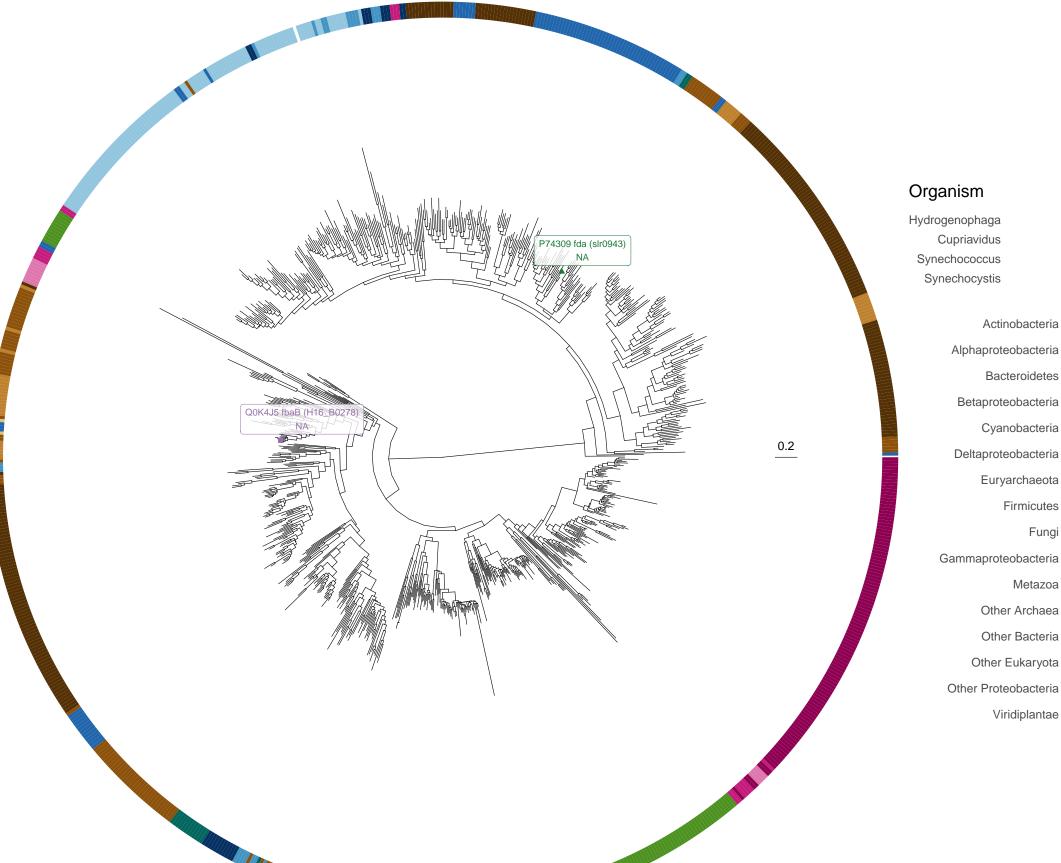
ALD K01623 ALDO; fructose-bisphosphate aldolase, class I [EC:4.1.2.13]



Cupriavidus Synechococcus

> Actinobacteria Alphaproteobacteria

> > Bacteroidetes

Betaproteobacteria

Cyanobacteria

Euryarchaeota

Firmicutes

Fungi

Metazoa

Other Archaea

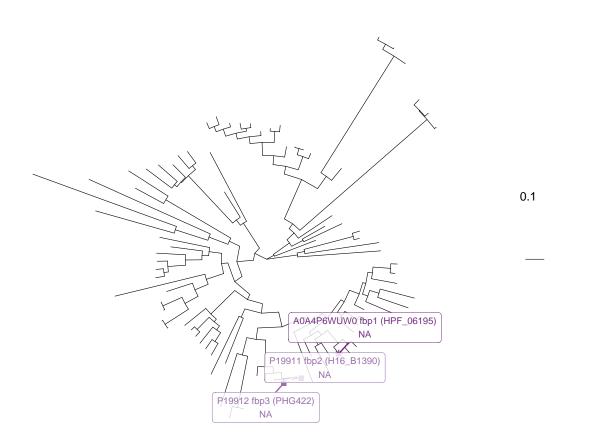
Other Bacteria

Other Eukaryota

Other Proteobacteria

FBP-SBPase_I

K01086 fbp-SEBP; fructose-1,6-bisphosphatase I / sedoheptulose-1,7-bisphosphatase [EC:3.1.3.11 3.1.3.37]



