glucose binding
positive regulation of glycoprotein biosynthetic process
hyaluronan metabolic process
glucose 6−phosphate metabolic process
deoxyribonucleotide biosynthetic process
positive regulation of glycogen biosynthetic process
negative regulation of glycogen biosynthetic process
sulfide:quinone oxidoreductase activity
oxidoreductase activity, acting on the CH−CH group of donors
oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor
oxidoreductase activity
glutamate−5−semialdehyde dehydrogenase activity
glutamate 5−kinase activity
carbonate dehydratase activity
proline catabolic process
ornithine biosynthetic process
methionyl−tRNA aminoacylation
methionine catabolic process
citrulline biosynthetic process
4−hydroxyproline catabolic process
amide biosynthetic process
negative regulation of cytoplasmic translational initiation in response to stress
RNA polymerase II intronic transcription regulatory region sequence−specific DNA binding
RNA polymerase II cis−regulatory region sequence−specific DNA binding
RNA−dependent DNA biosynthetic process
single−stranded 3'−5' DNA helicase activity
DNA recombination
negative regulation of double−strand break repair via nonhomologous end joining
DNA synthesis during double−strand break repair via homologous recombination
DNA double−strand break processing involved in repair via single−strand annealing
regulation of DNA endoreduplication
negative regulation of DNA endoreduplication
mitotic DNA replication
DNA unwinding involved in DNA replication
positive regulation of transcription of nucleolar large rRNA by RNA polymerase I
positive regulation of transcription from RNA polymerase II promoter in response to heat stress
catalysis of the reaction: 2 L−glutamate + NAD+ = 2−oxoglutarate + L−glutamine + H+ + NADH
glutamate dehydrogenase [NAD(P)+] activity
catalysis of the formation of L−glutamine and 2−oxoglutarate from L−glutamate
catalysis of the reaction: ATP + L−glutamate + NH4+ = ADP + H+ + L−glutamine + phosphate
Hsp90 protein binding
Hsp70 protein binding
regulation of mast cell activation
leukocyte migration involved in inflammatory response
complement activation, classical pathway
regulation of protein localization by the Cvt pathway
protein transport along microtubule
spermine acetylation
spermidine acetylation
regulation of protein metabolic process
putrescine acetylation
positive regulation of RNA biosynthetic process
nor−spermidine metabolic process
DNA binding
DNA metabolic process
DNA integration
negative regulation of chaperone−mediated protein folding
regulation of myosin−light−chain−phosphatase activity
protein adenylylation
peptidyl−tyrosine phosphorylation
peptidyl−lysine hydroxylation
negative regulation of protein kinase activity by protein phosphorylation
histone acetylation
regulation of hydrogen peroxide metabolic process
positive regulation of transcription from RNA polymerase II promoter in response to calcium ion
response to melanocyte−stimulating hormone
cellular response to histidine
cellular response to gonadotropin−releasing hormone
cellular response to diamide
cellular response to cGMP
cellular response to benomyl
response to food
positive regulation of cellular response to amino acid starvation
negative regulation of appetite
chemotaxis to folate
response to hypoxia
response to heat
positive regulation of transcription from RNA polymerase II promoter in response to heat stress
cellular stress response to acidic pH
innate immune response−activating signal transduction
glutathione biosynthetic process
RNA−directed DNA polymerase activity
DNA−directed DNA polymerase activity
glucose transmembrane transport
carbohydrate transmembrane transport
lipoprotein transport
D−glucose transmembrane transporter activity
bicarbonate transmembrane transporter activity

binding
carbohydrate derivative metabolic process
carbohydrate metabolic process
catalytic activity
cellular amino acid metabolic process
cellular nitrogen compound
cytoplasmic translation
DNA binding
DNA biosynthetic process
DNA helicase activity
DNA metabolic process
DNA repair
DNA replication
DNA−templated transcription
glutamate synthase (NADH) activity
glutamate synthase activity
glutamine synthetase activity
heat shock protein binding
immune system process
intracellular protein transport
microtubule−based movement
nitrogen compound metabolic process
nucleic acid binding
nucleic acid metabolic process
protein folding
protein modification process
regulation of reactive oxygen
regulation of transcription, DNA−templated transcription
response to nitrogen compound
response to nutrient levels
response to stress
signaling
sulfur compound metabolic process
transferase activity
transmembrane transport
transport
transporter activity

DEG.GO.terms
DMG.GO.terms
Method

Number of Genes
500
1000
1500
2000

Adjusted p−value
0.04
0.03
0.02
0.01