genes0.05_protein_wo_NA_trT_set00_StcNasMgh_S_baseMg_baseNaAllNa_Exp_noFilter_p1Sf_noNorm__Na_mM_Levels_kegg

Purine metabolism
padj:0.00000 N(−47/ +13/ 78)
Two−component system
padj:0.00000 N(−23/ +51/ 114)
ABC transporters
padj:0.00000 N(−50/ +34/ 153)
Pyrimidine metabolism
padj:0.00000 N(−36/ +2/ 52)
Ribosome
padj:0.00000 N(−46/ +0/ 54)
Aminoacyl−tRNA biosynthesis
padj:0.00000 N(−24/ +0/ 24)
Nitrogen metabolism
padj:0.00000 N(−11/ +17/ 33)
Phenylalanine, tyrosine and tryptophan biosynthesis
padj:0.00000 N(−20/ +1/ 21)
Arginine and proline metabolism
padj:0.00000 N(−23/ +7/ 36)
Glycine, serine and threonine metabolism
padj:0.00000 N(−18/ +8/ 30)
Pyruvate metabolism
padj:0.00000 N(−23/ +7/ 40)
Alanine, aspartate and glutamate metabolism
padj:0.00000 N(−19/ +5/ 28)
Cysteine and methionine metabolism
padj:0.00000 N(−19/ +4/ 23)
Amino sugar and nucleotide sugar metabolism
padj:0.00000 N(−21/ +8/ 35)
Valine, leucine and isoleucine biosynthesis
padj:0.00000 N(−18/ +1/ 19)
Starch and sucrose metabolism
padj:0.00000 N(−12/ +11/ 29)
Glycolysis / Gluconeogenesis
padj:0.00000 N(−20/ +5/ 32)
Glyoxylate and dicarboxylate metabolism
padj:0.00000 N(−9/ +15/ 35)
Pentose phosphate pathway
padj:0.00000 N(−18/ +4/ 28)
Glutathione metabolism
padj:0.00000 N(−13/ +2/ 16)
Sulfur metabolism
padj:0.00000 N(−12/ +1/ 13)
Oxidative phosphorylation
padj:0.00000 N(−21/ +2/ 41)
Citrate cycle (TCA cycle)
padj:0.00000 N(−14/ +5/ 26)
Selenoamino acid metabolism
padj:0.00000 N(−11/ +2/ 14)
Pentose and glucuronate interconversions
padj:0.00000 N(−5/ +13/ 24)
Propanoate metabolism
padj:0.00000 N(−9/ +10/ 25)
Fatty acid biosynthesis
padj:0.00000 N(−12/ +0/ 12)
Pantothenate and CoA biosynthesis
padj:0.00000 N(−14/ +1/ 16)
Fructose and mannose metabolism
padj:0.00000 N(−12/ +8/ 34)
Butanoate metabolism
padj:0.00000 N(−10/ +9/ 31)
Glycerophospholipid metabolism
padj:0.00000 N(−6/ +10/ 26)
RNA degradation
padj:0.00000 N(−11/ +1/ 13)
Nicotinate and nicotinamide metabolism
padj:0.00000 N(−13/ +0/ 16)
Phenylalanine metabolism
padj:0.00000 N(−3/ +10/ 17)
Bacterial secretion system
padj:0.00000 N(−12/ +5/ 30)
Histidine metabolism
padj:0.00001 N(−9/ +0/ 9)
Galactose metabolism
padj:0.00001 N(−8/ +9/ 31)
Peptidoglycan biosynthesis
padj:0.00001 N(−11/ +3/ 19)
Ubiquinone and other terpenoid−quinone biosynthesis
padj:0.00002 N(−7/ +5/ 17)
Protein export
padj:0.00004 N(−12/ +0/ 17)
One carbon pool by folate
padj:0.00007 N(−10/ +0/ 12)
Lysine biosynthesis
padj:0.00008 N(−11/ +0/ 14)
Phosphotransferase system (PTS)
padj:0.00008 N(−11/ +8/ 36)
Porphyrin and chlorophyll metabolism
padj:0.00012 N(−9/ +4/ 22)
Glycerolipid metabolism
padj:0.00015 N(−5/ +4/ 10)
Bacterial chemotaxis
padj:0.00029 N(−4/ +8/ 17)
Vitamin B6 metabolism
padj:0.00029 N(−8/ +0/ 9)
Folate biosynthesis
padj:0.00041 N(−7/ +2/ 10)
C5−Branched dibasic acid metabolism
padj:0.00050 N(−7/ +0/ 7)
Flagellar assembly
padj:0.00063 N(−15/ +1/ 19)
Nucleotide excision repair
padj:0.00178 N(−4/ +3/ 8)
Thiamine metabolism
padj:0.00194 N(−5/ +4/ 13)
Cyanoamino acid metabolism
padj:0.00334 N(−4/ +2/ 6)
Taurine and hypotaurine metabolism
padj:0.00334 N(−3/ +3/ 6)
Riboflavin metabolism
padj:0.01056 N(−5/ +2/ 9)
Base excision repair
padj:0.01539 N(−5/ +3/ 13)
Tryptophan metabolism
padj:0.02060 N(−3/ +4/ 9)
D−Glutamine and D−glutamate metabolism
padj:0.02151 N(−4/ +1/ 5)
beta−Alanine metabolism
padj:0.02553 N(−4/ +4/ 10)
Tyrosine metabolism
padj:0.04895 N(−4/ +2/ 9)
−50 −49 −48 −47 −46 −45 −44 −43 −42 −41 −40 −39 −38 −37 −36 −35 −34 −33 −32 −31 −30 −29 −28 −27 −26 −25 −24 −23 −22 −21 −20 −19 −18 −17 −16 −15 −14 −13 −12 −11 −10 −9 −8 −7 −6 −5 −4 −3 −2 −1 0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51
rank
−sign(cor)*P_log10
−10
0
10