| | genes_P0.05Fold2_mrna_trT_set02_StcNasMgh_S_baseNa_Exp_noFilter_p1Sf_noNormMg_mM_Levels_mf | |
|--|---|--|
| structural constituent of ribosome padj:0.00000 N(-44/ +0/ 57) | rps\$ rpIW rpIV rpmC rpIP rpsA rpmI rpsH rpmD rpsK rpIE rpsD rpsK rpIE rpsD rpsK rpIE rpsD rpsK rpIE rpsD rpsK rpII rpsC rpsD rpsD rpsC rpsD rpsD rpsC rpsD rpsD rpsD rpsD rpsD rpsD rpsD rpsD | |
| structural molecule activity _ padj:0.00000 N(-51/ +0/ 70) | fligl rpsS rpIW fligF rpIV fligG rpmC rpIP rpsA fligK fligL rpmI rpsH rpmD rpsK rpII rpsG rpsD rpsM rpIN rpsD rpsK rpII rpsG rpsD rpsM rpIN rpsD rpsK rpII rpsD rpsK rpIII rpsD rpsC rpsD rpsC rpsD rpsC rpsD rpsD rpsC rpsD rpsD rpsC rpsD rpsD rpsD rpsD rpsD rpsD rpsD rpsD | |
| rRNA binding padj:0.00000 N(-32/ +0/ 37) | rpsS rpIW rpIV rpmC rpIP rpsH rpsK rpIO rpsE rpmE rpIB rpIR rpsN rpsC rpIT rpsG rpsD rpsM rpIN rpsO rpIS rpIE rpIX rpIA rpsF rpsR rpII rpsL rpIK | |
| RNA binding padj:0.00000 N(-52/ +0/ 109) | pheT rps\$ rpIW rpIV rpmC rpIP rpsA rne trmD rpsH pnp rnr rpsK truA rpIO rpsE rpmE deaD rpID rpiC truB rpIF rpsB rpsD rpsC infC rpIT rpsG rpsD rpsC infC rpID rpsC rpsD rpsC infC rpID rpsC rpsD rpsC rpsD rpsC infC rpID rpsC rpsD | |
| tRNA binding _ padj:0.00000 N(-10/ +0/ 17) | pheT rpsS rpIP rpsG rpsM rpsI rpIA rpsL | |
| aminoacyl–tRNA ligase activity padj:0.00008 N(-9/ +0/ 32) | pheT asnA pheS valS lysS gltX alaS lleS glyS | |
| gase activity, forming aminoacyl–tRNA and related compounds | pheT asnA pheS valS lysS gltX alaS ileS glyS | |
| ligase activity, forming carbon–oxygen bonds | pheT asnA pheS valS lysS gltX alaS ileS glyS | |
| phenylalanine–tRNA ligase activity padj:0.00036 N(-2/ +0/ 4) | pheT pheS | |
| nucleotide binding _ padj:0.00056 N(-78/ +9/ 578) | pntB copA cysI fabG yjcD thrB ydiJ pheT rpIW secA cysD fecE mrp thrA cysN cysJ cysC atpD bipA gnd purD menE fusA pyrH cysA asnA uup thiD phoQ sfcA rfaE trmE deaD thIL murC livF pdxA pykF aroE infB nusA pheS asd leuB rnfG hisO mokB yjjK valS modF atpD bipA gnd purD menE fusA pyrH cysA asnA uup thiD phoQ sfcA rfaE trmE deaD thIL murC livF pdxA pykF aroE infB nusA pheS asd leuB rnfG hisO mokB yjjK valS modF atpD purC glnA wecC sms rhIE serA | alsK ugd nrdE ycdH aceK lldD gntK ssuB alsA |
| motor activity | figH figF figJ figG figK figE | |
| cation binding padj:0.01564 N(-63/ +11/ 639) | copA cysl pheT cueO fecD secA fecE fecC cysJ purD nth ruvC btuB nucl phoQ ilvD sfcA trmE cyoA ligA pepB rpmE rffH menC pdxA pykF pheS ppa leuB rnhB hisG mutT modF cyoB nei pdxY leuC ycdX yggW ycdB cusB hisD trmE cyoA ligA pepB rpmE rffH menC pdxA pykF pheS ppa leuB rnhB hisG mutT modF cyoB nei pdxY leuC ycdX yggW ycdB cusB hisD trmE cyoA ligA pepB rpmE rffH menC pdxA pykF pheS ppa leuB rnhB hisG mutT modF cyoB nei pdxY leuC ycdX yggW ycdB cusB hisD trmE cyoA ligA pepB rpmE rffH menC pdxA pykF pheS ppa leuB rnhB hisG mutT modF cyoB nei pdxY leuC ycdX yggW ycdB cusB hisD trmE cyoA ligA pepB rpmE rffH menC pdxA pykF pheS ppa leuB rnhB hisG mutT modF cyoB nei pdxY leuC ycdX yggW ycdB cusB hisD trmE cyoA ligA pepB rpmE rffH menC pdxA pykF pheS ppa leuB rnhB hisG mutT modF cyoB nei pdxY leuC ycdX yggW ycdB cusB hisD trmE cyoA ligA ppa leuB rnhB hisG mutT modF cyoB nei pdxY leuC ycdX yggW ycdB cusB hisD hisD hisD hisD hisD hisD hisD hisD | pyrl feoA gldA yjiL narl narG celA narH ydeN ydeM modA |