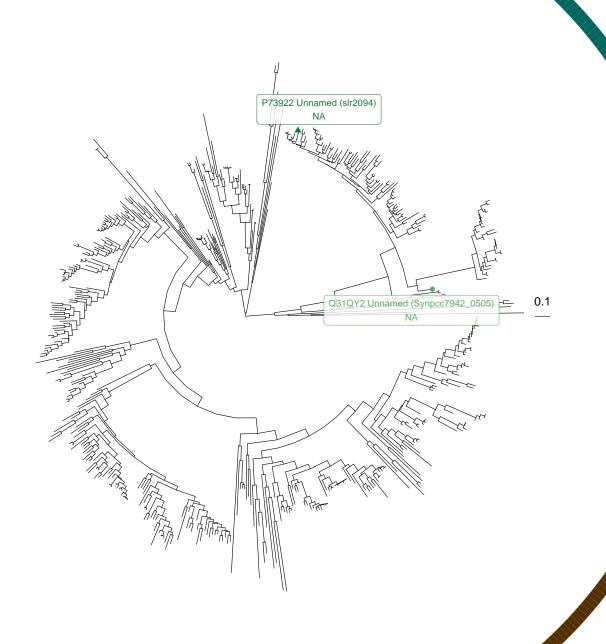
Organism

Synechocystis

Actinobacteria
Alphaproteobacteria
Bacteroidetes
Betaproteobacteria
Cyanobacteria
Deltaproteobacteria
Euryarchaeota
Firmicutes
Fungi
Gammaproteobacteria
Metazoa
Other Archaea
Other Bacteria
Other Eukaryota

FBP-SBPase_II_glpX

K11532 glpX-SEBP; fructose-1,6-bisphosphatase II / sedoheptulose-1,7-bisphosphatase [EC:3.1.3.11 3.1.3.37]



Organism

Hydrogenophaga *
Cupriavidus
Synechococcus

Synechocystis

Actinobacteria
Alphaproteobacteria
Bacteroidetes

Betaproteobacteria

Cyanobacteria

Deltaproteobacteria

Euryarchaeota

Firmicutes

Fungi

Gammaproteobacteria

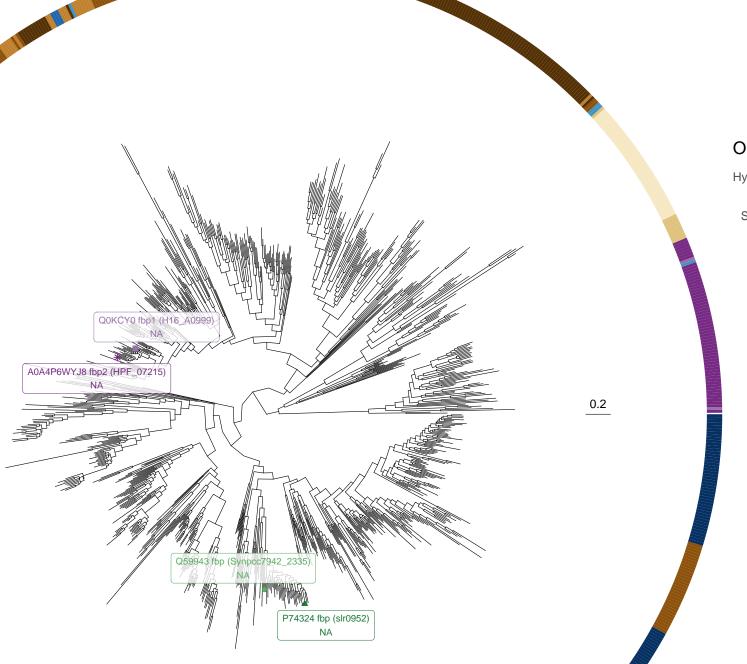
Metazoa

Other Archaea

Other Bacteria

Other Eukaryota
Other Proteobacteria

FBPase_I K03841 FBP, fbp; fructose–1,6–bisphosphatase I [EC:3.1.3.11]



