SD
SS0.45
95% confidence intervals
Vibrio cholerae pathogenic cycle 4.29e-7
Pantothenate and CoA biosynthesis 1.03e-6
Vitamin B6 metabolism 1.88e-6
RNA transport 3.14e-6
"Valine, leucine and isoleucine biosynthesis" 5.29e-6
MAPK signaling pathway - yeast 6.52e-6
Arginine and proline metabolism 7.09e-6
Glycan biosynthesis and metabolism 7.66e-6
Epithelial cell signaling in Helicobacter pylori i... 8.44e-6
Biosynthesis and biodegradation of secondary metab... 1.43e-5
Porphyrin and chlorophyll metabolism 1.45e-5
Bacterial chemotaxis 1.65e-5
Pentose phosphate pathway 1.67e-5
Other transporters 1.75e-5
Xylene degradation 1.81e-5
Glycerolipid metabolism 1.83e-5
Bacterial motility proteins 1.90e-5
Nitrogen metabolism 2.05e-5
Cell cycle - Caulobacter 2.22e-5
Atrazine degradation 2.34e-5
Two-component system 2.42e-5
Transcription machinery 2.49e-5
D-Alanine metabolism 2.58e-5
C5-Branched dibasic acid metabolism 3.23e-5
Cysteine and methionine metabolism 3.27e-5
"Phenylalanine, tyrosine and tryptophan biosynthesis" 3.30e-5
Glyoxylate and dicarboxylate metabolism 3.75e-5
Purine metabolism 3.88e-5
"Tropane, piperidine and pyridine alkaloid biosynt... 4.63e-5
Nucleotide excision repair 4.66e-5
Styrene degradation 4.75e-5
Aminoacyl-tRNA biosynthesis 4.83e-5
Methane metabolism 5.00e-5
Inositol phosphate metabolism 5.61e-5
Progesterone-mediated oocyte maturation 5.80e-5
Prostate cancer 5.80e-5
Antigen processing and presentation 5.80e-5
NOD-like receptor signaling pathway 5.83e-5
Phosphatidylinositol signaling system 5.86e-5
Energy metabolism 6.01e-5
Novobiocin biosynthesis 6.24e-5
Taurine and hypotaurine metabolism 6.25e-5
Ribosome 6.69e-5
Glycerophospholipid metabolism 6.86e-5
Proteasome 7.31e-5
Function unknown 7.36e-5
Glycolysis / Gluconeogenesis 7.43e-5
Zeatin biosynthesis 8.45e-5
Flagellar assembly 8.97e-5
DNA replication 9.06e-5
Staphylococcus aureus infection 9.57e-5
Dioxin degradation 9.84e-5
Glycosyltransferases 9.87e-5
RNA polymerase 1.08e-4
Selenocompound metabolism 1.09e-4
Pentose and glucuronate interconversions 1.14e-4
Renal cell carcinoma 1.29e-4
Sporulation 1.32e-4
Primary immunodeficiency 1.34e-4
Primary bile acid biosynthesis 1.47e-4
Polycyclic aromatic hydrocarbon degradation 1.49e-4
Toluene degradation 1.55e-4
Isoquinoline alkaloid biosynthesis 1.58e-4
Secondary bile acid biosynthesis 1.59e-4
Amino acid metabolism 1.60e-4
Peroxisome 1.69e-4
"Glycine, serine and threonine metabolism" 1.85e-4
Synthesis and degradation of ketone bodies 1.86e-4
Amino sugar and nucleotide sugar metabolism 2.02e-4
Ribosome Biogenesis 2.23e-4
Plant-pathogen interaction 2.25e-4
Cell division 2.29e-4
Protein export 2.31e-4
Translation factors 2.66e-4
Prenyltransferases 2.85e-4
Histidine metabolism 3.00e-4
Apoptosis 3.24e-4
Type I diabetes mellitus 3.41e-4
Terpenoid backbone biosynthesis 3.43e-4
ABC transporters 3.53e-4
Phosphonate and phosphinate metabolism 3.54e-4
Ion channels 4.44e-4
Phenylpropanoid biosynthesis 4.63e-4
Other ion-coupled transporters 4.97e-4
Transcription related proteins 5.22e-4
