-02 59 BP signaling  
## 1580 darkgrey 249 1.1e-05 8.9e-02 53 BP signal transduction  
## 1581 darkgrey 249 2.0e-05 1.7e-01 59 BP cell communication  
## 1582 darkgrey 249 3.3e-05 2.7e-01 13 BP small GTPase mediated signal transductio  
## 1583 darkgrey 249 3.5e-05 2.9e-01 14 BP endocytosis  
## 1584 darkgrey 249 1.1e-04 9.1e-01 13 MF mRNA binding  
## 1585 darkgrey 249 1.4e-04 1.0e+00 5 CC clathrin-coated vesicle  
## 1586 darkgrey 249 1.7e-04 1.0e+00 17 BP mRNA processing  
## 1587 darkgrey 249 2.9e-04 1.0e+00 5 BP positive regulation of Ras protein signa  
## 1588 darkgrey 249 3.1e-04 1.0e+00 11 MF phosphatase activity  
## 1589 darkgrey 249 3.9e-04 1.0e+00 6 MF Rho GTPase binding  
## 1590 darkgrey 249 3.9e-04 1.0e+00 11 BP dephosphorylation  
## 1591 darkgrey 249 4.4e-04 1.0e+00 6 BP receptor-mediated endocytosis  
## 1592 darkgrey 249 5.9e-04 1.0e+00 14 BP RNA splicing, via transesterification re  
## 1593 darkgrey 249 5.9e-04 1.0e+00 14 BP mRNA splicing, via spliceosome  
## 1594 darkgrey 249 6.2e-04 1.0e+00 5 MF protein tyrosine phosphatase activity  
## 1595 darkgrey 249 7.2e-04 1.0e+00 8 BP protein dephosphorylation  
## 1596 darkgrey 249 7.5e-04 1.0e+00 20 MF enzyme binding  
## 1597 darkgrey 249 8.5e-04 1.0e+00 16 BP regulation of catalytic activity  
## 1598 darkgrey 249 9.8e-04 1.0e+00 4 BP negative regulation of insulin receptor   
## 1599 darkgrey 249 1.1e-03 1.0e+00 34 CC endomembrane system  
## 1600 darkgrey 249 1.1e-03 1.0e+00 14 BP RNA splicing  
## 1601 darkgrey 249 1.2e-03 1.0e+00 21 BP vesicle-mediated transport  
## 1602 darkgrey 249 1.3e-03 1.0e+00 2 BP mitotic G1/S transition checkpoint  
## 1603 darkgrey 249 1.3e-03 1.0e+00 2 MF phosphatidylinositol-4-phosphate phospha  
## 1604 darkgrey 249 1.6e-03 1.0e+00 4 BP clathrin-dependent endocytosis  
## 1605 darkgrey 249 1.7e-03 1.0e+00 5 BP positive regulation of Wnt signaling pat  
## 1606 darkgrey 249 1.7e-03 1.0e+00 5 BP Rab protein signal transduction  
## 1607 darkgrey 249 1.7e-03 1.0e+00 11 MF phosphoric ester hydrolase activity  
## 1608 darkgrey 249 1.7e-03 1.0e+00 3 BP regulation of Rab protein signal transdu  
## 1609 darkgrey 249 2.1e-03 1.0e+00 3 BP phosphatidylinositol dephosphorylation  
## 1610 darkgrey 249 2.2e-03 1.0e+00 26 BP cell surface receptor signaling pathway  
## 1611 darkgrey 249 2.3e-03 1.0e+00 7 MF Rab GTPase binding  
## 1612 darkgrey 249 2.5e-03 1.0e+00 2 MF insulin-like growth factor binding  
## 1613 darkgrey 249 2.6e-03 1.0e+00 7 BP regulation of GTPase activity  
## 1614 darkgrey 249 2.7e-03 1.0e+00 3 BP negative regulation of G1/S transition o  
## 1615 darkgrey 249 2.7e-03 1.0e+00 3 MF phosphatidylinositol phosphate phosphata  
## 1616 darkgrey 249 2.8e-03 1.0e+00 4 MF Rho guanyl-nucleotide exchange factor ac  
## 1617 darkgrey 249 3.2e-03 1.0e+00 15 BP negative regulation of signal transducti  
## 1618 darkgrey 249 3.3e-03 1.0e+00 9 MF lipid binding  
## 1619 darkgrey 249 3.6e-03 1.0e+00 4 BP regulation of Rho protein signal transdu  
## 1620 darkgrey 249 3.9e-03 1.0e+00 37 BP cellular protein modification process  
## 1621 darkgrey 249 4.1e-03 1.0e+00 2 BP protein localization to synapse  
## 1622 darkgrey 249 4.1e-03 1.0e+00 2 MF Ral GTPase binding  
## 1623 darkgrey 249 4.1e-03 1.0e+00 17 CC vesicle  
## 1624 darkgrey 249 4.5e-03 1.0e+00 6 BP regulation of mRNA processing  
## 1625 darkgrey 249 4.7e-03 1.0e+00 7 MF phospholipid binding  
## 1626 darkgrey 249 4.8e-03 1.0e+00 3 BP positive regulation of smoothened signal  
## 1627 darkgrey 249 4.8e-03 1.0e+00 6 MF phosphoprotein phosphatase activity  
## 1628 darkgrey 249 4.8e-03 1.0e+00 14 BP regulation of growth  
## 1629 darkgrey 249 5.4e-03 1.0e+00 47 MF nucleic acid binding  
## 1630 darkgrey 249 5.7e-03 1.0e+00 4 BP regulation of insulin receptor signaling  
## 1631 darkgrey 249 6.1e-03 1.0e+00 2 BP clathrin-dependent endocytosis involved   
## 1632 darkgrey 249 6.3e-03 1.0e+00 21 MF RNA binding  
## 1633 darkgrey 249 6.5e-03 1.0e+00 23 BP intracellular signal transduction  
## 1634 darkgrey 249 6.7e-03 1.0e+00 13 BP synapse organization  
## 1635 darkgrey 249 6.8e-03 1.0e+00 5 BP alternative mRNA splicing, via spliceoso  
## 1636 darkgrey 249 6.8e-03 1.0e+00 5 BP regulation of alternative mRNA splicing,  
## 1637 darkgrey 249 6.9e-03 1.0e+00 14 CC Golgi apparatus  
## 1638 darkgrey 249 6.9e-03 1.0e+00 4 BP positive regulation of canonical Wnt sig  
## 1639 darkgrey 249 7.4e-03 1.0e+00 7 BP negative regulation of growth  
## 1640 darkgrey 249 7.7e-03 1.0e+00 3 BP proteoglycan biosynthetic process  
## 1641 darkgrey 249 7.7e-03 1.0e+00 3 BP positive regulation of circadian rhythm  
## 1642 darkgrey 249 7.9e-03 1.0e+00 15 CC cytoplasmic vesicle  
## 1643 darkgrey 249 8.3e-03 1.0e+00 14 BP appendage morphogenesis  
## 1644 darkgrey 249 8.4e-03 1.0e+00 2 BP plasma membrane tubulation  
## 1645 darkgrey 249 8.4e-03 1.0e+00 2 BP clathrin-dependent synaptic vesicle endo  
## 1646 darkgrey 249 8.4e-03 1.0e+00 2 MF GTPase activating protein binding  
## 1647 darkgrey 249 8.8e-03 1.0e+00 3 BP inositol phosphate metabolic process  
## 1648 darkgrey 249 8.8e-03 1.0e+00 3 BP phospholipid dephosphorylation  
## 1649 darkgrey 249 9.0e-03 1.0e+00 7 BP developmental pigmentation  
## 1650 darkgrey 249 9.1e-03 1.0e+00 17 BP growth  
## 1651 darkgrey 249 9.7e-03 1.0e+00 5 BP negative regulation of protein phosphory  
## 1652 darkgrey 249 9.7e-03 1.0e+00 5 CC coated vesicle  
## 1653 darkgrey 249 9.9e-03 1.0e+00 25 BP regulation of developmental process  
## 1654 darkgrey 249 9.9e-03 1.0e+00 4 BP regulation of smoothened signaling pathw  
## 1655 darkred 60 2.0e-43 1.7e-39 28 CC cytosolic ribosome  
## 1656 darkred 60 4.4e-39 3.7e-35 27 BP cytoplasmic translation  
## 1657 darkred 60 4.4e-35 3.7e-31 28 CC ribosome  
## 1658 darkred 60 1.3e-34 1.1e-30 27 MF structural constituent of ribosome  
## 1659 darkred 60 1.7e-28 1.5e-24 30 BP translation  
## 1660 darkred 60 8.4e-27 7.1e-23 17 CC cytosolic large ribosomal subunit  
## 1661 darkred 60 6.0e-25 5.0e-21 30 BP peptide metabolic process  
## 1662 darkred 60 7.0e-25 5.9e-21 31 CC cytosol  
## 1663 darkred 60 2.5e-24 2.1e-20 28 MF structural molecule activity  
## 1664 darkred 60 2.2e-23 1.9e-19 29 CC ribonucleoprotein complex  
## 1665 darkred 60 1.4e-21 1.2e-17 17 CC large ribosomal subunit  
## 1666 darkred 60 1.7e-16 1.4e-12 11 CC cytosolic small ribosomal subunit  
## 1667 darkred 60 2.5e-15 2.1e-11 41 CC protein-containing complex  
## 1668 darkred 60 1.0e-13 8.5e-10 46 CC cytoplasm  
## 1669 darkred 60 1.3e-13 1.1e-09 11 CC small ribosomal subunit  
## 1670 darkred 60 1.5e-11 1.3e-07 13 BP ribosome biogenesis  
## 1671 darkred 60 4.4e-10 3.7e-06 8 BP ribosomal large subunit biogenesis  
## 1672 darkred 60 4.5e-10 3.8e-06 33 BP protein metabolic process  
## 1673 darkred 60 1.4e-09 1.2e-05 32 BP gene expression  
## 1674 darkred 60 1.9e-09 1.6e-05 33 BP biosynthetic process  
## 1675 darkred 60 5.4e-08 4.5e-04 44 BP cellular metabolic process  
## 1676 darkred 60 1.7e-07 1.4e-03 43 CC intracellular organelle  
## 1677 darkred 60 4.9e-07 4.1e-03 9 CC mitochondrial inner membrane  
## 1678 darkred 60 5.9e-07 4.9e-03 47 CC intracellular  
## 1679 darkred 60 1.5e-06 1.2e-02 41 BP nitrogen compound metabolic process  
## 1680 darkred 60 2.8e-06 2.3e-02 9 CC mitochondrial membrane  
## 1681 darkred 60 2.9e-06 2.4e-02 7 BP ATP metabolic process  
## 1682 darkred 60 4.5e-06 3.8e-02 9 CC mitochondrial envelope  
## 1683 darkred 60 1.8e-05 1.5e-01 4 BP mitochondrial electron transport, NADH t  
## 1684 darkred 60 2.1e-05 1.8e-01 5 BP mitochondrial ATP synthesis coupled elec  
## 1685 darkred 60 2.3e-05 1.9e-01 5 BP ATP synthesis coupled electron transport  
## 1686 darkred 60 2.9e-05 2.4e-01 5 CC mitochondrial respiratory chain  
## 1687 darkred 60 3.0e-05 2.5e-01 12 MF RNA binding  
## 1688 darkred 60 3.1e-05 2.6e-01 7 BP generation of precursor metabolites and   
## 1689 darkred 60 3.5e-05 3.0e-01 5 BP respiratory electron transport chain  
## 1690 darkred 60 3.9e-05 3.3e-01 6 BP rRNA processing  
## 1691 darkred 60 4.3e-05 3.6e-01 5 BP electron transport chain  
## 1692 darkred 60 5.1e-05 4.3e-01 4 CC mitochondrial respiratory chain complex   
## 1693 darkred 60 5.1e-05 4.3e-01 4 CC NADH dehydrogenase complex  
## 1694 darkred 60 5.6e-05 4.7e-01 5 BP oxidative phosphorylation  
## 1695 darkred 60 8.6e-05 7.2e-01 11 CC organelle membrane  
## 1696 darkred 60 1.3e-04 1.0e+00 4 BP ribosome assembly  
## 1697 darkred 60 1.3e-04 1.0e+00 7 BP purine nucleotide metabolic process  
## 1698 darkred 60 1.3e-04 1.0e+00 7 BP ribonucleotide metabolic process  
## 1699 darkred 60 1.3e-04 1.0e+00 3 BP maturation of LSU-rRNA  
## 1700 darkred 60 1.6e-04 1.0e+00 7 BP ribose phosphate metabolic process  
## 1701 darkred 60 1.9e-04 1.0e+00 5 BP cellular respiration  
## 1702 darkred 60 2.0e-04 1.0e+00 3 BP ribosomal large subunit assembly  
## 1703 darkred 60 2.1e-04 1.0e+00 48 BP cellular process  
## 1704 darkred 60 2.5e-04 1.0e+00 4 BP ribosomal small subunit biogenesis  
## 1705 darkred 60 5.5e-04 1.0e+00 7 BP nucleotide metabolic process  
## 1706 darkred 60 5.8e-04 1.0e+00 3 MF NADH dehydrogenase activity  
## 1707 darkred 60 5.8e-04 1.0e+00 7 BP nucleoside phosphate metabolic process  
## 1708 darkred 60 5.9e-04 1.0e+00 10 BP RNA processing  
## 1709 darkred 60 2.2e-03 1.0e+00 3 MF oxidoreductase activity, acting on NAD(P  
## 1710 darkred 60 2.4e-03 1.0e+00 10 CC mitochondrion  
## 1711 darkred 60 2.8e-03 1.0e+00 2 MF intramolecular transferase activity  
## 1712 darkred 60 3.6e-03 1.0e+00 2 CC mitochondrial proton-transporting ATP sy  
## 1713 darkred 60 5.0e-03 1.0e+00 2 MF ribosome binding  
## 1714 darkred 60 5.2e-03 1.0e+00 4 BP ribonucleoprotein complex assembly  
## 1715 darkred 60 5.3e-03 1.0e+00 1 BP protein insertion into mitochondrial inn  
## 1716 darkred 60 5.3e-03 1.0e+00 1 BP positive regulation by host of viral gen  
## 1717 darkred 60 5.3e-03 1.0e+00 1 BP positive regulation of glycogen biosynth  
## 1718 darkred 60 5.3e-03 1.0e+00 1 BP IRES-dependent viral translational initi  
## 1719 darkred 60 5.3e-03 1.0e+00 1 CC mitochondrial processing peptidase compl  
## 1720 darkred 60 5.3e-03 1.0e+00 1 CC eRF1 methyltransferase complex  
## 1721 darkred 60 5.3e-03 1.0e+00 1 MF phosphoglycerate mutase activity  
## 1722 darkred 60 5.3e-03 1.0e+00 1 MF ribokinase activity  
## 1723 darkred 60 5.3e-03 1.0e+00 1 MF UFM1 transferase activity  
## 1724 darkred 60 6.7e-03 1.0e+00 54 MF molecular\_function  
## 1725 darkred 60 9.2e-03 1.0e+00 8 BP phosphorylation  
## 1726 darkturquoise 65 1.0e-05 8.6e-02 3 MF proteasome binding  
## 1727 darkturquoise 65 8.1e-05 6.8e-01 3 BP L-amino acid transport  
## 1728 darkturquoise 65 2.3e-04 1.0e+00 3 MF L-amino acid transmembrane transporter a  
## 1729 darkturquoise 65 2.1e-03 1.0e+00 2 MF polypeptide N-acetylgalactosaminyltransf  
## 1730 darkturquoise 65 2.7e-03 1.0e+00 3 BP amino acid transport  
## 1731 darkturquoise 65 3.2e-03 1.0e+00 3 MF amino acid transmembrane transporter act  
## 1732 darkturquoise 65 4.3e-03 1.0e+00 2 BP proteasome assembly  
## 1733 darkturquoise 65 5.8e-03 1.0e+00 1 BP peptidyl-pyrromethane cofactor linkage  
## 1734 darkturquoise 65 5.8e-03 1.0e+00 1 BP negative regulation of NF-kappaB transcr  
## 1735 darkturquoise 65 5.8e-03 1.0e+00 1 BP tRNA methylthiolation  
## 1736 darkturquoise 65 5.8e-03 1.0e+00 1 BP negative regulation of dopamine metaboli  
## 1737 darkturquoise 65 5.8e-03 1.0e+00 1 BP L-glutamate import  
## 1738 darkturquoise 65 5.8e-03 1.0e+00 1 BP proteasome core complex assembly  
## 1739 darkturquoise 65 5.8e-03 1.0e+00 1 MF dimethylallyltranstransferase activity  
## 1740 darkturquoise 65 5.8e-03 1.0e+00 1 MF geranyltranstransferase activity  
## 1741 darkturquoise 65 5.8e-03 1.0e+00 1 MF hydroxymethylbilane synthase activity  
## 1742 darkturquoise 65 5.8e-03 1.0e+00 1 MF pyroglutamyl-peptidase activity  
## 1743 darkturquoise 65 5.8e-03 1.0e+00 1 MF N6-threonylcarbomyladenosine methylthiot  
## 1744 darkturquoise 65 5.8e-03 1.0e+00 1 MF sphingolipid delta-4 desaturase activity  
## 1745 darkturquoise 65 5.8e-03 1.0e+00 1 MF betaine-homocysteine S-methyltransferase  
## 1746 darkturquoise 65 5.8e-03 1.0e+00 1 MF NF-kappaB binding  
## 1747 darkturquoise 65 8.4e-03 1.0e+00 2 MF acetylgalactosaminyltransferase activity  
## 1748 greenyellow 135 4.3e-60 3.6e-56 36 CC proteasome complex  
## 1749 greenyellow 135 1.7e-32 1.4e-28 35 BP proteasome-mediated ubiquitin-dependent   
## 1750 greenyellow 135 1.1e-31 9.5e-28 35 BP proteasomal protein catabolic process  
## 1751 greenyellow 135 1.3e-28 1.1e-24 15 CC proteasome core complex  
## 1752 greenyellow 135 1.8e-28 1.5e-24 36 BP ubiquitin-dependent protein catabolic pr  
## 1753 greenyellow 135 3.2e-28 2.7e-24 36 BP modification-dependent protein catabolic  
## 1754 greenyellow 135 1.1e-27 9.3e-24 15 MF threonine-type endopeptidase activity  
## 1755 greenyellow 135 9.2e-27 7.7e-23 36 BP proteolysis involved in cellular protein  
## 1756 greenyellow 135 1.5e-26 1.2e-22 36 BP cellular protein catabolic process  
## 1757 greenyellow 135 9.0e-26 7.5e-22 14 BP proteasomal ubiquitin-independent protei  
## 1758 greenyellow 135 1.7e-25 1.4e-21 16 CC proteasome regulatory particle  
## 1759 greenyellow 135 2.4e-25 2.0e-21 36 BP protein catabolic process  
## 1760 greenyellow 135 7.2e-20 6.0e-16 36 BP organonitrogen compound catabolic proces  
## 1761 greenyellow 135 6.5e-19 5.4e-15 47 BP catabolic process  
## 1762 greenyellow 135 3.7e-18 3.1e-14 43 BP proteolysis  
## 1763 greenyellow 135 8.5e-18 7.1e-14 42 BP organic substance catabolic process  
## 1764 greenyellow 135 3.9e-16 3.3e-12 8 CC proteasome core complex, alpha-subunit c  
## 1765 greenyellow 135 1.4e-14 1.2e-10 70 CC protein-containing complex  
## 1766 greenyellow 135 1.7e-14 1.4e-10 8 CC proteasome regulatory particle, lid subc  
## 1767 greenyellow 135 6.7e-13 5.6e-09 63 BP protein metabolic process  
## 1768 greenyellow 135 1.1e-12 9.2e-09 8 CC proteasome regulatory particle, base sub  
## 1769 greenyellow 135 7.0e-12 5.9e-08 104 CC intracellular  
## 1770 greenyellow 135 1.1e-11 9.2e-08 81 CC cytoplasm  
## 1771 greenyellow 135 2.0e-11 1.7e-07 6 CC proteasome core complex, beta-subunit co  
## 1772 greenyellow 135 2.4e-10 2.0e-06 6 MF proteasome-activating ATPase activity  
## 1773 greenyellow 135 8.8e-09 7.4e-05 24 BP protein-containing complex assembly  
## 1774 greenyellow 135 9.7e-09 8.2e-05 23 MF peptidase activity  
## 1775 greenyellow 135 1.4e-08 1.1e-04 5 BP positive regulation of RNA polymerase II  
## 1776 greenyellow 135 3.2e-08 2.7e-04 6 BP proteasome assembly  
## 1777 greenyellow 135 3.4e-08 2.9e-04 86 BP cellular metabolic process  
## 1778 greenyellow 135 6.0e-08 5.0e-04 5 BP regulation of RNA polymerase II transcri  
## 1779 greenyellow 135 9.6e-08 8.0e-04 18 MF endopeptidase activity  
## 1780 greenyellow 135 2.0e-07 1.7e-03 108 BP cellular process  
## 1781 greenyellow 135 4.6e-07 3.8e-03 5 BP positive regulation of transcription ini  
## 1782 greenyellow 135 6.7e-07 5.6e-03 81 BP nitrogen compound metabolic process  
## 1783 greenyellow 135 1.4e-06 1.2e-02 4 CC cytosolic proteasome complex  
## 1784 greenyellow 135 4.3e-06 3.6e-02 5 BP RNA polymerase II preinitiation complex   
## 1785 greenyellow 135 5.4e-06 4.5e-02 7 BP positive regulation of protein complex a  
## 1786 greenyellow 135 1.1e-05 9.5e-02 79 CC intracellular organelle  
## 1787 greenyellow 135 1.6e-05 1.4e-01 5 BP transcription preinitiation complex asse  
## 1788 greenyellow 135 2.2e-05 1.9e-01 69 CC intracellular membrane-bounded organelle  
## 1789 greenyellow 135 3.4e-05 2.9e-01 3 BP protein geranylgeranylation  
## 1790 greenyellow 135 6.0e-05 5.0e-01 3 BP protein prenylation  
## 1791 greenyellow 135 8.1e-05 6.8e-01 19 CC cytosol  
## 1792 greenyellow 135 1.2e-04 9.9e-01 36 MF hydrolase activity  
## 1793 greenyellow 135 1.3e-04 1.0e+00 4 BP lamellipodium assembly  
## 1794 greenyellow 135 1.5e-04 1.0e+00 2 CC CAAX-protein geranylgeranyltransferase c  
## 1795 greenyellow 135 1.5e-04 1.0e+00 2 MF CAAX-protein geranylgeranyltransferase a  
## 1796 greenyellow 135 2.0e-04 1.0e+00 3 BP cellular response to virus  
## 1797 greenyellow 135 2.0e-04 1.0e+00 3 CC ER membrane protein complex  
## 1798 greenyellow 135 2.7e-04 1.0e+00 3 BP protein folding in endoplasmic reticulum  
## 1799 greenyellow 135 4.4e-04 1.0e+00 2 BP regulation of dopamine metabolic process  
## 1800 greenyellow 135 5.1e-04 1.0e+00 6 BP protein-DNA complex assembly  
## 1801 greenyellow 135 5.8e-04 1.0e+00 3 MF TBP-class protein binding  
## 1802 greenyellow 135 8.7e-04 1.0e+00 2 BP peroxisome fission  
## 1803 greenyellow 135 8.7e-04 1.0e+00 2 BP molybdopterin cofactor biosynthetic proc  
## 1804 greenyellow 135 8.7e-04 1.0e+00 2 BP regulation of catecholamine metabolic pr  
## 1805 greenyellow 135 9.9e-04 1.0e+00 5 BP regulation of protein catabolic process  
## 1806 greenyellow 135 1.1e-03 1.0e+00 3 BP regulation of lamellipodium assembly  
## 1807 greenyellow 135 1.1e-03 1.0e+00 7 BP ribonucleoprotein complex assembly  
## 1808 greenyellow 135 1.2e-03 1.0e+00 6 BP neurotransmitter secretion  
## 1809 greenyellow 135 1.8e-03 1.0e+00 5 CC integral component of endoplasmic reticu  
## 1810 greenyellow 135 1.9e-03 1.0e+00 5 BP transcription initiation from RNA polyme  
## 1811 greenyellow 135 2.1e-03 1.0e+00 15 CC ribonucleoprotein complex  
## 1812 greenyellow 135 2.1e-03 1.0e+00 8 CC endoplasmic reticulum membrane  
## 1813 greenyellow 135 2.1e-03 1.0e+00 2 BP Mo-molybdopterin cofactor biosynthetic p  
## 1814 greenyellow 135 2.1e-03 1.0e+00 2 BP molybdopterin cofactor metabolic process  
## 1815 greenyellow 135 2.2e-03 1.0e+00 5 CC intrinsic component of endoplasmic retic  
## 1816 greenyellow 135 2.6e-03 1.0e+00 3 BP positive regulation of proteasomal ubiqu  
## 1817 greenyellow 135 2.9e-03 1.0e+00 4 BP ribosome assembly  
## 1818 greenyellow 135 3.0e-03 1.0e+00 2 MF vitamin transmembrane transporter activi  
## 1819 greenyellow 135 3.0e-03 1.0e+00 5 BP macroautophagy  
## 1820 greenyellow 135 3.0e-03 1.0e+00 5 CC mitochondrial ribosome  
## 1821 greenyellow 135 3.3e-03 1.0e+00 3 BP endoplasmic reticulum organization  
## 1822 greenyellow 135 3.3e-03 1.0e+00 3 BP positive regulation of proteasomal prote  
## 1823 greenyellow 135 3.4e-03 1.0e+00 5 BP DNA-templated transcription, initiation  
## 1824 greenyellow 135 3.6e-03 1.0e+00 59 MF catalytic activity  
## 1825 greenyellow 135 3.9e-03 1.0e+00 2 CC Arp2/3 protein complex  
## 1826 greenyellow 135 4.2e-03 1.0e+00 4 BP vacuole organization  
## 1827 greenyellow 135 4.2e-03 1.0e+00 3 BP positive regulation of ubiquitin-depende  
## 1828 greenyellow 135 4.3e-03 1.0e+00 7 MF structural constituent of ribosome  
## 1829 greenyellow 135 4.3e-03 1.0e+00 12 CC endoplasmic reticulum  
## 1830 greenyellow 135 4.9e-03 1.0e+00 10 MF ATPase activity  
## 1831 greenyellow 135 5.0e-03 1.0e+00 2 BP negative regulation of phosphatase activ  
## 1832 greenyellow 135 5.0e-03 1.0e+00 2 BP actin filament depolymerization  
## 1833 greenyellow 135 5.0e-03 1.0e+00 2 BP vitamin transport  
## 1834 greenyellow 135 5.0e-03 1.0e+00 2 CC lamellipodium  
## 1835 greenyellow 135 5.0e-03 1.0e+00 2 MF polyubiquitin modification-dependent pro  
## 1836 greenyellow 135 5.1e-03 1.0e+00 3 BP regulation of proteasomal ubiquitin-depe  
## 1837 greenyellow 135 5.1e-03 1.0e+00 3 BP positive regulation of proteolysis invol  
## 1838 greenyellow 135 5.7e-03 1.0e+00 6 BP signal release  
## 1839 greenyellow 135 5.7e-03 1.0e+00 4 BP actin filament polymerization  
## 1840 greenyellow 135 5.9e-03 1.0e+00 6 BP neurotransmitter transport  
## 1841 greenyellow 135 6.1e-03 1.0e+00 4 BP positive regulation of proteolysis  
## 1842 greenyellow 135 6.2e-03 1.0e+00 2 CC integral component of peroxisomal membra  
## 1843 greenyellow 135 6.2e-03 1.0e+00 2 MF sulfurtransferase activity  
## 1844 greenyellow 135 6.4e-03 1.0e+00 4 MF transferase activity, transferring alkyl  
## 1845 greenyellow 135 6.8e-03 1.0e+00 3 BP autophagosome assembly  
## 1846 greenyellow 135 6.8e-03 1.0e+00 3 BP positive regulation of cellular protein   
## 1847 greenyellow 135 6.8e-03 1.0e+00 3 CC mitochondrial small ribosomal subunit  
## 1848 greenyellow 135 6.8e-03 1.0e+00 16 CC mitochondrion  
## 1849 greenyellow 135 7.2e-03 1.0e+00 9 BP chemical synaptic transmission  
## 1850 greenyellow 135 7.4e-03 1.0e+00 3 BP regulation of proteasomal protein catabo  
## 1851 greenyellow 135 7.5e-03 1.0e+00 12 MF structural molecule activity  
## 1852 greenyellow 135 7.5e-03 1.0e+00 9 BP synaptic signaling  
## 1853 greenyellow 135 7.5e-03 1.0e+00 2 MF prenyltransferase activity  
## 1854 greenyellow 135 7.6e-03 