glucose binding — **binding**

positive regulation of glycoprotein biosynthetic process
hyaluronan metabolic process
glucose 6−phosphate metabolic process
deoxyribonucleotide biosynthetic process
— **carbohydrate derivative metabolic process**

positive regulation of glycogen biosynthetic process
negative regulation of glycogen biosynthetic process
— **carbohydrate metabolic 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
— **catalytic activity**

proline catabolic process
ornithine biosynthetic process
methionyl−tRNA aminoacylation
methionine catabolic process
citrulline biosynthetic process
4−hydroxyproline catabolic process
— **cellular amino acid metabolic process**

amide biosynthetic process — **cellular nitrogen compound**

negative regulation of cytoplasmic translational initiation in response to stress — **cytoplasmic translation**

RNA polymerase II intronic transcription regulatory region sequence−specific DNA binding
RNA polymerase II cis−regulatory region sequence−specific DNA binding
— **DNA binding**

RNA−dependent DNA biosynthetic process — **DNA biosynthetic process**

single−stranded 3'−5' DNA helicase activity — **DNA helicase activity**

DNA recombination — **DNA metabolic process**

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
— **DNA repair**

regulation of DNA endoreduplication
negative regulation of DNA endoreduplication
mitotic DNA replication
DNA unwinding involved in DNA replication
— **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
— **DNA−templated transcription**

Hsp90 protein binding
Hsp70 protein binding
— **heat shock protein binding**

regulation of mast cell activation
leukocyte migration involved in inflammatory response
complement activation, classical pathway
— **immune system process**

regulation of protein localization by the Cvt pathway — **intracellular protein transport**

protein transport along microtubule — **microtubule−based movement**

spermine acetylation
spermidine acetylation
regulation of protein metabolic process
putrescine acetylation
positive regulation of RNA biosynthetic process
nor−spermidine metabolic process
— **nitrogen compound metabolic process**

DNA binding — **nucleic acid binding**

DNA metabolic process
DNA integration
— **nucleic acid metabolic process**

negative regulation of chaperone−mediated protein folding — **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
— **protein modification process**

regulation of hydrogen peroxide metabolic process — **regulation of reactive oxygen**

positive regulation of transcription from RNA polymerase II promoter in response to calcium ion — **regulation of transcription, DNA−templated transcription**

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 nitrogen compound**

response to food
positive regulation of cellular response to amino acid starvation
negative regulation of appetite
chemotaxis to folate
— **response to nutrient levels**

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
— **response to stress**

innate immune response−activating signal transduction — **signaling**

glutathione biosynthetic process — **sulfur compound metabolic process**

RNA−directed DNA polymerase activity
DNA−directed DNA polymerase activity
— **transferase activity**

glucose transmembrane transport
carbohydrate transmembrane transport
— **transmembrane transport**

lipoprotein transport — **transport**

D−glucose transmembrane transporter activity
bicarbonate transmembrane transporter activity
— **transporter activity**

DEG.GO.terms
DMG.GO.terms

Method

Adjusted p−value
0.04
0.03
0.02
0.01

Number of Genes
100
200
300
400
500