genes_P0.05Fold2_protein_trT_set00_StcNasMgh_S_baseMg_baseNaAllNa_Sta_noFilter_p1Sf_noNorm__Na_mM_Levels_kegg

Ribosome
padj:0.00000 N(−47/ +0/ 54)
Alanine, aspartate and glutamate metabolism
padj:0.00000 N(−22/ +3/ 28)
Purine metabolism
padj:0.00000 N(−34/ +7/ 78)
Phenylalanine, tyrosine and tryptophan biosynthesis
padj:0.00000 N(−20/ +0/ 21)
Aminoacyl−tRNA biosynthesis
padj:0.00000 N(−22/ +0/ 24)
Pyruvate metabolism
padj:0.00000 N(−23/ +5/ 40)
Pyrimidine metabolism
padj:0.00000 N(−29/ +1/ 52)
Arginine and proline metabolism
padj:0.00000 N(−23/ +4/ 36)
Cysteine and methionine metabolism
padj:0.00000 N(−19/ +3/ 23)
ABC transporters
padj:0.00000 N(−36/ +21/ 153)
Two−component system
padj:0.00000 N(−17/ +29/ 114)
Nitrogen metabolism
padj:0.00000 N(−12/ +11/ 33)
Glycine, serine and threonine metabolism
padj:0.00000 N(−16/ +5/ 30)
Amino sugar and nucleotide sugar metabolism
padj:0.00000 N(−19/ +5/ 35)
Glycolysis / Gluconeogenesis
padj:0.00000 N(−21/ +1/ 32)
Pentose phosphate pathway
padj:0.00000 N(−16/ +3/ 28)
Valine, leucine and isoleucine biosynthesis
padj:0.00000 N(−16/ +0/ 19)
Starch and sucrose metabolism
padj:0.00000 N(−12/ +7/ 29)
Glyoxylate and dicarboxylate metabolism
padj:0.00000 N(−9/ +11/ 35)
Oxidative phosphorylation
padj:0.00000 N(−18/ +2/ 41)
Fructose and mannose metabolism
padj:0.00000 N(−12/ +7/ 34)
Glutathione metabolism
padj:0.00000 N(−11/ +2/ 16)
Fatty acid biosynthesis
padj:0.00000 N(−11/ +0/ 12)
Sulfur metabolism
padj:0.00000 N(−10/ +1/ 13)
Propanoate metabolism
padj:0.00000 N(−11/ +5/ 25)
Selenoamino acid metabolism
padj:0.00000 N(−9/ +2/ 14)
Histidine metabolism
padj:0.00000 N(−9/ +0/ 9)
Citrate cycle (TCA cycle)
padj:0.00000 N(−13/ +2/ 26)
One carbon pool by folate
padj:0.00001 N(−10/ +0/ 12)
Pantothenate and CoA biosynthesis
padj:0.00002 N(−12/ +0/ 16)
Phenylalanine metabolism
padj:0.00002 N(−3/ +8/ 17)
Lysine biosynthesis
padj:0.00007 N(−10/ +0/ 14)
Butanoate metabolism
padj:0.00019 N(−10/ +4/ 31)
Cyanoamino acid metabolism
padj:0.00079 N(−4/ +2/ 6)
Bacterial secretion system
padj:0.00150 N(−10/ +2/ 30)
Protein export
padj:0.00226 N(−9/ +0/ 17)
Phosphotransferase system (PTS)
padj:0.00382 N(−10/ +4/ 36)
RNA degradation
padj:0.00419 N(−7/ +1/ 13)
Pentose and glucuronate interconversions
padj:0.01122 N(−5/ +5/ 24)
Tyrosine metabolism
padj:0.01280 N(−5/ +1/ 9)
Methane metabolism
padj:0.01284 N(−2/ +5/ 13)
Peptidoglycan biosynthesis
padj:0.01626 N(−6/ +3/ 19)
Biosynthesis of siderophore group nonribosomal peptides
padj:0.01881 N(−4/ +1/ 6)
beta−Alanine metabolism
padj:0.03135 N(−5/ +2/ 10)
C5−Branched dibasic acid metabolism
padj:0.04012 N(−5/ +0/ 7)
Trinitrotoluene degradation
padj:0.04012 N(−2/ +3/ 5)
Bacterial chemotaxis
padj:0.04434 N(−4/ +4/ 17)
rank
−sign(cor)*P_log10
−5
0
5