genes_P0.05Fold2_mrna_trT_set02_StcNasMglMgh_S_baseMglowMg_baseNa_Exp_noFilter_p1Sf_noNorm__Mg_mM_Levels_kegg

Ribosome
padj:0.00000 N(−47/ +1/ 77)
Purine metabolism
padj:0.00000 N(−36/ +0/ 76)
ABC transporters
padj:0.00000 N(−47/ +3/ 153)
Pyrimidine metabolism
padj:0.00000 N(−27/ +0/ 52)
Aminoacyl−tRNA biosynthesis
padj:0.00000 N(−17/ +0/ 25)
Homologous recombination
padj:0.00000 N(−14/ +0/ 27)
Valine, leucine and isoleucine biosynthesis
padj:0.00000 N(−10/ +2/ 19)
Thiamine metabolism
padj:0.00000 N(−5/ +5/ 12)
Peptidoglycan biosynthesis
padj:0.00000 N(−12/ +0/ 19)
Fatty acid biosynthesis
padj:0.00000 N(−9/ +0/ 12)
Phenylalanine, tyrosine and tryptophan biosynthesis
padj:0.00000 N(−11/ +0/ 21)
Glycine, serine and threonine metabolism
padj:0.00003 N(−12/ +0/ 30)
Oxidative phosphorylation
padj:0.00006 N(−13/ +0/ 41)
One carbon pool by folate
padj:0.00006 N(−8/ +0/ 12)
Sulfur metabolism
padj:0.00006 N(−8/ +0/ 13)
Alanine, aspartate and glutamate metabolism
padj:0.00007 N(−10/ +1/ 28)
RNA degradation
padj:0.00021 N(−8/ +0/ 13)
Cysteine and methionine metabolism
padj:0.00044 N(−10/ +0/ 23)
Mismatch repair
padj:0.00045 N(−9/ +0/ 21)
DNA replication
padj:0.00057 N(−8/ +0/ 16)
Ubiquinone and other terpenoid−quinone biosynthesis
padj:0.00057 N(−8/ +0/ 17)
Arginine and proline metabolism
padj:0.00062 N(−11/ +1/ 35)
Vitamin B6 metabolism
padj:0.00143 N(−6/ +0/ 9)
Selenoamino acid metabolism
padj:0.00165 N(−7/ +0/ 14)
Bacterial secretion system
padj:0.00680 N(−9/ +0/ 30)
Nicotinate and nicotinamide metabolism
padj:0.00824 N(−7/ +0/ 16)
Protein export
padj:0.00824 N(−7/ +0/ 16)
Terpenoid backbone biosynthesis
padj:0.01183 N(−6/ +0/ 11)
Base excision repair
padj:0.01744 N(−6/ +0/ 12)
Lysine biosynthesis
padj:0.03411 N(−6/ +0/ 14)
rpsM
rplX
rplC
rpsG
rplW
rpsO
rpsF
rplD
rplJ
rplF
rpsS
rpmI
rpsJ
rpmB
rplI
rpsB
nrdA
holA
spoT
purL
purE
gsk
purB
guaB
dnaE
purM
adk
apt
purT
guaA
purH
ndk
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4
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rank
−sign(cor)*P_log10
−20
−10
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10
20