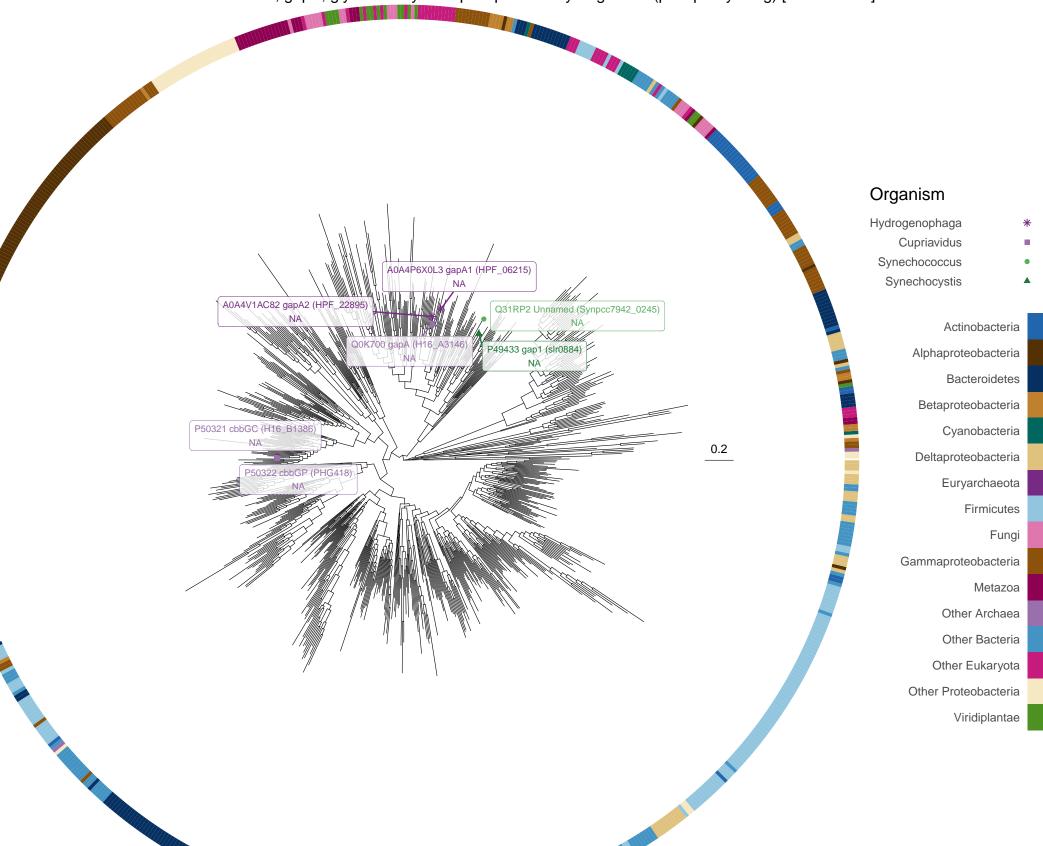
Organism

Hydrogenophaga *
Cupriavidus
Synechococcus
Synechocystis

Actinobacteria
Alphaproteobacteria
Bacteroidetes
Betaproteobacteria
Cyanobacteria
Deltaproteobacteria
Euryarchaeota
Firmicutes
Fungi
Gammaproteobacteria
Metazoa
Other Archaea
Other Bacteria

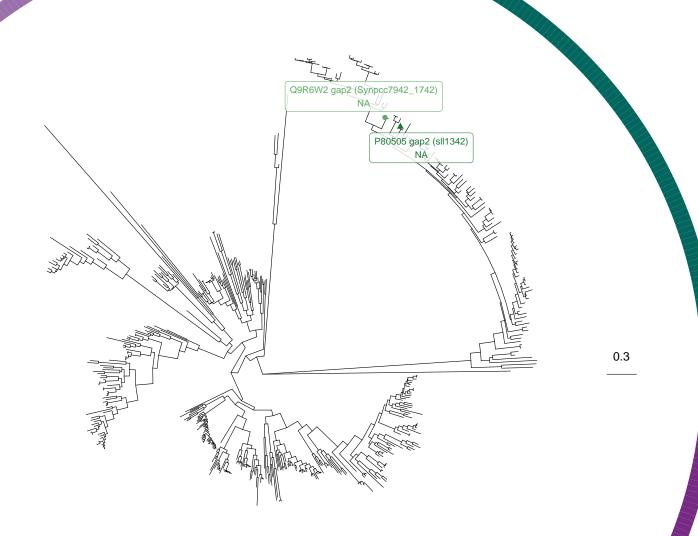
Other Proteobacteria

GAPDH K00134 GAPDH, gapA; glyceraldehyde 3–phosphate dehydrogenase (phosphorylating) [EC:1.2.1.12]



GAPDH2

K00150 gap2; glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) [EC:1.2.1.59]