| metal ion binding padj:0.01741 N(-62/ +10/ 625) | copA cysl pheT cueO fecD secA fecE fecC cysJ purD nth ruvC btuB nucl phoQ iivD sfcA trmE cyoA ligA pepB rpmE rffH menC pdxA pykF pheS ppa leuB rnhB hisG mutT modF cyoB nei pdxY leuC ycdX yggW ycdB cusB hisD sms hyaD ispD | pyrl feoA gldA yjiL narl narG narH ydeN ydeM modA |
| ion binding _ padj:0.01808 N(-63/ +11/ 641) | COPA CYSI PHET CUEO fecD SECA fecE fecC CYS.J PUTD nth rUVC bluB nucl phoQ iiVD SfcA trmE CYCA ligA pepB rpmE rffH menC pdxA pykF pheS ppa leuB rnhB hisG mutT modF cycB nei pdxY leuC ycdX yggW ycdB cusB hisD sms hyaD ispD | pyrl feoA gldA yjiL narl narG celA narH ydeN ydeM modA |
| purine ribonucleotide bindingpadj:0.01943 N(-57/ +6/ 450) | COPA YJCD thrB pheT secA cysD fecE mrp thrA cysN cysC atpD bipA purD menE fusA pyrH cysA asnA uup thiD phoQ rfaE trmE deaD thiL murC livF pykF infB pheS hisG mukB yjjK valS modF atpG accA pdxY purL guaA lpxK tauB lysS gltX alaS rtcA foiE lieS dppF glyS atpA dppD purC glnA sms rhiE | alsK nrdE aceK gntK ssuB alsA |
| ribonucleotide binding padj:0.01943 N(-57/ +6/ 450) | COPA YJCD thrB pheT secA cysD fecE mrp thrA cysN cysC atpD bipA purD menE fusA pyrH cysA asnA uup thiD phoQ rfaE trmE deaD thiL murC livF pykF infB pheS hisG mukB yJjK vaiS modF atpG accA pdxY purL guaA lpxK tauB lysS gltX alaS rtcA foiE lieS dppF glyS atpA dppD purC glnA sms rhiE | alsK nrdE aceK gntK ssuB alsA |
| NADP or NADPH binding padj:0.02140 N(-7/ +0/ 16) | pntB cysl thrA gnd aroE asd ilvC | |
| fatty-acid synthase activity _ padj:0.02720 N(-5/ +0/ 6) | fabG fabI fabD fabH fabF | |
| ATP binding padj:0.03997 N(-52/ +6/ 419) | copA yjcD thrB pheT secA cysD fecE mrp thrA cysN cysC atpD purD menE pyrH cysA asnA uup thiD phoQ rfaE deaD thiL murC livF pykF pheS hisG mukB yjjK valS modF atpG accA pdxY purL guaA lpxK tauB lysS gltX alaS rtcA ileS dppF glyS atpA dppD purC glnA sms rhIE | alsK nrdE aceK gntK ssuB alsA |
| adenyl ribonucleotide binding padj:0.04241 N(-52/ +6/ 420) | copA yjcD thrB pheT secA cysD fecE mrp thrA cysN cysC atpD purD menE pyrH cysA asnA uup thiD phoQ rfaE deaD thiL murC livF pykF pheS hisG mukB yjjK valS modF atpG accA pdxY purL guaA lpxK tauB lysS gltX alaS rtcA ileS dppF glyS atpA dppD purC glnA sms rhIE | alsK nrdE aceK gntK ssuB alsA |
| | -78 -77 -76 -75 -74 -73 -72 -71 -70 -68 -68 -67 -66 -65 -64 -63 -62 -61 -60 -58 -58 -57 -56 -55 -54 -53 -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 -89 -88 -57 -56 -55 -54 -53 -52 -54 -23 -22 -21 -20 -19 -18 -17 -16 -15 -14 -13 -12 -11 -10 -9 -18 -17 -16 -15 -14 -13 -12 -11 -10 -9 -18 -17 -16 -15 -14 -13 -12 -11 -10 -19 -18 -17 -10 -19 -19 -18 -17 -10 -19 -18 -17 -10 -19 -19 -18 -17 -10 -19 -19 -18 -17 -10 -19 -19 -19 -19 -19 -19 -19 -19 -19 -19 | 0 1 2 3 4 5 6 7 8 9 10 11 |