Carbon fixation pathways in prokaryotes 5.30e-4
Peptidoglycan biosynthesis 5.33e-4
DNA repair and recombination proteins 5.41e-4
Huntington's disease 6.50e-4
Nitrotoluene degradation 7.34e-4
Starch and sucrose metabolism 7.82e-4
Biotin metabolism 8.02e-4
Pyrimidine metabolism 8.02e-4
Arachidonic acid metabolism 8.20e-4
Phosphotransferase system (PTS) 8.34e-4
Carbon fixation in photosynthetic organisms 8.98e-4
Signal transduction mechanisms 9.51e-4
Others 9.63e-4
Chaperones and folding catalysts 9.85e-4
Ribosome biogenesis in eukaryotes 1.06e-3
Biosynthesis of ansamycins 1.08e-3
Glutathione metabolism 1.18e-3
Homologous recombination 1.33e-3
Alzheimer's disease 1.38e-3
Base excision repair 1.53e-3
Mismatch repair 1.55e-3
Cyanoamino acid metabolism 1.61e-3
Tyrosine metabolism 1.64e-3
Translation proteins 1.73e-3
Chromosome 1.78e-3
One carbon pool by folate 2.09e-3
Ubiquinone and other terpenoid-quinone biosynthesis 2.18e-3
Flavone and flavonol biosynthesis 2.34e-3
Lysine degradation 2.58e-3
Galactose metabolism 2.67e-3
Metabolism of cofactors and vitamins 2.97e-3
Phenylalanine metabolism 3.16e-3
Naphthalene degradation 3.34e-3
Penicillin and cephalosporin biosynthesis 3.41e-3
Insulin signaling pathway 3.85e-3
Lipoic acid metabolism 3.86e-3
Transcription factors 4.01e-3
Streptomycin biosynthesis 4.08e-3
beta-Alanine metabolism 4.53e-3
Sulfur relay system 4.65e-3
Oxidative phosphorylation 5.99e-3
Chlorocyclohexane and chlorobenzene degradation 6.08e-3
Adipocytokine signaling pathway 6.18e-3
Restriction enzyme 6.28e-3
Protein folding and associated processing 6.44e-3
Lipid metabolism 7.77e-3
RNA degradation 8.48e-3
RIG-I-like receptor signaling pathway 0.010
Carbohydrate digestion and absorption 0.010
Aminobenzoate degradation 0.011
Benzoate degradation 0.012
Fructose and mannose metabolism 0.012
Citrate cycle (TCA cycle) 0.013
Ether lipid metabolism 0.014
Lipopolysaccharide biosynthesis proteins 0.014
Nicotinate and nicotinamide metabolism 0.014
beta-Lactam resistance 0.014
Germination 0.015
Caprolactam degradation 0.015
Chloroalkane and chloroalkene degradation 0.016
General function prediction only 0.018
"Stilbenoid, diarylheptanoid and gingerol biosynth... 0.019
D-Arginine and D-ornithine metabolism 0.023
Amino acid related enzymes 0.023
D-Glutamine and D-glutamate metabolism 0.025
Protein processing in endoplasmic reticulum 0.026
"Alanine, aspartate and glutamate metabolism" 0.026
Amoebiasis 0.027
Bacterial secretion system 0.032
Limonene and pinene degradation 0.033
"Replication, recombination and repair proteins" 0.034
Nucleotide metabolism 0.034
African trypanosomiasis 0.042
DNA replication proteins 0.044
Chagas disease (American trypanosomiasis) 0.044
Prion diseases 0.045
Bisphenol degradation 0.047
Bladder cancer 0.047
Circadian rhythm - plant 0.048
Ethylbenzene degradation 0.048
G protein-coupled receptors 0.048
Biosynthesis of unsaturated fatty acids 0.049
p-value (corrected)
0.0
3.6
Mean proportion (%)
−1.5
−1.0
−0.5
0.0
0.5
1.0
Difference in mean proportions (%)