Organism

Hydrogenophaga *
Cupriavidus
Synechococcus
Synechocystis

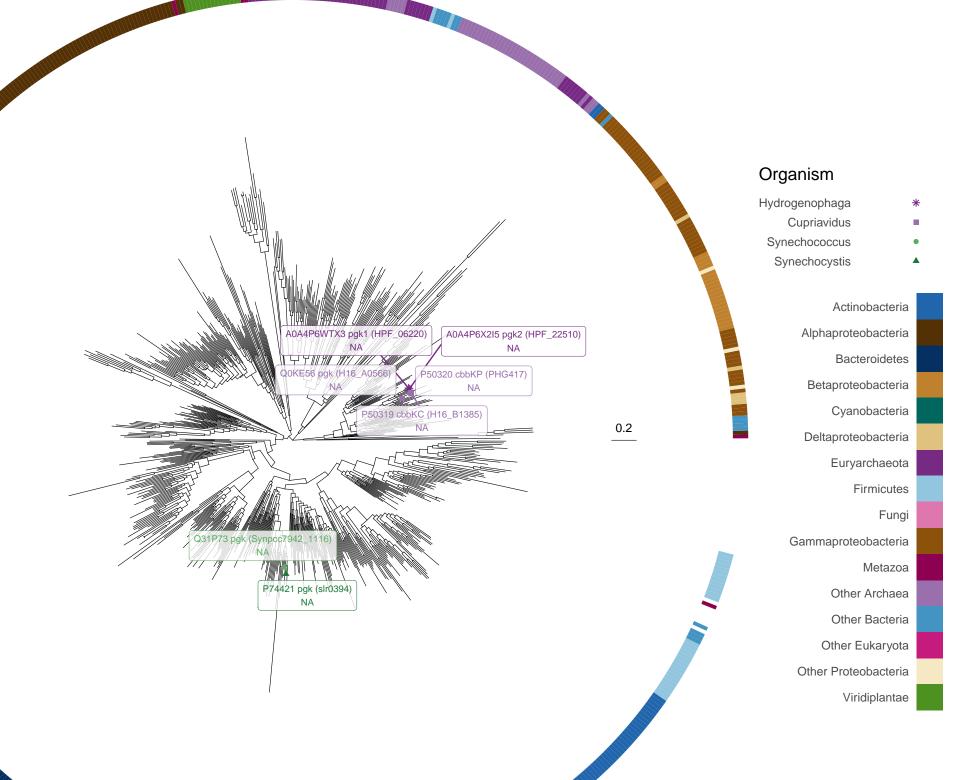
Actinobacteria
Alphaproteobacteria
Bacteroidetes
Betaproteobacteria
Cyanobacteria
Deltaproteobacteria
Euryarchaeota
Firmicutes
Fungi
Gammaproteobacteria

