	genes_P0.05Fold2_mrna_trT_set02_StcYtcNasMgh_SY_baseMg_baseNa_Exp_noFilter_p1Sf_noNormcarbonSource_mf
structural constituent of ribosome padj:0.00000 N(-50/ +0/ 57)	TPIL TPIY TPAS TPAN TPIS TPANS TPIN TPAS TPANS TPINS TPANS TPINS TPANS T
rRNA binding	TRAN TO
structural molecule activity padj:0.00000 N(-50/ +0/ 70)	TIPL TIPL TIPL TIPL TIPL TIPL TIPL TIPL
RNA binding	ers rluA yoʻiL ipiV rpiD irmD rpsS rpsD rpsG rpiC rpsH rpiC rpiC rpiC rpiC rpiC rpiC rpiC rpiC
tRNA binding padj:0.00000 N(-13/ +0/ 17)	rpsS rmpA tpIA rpIE rph rpIP rpsJ tpsG rpmG rpsM mwG rpsL
metal ion binding	miss and dapt cops met point feed again to got the got one of the got of the
cation binding	mish cold daspt copA met pyrt nirb nepA feeb yigh nepH spot entb modif meth feeb yigh nepH spot on the nepB mod spot on the nepB mod spot on the nepB mod spot entb prech spot on the nepB mod spot on
ion binding	mina cold dapt copi met park took gind gind gind gind gind gind gind gind
purine nucleotide binding	miss port yang era cops usup for the grad part the arch pa
nucleotide binding	misA IVC pyris yegD era copA usup folC nitS pyris polA modF thiL met your feeE nusA gris cyaD feeB yigG adik recQ yilD tasB cyaD feeB yild gris cyaD fe
purine ribonucleotide binding padj:0.00001 N(-88/ +8/ 450)	misit pyrid yegiD era copi usup folic dniss dmad post of the purk ment of the purk process of the purk ment of the purk ment of the purk ment of the purk purk purk purk ment of the purk purk purk purk purk purk purk purk
ribonucleotide bindingpadj:0.00001 N(-88/ +8/ 450)	miles pyre yegD era copA uup folC dnaB deaD ineA dnaJ ponB recQ gutQ yhoM menE recB thuS purC tesE thuS purC te
transition metal ion binding padj:0.00001 N(-76/ +12/ 473)	cold daspE copA metE nir® napA ispF cueO dnsJ fecA glmU alsS sims putsY yigB (gt fecB entB flucD entE yindD entB yigM yeeL metG yigM fecB entB flucD entB yigM fecB entB flucD entB yigM yeeL metG yigM fecB entB flucD entB yigM yeeL metG yigM fecB entB flucD entB yigM fecB entB flucD entB yigM yeeL metG yigM fecB entB flucD entB yigM fecB entB flucD entB yigM yeeL metG yigM fecB entB flucD entB yigM fecB entB flucD entB yigM yeeL metG yigM fecB entB flucD entB yigM yeeL metG yigM fecB entB flucD entB yigM yeeL metG yigM fecB entB flucD entB yigM fecB entB flucD entB yigM yeeL metG yigM fecB entB flucD entB yigM yeeL metG yigM fecB entB flucD entB yigM yeeL metG yigM yeeL metG yigM fecB entB flucD entB yigM yeeL metG yigM fecB entB flucD entB yigM yeeL metG yigM yeeL metG yigM yeeL metG yigM flucD entB yigM yeeL metG yigM fecB entB flucD entB yigM yeeL metG yigM flucD entB yigM yeeL metG yigM
nucleoside binding	miaA pyrH yegD copA uup folC niriB yhidG drasB desD insA drasA purO yicD yhidZ yncE girlX nrdA cmix bilS purC kesS purT fesE nich purK menE recB fhuC entE pyrG park yeb yeb yhidZ yncE girlX nrdA cmix bilS purC kesS purT fesE nich purK menE recB fhuC entE pyrG park fesE thrA coadD york fesE thrA coadD y
adenyl nucleotide bindingpadj:0.00002 N(-87/ +11/ 468)	THISA DAYS SHEET THE SHEET SHE