1.0e+00 7 CC ribosome  
## 1855 greenyellow 135 8.9e-03 1.0e+00 4 BP actin polymerization or depolymerization  
## 1856 greenyellow 135 9.5e-03 1.0e+00 5 BP mitochondrial translation  
## 1857 grey 1049 7.2e-18 6.0e-14 508 CC intracellular organelle  
## 1858 grey 1049 3.4e-17 2.8e-13 593 CC intracellular  
## 1859 grey 1049 8.2e-13 6.9e-09 423 CC intracellular membrane-bounded organelle  
## 1860 grey 1049 9.8e-12 8.2e-08 401 CC cytoplasm  
## 1861 grey 1049 1.2e-09 1.0e-05 87 CC organelle membrane  
## 1862 grey 1049 3.5e-09 2.9e-05 64 BP regulation of nervous system development  
## 1863 grey 1049 7.4e-09 6.2e-05 212 BP regulation of cellular metabolic process  
## 1864 grey 1049 8.0e-09 6.7e-05 38 BP small GTPase mediated signal transductio  
## 1865 grey 1049 1.5e-08 1.3e-04 79 BP vesicle-mediated transport  
## 1866 grey 1049 1.6e-08 1.3e-04 299 BP cellular component organization  
## 1867 grey 1049 3.1e-08 2.6e-04 40 CC mitochondrial inner membrane  
## 1868 grey 1049 3.4e-08 2.9e-04 49 BP regulation of neurogenesis  
## 1869 grey 1049 4.4e-08 3.7e-04 28 BP dorsal closure  
## 1870 grey 1049 5.6e-08 4.7e-04 650 BP cellular process  
## 1871 grey 1049 9.6e-08 8.1e-04 204 BP organelle organization  
## 1872 grey 1049 1.0e-07 8.6e-04 30 BP morphogenesis of embryonic epithelium  
## 1873 grey 1049 1.2e-07 9.7e-04 465 BP cellular metabolic process  
## 1874 grey 1049 2.3e-07 2.0e-03 139 BP nervous system development  
## 1875 grey 1049 2.6e-07 2.2e-03 67 BP regulation of cell differentiation  
## 1876 grey 1049 2.6e-07 2.2e-03 36 BP embryonic development via the syncytial   
## 1877 grey 1049 3.1e-07 2.6e-03 39 BP embryo development ending in birth or eg  
## 1878 grey 1049 3.9e-07 3.3e-03 32 BP Ras protein signal transduction  
## 1879 grey 1049 4.1e-07 3.4e-03 83 BP phosphorylation  
## 1880 grey 1049 4.8e-07 4.0e-03 221 BP regulation of metabolic process  
## 1881 grey 1049 5.7e-07 4.8e-03 43 CC mitochondrial membrane  
## 1882 grey 1049 5.8e-07 4.8e-03 20 CC mitochondrial respiratory chain  
## 1883 grey 1049 6.0e-07 5.1e-03 28 BP ATP metabolic process  
## 1884 grey 1049 7.2e-07 6.0e-03 91 BP intracellular transport  
## 1885 grey 1049 7.6e-07 6.4e-03 52 BP cell migration  
## 1886 grey 1049 8.0e-07 6.7e-03 124 CC endomembrane system  
## 1887 grey 1049 8.0e-07 6.7e-03 39 CC endosome  
## 1888 grey 1049 9.1e-07 7.6e-03 35 BP generation of precursor metabolites and   
## 1889 grey 1049 1.0e-06 8.8e-03 35 BP regulation of neuron differentiation  
## 1890 grey 1049 1.6e-06 1.3e-02 63 CC vesicle  
## 1891 grey 1049 1.7e-06 1.4e-02 58 CC cytoplasmic vesicle  
## 1892 grey 1049 1.8e-06 1.5e-02 122 BP phosphate-containing compound metabolic   
## 1893 grey 1049 2.0e-06 1.7e-02 142 BP cellular protein modification process  
## 1894 grey 1049 2.1e-06 1.7e-02 14 CC mitochondrial respiratory chain complex   
## 1895 grey 1049 2.1e-06 1.7e-02 14 CC NADH dehydrogenase complex  
## 1896 grey 1049 2.5e-06 2.1e-02 20 BP electron transport chain  
## 1897 grey 1049 2.6e-06 2.2e-02 268 CC protein-containing complex  
## 1898 grey 1049 3.0e-06 2.5e-02 43 CC mitochondrial envelope  
## 1899 grey 1049 3.2e-06 2.6e-02 20 BP negative regulation of neurogenesis  
## 1900 grey 1049 3.8e-06 3.2e-02 91 BP protein localization  
## 1901 grey 1049 4.3e-06 3.6e-02 18 BP mitochondrial ATP synthesis coupled elec  
## 1902 grey 1049 4.5e-06 3.8e-02 66 BP regulation of localization  
## 1903 grey 1049 4.9e-06 4.1e-02 67 BP establishment of protein localization  
## 1904 grey 1049 5.2e-06 4.4e-02 19 BP respiratory electron transport chain  
## 1905 grey 1049 5.5e-06 4.6e-02 18 BP ATP synthesis coupled electron transport  
## 1906 grey 1049 6.1e-06 5.1e-02 20 BP oxidative phosphorylation  
## 1907 grey 1049 6.3e-06 5.3e-02 90 CC mitochondrion  
## 1908 grey 1049 8.7e-06 7.3e-02 108 BP generation of neurons  
## 1909 grey 1049 9.3e-06 7.8e-02 112 BP neurogenesis  
## 1910 grey 1049 9.4e-06 7.9e-02 248 BP multicellular organism development  
## 1911 grey 1049 1.1e-05 8.9e-02 26 BP border follicle cell migration  
## 1912 grey 1049 1.1e-05 9.1e-02 23 BP cellular respiration  
## 1913 grey 1049 1.2e-05 1.0e-01 138 BP regulation of RNA metabolic process  
## 1914 grey 1049 1.6e-05 1.3e-01 129 BP regulation of transcription, DNA-templat  
## 1915 grey 1049 1.6e-05 1.3e-01 31 BP autophagy  
## 1916 grey 1049 1.6e-05 1.3e-01 27 BP ovarian follicle cell migration  
## 1917 grey 1049 1.7e-05 1.5e-01 21 BP regulation of GTPase activity  
## 1918 grey 1049 1.8e-05 1.5e-01 238 MF protein binding  
## 1919 grey 1049 1.8e-05 1.5e-01 7 BP late endosome to vacuole transport  
## 1920 grey 1049 2.0e-05 1.7e-01 52 BP cell motility  
## 1921 grey 1049 2.3e-05 1.9e-01 63 BP protein transport  
## 1922 grey 1049 2.4e-05 2.0e-01 20 BP Golgi organization  
## 1923 grey 1049 2.6e-05 2.2e-01 6 BP dorsal closure, spreading of leading edg  
## 1924 grey 1049 2.8e-05 2.4e-01 49 BP regulation of catalytic activity  
## 1925 grey 1049 3.1e-05 2.6e-01 53 BP intracellular protein transport  
## 1926 grey 1049 3.2e-05 2.7e-01 71 BP cellular protein localization  
## 1927 grey 1049 3.5e-05 2.9e-01 20 BP regulation of small GTPase mediated sign  
## 1928 grey 1049 4.0e-05 3.3e-01 13 BP regulation of epidermal growth factor re  
## 1929 grey 1049 4.4e-05 3.7e-01 94 BP regulation of developmental process  
## 1930 grey 1049 4.4e-05 3.7e-01 28 BP regulation of cytoskeleton organization  
## 1931 grey 1049 4.8e-05 4.0e-01 27 BP regulation of cell morphogenesis  
## 1932 grey 1049 4.9e-05 4.1e-01 20 CC adherens junction  
## 1933 grey 1049 5.3e-05 4.5e-01 34 CC polytene chromosome  
## 1934 grey 1049 5.4e-05 4.5e-01 4 BP protein transport to vacuole involved in  
## 1935 grey 1049 5.5e-05 4.6e-01 27 BP regulation of cell projection organizati  
## 1936 grey 1049 5.6e-05 4.7e-01 81 BP neuron development  
## 1937 grey 1049 5.8e-05 4.8e-01 39 BP embryonic morphogenesis  
## 1938 grey 1049 5.8e-05 4.9e-01 16 CC coated vesicle  
## 1939 grey 1049 5.9e-05 5.0e-01 26 BP negative regulation of cell differentiat  
## 1940 grey 1049 6.0e-05 5.0e-01 33 BP ameboidal-type cell migration  
## 1941 grey 1049 6.3e-05 5.3e-01 36 BP establishment or maintenance of cell pol  
## 1942 grey 1049 6.4e-05 5.4e-01 92 BP regulation of signal transduction  
## 1943 grey 1049 7.6e-05 6.4e-01 130 BP transcription, DNA-templated  
## 1944 grey 1049 7.8e-05 6.6e-01 11 BP actin cytoskeleton reorganization  
## 1945 grey 1049 8.1e-05 6.8e-01 20 BP regulation of autophagy  
## 1946 grey 1049 8.4e-05 7.1e-01 156 BP cell development  
## 1947 grey 1049 8.6e-05 7.2e-01 82 BP locomotion  
## 1948 grey 1049 8.9e-05 7.4e-01 270 BP anatomical structure development  
## 1949 grey 1049 9.0e-05 7.6e-01 10 BP negative regulation of epidermal growth   
## 1950 grey 1049 9.2e-05 7.7e-01 21 BP endosomal transport  
## 1951 grey 1049 9.3e-05 7.8e-01 93 BP neuron differentiation  
## 1952 grey 1049 1.1e-04 8.8e-01 75 BP cell morphogenesis  
## 1953 grey 1049 1.2e-04 9.7e-01 81 BP regulation of transcription by RNA polym  
## 1954 grey 1049 1.2e-04 1.0e+00 6 BP ubiquitin-dependent protein catabolic pr  
## 1955 grey 1049 1.2e-04 1.0e+00 10 BP mitochondrial electron transport, NADH t  
## 1956 grey 1049 1.3e-04 1.0e+00 32 BP endocytosis  
## 1957 grey 1049 1.3e-04 1.0e+00 137 BP animal organ development  
## 1958 grey 1049 1.3e-04 1.0e+00 279 BP developmental process  
## 1959 grey 1049 1.3e-04 1.0e+00 31 BP transmembrane receptor protein tyrosine   
## 1960 grey 1049 1.3e-04 1.0e+00 14 CC Golgi-associated vesicle  
## 1961 grey 1049 1.3e-04 1.0e+00 77 BP cytoskeleton organization  
## 1962 grey 1049 1.4e-04 1.0e+00 48 BP negative regulation of signal transducti  
## 1963 grey 1049 1.4e-04 1.0e+00 158 BP regulation of gene expression  
## 1964 grey 1049 1.5e-04 1.0e+00 15 BP epidermal growth factor receptor signali  
## 1965 grey 1049 1.5e-04 1.0e+00 60 BP growth  
## 1966 grey 1049 1.5e-04 1.0e+00 75 BP cellular macromolecule localization  
## 1967 grey 1049 1.6e-04 1.0e+00 72 CC chromosome  
## 1968 grey 1049 1.7e-04 1.0e+00 10 MF NADH dehydrogenase activity  
## 1969 grey 1049 1.8e-04 1.0e+00 13 MF oxidoreductase activity, acting on NAD(P  
## 1970 grey 1049 1.8e-04 1.0e+00 67 BP pattern specification process  
## 1971 grey 1049 2.0e-04 1.0e+00 14 BP regulation of microtubule-based process  
## 1972 grey 1049 2.0e-04 1.0e+00 55 BP eye development  
## 1973 grey 1049 2.3e-04 1.0e+00 48 BP axonogenesis  
## 1974 grey 1049 2.3e-04 1.0e+00 10 BP negative regulation of neuron differenti  
## 1975 grey 1049 2.3e-04 1.0e+00 122 BP multicellular organism reproduction  
## 1976 grey 1049 2.4e-04 1.0e+00 33 BP membrane organization  
## 1977 grey 1049 2.5e-04 1.0e+00 179 BP cell differentiation  
## 1978 grey 1049 2.5e-04 1.0e+00 41 CC chromatin  
## 1979 grey 1049 2.6e-04 1.0e+00 45 BP regulation of growth  
## 1980 grey 1049 2.6e-04 1.0e+00 22 BP stem cell proliferation  
## 1981 grey 1049 2.7e-04 1.0e+00 9 BP protein localization to endoplasmic reti  
## 1982 grey 1049 2.7e-04 1.0e+00 52 BP compound eye development  
## 1983 grey 1049 2.9e-04 1.0e+00 37 BP regulation of transport  
## 1984 grey 1049 3.0e-04 1.0e+00 7 MF oxidoreductase activity, acting on NAD(P  
## 1985 grey 1049 3.0e-04 1.0e+00 49 BP axon development  
## 1986 grey 1049 3.1e-04 1.0e+00 17 BP regulation of Ras protein signal transdu  
## 1987 grey 1049 3.1e-04 1.0e+00 83 BP transcription by RNA polymerase II  
## 1988 grey 1049 3.2e-04 1.0e+00 56 CC endoplasmic reticulum  
## 1989 grey 1049 3.5e-04 1.0e+00 28 CC cell junction  
## 1990 grey 1049 3.5e-04 1.0e+00 90 BP animal organ morphogenesis  
## 1991 grey 1049 3.5e-04 1.0e+00 46 CC Golgi apparatus  
## 1992 grey 1049 3.6e-04 1.0e+00 63 BP neuron projection development  
## 1993 grey 1049 3.6e-04 1.0e+00 40 BP regulation of cell death  
## 1994 grey 1049 3.7e-04 1.0e+00 16 BP regulation of cell migration  
## 1995 grey 1049 3.9e-04 1.0e+00 11 BP establishment or maintenance of apical/b  
## 1996 grey 1049 4.0e-04 1.0e+00 26 BP positive regulation of cell differentiat  
## 1997 grey 1049 4.0e-04 1.0e+00 84 BP organic substance transport  
## 1998 grey 1049 4.2e-04 1.0e+00 28 BP epithelial cell migration  
## 1999 grey 1049 4.3e-04 1.0e+00 59 BP cell morphogenesis involved in neuron di  
## 2000 grey 1049 4.3e-04 1.0e+00 14 BP regulation of axonogenesis  
## 2001 grey 1049 4.4e-04 1.0e+00 58 CC nucleoplasm  
## 2002 grey 1049 4.7e-04 1.0e+00 28 BP epithelium migration  
## 2003 grey 1049 4.8e-04 1.0e+00 63 BP sensory organ development  
## 2004 grey 1049 5.1e-04 1.0e+00 238 CC membrane  
## 2005 grey 1049 5.6e-04 1.0e+00 424 BP nitrogen compound metabolic process  
## 2006 grey 1049 5.8e-04 1.0e+00 42 BP actin filament-based process  
## 2007 grey 1049 6.0e-04 1.0e+00 8 BP endosome transport via multivesicular bo  
## 2008 grey 1049 6.2e-04 1.0e+00 14 BP regulation of cell shape  
## 2009 grey 1049 6.2e-04 1.0e+00 11 CC cell division site  
## 2010 grey 1049 6.3e-04 1.0e+00 3 CC ESCRT II complex  
## 2011 grey 1049 6.3e-04 1.0e+00 63 BP cell morphogenesis involved in different  
## 2012 grey 1049 6.3e-04 1.0e+00 30 CC endoplasmic reticulum membrane  
## 2013 grey 1049 6.5e-04 1.0e+00 33 BP purine nucleotide metabolic process  
## 2014 grey 1049 6.6e-04 1.0e+00 9 BP establishment or maintenance of epitheli  
## 2015 grey 1049 6.6e-04 1.0e+00 9 CC transcriptionally active chromatin  
## 2016 grey 1049 6.9e-04 1.0e+00 12 BP vacuolar transport  
## 2017 grey 1049 6.9e-04 1.0e+00 12 BP regulation of microtubule cytoskeleton o  
## 2018 grey 1049 6.9e-04 1.0e+00 780 CC cellular\_component  
## 2019 grey 1049 7.0e-04 1.0e+00 4 BP late endosome to vacuole transport via m  
## 2020 grey 1049 7.1e-04 1.0e+00 40 BP actin cytoskeleton organization  
## 2021 grey 1049 7.2e-04 1.0e+00 64 BP positive regulation of gene expression  
## 2022 grey 1049 7.6e-04 1.0e+00 162 BP anatomical structure morphogenesis  
## 2023 grey 1049 7.7e-04 1.0e+00 11 BP fatty acid catabolic process  
## 2024 grey 1049 8.1e-04 1.0e+00 18 BP lipid modification  
## 2025 grey 1049 8.1e-04 1.0e+00 26 BP learning or memory  
## 2026 grey 1049 8.2e-04 1.0e+00 8 BP endoplasmic reticulum organization  
## 2027 grey 1049 8.3e-04 1.0e+00 25 BP response to hormone  
## 2028 grey 1049 8.4e-04 1.0e+00 131 BP reproduction  
## 2029 grey 1049 8.9e-04 1.0e+00 57 MF enzyme binding  
## 2030 grey 1049 9.1e-04 1.0e+00 54 BP positive regulation of transcription, DN  
## 2031 grey 1049 9.3e-04 1.0e+00 16 BP histone acetylation  
## 2032 grey 1049 9.8e-04 1.0e+00 72 CC cytosol  
## 2033 grey 1049 9.9e-04 1.0e+00 6 BP negative regulation of photoreceptor cel  
## 2034 grey 1049 9.9e-04 1.0e+00 6 MF NADH dehydrogenase (ubiquinone) activity  
## 2035 grey 1049 1.0e-03 1.0e+00 13 CC endosome membrane  
## 2036 grey 1049 1.1e-03 1.0e+00 16 BP peptidyl-lysine acetylation  
## 2037 grey 1049 1.1e-03 1.0e+00 58 BP neuron projection morphogenesis  
## 2038 grey 1049 1.1e-03 1.0e+00 72 BP morphogenesis of an epithelium  
## 2039 grey 1049 1.1e-03 1.0e+00 9 BP fatty acid beta-oxidation  
## 2040 grey 1049 1.1e-03 1.0e+00 77 BP intracellular signal transduction  
## 2041 grey 1049 1.1e-03 1.0e+00 27 MF Ras GTPase binding  
## 2042 grey 1049 1.2e-03 1.0e+00 100 BP gamete generation  
## 2043 grey 1049 1.2e-03 1.0e+00 19 CC centrosome  
## 2044 grey 1049 1.2e-03 1.0e+00 33 BP ribose phosphate metabolic process  
## 2045 grey 1049 1.2e-03 1.0e+00 53 BP protein phosphorylation  
## 2046 grey 1049 1.3e-03 1.0e+00 37 BP positive regulation of cellular protein   
## 2047 grey 1049 1.3e-03 1.0e+00 10 BP adherens junction organization  
## 2048 grey 1049 1.3e-03 1.0e+00 109 BP epithelium development  
## 2049 grey 1049 1.3e-03 1.0e+00 32 BP ribonucleotide metabolic process  
## 2050 grey 1049 1.3e-03 1.0e+00 125 BP reproductive process  
## 2051 grey 1049 1.4e-03 1.0e+00 35 MF protein kinase activity  
## 2052 grey 1049 1.4e-03 1.0e+00 13 MF Ras guanyl-nucleotide exchange factor ac  
## 2053 grey 1049 1.4e-03 1.0e+00 8 CC COPII-coated ER to Golgi transport vesic  
## 2054 grey 1049 1.5e-03 1.0e+00 27 MF small GTPase binding  
## 2055 grey 1049 1.5e-03 1.0e+00 28 BP histone modification  
## 2056 grey 1049 1.6e-03 1.0e+00 34 BP regulation of programmed cell death  
## 2057 grey 1049 1.6e-03 1.0e+00 48 BP developmental growth  
## 2058 grey 1049 1.7e-03 1.0e+00 236 CC nucleus  
## 2059 grey 1049 1.7e-03 1.0e+00 177 BP cell communication  
## 2060 grey 1049 1.7e-03 1.0e+00 20 BP memory  
## 2061 grey 1049 1.8e-03 1.0e+00 27 BP neuromuscular junction development  
## 2062 grey 1049 1.8e-03 1.0e+00 47 BP cell proliferation  
## 2063 grey 1049 1.9e-03 1.0e+00 14 BP ER to Golgi vesicle-mediated transport  
## 2064 grey 1049 1.9e-03 1.0e+00 38 BP axon guidance  
## 2065 grey 1049 2.0e-03 1.0e+00 10 BP axo-dendritic transport  
## 2066 grey 1049 2.0e-03 1.0e+00 13 BP establishment of cell polarity  
## 2067 grey 1049 2.0e-03 1.0e+00 12 BP regulation of endocytosis  
## 2068 grey 1049 2.1e-03 1.0e+00 81 BP cell surface receptor signaling pathway  
## 2069 grey 1049 2.1e-03 1.0e+00 20 BP morphogenesis of a polarized epithelium  
## 2070 grey 1049 2.1e-03 1.0e+00 6 BP cell competition in a multicellular orga  
## 2071 grey 1049 2.1e-03 1.0e+00 6 BP negative regulation of small GTPase medi  
## 2072 grey 1049 2.1e-03 1.0e+00 6 CC mitochondrial proton-transporting ATP sy  
## 2073 grey 1049 2.2e-03 1.0e+00 5 BP lipid droplet organization  
## 2074 grey 1049 2.2e-03 1.0e+00 5 CC multivesicular body  
## 2075 grey 1049 2.2e-03 1.0e+00 9 CC recycling endosome  
## 2076 grey 1049 2.4e-03 1.0e+00 3 BP septum digestion after cytokinesis  
## 2077 grey 1049 2.4e-03 1.0e+00 3 BP stress granule assembly  
## 2078 grey 1049 2.4e-03 1.0e+00 3 CC CCR4-NOT core complex  
## 2079 grey 1049 2.4e-03 1.0e+00 3 MF acetyl-CoA C-acyltransferase activity  
## 2080 grey 1049 2.4e-03 1.0e+00 16 BP protein acetylation  
## 2081 grey 1049 2.4e-03 1.0e+00 10 BP Rab protein signal transduction  
## 2082 grey 1049 2.4e-03 1.0e+00 12 MF electron transfer activity  
## 2083 grey 1049 2.4e-03 1.0e+00 17 BP positive regulation of neurogenesis  
## 2084 grey 1049 2.4e-03 1.0e+00 222 BP protein metabolic process  
## 2085 grey 1049 2.5e-03 1.0e+00 71 BP oogenesis  
## 2086 grey 1049 2.7e-03 1.0e+00 19 BP regulation of locomotion  
## 2087 grey 1049 2.7e-03 1.0e+00 16 BP negative regulation of cell proliferatio  
## 2088 grey 1049 2.7e-03 1.0e+00 9 BP fatty acid oxidation  
## 2089 grey 1049 2.7e-03 1.0e+00 60 BP tube morphogenesis  
## 2090 grey 1049 2.8e-03 1.0e+00 38 BP wing disc morphogenesis  
## 2091 grey 1049 2.8e-03 1.0e+00 14 BP long-term memory  
## 2092 grey 1049 2.8e-03 1.0e+00 14 BP response to insulin  
## 2093 grey 1049 2.8e-03 1.0e+00 4 BP semaphorin-plexin signaling pathway  
## 2094 grey 1049 2.8e-03 1.0e+00 4 CC mitochondrial proton-transporting ATP sy  
## 2095 grey 1049 2.8e-03 1.0e+00 4 MF acyl-CoA dehydrogenase activity  
## 2096 grey 1049 2.8e-03 1.0e+00 37 BP imaginal disc-derived wing morphogenesis  
## 2097 grey 1049 2.9e-03 1.0e+00 28 MF GTPase binding  
## 2098 grey 1049 3.0e-03 1.0e+00 15 MF GTPase activator activity  
## 2099 grey 1049 3.0e-03 1.0e+00 8 BP segment specification  
## 2100 grey 1049 3.1e-03 1.0e+00 13 MF protein transporter activity  
## 2101 grey 1049 3.1e-03 1.0e+00 26 BP positive regulation of catalytic activit  
## 2102 grey 1049 3.1e-03 1.0e+00 7 BP autophagosome maturation  
## 2103 grey 1049 3.2e-03 1.0e+00 45 BP epithelial cell development  
## 2104 grey 1049 3.3e-03 1.0e+00 5 BP peptidyl-lysine trimethylation  
## 2105 grey 1049 3.3e-03 1.0e+00 9 BP lipid oxidation  
## 2106 grey 1049 3.3e-03 1.0e+00 15 BP macroautophagy  
## 2107 grey 1049 3.4e-03 1.0e+00 16 MF kinase binding  
## 2108 grey 1049 3.4e-03 1.0e+00 10 BP regulation of photoreceptor cell differe  
## 2109 grey 1049 3.5e-03 1.0e+00 49 BP imaginal disc morphogenesis  
## 2110 grey 1049 3.6e-03 1.0e+00 41 BP ovarian follicle cell development  
## 2111 grey 1049 3.6e-03 1.0e+00 171 BP signaling  
## 2112 grey 1049 3.7e-03 1.0e+00 18 BP establishment of planar polarity  
## 2113 grey 1049 3.7e-03 1.0e+00 18 BP establishment of tissue polarity  
## 2114 grey 1049 3.8e-03 1.0e+00 17 BP neuroblast proliferation  
## 2115 grey 1049 3.8e-03 1.0e+00 56 BP metamorphosis  
## 2116 grey 1049 4.0e-03 1.0e+00 43 BP imaginal disc-derived appendage developm  
## 2117 grey 1049 4.0e-03 1.0e+00 6 CC cell-cell adherens junction  
## 2118 grey 1049 4.0e-03 1.0e+00 9 BP negative regulation of stem cell prolife  
## 2119 grey 1049 4.1e-03 1.0e+00 10 BP positive regulation of cell cycle proces  
## 2120 grey 1049 4.1e-03 1.0e+00 47 BP cell death  
## 2121 grey 1049 4.3e-03 1.0e+00 61 BP protein-containing complex assembly  
## 2122 grey 1049 4.4e-03 1.0e+00 149 BP signal transduction  
## 2123 grey 1049 4.5e-03 1.0e+00 25 BP synapse assembly  
## 2124 grey 1049 4.6e-03 1.0e+00 13 CC late endosome  
## 2125 grey 1049 4.6e-03 1.0e+00 28 MF chromatin binding  
## 2126 grey 1049 4.6e-03 1.0e+00 8 CC P-body  
## 2127 grey 1049 4.7e-03 1.0e+00 20 BP oocyte construction  
## 2128 grey 1049 4.7e-03 1.0e+00 45 BP taxis  
## 2129 grey 1049 4.7e-03 1.0e+00 41 BP post-embryonic appendage morphogenesis  
## 2130 grey 1049 4.7e-03 1.0e+00 14 CC neuromuscular junction  
## 2131 grey 1049 4.8e-03 1.0e+00 5 BP regulation of histone acetylation  
## 2132 grey 1049 4.8e-03 1.0e+00 5 BP regulation of oviposition  
## 2133 grey 1049 4.8e-03 1.0e+00 5 BP nonassociative learning  
## 2134 grey 1049 4.8e-03 1.0e+00 5 MF TBP-class protein binding  
## 2135 grey 1049 4.8e-03 1.0e+00 4 BP regulation of post-mating oviposition  
## 2136 grey 1049 4.8e-03 1.0e+00 4 CC BLOC-1 complex  
## 2137 grey 1049 4.8e-03 1.0e+00 24 BP oocyte differentiation  
## 2138 grey 1049 5.0e-03 1.0e+00 12 BP cortical actin cytoskeleton organization  
## 2139 grey 1049 5.0e-03 1.0e+00 18 CC cell-cell junction  
## 2140 grey 1049 5.1e-03 1.0e+00 99 BP catabolic process  
## 2141 grey 1049 5.1e-03 1.0e+00 7 BP negative regulation of autophagy  
## 2142 grey 1049 5.1e-03 1.0e+00 7 BP regulation of cell fate specification  
## 2143 grey 1049 5.1e-03 1.0e+00 7 BP histone H3-K4 methylation  
## 2144 grey 1049 5.1e-03 1.0e+00 7 CC cytochrome complex  
## 2145 grey 1049 5.3e-03 1.0e+00 113 BP tissue development  
## 2146 grey 1049 5.3e-03 1.0e+00 39 BP compound eye morphogenesis  
## 2147 grey 1049 5.3e-03 1.0e+00 29 BP regulation of apoptotic process  
## 2148 grey 1049 5.3e-03 1.0e+00 21 BP Golgi vesicle transport  
## 2149 grey 1049 5.3e-03 1.0e+00 6 BP establishment of mitotic spindle orienta  
## 2150 grey 1049 5.3e-03 1.0e+00 14 MF guanyl-nucleotide exchange factor activi  
## 2151 grey 1049 5.4e-03 1.0e+00 15 