genes_P0.05Fold2_mrna_trT_set02_StcNasMgh_S_baseMghighMg_baseNa_Sta_noFilter_p1Sf_noNorm__Mg_mM_Levels_mf
structural constituent of ribosome padj:0.00000 N(−1/ +32/ 57)
rRNA binding padj:0.00000 N(−1/ +24/ 37)
structural molecule activity padj:0.00000 N(−2/ +32/ 70)
RNA binding padj:0.00000 N(−1/ +37/ 109)
ATP binding padj:0.00000 N(−9/ +79/ 419)
adenyl ribonucleotide binding padj:0.00000 N(−9/ +79/ 420)
purine ribonucleotide binding padj:0.00000 N(−9/ +82/ 450)
ribonucleotide binding padj:0.00000 N(−9/ +82/ 450)
inorganic anion transmembrane transporter activity padj:0.00000 N(−1/ +12/ 26)
adenyl nucleotide binding padj:0.00000 N(−10/ +83/ 468)
purine nucleoside binding padj:0.00000 N(−10/ +83/ 468)
nucleoside binding padj:0.00000 N(−10/ +84/ 475)
nucleotide binding padj:0.00000 N(−13/ +97/ 578)
purine nucleotide binding padj:0.00000 N(−10/ +86/ 498)
tRNA binding padj:0.00000 N(−1/ +9/ 17)
anion transmembrane transporter activity padj:0.00000 N(−2/ +12/ 37)
inorganic phosphate transmembrane transporter activity padj:0.00001 N(−1/ +4/ 10)
aminoacyl−tRNA ligase activity padj:0.00001 N(−1/ +10/ 32)
ATPase activity, coupled to transmembrane movement of ions padj:0.00001 N(−1/ +10/ 32)
ligase activity, forming aminoacyl−tRNA and related compounds padj:0.00001 N(−1/ +10/ 32)
ligase activity, forming carbon−oxygen bonds padj:0.00001 N(−1/ +10/ 32)
phosphate transmembrane−transporting ATPase activity padj:0.00002 N(−1/ +1/ 5)
anion transmembrane−transporting ATPase activity padj:0.00002 N(−1/ +6/ 13)
phosphate transmembrane transporter activity padj:0.00003 N(−1/ +4/ 11)
P−P−bond−hydrolysis−driven transmembrane transporter activity padj:0.00012 N(−3/ +16/ 75)
primary active transmembrane transporter activity padj:0.00012 N(−3/ +16/ 75)
ATPase activity, coupled to movement of substances padj:0.00023 N(−3/ +15/ 70)
ATPase activity, coupled to transmembrane movement of substances padj:0.00023 N(−3/ +15/ 70)
hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances padj:0.00057 N(−3/ +15/ 73)
metal ion binding padj:0.00067 N(−19/ +66/ 625)
ATPase activity, coupled padj:0.00071 N(−3/ +19/ 92)
cation binding padj:0.00119 N(−20/ +66/ 639)
hydrogen ion transmembrane transporter activity padj:0.00121 N(−1/ +10/ 20)
ion binding padj:0.00144 N(−20/ +66/ 641)
hydrogen ion transporting ATP synthase activity, rotational mechanism padj:0.00296 N(−1/ +7/ 8)
ATPase activity padj:0.00358 N(−3/ +30/ 144)
magnesium ion binding padj:0.00722 N(−6/ +18/ 147)
transition metal ion binding padj:0.00738 N(−14/ +50/ 473)
monovalent inorganic cation transmembrane transporter activity padj:0.00996 N(−1/ +10/ 27)
ribonuclease P activity padj:0.01990 N(−1/ +1/ 3)
unfolded protein binding padj:0.03137 N(−1/ +7/ 12)
sulfate transmembrane transporter activity padj:0.03654 N(−1/ +5/ 7)
ligase activity, forming carbon−nitrogen bonds padj:0.03870 N(−1/ +9/ 35)
phenylalanine−tRNA ligase activity padj:0.03888 N(−1/ +1/ 4)
tRNA−specific ribonuclease activity padj:0.03888 N(−1/ +1/ 4)
rank
−sign(cor)*P_log10
−5
0
5