Other Archaea
Other Bacteria

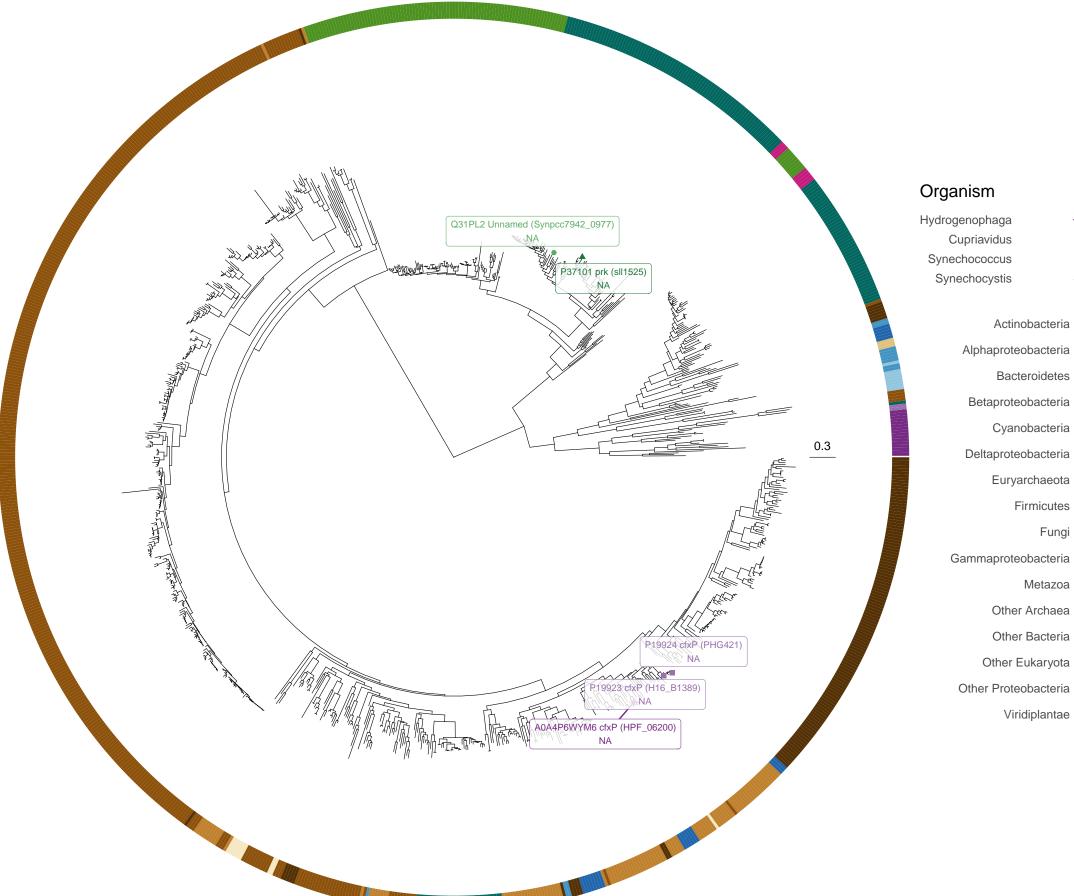
Metazoa

Other Eukaryota
Other Proteobacteria

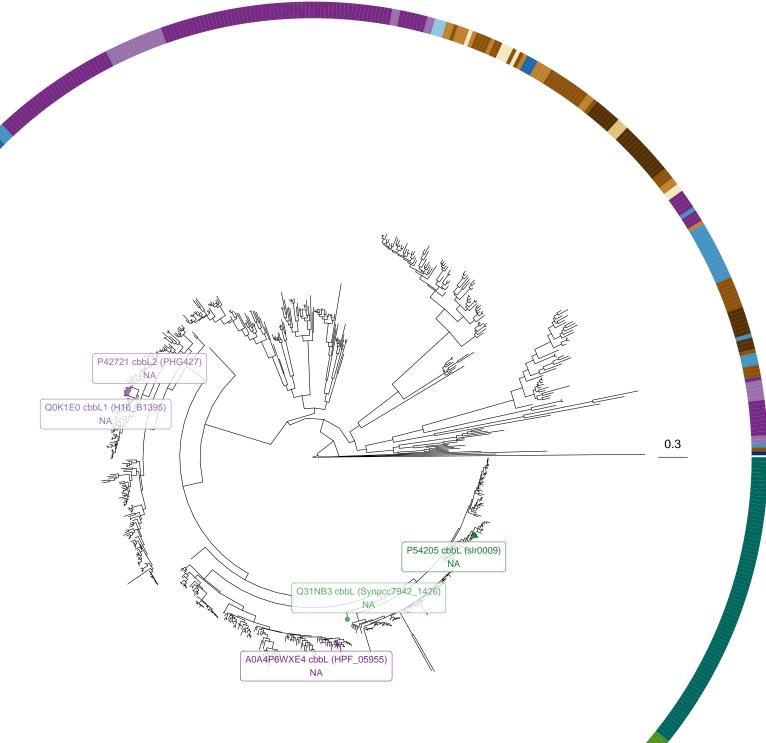
PGK K00927 PGK, pgk; phosphoglycerate kinase [EC:2.7.2.3]



PRK
K00855 PRK, prkB; phosphoribulokinase [EC:2.7.1.19]



rbcL K01601 rbcL, cbbL; ribulose–bisphosphate carboxylase large chain [EC:4.1.1.39]