CC transport vesicle  
## 2152 grey 1049 5.4e-03 1.0e+00 36 BP nucleotide metabolic process  
## 2153 grey 1049 5.5e-03 1.0e+00 3 BP lysosome localization  
## 2154 grey 1049 5.5e-03 1.0e+00 3 BP dorsal closure, leading edge cell differ  
## 2155 grey 1049 5.5e-03 1.0e+00 3 BP sensory neuron axon guidance  
## 2156 grey 1049 5.6e-03 1.0e+00 24 CC nuclear chromatin  
## 2157 grey 1049 5.7e-03 1.0e+00 29 BP protein localization to organelle  
## 2158 grey 1049 5.7e-03 1.0e+00 8 BP negative regulation of neuroblast prolif  
## 2159 grey 1049 5.7e-03 1.0e+00 8 CC cleavage furrow  
## 2160 grey 1049 5.7e-03 1.0e+00 25 BP regulation of synapse structure or activ  
## 2161 grey 1049 5.8e-03 1.0e+00 9 BP ATP biosynthetic process  
## 2162 grey 1049 5.9e-03 1.0e+00 39 MF enzyme regulator activity  
## 2163 grey 1049 5.9e-03 1.0e+00 13 BP cellular response to insulin stimulus  
## 2164 grey 1049 5.9e-03 1.0e+00 13 CC apical junction complex  
## 2165 grey 1049 6.0e-03 1.0e+00 79 BP tube development  
## 2166 grey 1049 6.1e-03 1.0e+00 24 CC cell cortex  
## 2167 grey 1049 6.1e-03 1.0e+00 229 BP biosynthetic process  
## 2168 grey 1049 6.1e-03 1.0e+00 25 MF protein serine/threonine kinase activity  
## 2169 grey 1049 6.3e-03 1.0e+00 34 CC nuclear chromosome  
## 2170 grey 1049 6.4e-03 1.0e+00 36 BP nucleoside phosphate metabolic process  
## 2171 grey 1049 6.5e-03 1.0e+00 78 BP germ cell development  
## 2172 grey 1049 6.6e-03 1.0e+00 27 BP axis specification  
## 2173 grey 1049 6.6e-03 1.0e+00 10 BP positive regulation of protein catabolic  
## 2174 grey 1049 6.6e-03 1.0e+00 5 BP ecdysone-mediated induction of salivary   
## 2175 grey 1049 6.6e-03 1.0e+00 5 MF intramolecular transferase activity  
## 2176 grey 1049 6.7e-03 1.0e+00 14 MF protein kinase binding  
## 2177 grey 1049 6.8e-03 1.0e+00 21 BP oocyte development  
## 2178 grey 1049 6.9e-03 1.0e+00 9 BP positive regulation of mitotic cell cycl  
## 2179 grey 1049 7.2e-03 1.0e+00 61 BP oxidation-reduction process  
## 2180 grey 1049 7.2e-03 1.0e+00 16 BP cell fate specification  
## 2181 grey 1049 7.3e-03 1.0e+00 2 BP regulation of glycolytic process  
## 2182 grey 1049 7.3e-03 1.0e+00 2 BP monoubiquitinated histone H2A deubiquiti  
## 2183 grey 1049 7.3e-03 1.0e+00 2 BP negative regulation of epithelial cell p  
## 2184 grey 1049 7.3e-03 1.0e+00 2 BP positive regulation of histone H3-K9 tri  
## 2185 grey 1049 7.3e-03 1.0e+00 2 BP semaphorin-plexin signaling pathway invo  
## 2186 grey 1049 7.3e-03 1.0e+00 2 BP replication-born double-strand break rep  
## 2187 grey 1049 7.3e-03 1.0e+00 2 BP semaphorin-plexin signaling pathway invo  
## 2188 grey 1049 7.3e-03 1.0e+00 2 BP negative regulation of sodium ion transm  
## 2189 grey 1049 7.3e-03 1.0e+00 2 CC semaphorin receptor complex  
## 2190 grey 1049 7.3e-03 1.0e+00 2 CC PR-DUB complex  
## 2191 grey 1049 7.3e-03 1.0e+00 2 CC BORC complex  
## 2192 grey 1049 7.3e-03 1.0e+00 2 MF glyceraldehyde-3-phosphate dehydrogenase  
## 2193 grey 1049 7.3e-03 1.0e+00 2 MF MAP kinase kinase kinase kinase activity  
## 2194 grey 1049 7.3e-03 1.0e+00 2 MF semaphorin receptor activity  
## 2195 grey 1049 7.3e-03 1.0e+00 2 MF SAM domain binding  
## 2196 grey 1049 7.3e-03 1.0e+00 2 MF phosphatidylinositol 3-kinase catalytic   
## 2197 grey 1049 7.3e-03 1.0e+00 2 MF RNA polymerase II sequence-specific DNA-  
## 2198 grey 1049 7.4e-03 1.0e+00 4 BP germ-band extension  
## 2199 grey 1049 7.4e-03 1.0e+00 4 BP post-mating behavior  
## 2200 grey 1049 7.4e-03 1.0e+00 4 CC CCR4-NOT complex  
## 2201 grey 1049 7.4e-03 1.0e+00 4 MF histone methyltransferase activity (H3-K  
## 2202 grey 1049 7.4e-03 1.0e+00 46 BP negative regulation of transcription, DN  
## 2203 grey 1049 7.6e-03 1.0e+00 14 BP regulation of cell growth  
## 2204 grey 1049 7.6e-03 1.0e+00 41 BP imaginal disc-derived appendage morphoge  
## 2205 grey 1049 7.7e-03 1.0e+00 19 BP oocyte axis specification  
## 2206 grey 1049 7.7e-03 1.0e+00 10 BP positive regulation of cell migration  
## 2207 grey 1049 7.8e-03 1.0e+00 37 BP synapse organization  
## 2208 grey 1049 7.8e-03 1.0e+00 54 BP epithelial tube morphogenesis  
## 2209 grey 1049 7.9e-03 1.0e+00 7 BP establishment of mitotic spindle localiz  
## 2210 grey 1049 7.9e-03 1.0e+00 7 CC Golgi-associated vesicle membrane  
## 2211 grey 1049 8.1e-03 1.0e+00 9 MF myosin binding  
## 2212 grey 1049 8.2e-03 1.0e+00 22 BP regulation of synapse organization  
## 2213 grey 1049 8.2e-03 1.0e+00 39 BP positive regulation of transcription by   
## 2214 grey 1049 8.5e-03 1.0e+00 17 BP regulation of cell size  
## 2215 grey 1049 8.7e-03 1.0e+00 73 BP female gamete generation  
## 2216 grey 1049 8.8e-03 1.0e+00 22 CC apical part of cell  
## 2217 grey 1049 8.9e-03 1.0e+00 10 BP Rho protein signal transduction  
## 2218 grey 1049 8.9e-03 1.0e+00 41 BP appendage morphogenesis  
## 2219 grey 1049 9.0e-03 1.0e+00 29 BP secretion by cell  
## 2220 grey 1049 9.0e-03 1.0e+00 5 BP positive regulation of mitotic nuclear d  
## 2221 grey 1049 9.0e-03 1.0e+00 5 BP negative regulation of Ras protein signa  
## 2222 grey 1049 9.1e-03 1.0e+00 62 BP instar larval or pupal development  
## 2223 grey 1049 9.1e-03 1.0e+00 28 BP photoreceptor cell differentiation  
## 2224 grey 1049 9.3e-03 1.0e+00 20 MF enzyme activator activity  
## 2225 grey 1049 9.3e-03 1.0e+00 64 BP imaginal disc development  
## 2226 grey 1049 9.5e-03 1.0e+00 13 BP positive regulation of neuron differenti  
## 2227 grey 1049 9.7e-03 1.0e+00 7 BP intestinal stem cell homeostasis  
## 2228 grey 1049 9.7e-03 1.0e+00 7 BP positive regulation of Ras protein signa  
## 2229 grey 1049 9.7e-03 1.0e+00 7 BP positive regulation of proteolysis invol  
## 2230 lightcyan 82 1.4e-10 1.2e-06 46 BP cellular component organization  
## 2231 lightcyan 82 5.2e-09 4.4e-05 40 BP multicellular organism development  
## 2232 lightcyan 82 6.6e-09 5.6e-05 16 BP chromatin organization  
## 2233 lightcyan 82 2.7e-08 2.3e-04 33 BP organelle organization  
## 2234 lightcyan 82 4.5e-08 3.8e-04 29 BP cell development  
## 2235 lightcyan 82 4.8e-08 4.0e-04 21 BP neuron differentiation  
## 2236 lightcyan 82 6.5e-08 5.4e-04 19 BP neuron development  
## 2237 lightcyan 82 6.6e-08 5.5e-04 41 BP anatomical structure development  
## 2238 lightcyan 82 1.3e-07 1.1e-03 34 BP regulation of metabolic process  
## 2239 lightcyan 82 1.6e-07 1.4e-03 18 BP chromosome organization  
## 2240 lightcyan 82 1.7e-07 1.5e-03 31 BP cell differentiation  
## 2241 lightcyan 82 2.3e-07 1.9e-03 41 BP developmental process  
## 2242 lightcyan 82 3.3e-07 2.8e-03 36 MF protein binding  
## 2243 lightcyan 82 4.1e-07 3.4e-03 21 BP generation of neurons  
## 2244 lightcyan 82 7.4e-07 6.2e-03 10 BP histone modification  
## 2245 lightcyan 82 8.8e-07 7.4e-03 21 BP neurogenesis  
## 2246 lightcyan 82 1.1e-06 9.6e-03 27 BP regulation of gene expression  
## 2247 lightcyan 82 1.3e-06 1.1e-02 68 BP cellular process  
## 2248 lightcyan 82 1.5e-06 1.3e-02 10 CC polytene chromosome  
## 2249 lightcyan 82 1.6e-06 1.3e-02 36 CC nucleus  
## 2250 lightcyan 82 2.0e-06 1.6e-02 30 BP regulation of cellular metabolic process  
## 2251 lightcyan 82 2.1e-06 1.8e-02 15 BP cell morphogenesis involved in different  
## 2252 lightcyan 82 3.0e-06 2.5e-02 16 BP cell morphogenesis  
## 2253 lightcyan 82 3.5e-06 3.0e-02 14 BP cell morphogenesis involved in neuron di  
## 2254 lightcyan 82 4.1e-06 3.4e-02 27 BP anatomical structure morphogenesis  
## 2255 lightcyan 82 4.3e-06 3.6e-02 14 BP neuron projection morphogenesis  
## 2256 lightcyan 82 5.7e-06 4.8e-02 6 MF histone binding  
## 2257 lightcyan 82 5.8e-06 4.8e-02 22 BP nervous system development  
## 2258 lightcyan 82 6.7e-06 5.6e-02 16 BP post-embryonic development  
## 2259 lightcyan 82 8.5e-06 7.1e-02 23 BP animal organ development  
## 2260 lightcyan 82 8.5e-06 7.1e-02 14 BP neuron projection development  
## 2261 lightcyan 82 1.5e-05 1.2e-01 13 CC nucleoplasm  
## 2262 lightcyan 82 1.6e-05 1.3e-01 52 BP cellular metabolic process  
## 2263 lightcyan 82 1.6e-05 1.3e-01 22 BP cellular protein modification process  
## 2264 lightcyan 82 1.8e-05 1.5e-01 4 MF methylated histone binding  
## 2265 lightcyan 82 2.0e-05 1.6e-01 32 BP gene expression  
## 2266 lightcyan 82 2.3e-05 1.9e-01 15 BP oogenesis  
## 2267 lightcyan 82 2.8e-05 2.3e-01 10 CC chromatin  
## 2268 lightcyan 82 3.3e-05 2.8e-01 16 BP germ cell development  
## 2269 lightcyan 82 3.7e-05 3.1e-01 50 BP nitrogen compound metabolic process  
## 2270 lightcyan 82 4.0e-05 3.4e-01 14 CC chromosome  
## 2271 lightcyan 82 4.8e-05 4.0e-01 15 BP locomotion  
## 2272 lightcyan 82 5.8e-05 4.9e-01 8 BP regulation of gene expression, epigeneti  
## 2273 lightcyan 82 6.1e-05 5.1e-01 15 BP female gamete generation  
## 2274 lightcyan 82 7.9e-05 6.6e-01 8 BP gene silencing  
## 2275 lightcyan 82 8.4e-05 7.1e-01 6 BP stem cell population maintenance  
## 2276 lightcyan 82 9.2e-05 7.7e-01 14 BP negative regulation of gene expression  
## 2277 lightcyan 82 9.7e-05 8.2e-01 8 BP posttranscriptional regulation of gene e  
## 2278 lightcyan 82 1.2e-04 9.8e-01 6 BP imaginal disc pattern formation  
## 2279 lightcyan 82 1.2e-04 1.0e+00 33 CC protein-containing complex  
## 2280 lightcyan 82 1.3e-04 1.0e+00 6 BP hemopoiesis  
## 2281 lightcyan 82 1.3e-04 1.0e+00 6 BP regulation of chromatin organization  
## 2282 lightcyan 82 1.3e-04 1.0e+00 13 BP instar larval or pupal development  
## 2283 lightcyan 82 1.3e-04 1.0e+00 3 CC polytene chromosome band  
## 2284 lightcyan 82 1.5e-04 1.0e+00 8 BP cellular response to DNA damage stimulus  
## 2285 lightcyan 82 1.5e-04 1.0e+00 17 BP gamete generation  
## 2286 lightcyan 82 1.5e-04 1.0e+00 10 BP axonogenesis  
## 2287 lightcyan 82 1.6e-04 1.0e+00 8 BP embryonic pattern specification  
## 2288 lightcyan 82 1.7e-04 1.0e+00 9 BP axon guidance  
## 2289 lightcyan 82 1.7e-04 1.0e+00 6 BP chromatin silencing  
## 2290 lightcyan 82 1.8e-04 1.0e+00 5 BP wing disc pattern formation  
## 2291 lightcyan 82 1.9e-04 1.0e+00 49 CC intracellular organelle  
## 2292 lightcyan 82 2.0e-04 1.0e+00 12 BP sensory organ development  
## 2293 lightcyan 82 2.1e-04 1.0e+00 10 BP axon development  
## 2294 lightcyan 82 2.2e-04 1.0e+00 4 CC polytene chromosome interband  
## 2295 lightcyan 82 2.4e-04 1.0e+00 31 BP biosynthetic process  
## 2296 lightcyan 82 2.5e-04 1.0e+00 10 BP taxis  
## 2297 lightcyan 82 3.4e-04 1.0e+00 3 BP cellular response to ecdysone  
## 2298 lightcyan 82 3.8e-04 1.0e+00 8 BP segmentation  
## 2299 lightcyan 82 4.6e-04 1.0e+00 3 BP germ-band shortening  
## 2300 lightcyan 82 4.7e-04 1.0e+00 18 BP tissue development  
## 2301 lightcyan 82 4.8e-04 1.0e+00 4 BP histone lysine methylation  
## 2302 lightcyan 82 5.2e-04 1.0e+00 17 BP epithelium development  
## 2303 lightcyan 82 5.6e-04 1.0e+00 7 BP blastoderm segmentation  
## 2304 lightcyan 82 5.6e-04 1.0e+00 7 MF chromatin binding  
## 2305 lightcyan 82 5.9e-04 1.0e+00 10 BP eye development  
## 2306 lightcyan 82 6.7e-04 1.0e+00 8 BP immune response  
## 2307 lightcyan 82 6.9e-04 1.0e+00 3 BP regulation of histone methylation  
## 2308 lightcyan 82 7.8e-04 1.0e+00 9 BP cell motility  
## 2309 lightcyan 82 7.9e-04 1.0e+00 2 BP regulation of histone H3-K27 methylation  
## 2310 lightcyan 82 8.5e-04 1.0e+00 4 CC histone methyltransferase complex  
## 2311 lightcyan 82 1.0e-03 1.0e+00 6 BP larval development  
## 2312 lightcyan 82 1.0e-03 1.0e+00 5 BP chromatin remodeling  
## 2313 lightcyan 82 1.1e-03 1.0e+00 6 BP regulation of chromosome organization  
## 2314 lightcyan 82 1.1e-03 1.0e+00 4 BP histone methylation  
## 2315 lightcyan 82 1.1e-03 1.0e+00 2 BP central nervous system neuron axonogenes  
## 2316 lightcyan 82 1.1e-03 1.0e+00 3 BP centriole replication  
## 2317 lightcyan 82 1.1e-03 1.0e+00 18 BP reproductive process  
## 2318 lightcyan 82 1.2e-03 1.0e+00 3 BP centriole assembly  
## 2319 lightcyan 82 1.3e-03 1.0e+00 28 BP protein metabolic process  
## 2320 lightcyan 82 1.4e-03 1.0e+00 17 BP multicellular organism reproduction  
## 2321 lightcyan 82 1.4e-03 1.0e+00 54 CC intracellular  
## 2322 lightcyan 82 1.5e-03 1.0e+00 2 BP histone demethylation  
## 2323 lightcyan 82 1.5e-03 1.0e+00 13 BP cell surface receptor signaling pathway  
## 2324 lightcyan 82 1.5e-03 1.0e+00 17 BP regulation of transcription, DNA-templat  
## 2325 lightcyan 82 1.6e-03 1.0e+00 9 BP negative regulation of transcription, DN  
## 2326 lightcyan 82 1.6e-03 1.0e+00 3 BP cellular response to hypoxia  
## 2327 lightcyan 82 1.6e-03 1.0e+00 3 CC P-body  
## 2328 lightcyan 82 1.6e-03 1.0e+00 8 BP cell migration  
## 2329 lightcyan 82 1.7e-03 1.0e+00 22 MF nucleic acid binding  
## 2330 lightcyan 82 1.8e-03 1.0e+00 6 BP anterior/posterior pattern specification  
## 2331 lightcyan 82 1.8e-03 1.0e+00 5 BP cellular response to hormone stimulus  
## 2332 lightcyan 82 1.9e-03 1.0e+00 2 BP protein demethylation  
## 2333 lightcyan 82 1.9e-03 1.0e+00 2 BP central nervous system neuron developmen  
## 2334 lightcyan 82 1.9e-03 1.0e+00 2 BP histone H3-K27 methylation  
## 2335 lightcyan 82 1.9e-03 1.0e+00 2 MF histone demethylase activity  
## 2336 lightcyan 82 1.9e-03 1.0e+00 2 MF nuclear hormone receptor binding  
## 2337 lightcyan 82 1.9e-03 1.0e+00 18 BP reproduction  
## 2338 lightcyan 82 1.9e-03 1.0e+00 4 BP long-term memory  
## 2339 lightcyan 82 1.9e-03 1.0e+00 3 CC nuclear membrane  
## 2340 lightcyan 82 2.0e-03 1.0e+00 8 BP ovarian follicle cell development  
## 2341 lightcyan 82 2.0e-03 1.0e+00 28 BP nucleobase-containing compound metabolic  
## 2342 lightcyan 82 2.0e-03 1.0e+00 8 BP eye morphogenesis  
## 2343 lightcyan 82 2.0e-03 1.0e+00 4 BP protein methylation  
## 2344 lightcyan 82 2.2e-03 1.0e+00 4 MF DNA-binding transcription repressor acti  
## 2345 lightcyan 82 2.2e-03 1.0e+00 13 BP regulation of signal transduction  
## 2346 lightcyan 82 2.2e-03 1.0e+00 5 BP oocyte construction  
## 2347 lightcyan 82 2.3e-03 1.0e+00 2 BP sex comb development  
## 2348 lightcyan 82 2.3e-03 1.0e+00 2 CC histone locus body  
## 2349 lightcyan 82 2.4e-03 1.0e+00 17 BP transcription, DNA-templated  
## 2350 lightcyan 82 2.4e-03 1.0e+00 5 BP response to alcohol  
## 2351 lightcyan 82 2.4e-03 1.0e+00 23 BP RNA metabolic process  
## 2352 lightcyan 82 2.6e-03 1.0e+00 4 BP centrosome cycle  
## 2353 lightcyan 82 2.6e-03 1.0e+00 5 BP regulation of translation  
## 2354 lightcyan 82 2.7e-03 1.0e+00 13 BP animal organ morphogenesis  
## 2355 lightcyan 82 2.7e-03 1.0e+00 14 MF DNA binding  
## 2356 lightcyan 82 2.7e-03 1.0e+00 20 BP signal transduction  
## 2357 lightcyan 82 2.8e-03 1.0e+00 2 BP ecdysone receptor-mediated signaling pat  
## 2358 lightcyan 82 2.8e-03 1.0e+00 2 BP convergent extension  
## 2359 lightcyan 82 2.8e-03 1.0e+00 2 BP demethylation  
## 2360 lightcyan 82 2.8e-03 1.0e+00 2 CC phosphatidylinositol 3-kinase complex  
## 2361 lightcyan 82 2.8e-03 1.0e+00 2 CC MLL3/4 complex  
## 2362 lightcyan 82 2.8e-03 1.0e+00 2 MF demethylase activity  
## 2363 lightcyan 82 3.1e-03 1.0e+00 3 BP centrosome duplication  
## 2364 lightcyan 82 3.1e-03 1.0e+00 3 BP regulation of TORC1 signaling  
## 2365 lightcyan 82 3.4e-03 1.0e+00 2 BP synaptonemal complex organization  
## 2366 lightcyan 82 3.4e-03 1.0e+00 17 BP regulation of RNA metabolic process  
## 2367 lightcyan 82 3.4e-03 1.0e+00 5 BP oocyte development  
## 2368 lightcyan 82 3.5e-03 1.0e+00 4 BP double-strand break repair  
## 2369 lightcyan 82 3.6e-03 1.0e+00 10 BP response to organic substance  
## 2370 lightcyan 82 3.7e-03 1.0e+00 10 BP pattern specification process  
## 2371 lightcyan 82 3.7e-03 1.0e+00 5 BP regulation of cell projection organizati  
## 2372 lightcyan 82 3.8e-03 1.0e+00 8 BP epithelial cell development  
## 2373 lightcyan 82 3.9e-03 1.0e+00 8 BP defense response  
## 2374 lightcyan 82 4.0e-03 1.0e+00 2 BP negative regulation of innate immune res  
## 2375 lightcyan 82 4.1e-03 1.0e+00 3 BP TORC1 signaling  
## 2376 lightcyan 82 4.1e-03 1.0e+00 22 BP cell communication  
## 2377 lightcyan 82 4.6e-03 1.0e+00 2 BP mucosal immune response  
## 2378 lightcyan 82 4.6e-03 1.0e+00 2 BP intracellular steroid hormone receptor s  
## 2379 lightcyan 82 4.6e-03 1.0e+00 2 BP cytoplasmic mRNA processing body assembl  
## 2380 lightcyan 82 4.6e-03 1.0e+00 3 BP response to ecdysone  
## 2381 lightcyan 82 4.6e-03 1.0e+00 4 BP microtubule organizing center organizati  
## 2382 lightcyan 82 4.7e-03 1.0e+00 5 BP response to hormone  
## 2383 lightcyan 82 5.2e-03 1.0e+00 3 MF histone acetyltransferase activity  
## 2384 lightcyan 82 5.3e-03 1.0e+00 2 BP male germ-line stem cell population main  
## 2385 lightcyan 82 5.3e-03 1.0e+00 2 BP steroid hormone mediated signaling pathw  
## 2386 lightcyan 82 5.3e-03 1.0e+00 2 CC pericentric heterochromatin  
## 2387 lightcyan 82 5.3e-03 1.0e+00 2 MF 3'-5'-exoribonuclease activity  
## 2388 lightcyan 82 5.6e-03 1.0e+00 8 BP wing disc development  
## 2389 lightcyan 82 5.8e-03 1.0e+00 3 BP wing disc dorsal/ventral pattern formati  
## 2390 lightcyan 82 5.8e-03 1.0e+00 3 CC heterochromatin  
## 2391 lightcyan 82 6.0e-03 1.0e+00 39 CC intracellular membrane-bounded organelle  
## 2392 lightcyan 82 6.0e-03 1.0e+00 2 BP axon extension involved in axon guidance  
## 2393 lightcyan 82 6.0e-03 1.0e+00 2 MF exoribonuclease activity  
## 2394 lightcyan 82 6.1e-03 1.0e+00 9 BP metamorphosis  
## 2395 lightcyan 82 6.2e-03 1.0e+00 3 BP positive regulation of protein kinase ac  
## 2396 lightcyan 82 6.2e-03 1.0e+00 3 BP regulation of cellular protein localizat  
## 2397 lightcyan 82 6.2e-03 1.0e+00 3 MF chromatin DNA binding  
## 2398 lightcyan 82 6.4e-03 1.0e+00 5 BP oocyte differentiation  
## 2399 lightcyan 82 6.4e-03 1.0e+00 7 BP regulation of cell cycle  
## 2400 lightcyan 82 6.5e-03 1.0e+00 5 BP Notch signaling pathway  
## 2401 lightcyan 82 6.7e-03 1.0e+00 5 CC nuclear chromatin  
## 2402 lightcyan 82 6.8e-03 1.0e+00 2 BP intrinsic apoptotic signaling pathway in  
## 2403 lightcyan 82 6.8e-03 1.0e+00 2 BP positive regulation of smoothened signal  
## 2404 lightcyan 82 6.9e-03 1.0e+00 3 BP positive regulation of kinase activity  
## 2405 lightcyan 82 7.1e-03 1.0e+00 5 BP dendrite morphogenesis  
## 2406 lightcyan 82 7.2e-03 1.0e+00 3 BP larval lymph gland hemopoiesis  
## 2407 lightcyan 82 7.4e-03 1.0e+00 1 BP meiotic DNA repair synthesis involved in  
## 2408 lightcyan 82 7.4e-03 1.0e+00 1 BP platelet activation  
## 2409 lightcyan 82 7.4e-03 1.0e+00 1 BP negative regulation of glial cell apopto  
## 2410 lightcyan 82 7.4e-03 1.0e+00 1 BP regulation of long-term neuronal synapti  
## 2411 lightcyan 82 7.4e-03 1.0e+00 1 BP histone H3-K27 demethylation  
## 2412 lightcyan 82 7.4e-03 1.0e+00 1 BP commissural neuron axon guidance  
## 2413 lightcyan 82 7.4e-03 1.0e+00 1 BP fasciculation of sensory neuron axon  
## 2414 lightcyan 82 7.4e-03 1.0e+00 1 BP positive regulation of intrinsic apoptot  
## 2415 lightcyan 82 7.4e-03 1.0e+00 1 BP positive regulation of intrinsic apoptot  
## 2416 lightcyan 82 7.4e-03 1.0e+00 1 BP negative regulation of histone H3-K27 tr  
## 2417 lightcyan 82 7.4e-03 1.0e+00 1 BP histone H2A phosphorylation  
## 2418 lightcyan 82 7.4e-03 1.0e+00 1 CC lamellipodium membrane  
## 2419 lightcyan 82 7.4e-03 1.0e+00 1 CC transcriptionally silent chromatin  
## 2420 lightcyan 82 7.4e-03 1.0e+00 1 CC PAS complex  
## 2421 lightcyan 82 7.4e-03 1.0e+00 1 MF glycerophosphodiester phosphodiesterase   
## 2422 lightcyan 82 7.4e-03 1.0e+00 1 MF histone demethylase activity (H4-R3 spec  
## 2423 lightcyan 82 7.4e-03 1.0e+00 1 MF histone acetyltransferase activity (H3-K  
## 2424 lightcyan 82 7.4e-03 1.0e+00 1 MF phosphatidylinositol-4,5-bisphosphate 3-  
## 2425 lightcyan 82 7.4e-03 1.0e+00 1 MF lysine-acetylated histone binding  
## 2426 lightcyan 82 7.4e-03 1.0e+00 1 MF histone demethylase activity (H3-K27 spe  
## 2427 lightcyan 82 7.4e-03 1.0e+00 10 BP imaginal disc development  
## 2428 lightcyan 82 7.6e-03 1.0e+00 2 BP lamellocyte differentiation  
## 2429 lightcyan 82 7.6e-03 1.0e+00 3 BP dorsal/ventral pattern formation, imagin  
## 2430 lightcyan 82 8.2e-03 1.0e+00 5 BP embryonic development via the syncytial   
## 2431 lightcyan 82 8.4e-03 1.0e+00 2 BP anterior/posterior pattern specification  
## 2432 lightcyan 82 8.4e-03 1.0e+00 2 BP negative regulation of cell growth  
## 2433 lightcyan 82 8.6e-03 1.0e+00 5 BP regulation of neuron differentiation  
## 2434 lightcyan 82 8.7e-03 1.0e+00 4 BP negative regulation of cell cycle  
## 2435 lightcyan 82 9.0e-03 1.0e+00 5 BP dendrite development  
## 2436 lightcyan 82 9.3e-03 1.0e+00 2 BP somatic stem cell population maintenance  
## 2437 lightcyan 82 9.3e-03 1.0e+00 2 BP positive regulation of circadian rhythm  
## 2438 lightcyan 82 9.9e-03 1.0e+00 7 BP negative regulation of signal transducti  
