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)
rplD
rplA
rpmE
rplR
rpmD
rpmC
rpmB
rplK
rpsG
rplO
rpmG
rplT
rpsH
rpsK
rplC
rpsL
rpsR
rplS
rpmI
purB
gltD
gltB
purA
pyrI
aspC
argH
glmS
asnA
pyrB
asnB
ansA
gabD
carB
gabT
carA
ybaS
−47
−46
−12
−11
−10
−9
−8
−7
−6
rank
−sign(cor)*P_log10
−5
0
5