genes_P0.05Fold2_protein_trT_set00_StcNasMgh_S_baseMghighMg_baseNa_Exp_noFilter_p1Sf_noNorm__Mg_mM_Levels_mf

metal ion binding padj:0.00000 N(−51/ +2/ 640)
mgtA thiM sfcA rnfB ribD fumB glcB yncD ygiQ zntA rumB acnA nadA poxB ydbK yajD rimO speD bfr fdx hypB dapE ubiD idi elaC nth cyoA phoQ yfbR gudD leuB bisC yibO ptr nudF pdxY manB bioB recR aroB yggG cpsG ade dps napA glpQ cutC uxaA lnt dxs speB fepB entA
ion binding padj:0.00000 N(−52/ +2/ 656)
mgtA thiM sfcA rnfB ribD fumB glcB yncD ygiQ zntA rumB acnA nadA poxB ydbK yajD rimO speD bfr fdx hypB dapE ubiD idi elaC nth cyoA phoQ yfbR gudD leuB bisC yibO ptr nudF pdxY manB bioB recR aroB yggG cpsG ade dps napA glpQ ynfJ cutC uxaA lnt dxs speB fepB entA
transition metal ion binding padj:0.00000 N(−40/ +2/ 485)
rnfB ribD fumB yncD ygiQ zntA rumB acnA nadA ydbK yajD rimO bfr fdx hypB dapE ubiD idi elaC nth cyoA yfbR leuB bisC yibO ptr nudF pdxY bioB recR aroB yggG ade dps napA cutC uxaA lnt dxs speB fepB entA
cation binding padj:0.00000 N(−51/ +2/ 654)
mgtA thiM sfcA rnfB ribD fumB glcB yncD ygiQ zntA rumB acnA nadA poxB ydbK yajD rimO speD bfr fdx hypB dapE ubiD idi elaC nth cyoA phoQ yfbR gudD leuB bisC yibO ptr nudF pdxY manB bioB recR aroB yggG cpsG ade dps napA glpQ cutC uxaA lnt dxs speB fepB entA
iron ion binding padj:0.00001 N(−17/ +2/ 236)
rnfB fumB yncD ygiQ rumB acnA nadA ydbK rimO bfr fdx nth cyoA bioB dps napA uxaA fepB entA
4 iron, 4 sulfur cluster binding padj:0.00001 N(−11/ +0/ 107)
rnfB fumB ygiQ rumB acnA nadA ydbK rimO nth bioB napA
iron−sulfur cluster binding padj:0.00059 N(−13/ +0/ 143)
rnfB fumB ygiQ rumB acnA nadA ydbK rimO fdx nth ydiJ bioB napA
metal cluster binding padj:0.00059 N(−13/ +0/ 143)
rnfB fumB ygiQ rumB acnA nadA ydbK rimO fdx nth ydiJ bioB napA
manganese ion binding padj:0.00192 N(−10/ +0/ 57)
ubiD idi yfbR leuB yibO nudF ade uxaA dxs speB
nucleotide binding padj:0.02022 N(−49/ +0/ 586)
mgtA rstB thiM wrbA sfcA udhA ribD tilS barA zntA sdhA mutL fadD acs ybaX hsdR frdA fldB wecC rbsK nadD sapD hypB pckA yjbN ycjX uup apbA hscA phoQ yfbR rep glgC tufA narP kdgK leuB gpsA ydiJ ydaO yjeA engB pdxY oppF yfhK narX gutQ era yrbF
magnesium ion binding padj:0.02464 N(−15/ +0/ 152)
mgtA thiM glcB zntA poxB speD idi phoQ gudD leuB ptr nudF manB cpsG dxs
hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds, in linear amides padj:0.04315 N(−7/ +0/ 32)
amiB flgJ yneH nagA dapE amiA amiC
−52 −51 −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
rank
−sign(cor)*P_log10
−10 −5 0 5 10