## 2439 lightgreen 102 6.7e-31 5.6e-27 24 CC mitochondrial ribosome  
## 2440 lightgreen 102 2.2e-29 1.8e-25 25 BP mitochondrial translation  
## 2441 lightgreen 102 2.7e-27 2.3e-23 27 CC mitochondrial matrix  
## 2442 lightgreen 102 6.6e-23 5.5e-19 25 CC ribosome  
## 2443 lightgreen 102 2.5e-21 2.1e-17 23 MF structural constituent of ribosome  
## 2444 lightgreen 102 1.9e-20 1.6e-16 37 CC mitochondrion  
## 2445 lightgreen 102 1.3e-19 1.1e-15 15 CC mitochondrial large ribosomal subunit  
## 2446 lightgreen 102 6.7e-18 5.6e-14 28 BP translation  
## 2447 lightgreen 102 1.0e-17 8.5e-14 31 BP peptide metabolic process  
## 2448 lightgreen 102 1.9e-14 1.6e-10 15 CC large ribosomal subunit  
## 2449 lightgreen 102 7.8e-14 6.5e-10 25 MF structural molecule activity  
## 2450 lightgreen 102 5.4e-12 4.5e-08 25 CC ribonucleoprotein complex  
## 2451 lightgreen 102 6.8e-12 5.7e-08 9 CC mitochondrial small ribosomal subunit  
## 2452 lightgreen 102 7.8e-09 6.5e-05 60 CC cytoplasm  
## 2453 lightgreen 102 2.2e-08 1.9e-04 9 CC small ribosomal subunit  
## 2454 lightgreen 102 2.7e-07 2.3e-03 42 BP protein metabolic process  
## 2455 lightgreen 102 9.5e-06 8.0e-02 40 BP biosynthetic process  
## 2456 lightgreen 102 2.9e-05 2.4e-01 54 CC intracellular membrane-bounded organelle  
## 2457 lightgreen 102 4.4e-05 3.7e-01 40 CC protein-containing complex  
## 2458 lightgreen 102 1.7e-04 1.0e+00 35 BP gene expression  
## 2459 lightgreen 102 3.2e-04 1.0e+00 5 MF translation factor activity, RNA binding  
## 2460 lightgreen 102 3.4e-04 1.0e+00 4 BP mitochondrial respiratory chain complex   
## 2461 lightgreen 102 3.4e-04 1.0e+00 67 CC intracellular  
## 2462 lightgreen 102 3.7e-04 1.0e+00 3 BP mitochondrial respiratory chain complex   
## 2463 lightgreen 102 6.3e-04 1.0e+00 57 CC intracellular organelle  
## 2464 lightgreen 102 9.1e-04 1.0e+00 57 BP cellular metabolic process  
## 2465 lightgreen 102 9.8e-04 1.0e+00 5 MF S-adenosylmethionine-dependent methyltra  
## 2466 lightgreen 102 1.2e-03 1.0e+00 7 BP mitochondrion organization  
## 2467 lightgreen 102 2.2e-03 1.0e+00 2 MF nucleotidase activity  
## 2468 lightgreen 102 2.6e-03 1.0e+00 54 BP nitrogen compound metabolic process  
## 2469 lightgreen 102 3.5e-03 1.0e+00 2 MF sulfurtransferase activity  
## 2470 lightgreen 102 3.8e-03 1.0e+00 5 MF methyltransferase activity  
## 2471 lightgreen 102 5.3e-03 1.0e+00 3 MF rRNA binding  
## 2472 lightgreen 102 6.0e-03 1.0e+00 2 CC eukaryotic translation initiation factor  
## 2473 lightgreen 102 6.9e-03 1.0e+00 3 MF translation initiation factor activity  
## 2474 lightgreen 102 6.9e-03 1.0e+00 3 MF RNA methyltransferase activity  
## 2475 lightgreen 102 9.1e-03 1.0e+00 1 BP angiogenesis  
## 2476 lightgreen 102 9.1e-03 1.0e+00 1 BP ecdysone-mediated polytene chromosome pu  
## 2477 lightgreen 102 9.1e-03 1.0e+00 1 BP dihydrofolate metabolic process  
## 2478 lightgreen 102 9.1e-03 1.0e+00 1 CC nuclear microtubule  
## 2479 lightgreen 102 9.1e-03 1.0e+00 1 CC methylcrotonoyl-CoA carboxylase complex  
## 2480 lightgreen 102 9.1e-03 1.0e+00 1 MF dihydrofolate reductase activity  
## 2481 lightgreen 102 9.1e-03 1.0e+00 1 MF Rab GDP-dissociation inhibitor activity  
## 2482 lightgreen 102 9.1e-03 1.0e+00 1 MF 3'(2'),5'-bisphosphate nucleotidase acti  
## 2483 lightgreen 102 9.1e-03 1.0e+00 1 MF translation release factor activity, cod  
## 2484 lightgreen 102 9.1e-03 1.0e+00 1 MF acireductone synthase activity  
## 2485 lightgreen 102 9.1e-03 1.0e+00 1 MF tRNA (cytosine-3-)-methyltransferase act  
## 2486 lightyellow 79 8.4e-11 7.0e-07 9 CC Golgi-associated vesicle  
## 2487 lightyellow 79 1.9e-10 1.6e-06 51 CC cytoplasm  
## 2488 lightyellow 79 3.6e-10 3.0e-06 9 CC coated vesicle  
## 2489 lightyellow 79 5.6e-10 4.7e-06 7 CC Golgi-associated vesicle membrane  
## 2490 lightyellow 79 1.6e-09 1.4e-05 5 CC COPI vesicle coat  
## 2491 lightyellow 79 1.6e-09 1.4e-05 5 CC COPI-coated vesicle  
## 2492 lightyellow 79 2.0e-08 1.7e-04 8 BP ER to Golgi vesicle-mediated transport  
## 2493 lightyellow 79 2.4e-08 2.0e-04 10 BP Golgi vesicle transport  
## 2494 lightyellow 79 1.7e-07 1.5e-03 7 CC cytoplasmic vesicle membrane  
## 2495 lightyellow 79 3.3e-07 2.8e-03 7 CC vesicle membrane  
## 2496 lightyellow 79 1.9e-06 1.6e-02 9 MF structural constituent of ribosome  
## 2497 lightyellow 79 2.6e-06 2.2e-02 13 BP translation  
## 2498 lightyellow 79 4.7e-06 3.9e-02 9 CC ribosome  
## 2499 lightyellow 79 7.9e-06 6.6e-02 13 MF structural molecule activity  
## 2500 lightyellow 79 8.3e-06 6.9e-02 16 CC mitochondrion  
## 2501 lightyellow 79 1.4e-05 1.1e-01 4 BP retrograde vesicle-mediated transport, G  
## 2502 lightyellow 79 2.0e-05 1.6e-01 4 BP intra-Golgi vesicle-mediated transport  
## 2503 lightyellow 79 2.0e-05 1.7e-01 12 CC endoplasmic reticulum  
## 2504 lightyellow 79 2.7e-05 2.3e-01 55 CC intracellular  
## 2505 lightyellow 79 3.2e-05 2.7e-01 4 CC COPII-coated ER to Golgi transport vesic  
## 2506 lightyellow 79 4.8e-05 4.1e-01 6 BP protein targeting  
## 2507 lightyellow 79 4.9e-05 4.1e-01 13 BP peptide metabolic process  
## 2508 lightyellow 79 6.2e-05 5.2e-01 10 CC Golgi apparatus  
## 2509 lightyellow 79 8.8e-05 7.4e-01 42 CC intracellular membrane-bounded organelle  
## 2510 lightyellow 79 9.6e-05 8.1e-01 14 BP intracellular transport  
## 2511 lightyellow 79 1.0e-04 8.4e-01 47 CC intracellular organelle  
## 2512 lightyellow 79 1.2e-04 1.0e+00 7 CC mitochondrial matrix  
## 2513 lightyellow 79 1.3e-04 1.0e+00 10 BP intracellular protein transport  
## 2514 lightyellow 79 1.7e-04 1.0e+00 4 BP regulation of lipid storage  
## 2515 lightyellow 79 1.7e-04 1.0e+00 11 BP protein transport  
## 2516 lightyellow 79 1.8e-04 1.0e+00 31 CC protein-containing complex  
## 2517 lightyellow 79 1.9e-04 1.0e+00 17 CC endomembrane system  
## 2518 lightyellow 79 2.3e-04 1.0e+00 12 CC organelle membrane  
## 2519 lightyellow 79 2.3e-04 1.0e+00 5 CC mitochondrial ribosome  
## 2520 lightyellow 79 2.3e-04 1.0e+00 11 BP establishment of protein localization  
## 2521 lightyellow 79 2.9e-04 1.0e+00 7 CC endoplasmic reticulum membrane  
## 2522 lightyellow 79 3.4e-04 1.0e+00 4 MF ribonucleoprotein complex binding  
## 2523 lightyellow 79 4.5e-04 1.0e+00 11 BP vesicle-mediated transport  
## 2524 lightyellow 79 4.6e-04 1.0e+00 2 BP vesicle fusion with Golgi apparatus  
## 2525 lightyellow 79 4.6e-04 1.0e+00 4 BP lipid storage  
## 2526 lightyellow 79 7.2e-04 1.0e+00 5 CC large ribosomal subunit  
## 2527 lightyellow 79 7.6e-04 1.0e+00 9 CC cytoplasmic vesicle  
## 2528 lightyellow 79 8.8e-04 1.0e+00 28 BP biosynthetic process  
## 2529 lightyellow 79 1.3e-03 1.0e+00 5 BP cytoplasmic translation  
## 2530 lightyellow 79 1.3e-03 1.0e+00 3 BP fatty acid beta-oxidation  
## 2531 lightyellow 79 1.6e-03 1.0e+00 2 MF enoyl-CoA hydratase activity  
## 2532 lightyellow 79 1.6e-03 1.0e+00 9 CC vesicle  
## 2533 lightyellow 79 1.9e-03 1.0e+00 3 BP fatty acid oxidation  
## 2534 lightyellow 79 1.9e-03 1.0e+00 4 BP alcohol metabolic process  
## 2535 lightyellow 79 2.0e-03 1.0e+00 4 CC Golgi membrane  
## 2536 lightyellow 79 2.0e-03 1.0e+00 3 BP lipid oxidation  
## 2537 lightyellow 79 2.5e-03 1.0e+00 2 BP regulation of tube diameter, open trache  
## 2538 lightyellow 79 2.5e-03 1.0e+00 10 BP cellular protein localization  
## 2539 lightyellow 79 2.9e-03 1.0e+00 2 BP larval salivary gland morphogenesis  
## 2540 lightyellow 79 2.9e-03 1.0e+00 2 CC ER to Golgi transport vesicle membrane  
## 2541 lightyellow 79 3.2e-03 1.0e+00 3 BP fatty acid catabolic process  
## 2542 lightyellow 79 3.2e-03 1.0e+00 3 MF translation initiation factor activity  
## 2543 lightyellow 79 3.3e-03 1.0e+00 10 CC ribonucleoprotein complex  
## 2544 lightyellow 79 3.5e-03 1.0e+00 2 BP regulation of reactive oxygen species me  
## 2545 lightyellow 79 3.5e-03 1.0e+00 2 CC eukaryotic translation initiation factor  
## 2546 lightyellow 79 4.0e-03 1.0e+00 2 BP SRP-dependent cotranslational protein ta  
## 2547 lightyellow 79 4.0e-03 1.0e+00 2 MF P-P-bond-hydrolysis-driven protein trans  
## 2548 lightyellow 79 4.6e-03 1.0e+00 3 BP ribosome assembly  
## 2549 lightyellow 79 4.6e-03 1.0e+00 3 MF oxidoreductase activity, acting on NAD(P  
## 2550 lightyellow 79 4.6e-03 1.0e+00 2 BP regulation of tube diameter  
## 2551 lightyellow 79 4.8e-03 1.0e+00 3 CC mitochondrial large ribosomal subunit  
## 2552 lightyellow 79 4.9e-03 1.0e+00 4 CC cytosolic ribosome  
## 2553 lightyellow 79 5.4e-03 1.0e+00 11 BP protein localization  
## 2554 lightyellow 79 5.8e-03 1.0e+00 10 BP cellular macromolecule localization  
## 2555 lightyellow 79 6.0e-03 1.0e+00 4 BP mitochondrial translation  
## 2556 lightyellow 79 6.4e-03 1.0e+00 10 CC cytosol  
## 2557 lightyellow 79 6.6e-03 1.0e+00 11 BP organic substance transport  
## 2558 lightyellow 79 6.6e-03 1.0e+00 2 MF protein transmembrane transporter activi  
## 2559 lightyellow 79 6.6e-03 1.0e+00 3 BP translational initiation  
## 2560 lightyellow 79 6.9e-03 1.0e+00 1 BP ethanol oxidation  
## 2561 lightyellow 79 6.9e-03 1.0e+00 1 BP thiamine metabolic process  
## 2562 lightyellow 79 6.9e-03 1.0e+00 1 BP heme a biosynthetic process  
## 2563 lightyellow 79 6.9e-03 1.0e+00 1 BP thiamine diphosphate biosynthetic proces  
## 2564 lightyellow 79 6.9e-03 1.0e+00 1 BP regulation of hydrogen peroxide metaboli  
## 2565 lightyellow 79 6.9e-03 1.0e+00 1 BP glycerol catabolic process  
## 2566 lightyellow 79 6.9e-03 1.0e+00 1 BP positive regulation of histone phosphory  
## 2567 lightyellow 79 6.9e-03 1.0e+00 1 BP glyceraldehyde-3-phosphate biosynthetic   
## 2568 lightyellow 79 6.9e-03 1.0e+00 1 BP proteasome regulatory particle assembly  
## 2569 lightyellow 79 6.9e-03 1.0e+00 1 BP regulation of nitric oxide metabolic pro  
## 2570 lightyellow 79 6.9e-03 1.0e+00 1 BP regulation of peptidyl-cysteine S-nitros  
## 2571 lightyellow 79 6.9e-03 1.0e+00 1 MF lactoylglutathione lyase activity  
## 2572 lightyellow 79 6.9e-03 1.0e+00 1 MF octanol dehydrogenase activity  
## 2573 lightyellow 79 6.9e-03 1.0e+00 1 MF thiamine diphosphokinase activity  
## 2574 lightyellow 79 6.9e-03 1.0e+00 1 MF triose-phosphate isomerase activity  
## 2575 lightyellow 79 6.9e-03 1.0e+00 1 MF thiamine binding  
## 2576 lightyellow 79 6.9e-03 1.0e+00 1 MF dehydrodolichyl diphosphate synthase act  
## 2577 lightyellow 79 6.9e-03 1.0e+00 1 MF S-(hydroxymethyl)glutathione dehydrogena  
## 2578 lightyellow 79 6.9e-03 1.0e+00 1 MF ADP-dependent NAD(P)H-hydrate dehydratas  
## 2579 lightyellow 79 6.9e-03 1.0e+00 1 MF S-nitrosoglutathione reductase activity  
## 2580 lightyellow 79 6.9e-03 1.0e+00 1 MF COPII adaptor activity  
## 2581 lightyellow 79 8.2e-03 1.0e+00 2 MF ribosome binding  
## 2582 lightyellow 79 9.0e-03 1.0e+00 4 BP fatty acid metabolic process  
## 2583 lightyellow 79 9.0e-03 1.0e+00 2 BP protein targeting to ER  
## 2584 lightyellow 79 9.0e-03 1.0e+00 2 MF peptide transmembrane transporter activi  
## 2585 pink 269 7.5e-13 6.3e-09 104 CC nucleus  
## 2586 pink 269 4.0e-12 3.4e-08 74 BP regulation of gene expression  
## 2587 pink 269 4.4e-12 3.6e-08 65 BP regulation of RNA metabolic process  
## 2588 pink 269 3.0e-11 2.5e-07 88 BP regulation of metabolic process  
## 2589 pink 269 6.1e-11 5.1e-07 94 BP gene expression  
## 2590 pink 269 9.6e-11 8.1e-07 81 BP RNA metabolic process  
## 2591 pink 269 1.3e-10 1.1e-06 59 BP regulation of transcription, DNA-templat  
## 2592 pink 269 4.1e-10 3.5e-06 95 BP nucleobase-containing compound metabolic  
## 2593 pink 269 5.8e-10 4.8e-06 176 CC intracellular  
## 2594 pink 269 7.5e-10 6.3e-06 79 BP regulation of cellular metabolic process  
## 2595 pink 269 1.9e-09 1.6e-05 58 BP transcription, DNA-templated  
## 2596 pink 269 2.5e-09 2.1e-05 34 MF zinc ion binding  
## 2597 pink 269 5.1e-09 4.3e-05 37 CC chromosome  
## 2598 pink 269 1.4e-08 1.2e-04 71 MF nucleic acid binding  
## 2599 pink 269 2.2e-08 1.8e-04 148 CC intracellular organelle  
## 2600 pink 269 3.0e-08 2.5e-04 20 CC polytene chromosome  
## 2601 pink 269 5.9e-08 4.9e-04 38 BP regulation of transcription by RNA polym  
## 2602 pink 269 9.5e-08 8.0e-04 39 BP transcription by RNA polymerase II  
## 2603 pink 269 1.3e-07 1.1e-03 128 CC intracellular membrane-bounded organelle  
## 2604 pink 269 3.7e-07 3.1e-03 35 BP negative regulation of gene expression  
## 2605 pink 269 1.0e-06 8.3e-03 140 BP nitrogen compound metabolic process  
## 2606 pink 269 1.1e-06 8.9e-03 192 BP cellular process  
## 2607 pink 269 2.1e-06 1.7e-02 25 BP negative regulation of transcription, DN  
## 2608 pink 269 3.1e-06 2.6e-02 45 MF cation binding  
## 2609 pink 269 3.8e-06 3.2e-02 44 MF metal ion binding  
## 2610 pink 269 5.6e-06 4.7e-02 141 BP cellular metabolic process  
## 2611 pink 269 5.8e-06 4.9e-02 29 BP positive regulation of gene expression  
## 2612 pink 269 5.8e-06 4.9e-02 34 MF transition metal ion binding  
## 2613 pink 269 1.1e-05 9.3e-02 25 BP positive regulation of transcription, DN  
## 2614 pink 269 4.2e-05 3.6e-01 30 BP chromosome organization  
## 2615 pink 269 4.5e-05 3.8e-01 90 BP cellular component organization  
## 2616 pink 269 4.5e-05 3.8e-01 22 BP chromatin organization  
## 2617 pink 269 4.8e-05 4.0e-01 38 MF DNA binding  
## 2618 pink 269 5.3e-05 4.4e-01 15 MF chromatin binding  
## 2619 pink 269 5.9e-05 5.0e-01 50 MF transferase activity  
## 2620 pink 269 7.0e-05 5.9e-01 18 CC chromatin  
## 2621 pink 269 8.2e-05 6.9e-01 47 BP cellular protein modification process  
## 2622 pink 269 8.3e-05 7.0e-01 24 CC nucleoplasm  
## 2623 pink 269 1.1e-04 9.0e-01 19 BP positive regulation of transcription by   
## 2624 pink 269 1.1e-04 9.1e-01 13 CC nuclear chromatin  
## 2625 pink 269 1.2e-04 9.8e-01 61 BP cell differentiation  
## 2626 pink 269 1.2e-04 9.9e-01 14 BP protein ubiquitination  
## 2627 pink 269 1.2e-04 1.0e+00 3 MF histone methyltransferase activity (H3-K  
## 2628 pink 269 1.3e-04 1.0e+00 79 BP biosynthetic process  
## 2629 pink 269 1.7e-04 1.0e+00 15 MF ubiquitin-like protein transferase activ  
## 2630 pink 269 2.4e-04 1.0e+00 5 MF histone-lysine N-methyltransferase activ  
## 2631 pink 269 2.5e-04 1.0e+00 14 BP protein modification by small protein co  
## 2632 pink 269 2.6e-04 1.0e+00 52 BP cell development  
## 2633 pink 269 2.6e-04 1.0e+00 33 BP neuron differentiation  
## 2634 pink 269 2.9e-04 1.0e+00 36 BP generation of neurons  
## 2635 pink 269 3.1e-04 1.0e+00 43 BP nervous system development  
## 2636 pink 269 3.1e-04 1.0e+00 61 BP organelle organization  
## 2637 pink 269 3.4e-04 1.0e+00 37 BP neurogenesis  
## 2638 pink 269 4.3e-04 1.0e+00 5 CC PcG protein complex  
## 2639 pink 269 4.5e-04 1.0e+00 23 BP metamorphosis  
## 2640 pink 269 5.1e-04 1.0e+00 5 MF protein-lysine N-methyltransferase activ  
## 2641 pink 269 5.5e-04 1.0e+00 2 BP isoleucyl-tRNA aminoacylation  
## 2642 pink 269 5.5e-04 1.0e+00 2 BP mitotic cohesin unloading  
## 2643 pink 269 5.5e-04 1.0e+00 2 MF isoleucine-tRNA ligase activity  
## 2644 pink 269 5.8e-04 1.0e+00 13 BP gene silencing  
## 2645 pink 269 8.0e-04 1.0e+00 18 BP imaginal disc-derived appendage developm  
## 2646 pink 269 8.6e-04 1.0e+00 26 BP cell morphogenesis  
## 2647 pink 269 8.8e-04 1.0e+00 11 BP dorsal/ventral pattern formation  
## 2648 pink 269 1.0e-03 1.0e+00 13 MF ubiquitin-protein transferase activity  
## 2649 pink 269 1.0e-03 1.0e+00 31 BP regulation of developmental process  
## 2650 pink 269 1.1e-03 1.0e+00 5 MF histone methyltransferase activity  
## 2651 pink 269 1.1e-03 1.0e+00 12 BP histone modification  
## 2652 pink 269 1.1e-03 1.0e+00 19 BP cell death  
## 2653 pink 269 1.2e-03 1.0e+00 17 BP post-embryonic appendage morphogenesis  
## 2654 pink 269 1.3e-03 1.0e+00 57 BP signaling  
## 2655 pink 269 1.3e-03 1.0e+00 3 BP protein monoubiquitination  
## 2656 pink 269 1.3e-03 1.0e+00 3 CC ESC/E(Z) complex  
## 2657 pink 269 1.6e-03 1.0e+00 2 BP negative regulation of mRNA polyadenylat  
## 2658 pink 269 1.6e-03 1.0e+00 2 CC Hedgehog signaling complex  
## 2659 pink 269 1.6e-03 1.0e+00 17 BP imaginal disc-derived appendage morphoge  
## 2660 pink 269 1.8e-03 1.0e+00 17 BP appendage morphogenesis  
## 2661 pink 269 1.8e-03 1.0e+00 3 BP apical constriction involved in gastrula  
## 2662 pink 269 1.8e-03 1.0e+00 3 BP histone ubiquitination  
## 2663 pink 269 1.9e-03 1.0e+00 16 BP mRNA processing  
## 2664 pink 269 1.9e-03 1.0e+00 50 BP signal transduction  
## 2665 pink 269 1.9e-03 1.0e+00 26 MF ATP binding  
## 2666 pink 269 2.3e-03 1.0e+00 6 CC histone methyltransferase complex  
## 2667 pink 269 2.4e-03 1.0e+00 11 MF protein serine/threonine kinase activity  
## 2668 pink 269 2.4e-03 1.0e+00 3 BP response to caffeine  
## 2669 pink 269 2.5e-03 1.0e+00 5 CC polytene chromosome interband  
## 2670 pink 269 2.6e-03 1.0e+00 26 BP neuron development  
## 2671 pink 269 2.7e-03 1.0e+00 18 BP wing disc development  
## 2672 pink 269 2.7e-03 1.0e+00 14 CC nuclear chromosome  
## 2673 pink 269 2.8e-03 1.0e+00 26 MF adenyl ribonucleotide binding  
## 2674 pink 269 2.9e-03 1.0e+00 4 BP cytoplasmic microtubule organization  
## 2675 pink 269 3.0e-03 1.0e+00 80 BP anatomical structure development  
## 2676 pink 269 3.0e-03 1.0e+00 3 BP regulation of development, heterochronic  
## 2677 pink 269 3.2e-03 1.0e+00 29 BP regulation of signal transduction  
## 2678 pink 269 3.2e-03 1.0e+00 2 BP negative regulation of mRNA 3'-end proce  
## 2679 pink 269 3.2e-03 1.0e+00 2 CC cohesin complex  
## 2680 pink 269 3.2e-03 1.0e+00 2 CC nBAF complex  
## 2681 pink 269 3.2e-03 1.0e+00 6 BP histone methylation  
## 2682 pink 269 3.3e-03 1.0e+00 17 BP epithelial cell development  
## 2683 pink 269 3.3e-03 1.0e+00 25 BP oogenesis  
## 2684 pink 269 3.4e-03 1.0e+00 4 MF damaged DNA binding  
## 2685 pink 269 3.4e-03 1.0e+00 51 BP anatomical structure morphogenesis  
## 2686 pink 269 3.6e-03 1.0e+00 56 BP cell communication  
## 2687 pink 269 3.7e-03 1.0e+00 23 BP instar larval or pupal development  
## 2688 pink 269 3.8e-03 1.0e+00 3 BP positive regulation of photoreceptor cel  
## 2689 pink 269 3.8e-03 1.0e+00 33 BP gamete generation  
## 2690 pink 269 4.0e-03 1.0e+00 26 BP intracellular signal transduction  
## 2691 pink 269 4.1e-03 1.0e+00 69 MF protein binding  
## 2692 pink 269 4.3e-03 1.0e+00 25 BP post-embryonic development  
## 2693 pink 269 4.3e-03 1.0e+00 18 BP imaginal disc morphogenesis  
## 2694 pink 269 4.4e-03 1.0e+00 82 BP developmental process  
## 2695 pink 269 4.5e-03 1.0e+00 14 BP imaginal disc-derived wing morphogenesis  
## 2696 pink 269 4.5e-03 1.0e+00 30 MF purine nucleotide binding  
## 2697 pink 269 4.7e-03 1.0e+00 71 BP multicellular organism development  
## 2698 pink 269 5.0e-03 1.0e+00 26 BP female gamete generation  
## 2699 pink 269 5.0e-03 1.0e+00 4 CC transcriptionally active chromatin  
## 2700 pink 269 5.1e-03 1.0e+00 5 BP SCF-dependent proteasomal ubiquitin-depe  
## 2701 pink 269 5.1e-03 1.0e+00 5 MF protein methyltransferase activity  
## 2702 pink 269 5.2e-03 1.0e+00 16 BP programmed cell death  
## 2703 pink 269 5.2e-03 1.0e+00 2 BP positive regulation of hh target transcr  
## 2704 pink 269 5.2e-03 1.0e+00 2 BP histone monoubiquitination  
## 2705 pink 269 5.2e-03 1.0e+00 2 BP determination of dorsal/ventral asymmetr  
## 2706 pink 269 5.2e-03 1.0e+00 2 BP microtubule severing  
## 2707 pink 269 5.2e-03 1.0e+00 2 MF microtubule-severing ATPase activity  
## 2708 pink 269 5.2e-03 1.0e+00 13 BP RNA splicing, via transesterification re  
## 2709 pink 269 5.2e-03 1.0e+00 13 BP mRNA splicing, via spliceosome  
## 2710 pink 269 5.3e-03 1.0e+00 11 BP axis specification  
## 2711 pink 269 5.3e-03 1.0e+00 21 BP cell morphogenesis involved in different  
## 2712 pink 269 5.4e-03 1.0e+00 10 CC transcription factor complex  
## 2713 pink 269 5.6e-03 1.0e+00 9 MF transcription coregulator activity  
## 2714 pink 269 5.6e-03 1.0e+00 4 BP nuclear migration  
## 2715 pink 269 5.7e-03 1.0e+00 3 BP terminal region determination  
## 2716 pink 269 5.7e-03 1.0e+00 3 BP positive regulation of protein ubiquitin  
## 2717 pink 269 5.7e-03 1.0e+00 3 MF steroid hormone receptor activity  
## 2718 pink 269 5.9e-03 1.0e+00 23 BP imaginal disc development  
## 2719 pink 269 6.0e-03 1.0e+00 75 CC protein-containing complex  
## 2720 pink 269 6.0e-03 1.0e+00 27 BP germ cell development  
## 2721 pink 269 6.0e-03 1.0e+00 14 BP wing disc morphogenesis  
## 2722 pink 269 6.1e-03 1.0e+00 5 BP double-strand break repair via homologou  
## 2723 pink 269 6.1e-03 1.0e+00 5 BP recombinational repair  
## 2724 pink 269 6.1e-03 1.0e+00 5 BP histone lysine methylation  
## 2725 pink 269 6.3e-03 1.0e+00 4 BP epithelial cell morphogenesis  
## 2726 pink 269 6.7e-03 1.0e+00 6 CC histone acetyltransferase complex  
## 2727 pink 269 6.8e-03 1.0e+00 3 MF nuclear receptor