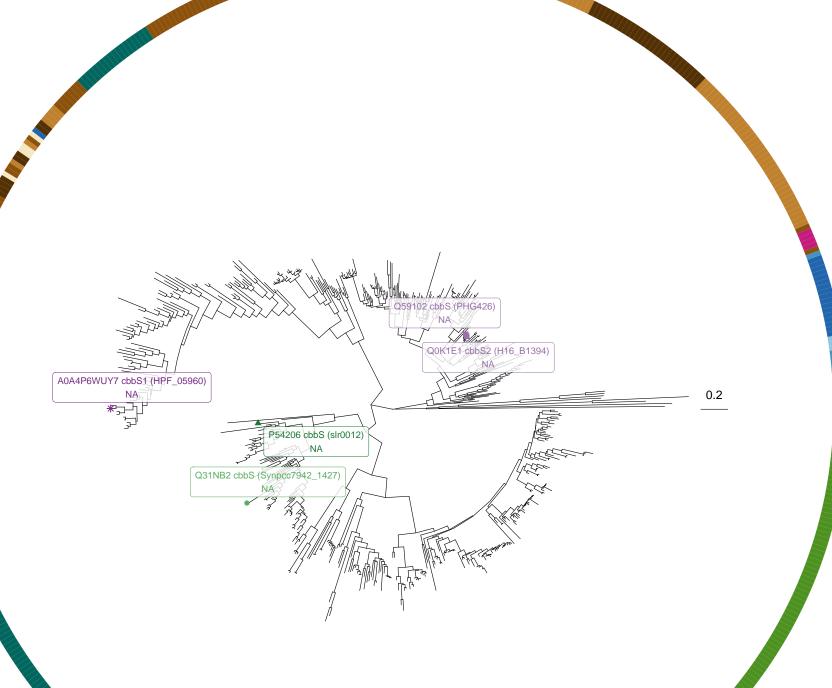


Organism

Hydrogenophaga *
Cupriavidus
Synechococcus
Synechocystis

Actinobacteria
Alphaproteobacteria
Bacteroidetes
Betaproteobacteria
Cyanobacteria
Deltaproteobacteria
Euryarchaeota
Firmicutes
Fungi
Gammaproteobacteria
Metazoa
Other Archaea
Other Bacteria
Other Eukaryota

rbcS K01602 rbcS, cbbS; ribulose–bisphosphate carboxylase small chain [EC:4.1.1.39]



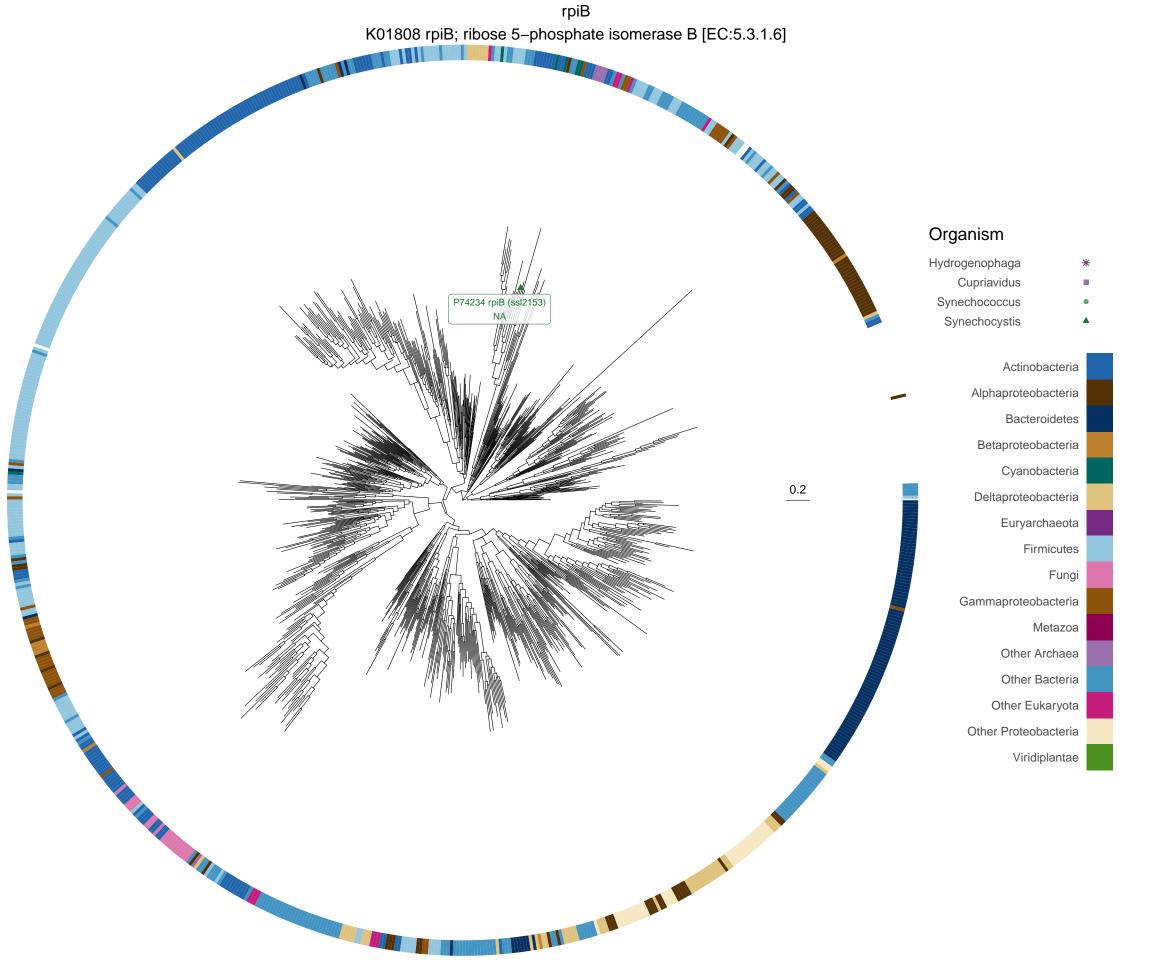
Organism

Actinobacteria
Alphaproteobacteria
Bacteroidetes
Betaproteobacteria
Cyanobacteria
Deltaproteobacteria
Euryarchaeota
Firmicutes
Fungi
Gammaproteobacteria
Metazoa
Other Archaea
Other Bacteria

