genes0.05_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:0.00001 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:0.00013 N(−3/ +16/ 75)
primary active transmembrane transporter activity
padj:0.00013 N(−3/ +16/ 75)
ATPase activity, coupled to movement of substances
padj:0.00026 N(−3/ +15/ 70)
ATPase activity, coupled to transmembrane movement of substances
padj:0.00026 N(−3/ +15/ 70)
hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances
padj:0.00064 N(−3/ +15/ 73)
ATPase activity, coupled
padj:0.00081 N(−3/ +19/ 92)
metal ion binding
padj:0.00091 N(−19/ +66/ 625)
hydrogen ion transmembrane transporter activity
padj:0.00129 N(−1/ +10/ 20)
cation binding
padj:0.00160 N(−20/ +66/ 639)
ion binding
padj:0.00193 N(−20/ +66/ 641)
hydrogen ion transporting ATP synthase activity, rotational mechanism
padj:0.00309 N(−1/ +7/ 8)
ATPase activity
padj:0.00423 N(−3/ +30/ 144)
magnesium ion binding
padj:0.00808 N(−6/ +18/ 147)
transition metal ion binding
padj:0.00912 N(−14/ +50/ 473)
monovalent inorganic cation transmembrane transporter activity
padj:0.01054 N(−1/ +10/ 27)
ribonuclease P activity
padj:0.02023 N(−1/ +1/ 3)
unfolded protein binding
padj:0.03263 N(−1/ +7/ 12)
sulfate transmembrane transporter activity
padj:0.03760 N(−1/ +5/ 7)
phenylalanine−tRNA ligase activity
padj:0.03951 N(−1/ +1/ 4)
tRNA−specific ribonuclease activity
padj:0.03951 N(−1/ +1/ 4)
ligase activity, forming carbon−nitrogen bonds
padj:0.04075 N(−1/ +9/ 35)
rplD
rplX
rpsN
rplR
rpsD
rplJ
rplF
rpsM
rpsJ
rpsF
−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 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97
rank
−sign(cor)*P_log10
−5
0
5