activity  
## 2728 pink 269 6.8e-03 1.0e+00 8 BP cellular response to hormone stimulus  
## 2729 pink 269 7.0e-03 1.0e+00 4 BP hormone-mediated signaling pathway  
## 2730 pink 269 7.0e-03 1.0e+00 4 BP positive regulation of establishment of   
## 2731 pink 269 7.1e-03 1.0e+00 6 BP protein methylation  
## 2732 pink 269 7.2e-03 1.0e+00 7 BP DNA recombination  
## 2733 pink 269 7.7e-03 1.0e+00 2 BP negative regulation of DNA binding  
## 2734 pink 269 7.7e-03 1.0e+00 2 BP mesectoderm development  
## 2735 pink 269 7.8e-03 1.0e+00 10 BP dendrite development  
## 2736 pink 269 8.0e-03 1.0e+00 3 BP positive regulation of protein secretion  
## 2737 pink 269 8.2e-03 1.0e+00 16 BP regulation of nervous system development  
## 2738 pink 269 8.3e-03 1.0e+00 9 BP response to hormone  
## 2739 pink 269 8.6e-03 1.0e+00 6 BP dorsal/ventral axis specification  
## 2740 pink 269 8.7e-03 1.0e+00 4 BP positive regulation of secretion  
## 2741 pink 269 8.8e-03 1.0e+00 20 BP neuron projection development  
## 2742 pink 269 9.0e-03 1.0e+00 18 BP regulation of cell differentiation  
## 2743 pink 269 9.0e-03 1.0e+00 13 BP RNA splicing  
## 2744 pink 269 9.1e-03 1.0e+00 5 BP neuron remodeling  
## 2745 pink 269 9.6e-03 1.0e+00 67 BP protein metabolic process  
## 2746 pink 269 9.8e-03 1.0e+00 13 BP apoptotic process  
## 2747 pink 269 9.9e-03 1.0e+00 8 BP response to alcohol  
## 2748 red 759 4.4e-31 3.7e-27 106 BP nervous system process  
## 2749 red 759 1.9e-30 1.6e-26 61 BP sensory perception of chemical stimulus  
## 2750 red 759 3.8e-30 3.2e-26 46 BP detection of stimulus involved in sensor  
## 2751 red 759 1.1e-29 9.6e-26 103 CC cell projection  
## 2752 red 759 1.3e-29 1.1e-25 39 BP detection of chemical stimulus involved   
## 2753 red 759 2.5e-28 2.1e-24 43 BP detection of chemical stimulus  
## 2754 red 759 1.7e-27 1.4e-23 31 MF olfactory receptor activity  
## 2755 red 759 9.3e-27 7.8e-23 43 BP sensory perception of smell  
## 2756 red 759 2.8e-26 2.4e-22 31 BP detection of chemical stimulus involved   
## 2757 red 759 1.4e-23 1.2e-19 35 MF odorant binding  
## 2758 red 759 1.7e-22 1.5e-18 27 CC dendrite membrane  
## 2759 red 759 2.9e-19 2.4e-15 30 CC neuron projection membrane  
## 2760 red 759 4.1e-19 3.4e-15 27 BP phototransduction  
## 2761 red 759 8.6e-19 7.3e-15 22 CC rhabdomere  
## 2762 red 759 1.0e-18 8.5e-15 42 CC dendrite  
## 2763 red 759 2.3e-18 1.9e-14 67 MF signaling receptor activity  
## 2764 red 759 5.5e-18 4.6e-14 59 MF transmembrane signaling receptor activit  
## 2765 red 759 1.2e-16 1.0e-12 23 BP cellular response to light stimulus  
## 2766 red 759 2.0e-16 1.7e-12 19 BP phototransduction, visible light  
## 2767 red 759 2.9e-16 2.4e-12 65 CC neuron projection  
## 2768 red 759 1.1e-15 9.0e-12 31 CC cell leading edge  
## 2769 red 759 3.7e-15 3.1e-11 20 BP detection of visible light  
## 2770 red 759 3.0e-14 2.6e-10 15 BP rhodopsin mediated signaling pathway  
## 2771 red 759 1.8e-13 1.5e-09 35 BP response to light stimulus  
## 2772 red 759 6.0e-13 5.0e-09 120 CC plasma membrane  
## 2773 red 759 1.8e-12 1.5e-08 23 BP cellular response to radiation  
## 2774 red 759 6.6e-12 5.6e-08 12 BP deactivation of rhodopsin mediated signa  
## 2775 red 759 9.4e-12 7.9e-08 15 BP sensory perception of light stimulus  
## 2776 red 759 1.9e-11 1.6e-07 12 BP regulation of rhodopsin mediated signali  
## 2777 red 759 6.6e-11 5.5e-07 36 BP response to radiation  
## 2778 red 759 7.0e-11 5.9e-07 9 CC inaD signaling complex  
## 2779 red 759 1.1e-10 9.2e-07 13 BP visual perception  
## 2780 red 759 2.1e-10 1.8e-06 123 CC cell periphery  
## 2781 red 759 2.4e-09 2.0e-05 36 BP G protein-coupled receptor signaling pat  
## 2782 red 759 3.5e-09 2.9e-05 195 CC membrane  
## 2783 red 759 6.4e-09 5.3e-05 12 BP regulation of G protein-coupled receptor  
## 2784 red 759 9.4e-09 7.9e-05 117 CC integral component of membrane  
## 2785 red 759 1.2e-08 1.0e-04 118 CC intrinsic component of membrane  
## 2786 red 759 5.2e-08 4.3e-04 8 MF photoreceptor activity  
## 2787 red 759 8.5e-08 7.2e-04 31 MF ion channel activity  
## 2788 red 759 2.1e-07 1.8e-03 146 BP cell communication  
## 2789 red 759 2.3e-07 1.9e-03 7 MF AMPA glutamate receptor activity  
## 2790 red 759 2.5e-07 2.1e-03 25 BP mating  
## 2791 red 759 2.8e-07 2.4e-03 8 CC sensory dendrite  
## 2792 red 759 2.9e-07 2.4e-03 31 MF channel activity  
## 2793 red 759 3.5e-07 2.9e-03 24 BP mating behavior  
## 2794 red 759 4.8e-07 4.0e-03 142 BP signaling  
## 2795 red 759 5.2e-07 4.4e-03 16 BP sensory perception of sound  
## 2796 red 759 6.0e-07 5.0e-03 7 CC AMPA glutamate receptor complex  
## 2797 red 759 6.4e-07 5.3e-03 21 CC cilium  
## 2798 red 759 7.1e-07 5.9e-03 11 MF glutamate receptor activity  
## 2799 red 759 9.8e-07 8.2e-03 6 CC rhabdomere membrane  
## 2800 red 759 9.8e-07 8.2e-03 6 MF G protein-coupled photoreceptor activity  
## 2801 red 759 2.8e-06 2.3e-02 6 BP response to light intensity  
## 2802 red 759 3.1e-06 2.6e-02 24 BP reproductive behavior  
## 2803 red 759 3.8e-06 3.2e-02 5 BP detection of UV  
## 2804 red 759 4.6e-06 3.8e-02 122 BP signal transduction  
## 2805 red 759 5.5e-06 4.6e-02 8 BP retina homeostasis  
## 2806 red 759 6.9e-06 5.8e-02 11 CC extrinsic component of plasma membrane  
## 2807 red 759 8.6e-06 7.2e-02 16 BP sensory perception of mechanical stimulu  
## 2808 red 759 1.1e-05 9.6e-02 4 BP adaptation of rhodopsin mediated signali  
## 2809 red 759 1.1e-05 9.6e-02 4 BP protein localization to rhabdomere  
## 2810 red 759 1.1e-05 9.6e-02 4 CC subrhabdomeral cisterna  
## 2811 red 759 1.2e-05 1.0e-01 16 MF ligand-gated ion channel activity  
## 2812 red 759 1.3e-05 1.1e-01 5 CC rhabdomere microvillus  
## 2813 red 759 1.5e-05 1.2e-01 13 CC cation channel complex  
## 2814 red 759 1.9e-05 1.6e-01 9 MF ionotropic glutamate receptor activity  
## 2815 red 759 2.2e-05 1.8e-01 18 BP chemosensory behavior  
## 2816 red 759 2.7e-05 2.2e-01 13 CC synaptic vesicle  
## 2817 red 759 3.5e-05 2.9e-01 17 BP courtship behavior  
## 2818 red 759 4.0e-05 3.4e-01 7 BP thermotaxis  
## 2819 red 759 4.8e-05 4.1e-01 16 BP male mating behavior  
## 2820 red 759 5.2e-05 4.4e-01 21 MF cation channel activity  
## 2821 red 759 5.5e-05 4.6e-01 4 BP phototransduction, UV  
## 2822 red 759 5.5e-05 4.6e-01 4 BP metarhodopsin inactivation  
## 2823 red 759 5.6e-05 4.7e-01 13 CC exocytic vesicle  
## 2824 red 759 5.7e-05 4.8e-01 8 BP clathrin-dependent endocytosis  
## 2825 red 759 6.7e-05 5.7e-01 15 BP male courtship behavior  
## 2826 red 759 7.3e-05 6.1e-01 45 CC integral component of plasma membrane  
## 2827 red 759 7.4e-05 6.2e-01 46 CC intrinsic component of plasma membrane  
## 2828 red 759 7.6e-05 6.4e-01 11 BP receptor-mediated endocytosis  
## 2829 red 759 8.0e-05 6.7e-01 9 MF calmodulin binding  
## 2830 red 759 9.3e-05 7.8e-01 32 CC synapse  
## 2831 red 759 1.2e-04 1.0e+00 21 CC presynapse  
## 2832 red 759 1.4e-04 1.0e+00 11 MF extracellular ligand-gated ion channel a  
## 2833 red 759 1.4e-04 1.0e+00 14 BP olfactory behavior  
## 2834 red 759 1.6e-04 1.0e+00 4 BP bulk synaptic vesicle endocytosis  
## 2835 red 759 1.7e-04 1.0e+00 9 BP calcium-mediated signaling  
## 2836 red 759 1.9e-04 1.0e+00 6 BP photoreceptor cell maintenance  
## 2837 red 759 2.0e-04 1.0e+00 3 BP retinoid metabolic process  
## 2838 red 759 2.0e-04 1.0e+00 15 BP compound eye photoreceptor development  
## 2839 red 759 2.2e-04 1.0e+00 14 CC receptor complex  
## 2840 red 759 2.2e-04 1.0e+00 17 BP photoreceptor cell development  
## 2841 red 759 2.3e-04 1.0e+00 5 BP entrainment of circadian clock by photop  
## 2842 red 759 3.0e-04 1.0e+00 21 BP adult behavior  
## 2843 red 759 3.2e-04 1.0e+00 7 CC ionotropic glutamate receptor complex  
## 2844 red 759 3.2e-04 1.0e+00 9 BP sensory perception of taste  
## 2845 red 759 3.3e-04 1.0e+00 14 BP synaptic vesicle localization  
## 2846 red 759 3.3e-04 1.0e+00 15 BP eye photoreceptor cell development  
## 2847 red 759 3.5e-04 1.0e+00 4 BP sequestering of calcium ion  
## 2848 red 759 3.5e-04 1.0e+00 4 BP clathrin-dependent synaptic vesicle endo  
## 2849 red 759 3.5e-04 1.0e+00 4 CC smooth endoplasmic reticulum  
## 2850 red 759 3.7e-04 1.0e+00 5 BP photoperiodism  
## 2851 red 759 3.7e-04 1.0e+00 5 BP detection of light stimulus involved in   
## 2852 red 759 3.7e-04 1.0e+00 5 CC microvillus  
## 2853 red 759 5.2e-04 1.0e+00 15 BP cilium organization  
## 2854 red 759 5.5e-04 1.0e+00 7 MF taste receptor activity  
## 2855 red 759 5.8e-04 1.0e+00 12 MF neurotransmitter receptor activity  
## 2856 red 759 6.0e-04 1.0e+00 13 CC secretory vesicle  
## 2857 red 759 6.7e-04 1.0e+00 4 BP regulation of clathrin-dependent endocyt  
## 2858 red 759 7.4e-04 1.0e+00 6 BP cyclic nucleotide biosynthetic process  
## 2859 red 759 7.4e-04 1.0e+00 6 BP entrainment of circadian clock  
## 2860 red 759 7.4e-04 1.0e+00 6 BP response to pheromone  
## 2861 red 759 8.6e-04 1.0e+00 5 BP transmission of nerve impulse  
## 2862 red 759 8.6e-04 1.0e+00 13 BP synaptic vesicle transport  
## 2863 red 759 9.0e-04 1.0e+00 7 BP regulation of protein secretion  
## 2864 red 759 1.0e-03 1.0e+00 30 BP synaptic signaling  
## 2865 red 759 1.0e-03 1.0e+00 14 CC transmembrane transporter complex  
## 2866 red 759 1.2e-03 1.0e+00 13 CC transport vesicle  
## 2867 red 759 1.2e-03 1.0e+00 5 BP detection of chemical stimulus involved   
## 2868 red 759 1.2e-03 1.0e+00 56 BP intracellular signal transduction  
## 2869 red 759 1.3e-03 1.0e+00 16 BP synaptic vesicle cycle  
## 2870 red 759 1.4e-03 1.0e+00 13 BP adult locomotory behavior  
## 2871 red 759 1.4e-03 1.0e+00 22 BP endocytosis  
## 2872 red 759 1.6e-03 1.0e+00 11 BP regulated exocytosis  
## 2873 red 759 1.7e-03 1.0e+00 6 MF ATP-dependent microtubule motor activity  
## 2874 red 759 1.7e-03 1.0e+00 5 BP synaptic vesicle priming  
## 2875 red 759 1.7e-03 1.0e+00 5 BP R7 cell development  
## 2876 red 759 1.8e-03 1.0e+00 3 BP nitric oxide mediated signal transductio  
## 2877 red 759 1.8e-03 1.0e+00 3 BP negative regulation of protein secretion  
## 2878 red 759 1.8e-03 1.0e+00 3 CC rhabdomere microvillus membrane  
## 2879 red 759 1.8e-03 1.0e+00 3 MF pheromone binding  
## 2880 red 759 1.8e-03 1.0e+00 4 BP cGMP biosynthetic process  
## 2881 red 759 1.8e-03 1.0e+00 17 BP signal release  
## 2882 red 759 1.9e-03 1.0e+00 29 BP chemical synaptic transmission  
## 2883 red 759 1.9e-03 1.0e+00 15 MF G protein-coupled receptor activity  
## 2884 red 759 2.1e-03 1.0e+00 13 BP cilium assembly  
## 2885 red 759 2.2e-03 1.0e+00 8 MF hormone activity  
## 2886 red 759 2.2e-03 1.0e+00 40 MF ion transmembrane transporter activity  
## 2887 red 759 2.3e-03 1.0e+00 10 BP regulation of protein transport  
## 2888 red 759 2.3e-03 1.0e+00 5 BP rhodopsin metabolic process  
## 2889 red 759 2.3e-03 1.0e+00 5 BP positive regulation of receptor-mediated  
## 2890 red 759 2.6e-03 1.0e+00 8 BP rhabdomere development  
## 2891 red 759 2.6e-03 1.0e+00 6 BP cyclic nucleotide metabolic process  
## 2892 red 759 2.9e-03 1.0e+00 11 CC extrinsic component of membrane  
## 2893 red 759 2.9e-03 1.0e+00 10 BP synaptic vesicle exocytosis  
## 2894 red 759 3.2e-03 1.0e+00 22 CC axon  
## 2895 red 759 3.3e-03 1.0e+00 10 BP regulation of establishment of protein l  
## 2896 red 759 3.4e-03 1.0e+00 2 BP desensitization of G protein-coupled rec  
## 2897 red 759 3.4e-03 1.0e+00 2 BP activation of phospholipase C activity  
## 2898 red 759 3.4e-03 1.0e+00 2 BP light-induced release of internally sequ  
## 2899 red 759 3.4e-03 1.0e+00 2 BP response to acetate  
## 2900 red 759 3.4e-03 1.0e+00 2 BP response to chlorate  
## 2901 red 759 3.4e-03 1.0e+00 2 BP retinal metabolic process  
## 2902 red 759 3.4e-03 1.0e+00 2 BP cellular response to acetate  
## 2903 red 759 3.4e-03 1.0e+00 2 BP cellular response to anoxia  
## 2904 red 759 3.4e-03 1.0e+00 2 BP dendritic spine maintenance  
## 2905 red 759 3.4e-03 1.0e+00 2 BP positive regulation of protein polyubiqu  
## 2906 red 759 3.4e-03 1.0e+00 2 BP dense core granule exocytosis  
## 2907 red 759 3.4e-03 1.0e+00 2 BP positive regulation of DNA topoisomerase  
## 2908 red 759 3.4e-03 1.0e+00 2 MF opsin binding  
## 2909 red 759 3.4e-03 1.0e+00 2 MF light-activated ion channel activity  
## 2910 red 759 3.4e-03 1.0e+00 2 MF extracellular phenylacetaldehyde-gated i  
## 2911 red 759 3.5e-03 1.0e+00 3 BP positive regulation of clathrin-dependen  
## 2912 red 759 3.5e-03 1.0e+00 3 CC microvillus membrane  
## 2913 red 759 3.9e-03 1.0e+00 4 BP regulation of ATPase activity  
## 2914 red 759 3.9e-03 1.0e+00 4 MF guanylate cyclase activity  
## 2915 red 759 4.0e-03 1.0e+00 6 BP axoneme assembly  
## 2916 red 759 4.0e-03 1.0e+00 13 BP regulation of protein localization  
## 2917 red 759 4.1e-03 1.0e+00 10 BP calcium ion regulated exocytosis  
## 2918 red 759 4.4e-03 1.0e+00 13 BP neurotransmitter secretion  
## 2919 red 759 4.8e-03 1.0e+00 6 CC axoneme  
## 2920 red 759 5.4e-03 1.0e+00 4 BP cellular response to UV  
## 2921 red 759 5.4e-03 1.0e+00 4 BP cGMP metabolic process  
## 2922 red 759 5.8e-03 1.0e+00 6 BP female mating behavior  
## 2923 red 759 5.8e-03 1.0e+00 3 BP negative regulation of compound eye reti  
## 2924 red 759 5.8e-03 1.0e+00 3 BP regulation of short-term neuronal synapt  
## 2925 red 759 6.3e-03 1.0e+00 20 BP locomotory behavior  
## 2926 red 759 6.8e-03 1.0e+00 9 BP tissue homeostasis  
## 2927 red 759 6.8e-03 1.0e+00 42 BP vesicle-mediated transport  
## 2928 red 759 7.6e-03 1.0e+00 5 BP cilium movement  
## 2929 red 759 8.5e-03 1.0e+00 21 BP photoreceptor cell differentiation  
## 2930 red 759 8.9e-03 1.0e+00 3 BP imaginal disc-derived wing expansion  
## 2931 red 759 8.9e-03 1.0e+00 3 MF sweet taste receptor activity  
## 2932 red 759 9.3e-03 1.0e+00 5 BP dosage compensation  
## 2933 red 759 9.3e-03 1.0e+00 5 BP synaptic transmission, glutamatergic  
## 2934 red 759 9.3e-03 1.0e+00 4 BP dosage compensation by hyperactivation o  
## 2935 red 759 9.3e-03 1.0e+00 4 BP cGMP-mediated signaling  
## 2936 red 759 9.8e-03 1.0e+00 2 BP conditioned taste aversion  
## 2937 red 759 9.8e-03 1.0e+00 2 BP regulation of cilium movement  
## 2938 red 759 9.8e-03 1.0e+00 2 BP manganese ion transport  
## 2939 red 759 9.8e-03 1.0e+00 2 BP gamma-aminobutyric acid signaling pathwa  
## 2940 red 759 9.8e-03 1.0e+00 2 BP synaptic vesicle maturation  
## 2941 red 759 9.8e-03 1.0e+00 2 BP negative regulation of protein binding  
## 2942 red 759 9.8e-03 1.0e+00 2 BP Rap protein signal transduction  
## 2943 red 759 9.8e-03 1.0e+00 2 BP SNARE complex disassembly  
## 2944 red 759 9.8e-03 1.0e+00 2 CC G protein-coupled receptor heterodimeric  
## 2945 red 759 9.8e-03 1.0e+00 2 CC dendrite terminus  
## 2946 red 759 9.8e-03 1.0e+00 2 CC neuromuscular junction of somatic muscle  
## 2947 red 759 9.8e-03 1.0e+00 2 CC messenger ribonucleoprotein complex  
## 2948 red 759 9.8e-03 1.0e+00 2 MF phosphatidylinositol phospholipase C act  
## 2949 red 759 9.8e-03 1.0e+00 2 MF phospholipase C activity  
## 2950 red 759 9.8e-03 1.0e+00 2 MF soluble NSF attachment protein activity  
## 2951 red 759 9.8e-03 1.0e+00 2 MF ecdysis-triggering hormone activity  
## 2952 royalblue 85 1.0e-10 8.4e-07 41 BP regulation of metabolic process  
## 2953 royalblue 85 2.0e-09 1.7e-05 33 BP regulation of gene expression  
## 2954 royalblue 85 1.1e-08 9.0e-05 28 BP transcription, DNA-templated  
## 2955 royalblue 85 1.5e-08 1.3e-04 8 CC histone methyltransferase complex  
## 2956 royalblue 85 2.7e-08 2.3e-04 35 BP regulation of cellular metabolic process  
## 2957 royalblue 85 8.3e-08 7.0e-04 26 BP regulation of transcription, DNA-templat  
## 2958 royalblue 85 9.0e-08 7.6e-04 14 BP cell migration  
## 2959 royalblue 85 9.7e-08 8.1e-04 27 BP regulation of RNA metabolic process  
## 2960 royalblue 85 1.8e-07 1.5e-03 38 BP gene expression  
## 2961 royalblue 85 2.9e-07 2.5e-03 20 BP germ cell development  
## 2962 royalblue 85 3.3e-07 2.8e-03 33 BP RNA metabolic process  
## 2963 royalblue 85 3.5e-07 2.9e-03 14 BP cell motility  
## 2964 royalblue 85 6.7e-07 5.6e-03 22 BP gamete generation  
## 2965 royalblue 85 1.2e-06 9.7e-03 65 CC intracellular  
## 2966 royalblue 85 3.3e-06 2.8e-02 17 BP oogenesis  
## 2967 royalblue 85 4.2e-06 3.5e-02 23 BP tissue development  
## 2968 royalblue 85 5.4e-06 4.5e-02 24 BP cellular protein modification process  
## 2969 royalblue 85 1.0e-05 8.5e-02 17 BP female gamete generation  
## 2970 royalblue 85 1.4e-05 1.2e-01 21 BP epithelium development  
## 2971 royalblue 85 1.5e-05 1.2e-01 55 CC intracellular organelle  
## 2972 royalblue 85 1.5e-05 1.3e-01 22 BP multicellular organism reproduction  
## 2973 royalblue 85 2.2e-05 1.9e-01 55 BP cellular metabolic process  
## 2974 royalblue 85 2.3e-05 2.0e-01 9 CC polytene chromosome  
## 2975 royalblue 85 3.2e-05 2.7e-01 11 BP ovarian follicle cell development  
## 2976 royalblue 85 3.7e-05 3.1e-01 35 CC nucleus  
## 2977 royalblue 85 3.8e-05 3.2e-01 25 BP cell development  
## 2978 royalblue 85 3.9e-05 3.3e-01 70 BP cellular process  
## 2979 royalblue 85 4.5e-05 3.7e-01 5 BP histone lysine methylation  
## 2980 royalblue 85 4.7e-05 4.0e-01 34 BP nucleobase-containing compound metabolic  
## 2981 royalblue 85 4.7e-05 4.0e-01 22 BP reproductive process  
## 2982 royalblue 85 4.8e-05 4.0e-01 4 BP histone H3-K4 methylation  
## 2983 royalblue 85 5.1e-05 4.3e-01 8 BP epithelial cell migration  
## 2984 royalblue 85 5.3e-05 4.4e-01 8 BP epithelium migration  
## 2985 royalblue 85 5.7e-05 4.8e-01 15 BP negative regulation of gene expression  
## 2986 royalblue 85 8.1e-05 6.8e-01 7 BP ovarian follicle cell migration  
## 2987 royalblue 85 8.6e-05 7.2e-01 11 BP epithelial cell development  
## 2988 royalblue 85 9.0e-05 7.5e-01 22 BP reproduction  
## 2989 royalblue 85 1.0e-04 8.6e-01 22 BP animal organ development  
## 2990 royalblue 85 1.2e-04 1.0e+00 35 CC protein-containing complex  
## 2991 royalblue 85 1.2e-04 1.0e+00 8 BP ameboidal-type cell migration  
## 2992 royalblue 85 1.3e-04 1.0e+00 5 BP histone methylation  
## 2993 royalblue 85 1.4e-04 1.0e+00 11 BP chromatin organization  
## 2994 royalblue 85 1.5e-04 1.0e+00 12 CC nucleoplasm  
## 2995 royalblue 85 1.5e-04 1.0e+00 16 BP regulation of signal transduction  
## 2996 royalblue 85 1.8e-04 1.0e+00 6 BP chromatin remodeling  
## 2997 royalblue 85 2.5e-04 1.0e+00 36 BP cellular component organization  
## 2998 royalblue 85 2.6e-04 1.0e+00 51 BP nitrogen compound metabolic process  
## 2999 royalblue 85 2.7e-04 1.0e+00 5 BP protein methylation  
## 3000 royalblue 85 2.8e-04 1.0e+00 26 BP cell differentiation  
## 3001 royalblue 85 4.0e-04 1.0e+00 6 BP border follicle cell migration  
## 3002 royalblue 85 4.2e-04 1.0e+00 14 BP locomotion  
## 3003 royalblue 85 4.3e-04 1.0e+00 31 MF protein binding  
## 3004 royalblue 85 4.9e-04 1.0e+00 26 BP organelle organization  
## 3005 royalblue 85 5.5e-04 1.0e+00 4 MF histone acetyltransferase activity  
## 3006 royalblue 85 5.5e-04 1.0e+00 12 BP positive regulation of gene expression  
## 3007 royalblue 85 5.7e-04 1.0e+00 7 BP histone modification  
## 3008 royalblue 85 6.2e-04 1.0e+00 11 BP growth  
## 3009 royalblue 85 6.2e-04 1.0e+00 7 BP regulation of gene expression, epigeneti  
## 3010 royalblue 85 6.6e-04 1.0e+00 13 BP chromosome organization  
## 3011 royalblue 85 8.0e-04 1.0e+00 7 BP gene silencing  
## 3012 royalblue 85 8.2e-04 1.0e+00 34 BP anatomical structure development  
## 3013 royalblue 85 8.7e-04 1.0e+00 31 BP multicellular organism development  
## 3014 royalblue 85 1.1e-03 1.0e+00 31 BP biosynthetic process  
## 3015 royalblue 85 1.2e-03 1.0e+00 12 CC chromosome  
## 3016 royalblue 85 1.3e-03 1.0e+00 2 CC WASH complex  
## 3017 royalblue 85 1.3e-03 1.0e+00 13 BP regulation of transcription by RNA polym  
## 3018 royalblue 85 1.4e-03 1.0e+00 10 BP positive regulation of transcription, DN  
## 3019 royalblue 85 1.4e-03 1.0e+00 4 MF proximal promoter DNA-binding transcript  
## 3020 royalblue 85 1.5e-03 1.0e+00 3 BP glial cell migration  
## 3021 royalblue 85 1.7e-03 1.0e+00 3 BP histone H3 acetylation  
## 3022 royalblue 85 1.8e-03 1.0e+00 34 BP developmental process  
## 3023 royalblue 85 1.8e-03 1.0e+00 3 BP nuclear migration  
## 3024 royalblue 85 2.2e-03 1.0e+00 2 BP chromatin-mediated maintenance of transc  
## 3025 royalblue 85 2.2e-03 1.0e+00 13 BP transcription by RNA polymerase II  
## 3026 royalblue 85 2.2e-03 1.0e+00 3 BP endocytic recycling  
## 3027 royalblue 85 2.3e-03 1.0e+00 6 BP embryonic development via the syncytial   
## 3028 royalblue 85 2.3e-03 1.0e+00 4 MF N-acetyltransferase activity  
## 3029 royalblue 85 2.3e-03 1.0e+00 10 MF enzyme binding  
## 3030 royalblue 85 2.5e-03 1.0e+00 8 BP compound eye morphogenesis  
## 3031 royalblue 85 2.5e-03 1.0e+00 