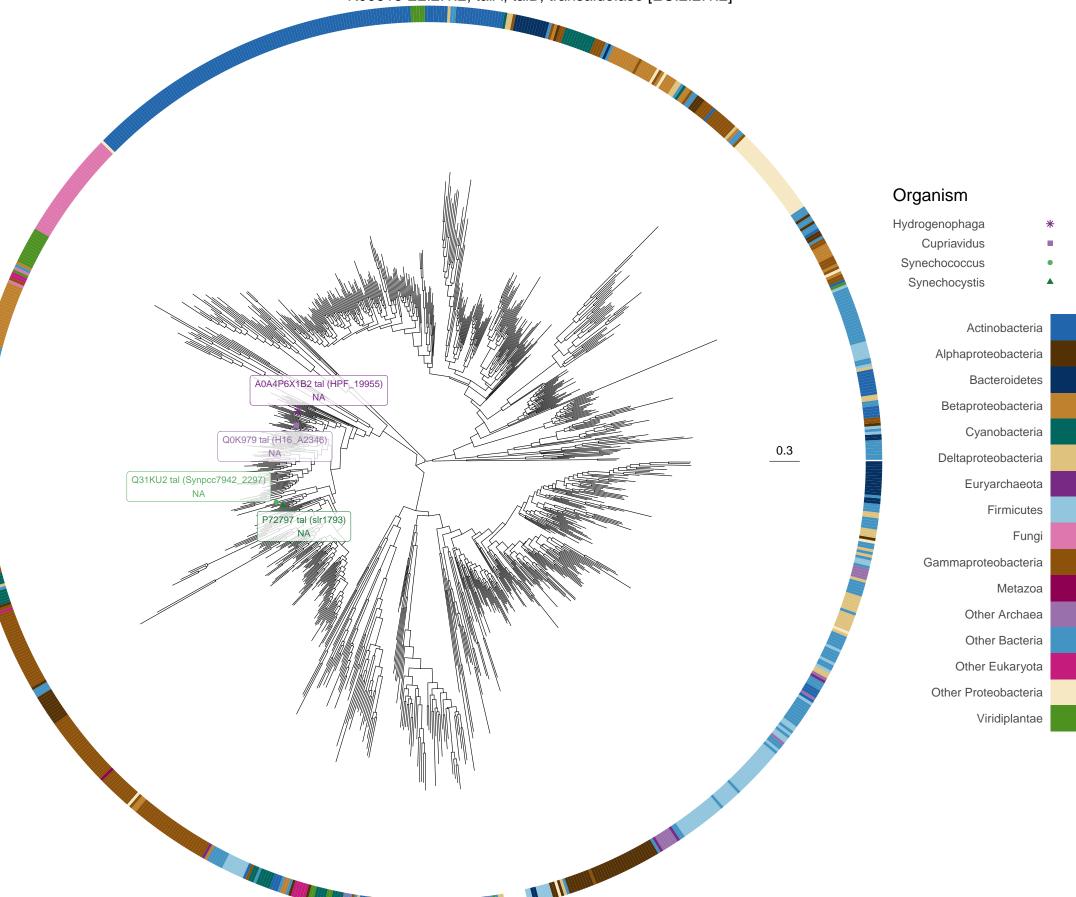
Other Proteobacteria

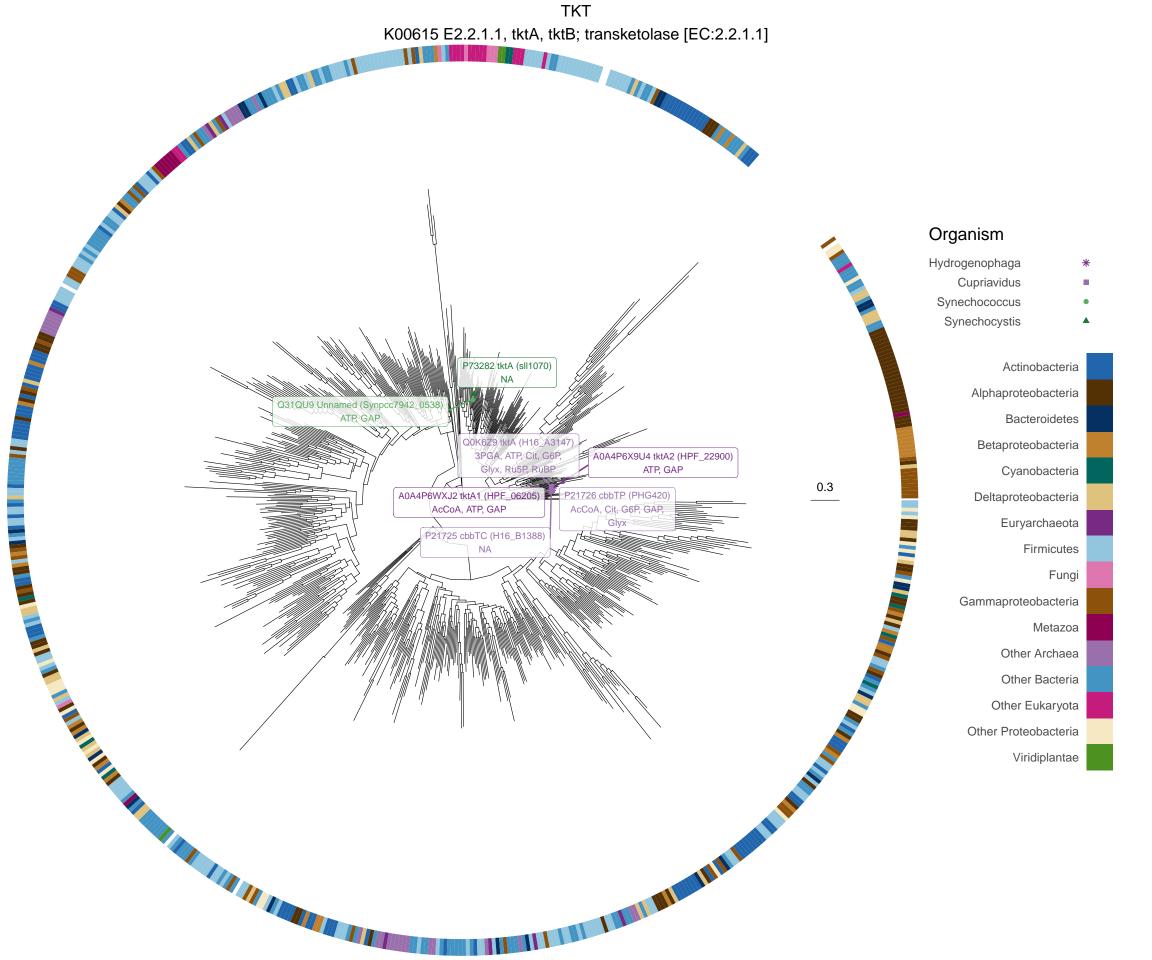
RPE K01783 rpe, RPE; ribulose-phosphate 3-epimerase [EC:5.1.3.1] Organism Hydrogenophaga Cupriavidus Synechococcus Synechocystis A0A4P6WXZ9 rpe1 (HPF_06190) Q0K6I5 rpe (H16_43317) Actinobacteria P40117 rpe1 (H16_B1391) Alphaproteobacteria NA Bacteroidetes A0A4P6X8Y2 rpe2 (HPF_21630) Betaproteobacteria Cyanobacteria 0.2 Deltaproteobacteria Euryarchaeota Firmicutes Fungi Gammaproteobacteria Metazoa Other Archaea Other Bacteria Other Eukaryota Other Proteobacteria Viridiplantae

rpiA K01807 rpiA; ribose 5-phosphate isomerase A [EC:5.3.1.6] Organism Hydrogenophaga Cupriavidus Synechococcus Synechocystis A0A4V1ABS0 rpiA (HPF_14625) NA Actinobacteria Q0K980 ipiA (H16, A2345) Alphaproteobacteria Q55766 rpiA (slr0194) NA Bacteroidetes Betaproteobacteria 1QQ3 rpiA (Synpec7942_0584) Cyanobacteria 0.2 Deltaproteobacteria Euryarchaeota Firmicutes Fungi Gammaproteobacteria Metazoa Other Archaea Other Bacteria Other Eukaryota Other Proteobacteria Viridiplantae



TAL K00616 E2.2.1.2, talA, talB; transaldolase [EC:2.2.1.2]





TPI K01803 TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1] Organism Hydrogenophaga Cupriavidus Synechococcus Synechocystis Actinobacteria Alphaproteobacteria Bacteroidetes Betaproteobacteria Cyanobacteria 0.4 Deltaproteobacteria Euryarchaeota Firmicutes Fungi A0A4P6WY50 tpiA (HPF_07480) NA Q31NS8 tpiA (Synpcc7942_1261) Gammaproteobacteria Metazoa Other Archaea Q59994 tpiA (slr0783) Other Bacteria Other Eukaryota Other Proteobacteria Viridiplantae