purine nucleoside binding padj:0.00002 N(-87/ +11/ 468)	miaA pyrH yegD copA usip folG nirB yhdG dnaB deaD inaA dnaJ gidA ponB risE nreC gulQ yheN metG feeE thrA coaD yehi liyeS cysD adk recG ynpD tainB cysN fueK hisG thrB cysC recF yejl griA mgiA mgiA gipA invB kdpA rhaB acoiK lyxK gicE bax gipK
iron ion binding padj:0.00003 N(-41/ +6/ 226)	nit napA fecA yfg8 fecR fecC rnfC fecB ygiQ fecB entB fhuC entB fecB shib mufY entC fecB napH yggW yggX fecE fhuB mufY entC fecB ygiQ fecB ontB fhuC garL ceiD hcaE yeaW mhp8 gipC
ATP binding	misA pyrM yegD copA uup folC druB deaD inaA dru yet secA gak druA coaD lys6 cycD adk recG yngD touB cycD yet secA gak druA purb yet secA gak druA coaD lys6 cycD adk recG yngD touB cycD yet secA gak druA coaD lys6 cycD adk recG yngD touB guaA tepE phos recQ gutQ yheM metG feeE thrA coaD lys6 cycD adk recG yngD touB gutA touB cycD proxA uhpB guaA tepE phos recQ gutQ yheM metG feeE thrA coaD lys6 cycD adk recG yngD touB gutA touB cycD proxA uhpB guaA tepE phos recQ gutQ yheM metG feeE thrA coaD lys6 cycD adk recG yngD touB gutA touB cycD proxA uhpB guaA tepE phos recQ gutQ yheM metG feeE thrA coaD lys6 cycD adk recG yngD touB gutA touB cycD proxA uhpB guaA tepE phos recQ gutQ yheM metG feeE thrA coaD lys6 cycD adk recG yngD touB gutA touB cycD proxA uhpB guaA tepE phos recQ gutQ yheM metG feeE thrA coaD lys6 cycD adk recG yngD touB gutA touB cycD proxA uhpB guaA tepE phos recQ gutQ yheM metG feeE thrA coaD lys6 cycD adk recG yngD touB gutA touB cycD proxA uhpB guaA tepE phos recQ gutQ yheM metG feeE thrA coaD lys6 cycD adk recG yngD touB gutA touB cycD proxA uhpB guaA tepE phos recQ gutQ yheM metG feeE thrA coaD lys6 cycD adk recG yngD proxA uhpB gutA touB cycD proxA uhpB
adenyl ribonucleotide binding padj:0.00004 N(-80/ +8/ 420)	THIBAD BY THE SHOPE COORD BLUE TOTAL COUNT TOTAL CHILD STATE STORE STATE STATE STORE STATE STATE STORE STATE STATE STORE STATE STATE STATE STORE STATE
aminoacyl–tRNA ligase activity padj:0.00016 N(-10/ +0/ 32)	ataS angS sapS tyrS gttX titS feuS phieS matiG lysS
ase activity, forming aminoacyl–tRNA and related compounds padj:0.00018 N(-10/ +0/ 32)	ala\$ arg\$ asp\$ tyr\$ gltX til5 leuS phe\$ motG lys\$
ligase activity, forming carbon–oxygen bonds	atuS angS angS tyrS gritX tilS fau.S pheS meetG byuS
tRNA-specific ribonuclease activity	mpA rph
magnesium ion binding	miaA copA pyrE speD upp ispF gimU psal stoL livi medK purD aceE purF purT suitB prsA entD pheS ruvC lysS yijG hisG ispD mutT gard. livB apitA glbF
transferase activity, transferring pentosyl groups	pyrE upp cohT tgi purF mreA apt hisG yelf2
adenylyltransferase activity	ponition madiff entities could cyell cyell
translation factor activity, nucleic acid bindingpadj:0.00917 N(-9/ +0/ 19)	yolH greA prfB infA fusA nusA tsf prfC infB
glycerol-3-phosphate dehydrogenase activity padj:0.01129 N(-1/ +4/ 4)	glpA glpD glpB glpC
ribonuclease P activity	
	-107 -106 -105 -104 -105 -104 -105 -104 -105 -104 -105 -104 -105 -104 -105 -104 -105 -104 -105 -104 -105 -104 -105 -104 -105 -105 -104 -105 -104 -105 -105 -104 -105 -104 -105 -105 -104 -105 -104 -105 -105 -105 -105 -105 -105 -105 -105