4 CC histone acetyltransferase complex  
## 3032 royalblue 85 2.5e-03 1.0e+00 8 MF transcription regulatory region DNA bind  
## 3033 royalblue 85 2.6e-03 1.0e+00 9 BP wing disc development  
## 3034 royalblue 85 2.6e-03 1.0e+00 3 MF thiol-dependent ubiquitin-specific prote  
## 3035 royalblue 85 2.6e-03 1.0e+00 3 MF thiol-dependent ubiquitinyl hydrolase ac  
## 3036 royalblue 85 2.6e-03 1.0e+00 4 BP regulation of cell migration  
## 3037 royalblue 85 2.7e-03 1.0e+00 9 BP compound eye development  
## 3038 royalblue 85 2.7e-03 1.0e+00 9 BP negative regulation of transcription, DN  
## 3039 royalblue 85 2.8e-03 1.0e+00 4 MF N-acyltransferase activity  
## 3040 royalblue 85 2.9e-03 1.0e+00 5 BP methylation  
## 3041 royalblue 85 2.9e-03 1.0e+00 4 MF DNA-binding transcription repressor acti  
## 3042 royalblue 85 3.0e-03 1.0e+00 13 BP cell surface receptor signaling pathway  
## 3043 royalblue 85 3.0e-03 1.0e+00 8 BP regulation of growth  
## 3044 royalblue 85 3.0e-03 1.0e+00 10 MF DNA-binding transcription factor activit  
## 3045 royalblue 85 3.1e-03 1.0e+00 21 BP signal transduction  
## 3046 royalblue 85 3.2e-03 1.0e+00 13 BP tube development  
## 3047 royalblue 85 3.2e-03 1.0e+00 8 BP eye morphogenesis  
## 3048 royalblue 85 3.3e-03 1.0e+00 2 BP growth of a germarium-derived egg chambe  
## 3049 royalblue 85 3.3e-03 1.0e+00 2 CC MLL3/4 complex  
## 3050 royalblue 85 3.3e-03 1.0e+00 3 BP nucleus localization  
## 3051 royalblue 85 3.7e-03 1.0e+00 4 CC protein acetyltransferase complex  
## 3052 royalblue 85 3.9e-03 1.0e+00 3 BP cellular response to topologically incor  
## 3053 royalblue 85 4.0e-03 1.0e+00 9 BP eye development  
## 3054 royalblue 85 4.0e-03 1.0e+00 4 MF acetyltransferase activity  
## 3055 royalblue 85 4.1e-03 1.0e+00 3 BP protein deubiquitination  
## 3056 royalblue 85 4.1e-03 1.0e+00 3 BP negative regulation of proteolysis  
## 3057 royalblue 85 4.2e-03 1.0e+00 6 BP embryo development ending in birth or eg  
## 3058 royalblue 85 4.4e-03 1.0e+00 4 BP gliogenesis  
## 3059 royalblue 85 4.4e-03 1.0e+00 4 BP canonical Wnt signaling pathway  
## 3060 royalblue 85 4.6e-03 1.0e+00 2 BP protein quality control for misfolded or  
## 3061 royalblue 85 4.6e-03 1.0e+00 42 CC intracellular membrane-bounded organelle  
## 3062 royalblue 85 4.7e-03 1.0e+00 3 CC polytene chromosome puff  
## 3063 royalblue 85 4.8e-03 1.0e+00 10 BP sensory organ development  
## 3064 royalblue 85 5.0e-03 1.0e+00 3 BP regulation of photoreceptor cell differe  
## 3065 royalblue 85 5.7e-03 1.0e+00 3 BP regulation of epithelial cell migration  
## 3066 royalblue 85 6.4e-03 1.0e+00 11 BP morphogenesis of an epithelium  
## 3067 royalblue 85 6.8e-03 1.0e+00 3 BP positive regulation of cell migration  
## 3068 royalblue 85 6.8e-03 1.0e+00 3 BP dorsal appendage formation  
## 3069 royalblue 85 6.9e-03 1.0e+00 2 BP cell-cell adhesion mediated by cadherin  
## 3070 royalblue 85 7.0e-03 1.0e+00 6 BP establishment or maintenance of cell pol  
## 3071 royalblue 85 7.1e-03 1.0e+00 7 MF DNA-binding transcription factor activit  
## 3072 royalblue 85 7.8e-03 1.0e+00 2 BP regulation of DNA binding  
## 3073 royalblue 85 7.9e-03 1.0e+00 1 BP suture of dorsal opening  
## 3074 royalblue 85 7.9e-03 1.0e+00 1 BP sternite morphogenesis  
## 3075 royalblue 85 7.9e-03 1.0e+00 1 BP mystery cell differentiation  
## 3076 royalblue 85 7.9e-03 1.0e+00 1 BP defecation  
## 3077 royalblue 85 7.9e-03 1.0e+00 1 BP conversion of ds siRNA to ss siRNA invol  
## 3078 royalblue 85 7.9e-03 1.0e+00 1 BP histone H3-K79 methylation  
## 3079 royalblue 85 7.9e-03 1.0e+00 1 BP nuclear cortical migration  
## 3080 royalblue 85 7.9e-03 1.0e+00 1 BP histone H3-K18 acetylation  
## 3081 royalblue 85 7.9e-03 1.0e+00 1 BP R1/R6 development  
## 3082 royalblue 85 7.9e-03 1.0e+00 1 BP compound eye corneal lens morphogenesis  
## 3083 royalblue 85 7.9e-03 1.0e+00 1 BP anterior mRNA localization involved in a  
## 3084 royalblue 85 7.9e-03 1.0e+00 1 BP histone H3-K36 dimethylation  
## 3085 royalblue 85 7.9e-03 1.0e+00 1 BP protein localization to cell leading edg  
## 3086 royalblue 85 7.9e-03 1.0e+00 1 BP positive regulation of receptor localiza  
## 3087 royalblue 85 7.9e-03 1.0e+00 1 CC mitochondrial DNA-directed RNA polymeras  
## 3088 royalblue 85 7.9e-03 1.0e+00 1 CC lateral cell cortex  
## 3089 royalblue 85 7.9e-03 1.0e+00 1 MF mitochondrial promoter sequence-specific  
## 3090 royalblue 85 7.9e-03 1.0e+00 1 MF UDP-glucose:glycoprotein glucosyltransfe  
## 3091 royalblue 85 7.9e-03 1.0e+00 1 MF elongation factor-2 kinase activity  
## 3092 royalblue 85 7.9e-03 1.0e+00 1 MF histone methyltransferase activity (H3-K  
## 3093 royalblue 85 7.9e-03 1.0e+00 1 MF DNA 5'-adenosine monophosphate hydrolase  
## 3094 royalblue 85 7.9e-03 1.0e+00 1 MF histone acetyltransferase activity (H3-K  
## 3095 royalblue 85 7.9e-03 1.0e+00 1 MF histone acetyltransferase activity (H3-K  
## 3096 royalblue 85 7.9e-03 1.0e+00 1 MF single-strand break-containing DNA bindi  
## 3097 royalblue 85 7.9e-03 1.0e+00 1 MF histone methyltransferase binding  
## 3098 royalblue 85 8.0e-03 1.0e+00 8 BP developmental growth  
## 3099 royalblue 85 8.1e-03 1.0e+00 4 BP endosomal transport  
## 3100 royalblue 85 8.3e-03 1.0e+00 7 BP proteolysis involved in cellular protein  
## 3101 royalblue 85 8.4e-03 1.0e+00 22 BP signaling  
## 3102 royalblue 85 8.8e-03 1.0e+00 2 BP positive regulation of hippo signaling  
## 3103 royalblue 85 9.0e-03 1.0e+00 7 BP cellular protein catabolic process  
## 3104 royalblue 85 9.1e-03 1.0e+00 27 BP protein metabolic process  
## 3105 royalblue 85 9.9e-03 1.0e+00 5 CC cell junction  
## 3106 salmon 114 1.5e-04 1.0e+00 3 BP anterograde axonal transport  
## 3107 salmon 114 2.8e-04 1.0e+00 8 BP synapse assembly  
## 3108 salmon 114 4.3e-04 1.0e+00 7 BP synaptic growth at neuromuscular junctio  
## 3109 salmon 114 5.9e-04 1.0e+00 2 BP anterograde synaptic vesicle transport  
## 3110 salmon 114 8.9e-04 1.0e+00 22 BP nervous system development  
## 3111 salmon 114 1.6e-03 1.0e+00 9 BP imaginal disc-derived wing morphogenesis  
## 3112 salmon 114 1.8e-03 1.0e+00 7 BP neuromuscular junction development  
## 3113 salmon 114 1.8e-03 1.0e+00 7 BP dendrite development  
## 3114 salmon 114 2.0e-03 1.0e+00 9 BP wing disc morphogenesis  
## 3115 salmon 114 2.2e-03 1.0e+00 36 BP multicellular organism development  
## 3116 salmon 114 2.4e-03 1.0e+00 9 BP synapse organization  
## 3117 salmon 114 2.4e-03 1.0e+00 3 BP axonal transport  
## 3118 salmon 114 2.7e-03 1.0e+00 2 BP glycosphingolipid biosynthetic process  
## 3119 salmon 114 2.8e-03 1.0e+00 16 BP animal organ morphogenesis  
## 3120 salmon 114 3.4e-03 1.0e+00 2 BP positive regulation of lamellipodium ass  
## 3121 salmon 114 3.4e-03 1.0e+00 2 MF non-membrane spanning protein tyrosine k  
## 3122 salmon 114 4.5e-03 1.0e+00 9 BP post-embryonic appendage morphogenesis  
## 3123 salmon 114 4.6e-03 1.0e+00 4 BP positive regulation of cell projection o  
## 3124 salmon 114 5.2e-03 1.0e+00 2 BP vesicle transport along microtubule  
## 3125 salmon 114 5.4e-03 1.0e+00 9 BP imaginal disc-derived appendage morphoge  
## 3126 salmon 114 5.7e-03 1.0e+00 9 BP appendage morphogenesis  
## 3127 salmon 114 5.9e-03 1.0e+00 13 BP morphogenesis of an epithelium  
## 3128 salmon 114 6.0e-03 1.0e+00 3 MF protein tyrosine kinase activity  
## 3129 salmon 114 6.2e-03 1.0e+00 6 BP dendrite morphogenesis  
## 3130 salmon 114 6.2e-03 1.0e+00 9 BP imaginal disc-derived appendage developm  
## 3131 salmon 114 6.2e-03 1.0e+00 2 BP retinal ganglion cell axon guidance  
## 3132 salmon 114 7.3e-03 1.0e+00 2 BP axon target recognition  
## 3133 salmon 114 8.0e-03 1.0e+00 3 BP axo-dendritic transport  
## 3134 salmon 114 8.1e-03 1.0e+00 7 BP regulation of developmental growth  
## 3135 salmon 114 8.8e-03 1.0e+00 13 BP neuron development  
## 3136 skyblue 44 5.9e-27 4.9e-23 18 CC cytosolic ribosome  
## 3137 skyblue 44 1.2e-23 1.0e-19 17 BP cytoplasmic translation  
## 3138 skyblue 44 7.7e-22 6.4e-18 18 CC ribosome  
## 3139 skyblue 44 5.7e-21 4.8e-17 17 MF structural constituent of ribosome  
## 3140 skyblue 44 1.2e-17 9.6e-14 21 BP peptide metabolic process  
## 3141 skyblue 44 3.1e-17 2.6e-13 19 BP translation  
## 3142 skyblue 44 4.3e-15 3.6e-11 18 MF structural molecule activity  
## 3143 skyblue 44 3.0e-14 2.5e-10 9 CC cytosolic small ribosomal subunit  
## 3144 skyblue 44 3.6e-14 3.0e-10 19 CC cytosol  
## 3145 skyblue 44 1.1e-13 9.6e-10 18 CC ribonucleoprotein complex  
## 3146 skyblue 44 3.2e-13 2.7e-09 9 CC cytosolic large ribosomal subunit  
## 3147 skyblue 44 6.1e-12 5.1e-08 9 CC small ribosomal subunit  
## 3148 skyblue 44 1.2e-10 1.0e-06 9 CC large ribosomal subunit  
## 3149 skyblue 44 1.7e-09 1.4e-05 32 CC cytoplasm  
## 3150 skyblue 44 9.9e-08 8.3e-04 25 CC protein-containing complex  
## 3151 skyblue 44 9.4e-07 7.9e-03 32 CC intracellular organelle  
## 3152 skyblue 44 4.2e-06 3.5e-02 22 BP biosynthetic process  
## 3153 skyblue 44 5.3e-06 4.4e-02 21 BP gene expression  
## 3154 skyblue 44 9.0e-06 7.6e-02 34 CC intracellular  
## 3155 skyblue 44 1.4e-05 1.2e-01 2 BP endonucleolytic cleavage to generate mat  
## 3156 skyblue 44 3.1e-05 2.6e-01 30 BP cellular metabolic process  
## 3157 skyblue 44 3.3e-05 2.7e-01 20 BP protein metabolic process  
## 3158 skyblue 44 5.4e-05 4.5e-01 3 MF ribosome binding  
## 3159 skyblue 44 2.9e-04 1.0e+00 2 BP endonucleolytic cleavage in ITS1 to sepa  
## 3160 skyblue 44 7.2e-04 1.0e+00 5 BP ribosome biogenesis  
## 3161 skyblue 44 8.1e-04 1.0e+00 3 BP ribosome assembly  
## 3162 skyblue 44 8.1e-04 1.0e+00 3 MF ribonucleoprotein complex binding  
## 3163 skyblue 44 1.2e-03 1.0e+00 2 BP maturation of 5.8S rRNA from tricistroni  
## 3164 skyblue 44 1.3e-03 1.0e+00 3 BP ribosomal small subunit biogenesis  
## 3165 skyblue 44 1.4e-03 1.0e+00 2 BP RNA phosphodiester bond hydrolysis, endo  
## 3166 skyblue 44 1.6e-03 1.0e+00 2 BP cleavage involved in rRNA processing  
## 3167 skyblue 44 1.8e-03 1.0e+00 2 BP maturation of 5.8S rRNA  
## 3168 skyblue 44 2.0e-03 1.0e+00 2 BP ribosomal small subunit assembly  
## 3169 skyblue 44 2.6e-03 1.0e+00 5 CC nuclear chromosome  
## 3170 skyblue 44 3.8e-03 1.0e+00 1 BP rRNA export from nucleus  
## 3171 skyblue 44 3.8e-03 1.0e+00 1 BP S-adenosyl-L-methionine transport  
## 3172 skyblue 44 3.8e-03 1.0e+00 1 BP positive regulation of translational fid  
## 3173 skyblue 44 3.8e-03 1.0e+00 1 BP regulation of plasma membrane sterol dis  
## 3174 skyblue 44 3.8e-03 1.0e+00 1 CC cortical endoplasmic reticulum  
## 3175 skyblue 44 3.8e-03 1.0e+00 1 MF S-adenosyl-L-methionine transmembrane tr  
## 3176 skyblue 44 4.6e-03 1.0e+00 7 MF RNA binding  
## 3177 skyblue 44 5.6e-03 1.0e+00 2 BP maturation of SSU-rRNA from tricistronic  
## 3178 skyblue 44 5.6e-03 1.0e+00 2 BP translational elongation  
## 3179 skyblue 44 6.1e-03 1.0e+00 4 CC nucleolus  
## 3180 skyblue 44 6.4e-03 1.0e+00 33 BP cellular process  
## 3181 skyblue 44 7.5e-03 1.0e+00 1 MF fumarate hydratase activity  
## 3182 skyblue 44 7.5e-03 1.0e+00 1 MF inorganic diphosphatase activity  
## 3183 skyblue 44 7.5e-03 1.0e+00 1 MF phosphoglycerate kinase activity  
## 3184 skyblue 44 7.5e-03 1.0e+00 1 MF oxidized purine nucleobase lesion DNA N-  
## 3185 skyblue 44 7.5e-03 1.0e+00 1 MF cysteine desulfurase activity  
## 3186 skyblue 44 7.5e-03 1.0e+00 1 MF large ribosomal subunit rRNA binding  
## 3187 skyblue 44 9.4e-03 1.0e+00 2 BP maturation of SSU-rRNA  
## 3188 skyblue 44 9.4e-03 1.0e+00 2 BP regulation of hemocyte proliferation  
## 3189 skyblue 44 9.4e-03 1.0e+00 2 MF rRNA binding  
## 3190 steelblue 39 2.1e-06 1.8e-02 3 BP protein localization to Golgi apparatus  
## 3191 steelblue 39 3.5e-05 3.0e-01 2 BP protein retention in Golgi apparatus  
## 3192 steelblue 39 9.3e-05 7.8e-01 24 CC cytoplasm  
## 3193 steelblue 39 1.2e-04 9.8e-01 2 BP perineurial glial growth  
## 3194 steelblue 39 2.1e-04 1.0e+00 4 BP regulation of Wnt signaling pathway  
## 3195 steelblue 39 2.5e-04 1.0e+00 2 BP positive regulation of ion transmembrane  
## 3196 steelblue 39 2.8e-04 1.0e+00 5 MF Ras GTPase binding  
## 3197 steelblue 39 3.0e-04 1.0e+00 5 MF small GTPase binding  
## 3198 steelblue 39 3.3e-04 1.0e+00 2 BP glial cell growth  
## 3199 steelblue 39 4.1e-04 1.0e+00 3 BP positive regulation of Wnt signaling pat  
## 3200 steelblue 39 4.6e-04 1.0e+00 5 MF GTPase binding  
## 3201 steelblue 39 5.9e-04 1.0e+00 4 BP Wnt signaling pathway  
## 3202 steelblue 39 6.6e-04 1.0e+00 9 BP regulation of signal transduction  
## 3203 steelblue 39 6.8e-04 1.0e+00 3 BP Rho protein signal transduction  
## 3204 steelblue 39 7.0e-04 1.0e+00 7 BP regulation of localization  
## 3205 steelblue 39 7.6e-04 1.0e+00 2 BP protein targeting to vacuole  
## 3206 steelblue 39 1.3e-03 1.0e+00 7 BP vesicle-mediated transport  
## 3207 steelblue 39 1.3e-03 1.0e+00 5 BP regulation of transport  
## 3208 steelblue 39 1.5e-03 1.0e+00 16 MF protein binding  
## 3209 steelblue 39 1.5e-03 1.0e+00 4 BP Ras protein signal transduction  
## 3210 steelblue 39 2.4e-03 1.0e+00 4 BP small GTPase mediated signal transductio  
## 3211 steelblue 39 2.4e-03 1.0e+00 2 MF channel regulator activity  
## 3212 steelblue 39 2.4e-03 1.0e+00 28 CC intracellular  
## 3213 steelblue 39 2.6e-03 1.0e+00 3 BP regulation of Ras protein signal transdu  
## 3214 steelblue 39 2.7e-03 1.0e+00 3 MF GTPase activator activity  
## 3215 steelblue 39 3.4e-03 1.0e+00 3 BP regulation of small GTPase mediated sign  
## 3216 steelblue 39 3.5e-03 1.0e+00 3 MF Rab GTPase binding  
## 3217 steelblue 39 3.5e-03 1.0e+00 1 BP detection of calcium ion  
## 3218 steelblue 39 3.5e-03 1.0e+00 1 BP activation of store-operated calcium cha  
## 3219 steelblue 39 3.5e-03 1.0e+00 1 BP locomotory exploration behavior  
## 3220 steelblue 39 3.5e-03 1.0e+00 1 BP negative regulation of gluconeogenesis  
## 3221 steelblue 39 3.5e-03 1.0e+00 1 BP positive regulation of adenylate cyclase  
## 3222 steelblue 39 3.5e-03 1.0e+00 1 BP positive regulation of protein desumoyla  
## 3223 steelblue 39 3.5e-03 1.0e+00 1 BP positive regulation of potassium ion imp  
## 3224 steelblue 39 3.5e-03 1.0e+00 1 BP negative regulation of non-canonical Wnt  
## 3225 steelblue 39 3.5e-03 1.0e+00 1 BP positive regulation of sodium ion transm  
## 3226 steelblue 39 3.5e-03 1.0e+00 1 MF chloride channel inhibitor activity  
## 3227 steelblue 39 3.5e-03 1.0e+00 1 MF potassium channel inhibitor activity  
## 3228 steelblue 39 3.5e-03 1.0e+00 1 MF ubiquitin-dependent protein binding  
## 3229 steelblue 39 3.6e-03 1.0e+00 3 BP spermatid differentiation  
## 3230 steelblue 39 3.7e-03 1.0e+00 6 MF enzyme binding  
## 3231 steelblue 39 3.9e-03 1.0e+00 2 BP retrograde transport, endosome to Golgi  
## 3232 steelblue 39 4.0e-03 1.0e+00 4 BP endocytosis  
## 3233 steelblue 39 4.5e-03 1.0e+00 2 MF Rho guanyl-nucleotide exchange factor ac  
## 3234 steelblue 39 5.1e-03 1.0e+00 2 BP regulation of Rho protein signal transdu  
## 3235 steelblue 39 5.3e-03 1.0e+00 4 MF ubiquitin-protein transferase activity  
## 3236 steelblue 39 5.5e-03 1.0e+00 2 BP maintenance of protein location in cell  
## 3237 steelblue 39 5.5e-03 1.0e+00 2 BP regulation of hemocyte differentiation  
## 3238 steelblue 39 6.5e-03 1.0e+00 4 MF ubiquitin-like protein transferase activ  
## 3239 steelblue 39 7.0e-03 1.0e+00 1 BP asparaginyl-tRNA aminoacylation  
## 3240 steelblue 39 7.0e-03 1.0e+00 1 BP negative regulation of terminal cell fat  
## 3241 steelblue 39 7.0e-03 1.0e+00 1 BP negative regulation of fusion cell fate   
## 3242 steelblue 39 7.0e-03 1.0e+00 1 BP negative regulation of inflammatory resp  
## 3243 steelblue 39 7.0e-03 1.0e+00 1 BP oenocyte delamination  
## 3244 steelblue 39 7.0e-03 1.0e+00 1 BP negative regulation of histone H2A K63-l  
## 3245 steelblue 39 7.0e-03 1.0e+00 1 BP response to rotenone  
## 3246 steelblue 39 7.0e-03 1.0e+00 1 BP ribosome-associated ubiquitin-dependent   
## 3247 steelblue 39 7.0e-03 1.0e+00 1 CC GID complex  
## 3248 steelblue 39 7.0e-03 1.0e+00 1 CC RQC complex  
## 3249 steelblue 39 7.0e-03 1.0e+00 1 MF asparagine-tRNA ligase activity  
## 3250 steelblue 39 7.0e-03 1.0e+00 1 MF calcium-induced calcium release activity  
## 3251 steelblue 39 7.3e-03 1.0e+00 2 BP positive regulation of canonical Wnt sig  
## 3252 steelblue 39 7.7e-03 1.0e+00 2 CC P granule  
## 3253 steelblue 39 7.7e-03 1.0e+00 4 BP muscle structure development  
## 3254 steelblue 39 7.7e-03 1.0e+00 5 CC cytoplasmic vesicle  
## 3255 steelblue 39 8.1e-03 1.0e+00 2 BP maintenance of protein location  
## 3256 steelblue 39 8.5e-03 1.0e+00 2 CC germ plasm  
## 3257 steelblue 39 8.9e-03 1.0e+00 7 BP cell surface receptor signaling pathway  
## 3258 tan 123 1.1e-05 9.1e-02 17 BP vesicle-mediated transport  
## 3259 tan 123 3.9e-05 3.2e-01 4 BP ommochrome biosynthetic process  
## 3260 tan 123 3.9e-05 3.2e-01 4 BP ocellus pigment biosynthetic process  
## 3261 tan 123 4.6e-04 1.0e+00 3 CC AP-type membrane coat adaptor complex  
## 3262 tan 123 5.7e-04 1.0e+00 4 BP eye pigment biosynthetic process  
## 3263 tan 123 6.1e-04 1.0e+00 6 BP endosomal transport  
## 3264 tan 123 6.4e-04 1.0e+00 2 CC AP-3 adaptor complex  
## 3265 tan 123 7.0e-04 1.0e+00 4 BP eye pigment metabolic process  
## 3266 tan 123 1.1e-03 1.0e+00 5 CC small nuclear ribonucleoprotein complex  
## 3267 tan 123 1.1e-03 1.0e+00 3 BP compound eye pigmentation  
## 3268 tan 123 2.2e-03 1.0e+00 2 BP heart formation  
## 3269 tan 123 2.7e-03 1.0e+00 3 BP retrograde transport, endosome to Golgi  
## 3270 tan 123 3.7e-03 1.0e+00 2 BP chromatin-mediated maintenance of transc  
## 3271 tan 123 3.7e-03 1.0e+00 2 MF nuclear hormone receptor binding  
## 3272 tan 123 4.0e-03 1.0e+00 4 CC nuclear body  
## 3273 tan 123 4.6e-03 1.0e+00 2 BP SNARE complex assembly  
## 3274 tan 123 4.7e-03 1.0e+00 4 MF protein transporter activity  
## 3275 tan 123 5.6e-03 1.0e+00 2 BP negative regulation of lipid storage  
## 3276 tan 123 6.5e-03 1.0e+00 5 BP developmental pigmentation  
## 3277 tan 123 6.7e-03 1.0e+00 14 BP intracellular transport  
## 3278 tan 123 7.1e-03 1.0e+00 7 BP secretion by cell  
## 3279 tan 123 7.7e-03 1.0e+00 3 BP meiotic spindle organization  
## 3280 tan 123 8.9e-03 1.0e+00 3 BP regulation of lipid storage  
## 3281 tan 123 8.9e-03 1.0e+00 37 CC protein-containing complex  
## 3282 turquoise 3240 2.4e-47 2.0e-43 394 CC extracellular region  
## 3283 turquoise 3240 3.7e-36 3.1e-32 233 CC extracellular space  
## 3284 turquoise 3240 5.2e-31 4.3e-27 245 BP oxidation-reduction process  
## 3285 turquoise 3240 1.3e-30 1.1e-26 250 MF oxidoreductase activity  
## 3286 turquoise 3240 2.2e-19 1.8e-15 161 MF cofactor binding  
## 3287 turquoise 3240 6.1e-19 5.1e-15 107 BP response to bacterium  
## 3288 turquoise 3240 1.7e-16 1.4e-12 81 MF iron ion binding  
## 3289 turquoise 3240 7.3e-16 6.1e-12 152 BP defense response  
## 3290 turquoise 3240 2.0e-15 1.7e-11 163 BP carboxylic acid metabolic process  
## 3291 turquoise 3240 3.1e-15 2.6e-11 168 BP organic acid metabolic process  
## 3292 turquoise 3240 6.4e-15 5.4e-11 71 MF heme binding  
## 3293 turquoise 3240 1.6e-14 1.3e-10 112 BP carbohydrate metabolic process  
## 3294 turquoise 3240 1.7e-14 1.5e-10 40 BP defense response to Gram-positive bacter  
## 3295 turquoise 3240 1.5e-13 1.2e-09 87 BP defense response to bacterium  
## 3296 turquoise 3240 1.6e-13 1.3e-09 80 MF oxidoreductase activity, acting on paire  
## 3297 turquoise 3240 1.9e-13 1.6e-09 113 BP defense response to other organism  
## 3298 turquoise 3240 4.2e-12 3.5e-08 83 BP generation of precursor metabolites and   
## 3299 turquoise 3240 6.4e-12 5.3e-08 42 MF endopeptidase inhibitor activity  
## 3300 turquoise 3240 1.0e-11 8.7e-08 43 MF peptidase inhibitor activity  
## 3301 turquoise 3240 7.9e-10 6.6e-06 31 BP aerobic respiration  
## 3302 turquoise 3240 9.1e-10 7.6e-06 45 BP defense response to Gram-negative bacter  
## 3303 turquoise 3240 3.2e-09 2.7e-05 52 BP cellular respiration  
## 3304 turquoise 3240 1.6e-08 1.4e-04 31 MF serine-type endopeptidase inhibitor acti  
## 3305 turquoise 3240 3.5e-08 2.9e-04 46 MF receptor ligand activity  
## 3306 turquoise 3240 6.2e-08 5.2e-04 33 CC myofibril  
## 3307 turquoise 3240 7.2e-08 6.1e-04 28 BP antibacterial humoral response  
## 3308 turquoise 3240 7.6e-08 6.3e-04 17 BP aromatic amino acid family metabolic pro  
## 3309 turquoise 3240 8.2e-08 6.9e-04 46 BP cellular carbohydrate metabolic process  
## 3310 turquoise 3240 1.8e-07 1.5e-03 11 BP tyrosine metabolic process  
## 3311 turquoise 3240 1.8e-07 1.5e-03 372 CC intrinsic component of membrane  
## 3312 turquoise 3240 2.2e-07 1.9e-03 19 BP tricarboxylic acid cycle  
## 3313 turquoise 3240 3.4e-07 2.9e-03 36 CC mitochondrial respiratory