GO:0034641 − cellular nitrogen compound metabolic process
GO:0090304 − nucleic acid metabolic process
GO:0046483 − heterocycle metabolic process
GO:0006725 − cellular aromatic compound metabolic process
GO:0006139 − nucleobase−containing compound metabolic process
GO:0016071 − mRNA metabolic process
GO:1901361 − organic cyclic compound catabolic process
GO:0046700 − heterocycle catabolic process
GO:0044270 − cellular nitrogen compound catabolic process
GO:0044265 − cellular macromolecule catabolic process
GO:0034655 − nucleobase−containing compound catabolic process
GO:0019439 − aromatic compound catabolic process
GO:0010608 − posttranscriptional regulation of gene expression
GO:0009057 − macromolecule catabolic process
GO:0006402 − mRNA catabolic process
GO:0006401 − RNA catabolic process
GO:0043604 − amide biosynthetic process
GO:0043043 − peptide biosynthetic process
GO:0031329 − regulation of cellular catabolic process
GO:0009894 − regulation of catabolic process
GO:0006518 − peptide metabolic process
GO:0006413 − translational initiation
GO:0006412 − translation
GO:1903311 − regulation of mRNA metabolic process
GO:0061013 − regulation of mRNA catabolic process
GO:0043488 − regulation of mRNA stability
GO:0043487 − regulation of RNA stability
GO:0034248 − regulation of cellular amide metabolic process
GO:0006417 − regulation of translation
GO:1901989 − positive regulation of cell cycle phase transition
GO:0061641 − CENP−A containing chromatin organization
GO:0043486 − histone exchange
GO:0043044 − ATP−dependent chromatin remodeling
GO:0042273 − ribosomal large subunit biogenesis
GO:0042255 − ribosome assembly
GO:0034724 − DNA replication−independent nucleosome organization
GO:0034508 − centromere complex assembly
GO:0034080 − CENP−A containing nucleosome assembly
GO:0031055 − chromatin remodeling at centromere
GO:0006614 − SRP−dependent cotranslational protein targeting to membrane
GO:0006613 − cotranslational protein targeting to membrane
GO:0006446 − regulation of translational initiation
GO:0006336 − DNA replication−independent nucleosome assembly
GO:2000815 − regulation of mRNA stability involved in response to oxidative stress
GO:1902629 − regulation of mRNA stability involved in cellular response to UV
GO:0097698 − telomere maintenance via base−excision repair
GO:0097010 − eukaryotic translation initiation factor 4F complex assembly
GO:0060735 − regulation of eIF2 alpha phosphorylation by dsRNA
GO:0006407 − rRNA export from nucleus
GO:0006286 − base−excision repair, base−free sugar−phosphate removal
0
Number of genes
p−value
1e−07
1e−06
1e−05
1e−04
0.001