chain  
## 3314 turquoise 3240 4.8e-07 4.0e-03 30 CC sarcomere  
## 3315 turquoise 3240 5.0e-07 4.2e-03 364 CC integral component of membrane  
## 3316 turquoise 3240 5.8e-07 4.8e-03 19 BP citrate metabolic process  
## 3317 turquoise 3240 5.8e-07 4.8e-03 185 MF transmembrane transporter activity  
## 3318 turquoise 3240 7.4e-07 6.2e-03 89 MF signaling receptor binding  
## 3319 turquoise 3240 7.5e-07 6.3e-03 59 BP humoral immune response  
## 3320 turquoise 3240 7.6e-07 6.4e-03 84 BP purine nucleotide metabolic process  
## 3321 turquoise 3240 1.1e-06 9.0e-03 86 BP ribose phosphate metabolic process  
## 3322 turquoise 3240 1.2e-06 9.9e-03 45 MF enzyme inhibitor activity  
## 3323 turquoise 3240 1.2e-06 1.0e-02 27 BP myofibril assembly  
## 3324 turquoise 3240 1.4e-06 1.2e-02 33 BP muscle cell development  
## 3325 turquoise 3240 1.9e-06 1.6e-02 21 BP response to unfolded protein  
## 3326 turquoise 3240 2.4e-06 2.0e-02 20 BP cellular response to unfolded protein  
## 3327 turquoise 3240 2.6e-06 2.2e-02 52 BP ATP metabolic process  
## 3328 turquoise 3240 2.9e-06 2.4e-02 22 BP muscle system process  
## 3329 turquoise 3240 3.0e-06 2.5e-02 9 BP one-carbon metabolic process  
## 3330 turquoise 3240 3.0e-06 2.5e-02 97 BP immune response  
## 3331 turquoise 3240 3.2e-06 2.7e-02 82 BP ribonucleotide metabolic process  
## 3332 turquoise 3240 3.2e-06 2.7e-02 29 BP neuropeptide signaling pathway  
## 3333 turquoise 3240 3.9e-06 3.2e-02 86 CC mitochondrial membrane  
## 3334 turquoise 3240 4.3e-06 3.6e-02 35 BP respiratory electron transport chain  
## 3335 turquoise 3240 4.7e-06 3.9e-02 36 BP electron transport chain  
## 3336 turquoise 3240 6.6e-06 5.5e-02 72 CC mitochondrial inner membrane  
## 3337 turquoise 3240 6.6e-06 5.6e-02 99 BP nucleoside phosphate metabolic process  
## 3338 turquoise 3240 7.0e-06 5.8e-02 165 BP response to organic substance  
## 3339 turquoise 3240 7.1e-06 5.9e-02 98 BP nucleotide metabolic process  
## 3340 turquoise 3240 7.3e-06 6.1e-02 21 BP triglyceride metabolic process  
## 3341 turquoise 3240 7.3e-06 6.2e-02 23 BP cellular response to topologically incor  
## 3342 turquoise 3240 7.4e-06 6.2e-02 210 CC mitochondrion  
## 3343 turquoise 3240 8.0e-06 6.7e-02 204 MF transporter activity  
## 3344 turquoise 3240 8.3e-06 7.0e-02 29 MF electron transfer activity  
## 3345 turquoise 3240 8.4e-06 7.0e-02 26 BP carbohydrate catabolic process  
## 3346 turquoise 3240 1.1e-05 9.6e-02 32 BP ATP synthesis coupled electron transport  
## 3347 turquoise 3240 1.3e-05 1.1e-01 167 BP transmembrane transport  
## 3348 turquoise 3240 1.3e-05 1.1e-01 19 BP negative regulation of peptidase activit  
## 3349 turquoise 3240 1.4e-05 1.2e-01 35 MF oxidoreductase activity, acting on CH-OH  
## 3350 turquoise 3240 1.4e-05 1.2e-01 70 BP cellular amino acid metabolic process  
## 3351 turquoise 3240 1.6e-05 1.3e-01 88 CC mitochondrial envelope  
## 3352 turquoise 3240 1.7e-05 1.4e-01 84 BP cuticle development  
## 3353 turquoise 3240 1.7e-05 1.4e-01 15 BP protein refolding  
## 3354 turquoise 3240 1.9e-05 1.6e-01 25 BP cellular amino acid biosynthetic process  
## 3355 turquoise 3240 2.0e-05 1.7e-01 35 BP lipid transport  
## 3356 turquoise 3240 2.1e-05 1.7e-01 36 BP oxidative phosphorylation  
## 3357 turquoise 3240 2.1e-05 1.8e-01 142 MF ion transmembrane transporter activity  
## 3358 turquoise 3240 2.2e-05 1.8e-01 23 BP chaperone-mediated protein folding  
## 3359 turquoise 3240 2.2e-05 1.8e-01 23 MF iron-sulfur cluster binding  
## 3360 turquoise 3240 2.3e-05 1.9e-01 17 BP muscle contraction  
## 3361 turquoise 3240 2.3e-05 1.9e-01 17 MF monocarboxylic acid transmembrane transp  
## 3362 turquoise 3240 2.3e-05 2.0e-01 82 BP open tracheal system development  
## 3363 turquoise 3240 2.4e-05 2.0e-01 31 BP mitochondrial ATP synthesis coupled elec  
## 3364 turquoise 3240 2.7e-05 2.2e-01 49 BP antimicrobial humoral response  
## 3365 turquoise 3240 2.8e-05 2.3e-01 28 MF oxidoreductase activity, acting on the C  
## 3366 turquoise 3240 3.0e-05 2.5e-01 16 CC collagen-containing extracellular matrix  
## 3367 turquoise 3240 3.0e-05 2.5e-01 16 MF growth factor activity  
## 3368 turquoise 3240 3.0e-05 2.5e-01 11 MF misfolded protein binding  
## 3369 turquoise 3240 3.3e-05 2.8e-01 20 BP heart contraction  
## 3370 turquoise 3240 3.3e-05 2.8e-01 18 BP negative regulation of endopeptidase act  
## 3371 turquoise 3240 4.2e-05 3.6e-01 24 BP heart process  
## 3372 turquoise 3240 5.0e-05 4.2e-01 22 BP negative regulation of proteolysis  
## 3373 turquoise 3240 5.6e-05 4.7e-01 64 CC extracellular matrix  
## 3374 turquoise 3240 5.7e-05 4.8e-01 20 BP sarcomere organization  
## 3375 turquoise 3240 6.1e-05 5.1e-01 18 MF neuropeptide hormone activity  
## 3376 turquoise 3240 7.0e-05 5.8e-01 60 BP chitin-based cuticle development  
## 3377 turquoise 3240 8.1e-05 6.8e-01 71 MF serine-type endopeptidase activity  
## 3378 turquoise 3240 8.3e-05 7.0e-01 17 BP monocarboxylic acid transport  
## 3379 turquoise 3240 8.6e-05 7.2e-01 56 BP innate immune response  
## 3380 turquoise 3240 8.6e-05 7.2e-01 8 MF sterol-transporting ATPase activity  
## 3381 turquoise 3240 8.8e-05 7.4e-01 11 MF protein binding involved in protein fold  
## 3382 turquoise 3240 9.9e-05 8.3e-01 40 MF organic anion transmembrane transporter   
## 3383 turquoise 3240 1.0e-04 8.7e-01 14 BP chaperone cofactor-dependent protein ref  
## 3384 turquoise 3240 1.4e-04 1.0e+00 13 MF 4 iron, 4 sulfur cluster binding  
## 3385 turquoise 3240 1.5e-04 1.0e+00 147 BP lipid metabolic process  
## 3386 turquoise 3240 1.5e-04 1.0e+00 49 BP muscle cell differentiation  
## 3387 turquoise 3240 1.8e-04 1.0e+00 100 BP cellular response to organic substance  
## 3388 turquoise 3240 1.9e-04 1.0e+00 28 BP response to fungus  
## 3389 turquoise 3240 2.1e-04 1.0e+00 6 BP carnitine metabolic process  
## 3390 turquoise 3240 2.1e-04 1.0e+00 6 MF imaginal disc growth factor receptor bin  
## 3391 turquoise 3240 2.1e-04 1.0e+00 109 MF endopeptidase activity  
## 3392 turquoise 3240 2.2e-04 1.0e+00 19 BP pyruvate metabolic process  
## 3393 turquoise 3240 2.3e-04 1.0e+00 79 BP muscle structure development  
## 3394 turquoise 3240 2.3e-04 1.0e+00 24 MF lipid transporter activity  
## 3395 turquoise 3240 2.5e-04 1.0e+00 65 MF coenzyme binding  
## 3396 turquoise 3240 2.5e-04 1.0e+00 20 BP acyl-CoA metabolic process  
## 3397 turquoise 3240 2.7e-04 1.0e+00 10 BP glycosaminoglycan catabolic process  
## 3398 turquoise 3240 2.7e-04 1.0e+00 10 BP central nervous system morphogenesis  
## 3399 turquoise 3240 2.8e-04 1.0e+00 15 CC cytochrome complex  
## 3400 turquoise 3240 3.0e-04 1.0e+00 56 BP sulfur compound metabolic process  
## 3401 turquoise 3240 3.1e-04 1.0e+00 9 MF transaminase activity  
## 3402 turquoise 3240 3.1e-04 1.0e+00 9 MF cholesterol transporter activity  
## 3403 turquoise 3240 3.2e-04 1.0e+00 7 BP glycine metabolic process  
## 3404 turquoise 3240 3.2e-04 1.0e+00 7 BP tetrahydrofolate metabolic process  
## 3405 turquoise 3240 3.2e-04 1.0e+00 7 MF quinone binding  
## 3406 turquoise 3240 3.5e-04 1.0e+00 19 CC Z disc  
## 3407 turquoise 3240 3.5e-04 1.0e+00 19 CC I band  
## 3408 turquoise 3240 3.5e-04 1.0e+00 16 BP glycogen metabolic process  
## 3409 turquoise 3240 3.7e-04 1.0e+00 12 MF signaling pattern recognition receptor a  
## 3410 turquoise 3240 3.7e-04 1.0e+00 12 MF peptidoglycan binding  
## 3411 turquoise 3240 3.8e-04 1.0e+00 949 MF catalytic activity  
## 3412 turquoise 3240 3.8e-04 1.0e+00 14 BP 'de novo' protein folding  
## 3413 turquoise 3240 3.9e-04 1.0e+00 118 BP cellular lipid metabolic process  
## 3414 turquoise 3240 4.7e-04 1.0e+00 623 CC membrane  
## 3415 turquoise 3240 5.0e-04 1.0e+00 72 MF active transmembrane transporter activit  
## 3416 turquoise 3240 5.6e-04 1.0e+00 41 MF carbohydrate binding  
## 3417 turquoise 3240 5.9e-04 1.0e+00 34 MF hydrolase activity, hydrolyzing O-glycos  
## 3418 turquoise 3240 6.0e-04 1.0e+00 74 MF serine-type peptidase activity  
## 3419 turquoise 3240 6.1e-04 1.0e+00 39 BP muscle organ development  
## 3420 turquoise 3240 6.9e-04 1.0e+00 74 MF serine hydrolase activity  
## 3421 turquoise 3240 7.6e-04 1.0e+00 34 BP regulation of tube architecture, open tr  
## 3422 turquoise 3240 8.5e-04 1.0e+00 5 MF hydroxymethyl-, formyl- and related tran  
## 3423 turquoise 3240 9.3e-04 1.0e+00 47 BP response to oxidative stress  
## 3424 turquoise 3240 1.1e-03 1.0e+00 135 CC intrinsic component of plasma membrane  
## 3425 turquoise 3240 1.1e-03 1.0e+00 7 BP glycerol metabolic process  
## 3426 turquoise 3240 1.1e-03 1.0e+00 7 BP striated muscle contraction  
## 3427 turquoise 3240 1.1e-03 1.0e+00 7 BP central nervous system formation  
## 3428 turquoise 3240 1.1e-03 1.0e+00 7 BP pericardial nephrocyte differentiation  
## 3429 turquoise 3240 1.1e-03 1.0e+00 7 MF cysteine-type endopeptidase inhibitor ac  
## 3430 turquoise 3240 1.1e-03 1.0e+00 18 MF monooxygenase activity  
## 3431 turquoise 3240 1.1e-03 1.0e+00 6 BP regulation of melanization defense respo  
## 3432 turquoise 3240 1.1e-03 1.0e+00 6 CC cytoneme  
## 3433 turquoise 3240 1.2e-03 1.0e+00 39 MF structural constituent of cuticle  
## 3434 turquoise 3240 1.3e-03 1.0e+00 21 MF G protein-coupled peptide receptor activ  
## 3435 turquoise 3240 1.3e-03 1.0e+00 22 BP regulation of tube size, open tracheal s  
## 3436 turquoise 3240 1.4e-03 1.0e+00 44 BP fatty acid metabolic process  
## 3437 turquoise 3240 1.5e-03 1.0e+00 42 BP developmental pigmentation  
## 3438 turquoise 3240 1.6e-03 1.0e+00 17 BP regulation of tube length, open tracheal  
## 3439 turquoise 3240 1.7e-03 1.0e+00 19 MF hormone activity  
## 3440 turquoise 3240 1.7e-03 1.0e+00 9 BP negative regulation of natural killer ce  
## 3441 turquoise 3240 1.7e-03 1.0e+00 9 BP response to hyperoxia  
## 3442 turquoise 3240 1.7e-03 1.0e+00 9 CC respiratory chain complex IV  
## 3443 turquoise 3240 1.7e-03 1.0e+00 9 MF N-acetylmuramoyl-L-alanine amidase activ  
## 3444 turquoise 3240 1.7e-03 1.0e+00 9 MF sterol transporter activity  
## 3445 turquoise 3240 1.7e-03 1.0e+00 9 MF peptidoglycan receptor activity  
## 3446 turquoise 3240 1.8e-03 1.0e+00 20 BP carbohydrate homeostasis  
## 3447 turquoise 3240 1.8e-03 1.0e+00 20 MF neuropeptide receptor activity  
## 3448 turquoise 3240 1.8e-03 1.0e+00 23 BP cuticle pigmentation  
## 3449 turquoise 3240 1.8e-03 1.0e+00 11 BP chitin-based embryonic cuticle biosynthe  
## 3450 turquoise 3240 1.8e-03 1.0e+00 11 CC lipid droplet  
## 3451 turquoise 3240 2.2e-03 1.0e+00 16 CC fusome  
## 3452 turquoise 3240 2.2e-03 1.0e+00 12 BP regulation of female receptivity  
## 3453 turquoise 3240 2.3e-03 1.0e+00 8 BP peptidoglycan metabolic process  
## 3454 turquoise 3240 2.3e-03 1.0e+00 8 BP peptidoglycan catabolic process  
## 3455 turquoise 3240 2.3e-03 1.0e+00 8 BP triglyceride biosynthetic process  
## 3456 turquoise 3240 2.3e-03 1.0e+00 8 CC tricarboxylic acid cycle enzyme complex  
## 3457 turquoise 3240 2.4e-03 1.0e+00 18 BP muscle attachment  
## 3458 turquoise 3240 2.4e-03 1.0e+00 18 BP negative regulation of immune response  
## 3459 turquoise 3240 2.4e-03 1.0e+00 18 CC mitochondrial respiratory chain complex   
## 3460 turquoise 3240 2.4e-03 1.0e+00 18 CC NADH dehydrogenase complex  
## 3461 turquoise 3240 2.4e-03 1.0e+00 22 MF peptide receptor activity  
## 3462 turquoise 3240 2.5e-03 1.0e+00 10 MF cytochrome-c oxidase activity  
## 3463 turquoise 3240 2.5e-03 1.0e+00 10 MF cytokine activity  
## 3464 turquoise 3240 2.5e-03 1.0e+00 96 MF cation transmembrane transporter activit  
## 3465 turquoise 3240 2.7e-03 1.0e+00 36 CC peroxisome  
## 3466 turquoise 3240 2.9e-03 1.0e+00 137 BP metamorphosis  
## 3467 turquoise 3240 3.0e-03 1.0e+00 7 BP UDP-glucose metabolic process  
## 3468 turquoise 3240 3.0e-03 1.0e+00 7 BP hemolymph coagulation  
## 3469 turquoise 3240 3.0e-03 1.0e+00 7 BP regulation of female receptivity, post-m  
## 3470 turquoise 3240 3.0e-03 1.0e+00 34 MF hydrolase activity, acting on glycosyl b  
## 3471 turquoise 3240 3.1e-03 1.0e+00 15 MF NADH dehydrogenase activity  
## 3472 turquoise 3240 3.1e-03 1.0e+00 11 BP decapentaplegic signaling pathway  
## 3473 turquoise 3240 3.3e-03 1.0e+00 158 BP instar larval or pupal development  
## 3474 turquoise 3240 3.3e-03 1.0e+00 36 BP mesoderm development  
## 3475 turquoise 3240 3.3e-03 1.0e+00 21 BP genital disc development  
## 3476 turquoise 3240 3.3e-03 1.0e+00 17 MF sodium channel activity  
## 3477 turquoise 3240 3.4e-03 1.0e+00 18 BP epithelial cell migration, open tracheal  
## 3478 turquoise 3240 3.4e-03 1.0e+00 9 BP antifungal humoral response  
## 3479 turquoise 3240 3.5e-03 1.0e+00 4 BP skeletal muscle contraction  
## 3480 turquoise 3240 3.5e-03 1.0e+00 4 BP pyrimidine nucleobase catabolic process  
## 3481 turquoise 3240 3.5e-03 1.0e+00 4 BP glycine catabolic process  
## 3482 turquoise 3240 3.5e-03 1.0e+00 4 BP melanin biosynthetic process from tyrosi  
## 3483 turquoise 3240 3.5e-03 1.0e+00 4 BP pyruvate transport  
## 3484 turquoise 3240 3.5e-03 1.0e+00 4 BP labial disc development  
## 3485 turquoise 3240 3.5e-03 1.0e+00 4 BP tetrahydrofolate interconversion  
## 3486 turquoise 3240 3.5e-03 1.0e+00 4 BP pheromone biosynthetic process  
## 3487 turquoise 3240 3.5e-03 1.0e+00 4 BP carnitine biosynthetic process  
## 3488 turquoise 3240 3.5e-03 1.0e+00 4 BP positive regulation of cysteine-type end  
## 3489 turquoise 3240 3.5e-03 1.0e+00 4 CC larval serum protein complex  
## 3490 turquoise 3240 3.5e-03 1.0e+00 4 CC glycine cleavage complex  
## 3491 turquoise 3240 3.5e-03 1.0e+00 4 CC phosphatidylinositol 3-kinase complex, c  
## 3492 turquoise 3240 3.5e-03 1.0e+00 4 MF pyruvate transmembrane transporter activ  
## 3493 turquoise 3240 3.5e-03 1.0e+00 131 BP ion transport  
## 3494 turquoise 3240 3.5e-03 1.0e+00 38 BP lipid catabolic process  
## 3495 turquoise 3240 3.6e-03 1.0e+00 128 CC integral component of plasma membrane  
## 3496 turquoise 3240 3.6e-03 1.0e+00 12 BP cholesterol transport  
## 3497 turquoise 3240 3.6e-03 1.0e+00 12 MF transmembrane receptor protein tyrosine   
## 3498 turquoise 3240 3.6e-03 1.0e+00 12 MF carboxy-lyase activity  
## 3499 turquoise 3240 3.6e-03 1.0e+00 6 CC mitochondrial proton-transporting ATP sy  
## 3500 turquoise 3240 3.6e-03 1.0e+00 6 CC proton-transporting ATP synthase complex  
## 3501 turquoise 3240 3.6e-03 1.0e+00 6 MF Toll binding  
## 3502 turquoise 3240 3.6e-03 1.0e+00 6 MF gamma-aminobutyric acid:sodium symporter  
## 3503 turquoise 3240 3.7e-03 1.0e+00 43 BP regulation of immune response  
## 3504 turquoise 3240 3.7e-03 1.0e+00 26 MF metalloendopeptidase activity  
## 3505 turquoise 3240 3.9e-03 1.0e+00 91 MF inorganic cation transmembrane transport  
## 3506 turquoise 3240 4.0e-03 1.0e+00 29 MF structural constituent of chitin-based l  
## 3507 turquoise 3240 4.0e-03 1.0e+00 13 BP regulation of Toll signaling pathway  
## 3508 turquoise 3240 4.0e-03 1.0e+00 13 BP sterol transport  
## 3509 turquoise 3240 4.0e-03 1.0e+00 13 BP regulation of developmental pigmentation  
## 3510 turquoise 3240 4.1e-03 1.0e+00 5 BP galactose metabolic process  
## 3511 turquoise 3240 4.1e-03 1.0e+00 5 BP tryptophan metabolic process  
## 3512 turquoise 3240 4.1e-03 1.0e+00 5 BP equator specification  
## 3513 turquoise 3240 4.1e-03 1.0e+00 5 CC striated muscle thin filament  
## 3514 turquoise 3240 4.1e-03 1.0e+00 5 MF ubiquinone binding  
## 3515 turquoise 3240 4.1e-03 1.0e+00 101 BP appendage morphogenesis  
## 3516 turquoise 3240 4.3e-03 1.0e+00 102 BP imaginal disc-derived appendage developm  
## 3517 turquoise 3240 4.3e-03 1.0e+00 35 BP purine nucleotide biosynthetic process  
## 3518 turquoise 3240 4.3e-03 1.0e+00 14 BP regulation of heart contraction  
## 3519 turquoise 3240 4.3e-03 1.0e+00 14 MF oxidoreductase activity, acting on the a  
## 3520 turquoise 3240 4.4e-03 1.0e+00 10 MF amino acid:sodium symporter activity  
## 3521 turquoise 3240 4.4e-03 1.0e+00 100 BP imaginal disc-derived appendage morphoge  
## 3522 turquoise 3240 4.7e-03 1.0e+00 18 BP ventral cord development  
## 3523 turquoise 3240 4.7e-03 1.0e+00 8 BP glycerol-3-phosphate metabolic process  
## 3524 turquoise 3240 4.7e-03 1.0e+00 8 BP regulation of muscle contraction  
## 3525 turquoise 3240 4.7e-03 1.0e+00 8 BP wing and notum subfield formation  
## 3526 turquoise 3240 4.7e-03 1.0e+00 8 CC mitochondrial respiratory chain complex   
## 3527 turquoise 3240 4.7e-03 1.0e+00 8 MF polysaccharide binding  
## 3528 turquoise 3240 4.7e-03 1.0e+00 144 BP tube morphogenesis  
## 3529 turquoise 3240 5.2e-03 1.0e+00 32 MF sodium ion transmembrane transporter act  
## 3530 turquoise 3240 5.2e-03 1.0e+00 35 MF structural constituent of chitin-based c  
## 3531 turquoise 3240 5.3e-03 1.0e+00 134 BP epithelial tube morphogenesis  
## 3532 turquoise 3240 6.0e-03 1.0e+00 20 BP Toll signaling pathway  
## 3533 turquoise 3240 6.2e-03 1.0e+00 9 MF lysozyme activity  
## 3534 turquoise 3240 6.2e-03 1.0e+00 9 MF neurotransmitter binding  
## 3535 turquoise 3240 6.3e-03 1.0e+00 14 BP mitochondrial electron transport, NADH t  
## 3536 turquoise 3240 6.4e-03 1.0e+00 17 MF glycosaminoglycan binding  
## 3537 turquoise 3240 6.4e-03 1.0e+00 15 MF carbon-carbon lyase activity  
## 3538 turquoise 3240 6.4e-03 1.0e+00 15 MF pyridoxal phosphate binding  
## 3539 turquoise 3240 6.4e-03 1.0e+00 7 BP oenocyte differentiation  
## 3540 turquoise 3240 6.4e-03 1.0e+00 7 BP mitochondrial electron transport, cytoch  
## 3541 turquoise 3240 6.4e-03 1.0e+00 7 BP fatty acid transport  
## 3542 turquoise 3240 6.4e-03 1.0e+00 7 BP wing disc anterior/posterior pattern for  
## 3543 turquoise 3240 6.4e-03 1.0e+00 7 BP regulation of epithelial cell migration,  
## 3544 turquoise 3240 6.5e-03 1.0e+00 16 BP cellular response to oxidative stress  
## 3545 turquoise 3240 6.5e-03 1.0e+00 16 BP glucose homeostasis  
## 3546 turquoise 3240 6.7e-03 1.0e+00 31 BP response to heat  
## 3547 turquoise 3240 6.9e-03 1.0e+00 23 BP hindgut morphogenesis  
## 3548 turquoise 3240 7.0e-03 1.0e+00 59 MF metal ion transmembrane transporter acti  
## 3549 turquoise 3240 7.2e-03 1.0e+00 33 MF ATPase activity, coupled to transmembran  
## 3550 turquoise 3240 7.2e-03 1.0e+00 174 BP post-embryonic development  
## 3551 turquoise 3240 7.3e-03 1.0e+00 10 BP apposition of dorsal and ventral imagina  
## 3552 turquoise 3240 7.3e-03 1.0e+00 10 MF amino acid:cation symporter activity  
## 3553 turquoise 3240 8.0e-03 1.0e+00 11 BP proximal/distal pattern formation, imagi  
## 3554 turquoise 3240 8.0e-03 1.0e+00 11 BP nucleotide-sugar metabolic process  
## 3555 turquoise 3240 8.2e-03 1.0e+00 41 BP organic anion transport  
## 3556 turquoise 3240 8.5e-03 1.0e+00 12 BP larval midgut cell programmed cell death  
## 3557 turquoise 3240 8.7e-03 1.0e+00 6 BP long-chain fatty acid metabolic process  
## 3558 turquoise 3240 8.7e-03 1.0e+00 6 BP determination of muscle attachment site  
## 3559 turquoise 3240 8.7e-03 1.0e+00 6 BP regulation of transforming growth factor  
## 3560 turquoise 3240 8.7e-03 1.0e+00 6 BP heat shock-mediated polytene chromosome   
## 3561 turquoise 3240 8.7e-03 1.0e+00 6 BP epithelial tube formation  
## 3562 turquoise 3240 8.7e-03 1.0e+00 6 MF phosphatidate phosphatase activity  
## 3563 turquoise 3240 8.7e-03 1.0e+00 6 MF gamma-aminobutyric acid transmembrane tr  
## 3564 turquoise 3240 8.7e-03 1.0e+00 17 BP ATP biosynthetic process  
## 3565 turquoise 3240 8.7e-03 1.0e+00 17 BP cellular response to heat  
## 3566 turquoise 3240 8.8e-03 1.0e+00 13 BP glycosaminoglycan metabolic process  
## 3567 turquoise 3240 8.8e-03 1.0e+00 13 CC integral component of mitochondrial memb  
## 3568 turquoise 3240 8.8e-03 1.0e+00 13 MF transmembrane receptor protein kinase ac  
## 3569 turquoise 3240 9.1e-03 1.0e+00 137 MF peptidase activity  
## 3570 turquoise 3240 9.6e-03 1.0e+00 34 BP wound healing  
## 3571 white 54 5.8e-30 4.8e-26 19 MF structural constituent of chitin-based c  
## 3572 white 54 2.0e-29 1.7e-25 19 MF structural constituent of cuticle  
## 3573 white 54 7.4e-27 6.2e-23 20 CC extracellular matrix  
## 3574 white 54 1.3e-25 1.1e-21 19 BP chitin-based cuticle development  
## 3575 white 54 2.2e-22 1.8e-18 19 BP cuticle development  
## 3576 white 54 2.0e-20 1.6e-16 26 CC extracellular region  
## 3577 white 54 1.6e-19 1.4e-15 13 MF structural constituent of chitin-based l  
## 3578 white 54 2.1e-18 1.8e-14 20 MF structural molecule activity  
## 3579 white 54 5.0e-09 4.2e-05 5 BP body morphogenesis  
## 3580 white 54 2.2e-05 1.8e-01 20 BP multicellular organism development  
## 3581 white 54 1.5e-04 1.0e+00 20 BP anatomical structure development  
## 3582 white 54 2.8e-04 1.0e+00 20 BP developmental process  
## 3583 white 54 5.3e-03 1.0e+00 6 CC extracellular space

subset(screenTab, module == "black" & termName == "nucleus")

## module size p-val Bonf nInTerm ont termName  
## 1 black 2886 3.9e-160 3.2e-156 1095 CC nucleus

write.csv(screenTab, file = "../../processed/DESEQ/Coexpression/resampMods/GOEnrichTab\_Resamp\_simple.csv",  
 row.names = FALSE)

# Notes for each module

ff <- unique(screenTab$module)  
  
ff.list <- vector(mode='list', length=length(ff))  
names(ff.list) <- ff  
  
for (ii in 1:length(ff))   
 {  
   
 ffc <- subset(screenTab,screenTab==ff[ii] )  
  
 ff.list[[ii]] <- ffc  
   
}  
  
# Note: # substitute 'screenTab' for 'tab' to see full details  
  
#lapply(ff.list[[ii]], head)

## Black (M1)

* 2956 genes in module; 771 GO terms across all GO categories
* BP: nucleobase metabolic process, gene expression, RNA processing, organelle organization, cellular metabolic process, cellular process, female gamete generation, germ cell development, reproduction, reproductive process, cellular protein modification process, cell communication, cell cycle, etc

## Blue (M2)

* 1747 genes, 311 GO terms
* BP: signalling, cell communication, nervous system process, ion transport, signal transduction, locomotion, neuron differentiation, neuron development, nervous system development, neurogenesis, cell morphogenesis, etc

## Brown (M3)

* 1084 genes, 116 terms
* BP: proteolysis, chitin metabolic process, fatty acid metabolic process, transmembrane transpoort, lipid metabolic process, lipid biosynthetic process, cellular lipid metabolic process, sulfur compound metabolic process, etc

## Cyan (M4)

* 507 genes, 98 terms
* BP: transmembrane transport, chitin metabolic process, ion transport, homeostatic process, heart development, fatty acid metabolic process, digestive tract development, response to toxic substance, etc ## Darkgreen (M5)
* 199 genes, 273 terms
* BP: multicellular organism development, anatomical structure development, signaling, cell communication, developmental process, signal transduction, neurogenesis, cell differentiation, organ development, etc

## Darkgrey (M6)

* 309 genes, 85 terms
* BP: signaling, regulation of signal transduction, regulation of Ras protein signal transduction, regulation of small GTPase mediated signal transduction, cell communication, etc

## Darkred (M7)

* 84 genes, 71 terms
* BP: cytoplasmic translation, translation, peptide metabolic process, cytosolic ribosome activity, cellular process, nitrogen compound metabolic process, cellular metabolic process, biosynthetic process, gene expression, protein metabolic process, ribosome biogenesis, etc

## Darkturquoise (M8)

* 79 genes, 22 terms
* BP: L-amino acid transport, amino acid transport, proteasome assembly, etc

## Greenyellow (M9)

* 165 genes, 109 terms
* BP: proteasome-mediated ubiquitin-dependent, proteasome catabolic process, ubiquitin processes, ubiquitin-dependent protein catabolic process, modification-dependent protein catabolic process, proteolysis involved in cellular protein, cellular protein catabolic process, proteasomal ubiquitin-independent protein catabolic process, protein catabolic process, organonitrogen compound catabolic proces, catabolic process, proteolysis, organic substance catabolic process, protein-containing complex assembly, etc

## Grey (M10)

* 45 + 1011 genes, 373 terms

## Lightcyan (M11)

* 117 genes, 209 terms
* BP: cellular component organization, multicellular organism development, organelle organization, cell development, anatomical structure development, regulation of metabolic process, developmental process, cellular process, cellular metabolic process, etc

## Lightgreen (M12)

* 107 genes, 47 terms
* BP: mitochondrial translation, translation, peptide metabolic process, protein metabolic process, biosynthetic process, gene expression, cellular metabolic process, nitrogen compound metabolic process, etc

## Lightyellow (M13)

* 107 genes, 99 terms
* BP: Golgi vesicle transport, ER to Golgi vesicle-mediated transport, translation, peptide metabolic process,intracellular transport, intracellular protein transport, protein transport, establishment of protein localization, vesicle-mediated transport, biosythetic process, cellular macromolecule localization, organic substance transport, etc

## Pink (M14)

* 382 genes, 163 terms
* BP: regulation of gene expression, regulation of metabolic process, regulation of RNA metabolic process, gene expression, RNA metabolic process, nucleobase-containing compound metabolic process, regulation of cellular metabolic process, transcription, nitrogen compound metabolic process, cellular process, cellular metabolic process, cellular protein modification process, cell differentiation, nervous system development, organelle organization, signaling, signal transduction, anatomical structure development, anatomical structure morphogenesis, gamete generation, etc, etc.

## Red (M15)

* 787 genes, 204 terms
* BP: nervous system process, sensory perception of chemical stimulus, detection of stimulus involved in sensory perception, detection of chemical stimulus, olfactory and sensory perception of smell, sensory perception of smell, phototransduction, response to light stimulus, cell communication, signaling, signal transduction, etc, etc.

## Royalblue (M16)

* 132 genes, 154 terms
* BP: regulation of metabolic process, regulation of gene expression, transcription, regulation of cellular metabolic process, regulation of transcription, regulation of RNA metabolic process, gene expression, germ cell development, RNA metabolic process, cellular metabolic process, nitrogen compound metabolic process, oogenesis, female gamete generation, ovarian follicle, etc, etc.

## Salmon (M17)

* 157 genes, 30 terms
* BP: nervous system development, neuron development, synapse assembly, synaptic growth at neuromuscular junction, anterograde axonal transport, multicellular organism development, animal organ morphogenesis, morphogenesis of an epithelium, etc.

## Skyblue (M18)

* 52 genes, 54 tems
* BP: cytoplasmic translation, peptide metabolic process, translation, biosynthetic process, gene expression, cellular metabolic process, protein metabolic process, ribosome biogenesis, cellular process, etc.

## Steelblue (M19)

* 44 genes, 68 terms
* BP: protein localization Golgi apparatus, protein retention in Golgi apparatus, Wnt signaling pathway, regulation of signal transduction, endocytosis, cell surface receptor signaling pathway, etc.

## Tan (M20)

* 163 genes, 24 terms
* BP: vesicle-mediated transport, ommochrome biosynthetic process, ocellus pigment biosynthetic process, eye pigment biosynthetic process, endosomal transport, eye pigment metabolic process, compound eye pigmentation, developmental pigmentation, intracellular transport, secretion by cell, regulation of lipid storage, etc.

## Turquoise (M21)

* 3337 genes, 289 terms
* BP: oxidation-reduction process, response to bacterium, defence response, carboxylic acid metabolic - process, organic acid metabolic process, carbohydrate metabolic process, defense response to bacterium, defense response to other organism, cellular respiration, cellular carbohydrate metabolic process, ribose phosphate metabolic process, immune response, nucleoside phosphate metabolic process, nucleoside phosphate metabolic process, response to organic substance, nucleotide metabolic process, transmembrane transport, chitin-based cuticle development, lipid metabolic process, cellular lipid metabolic process, response to oxidative stress, fatty acid metabolic process, developmental pigmentation, ion transport, etc, etc, etc.

## White (M22)

* 54 genes, 13 terms
* BP: chitin-based cuticle development, cuticle development, body morphogenesis, multicellular organism development, anatomical structure development, developmental process.