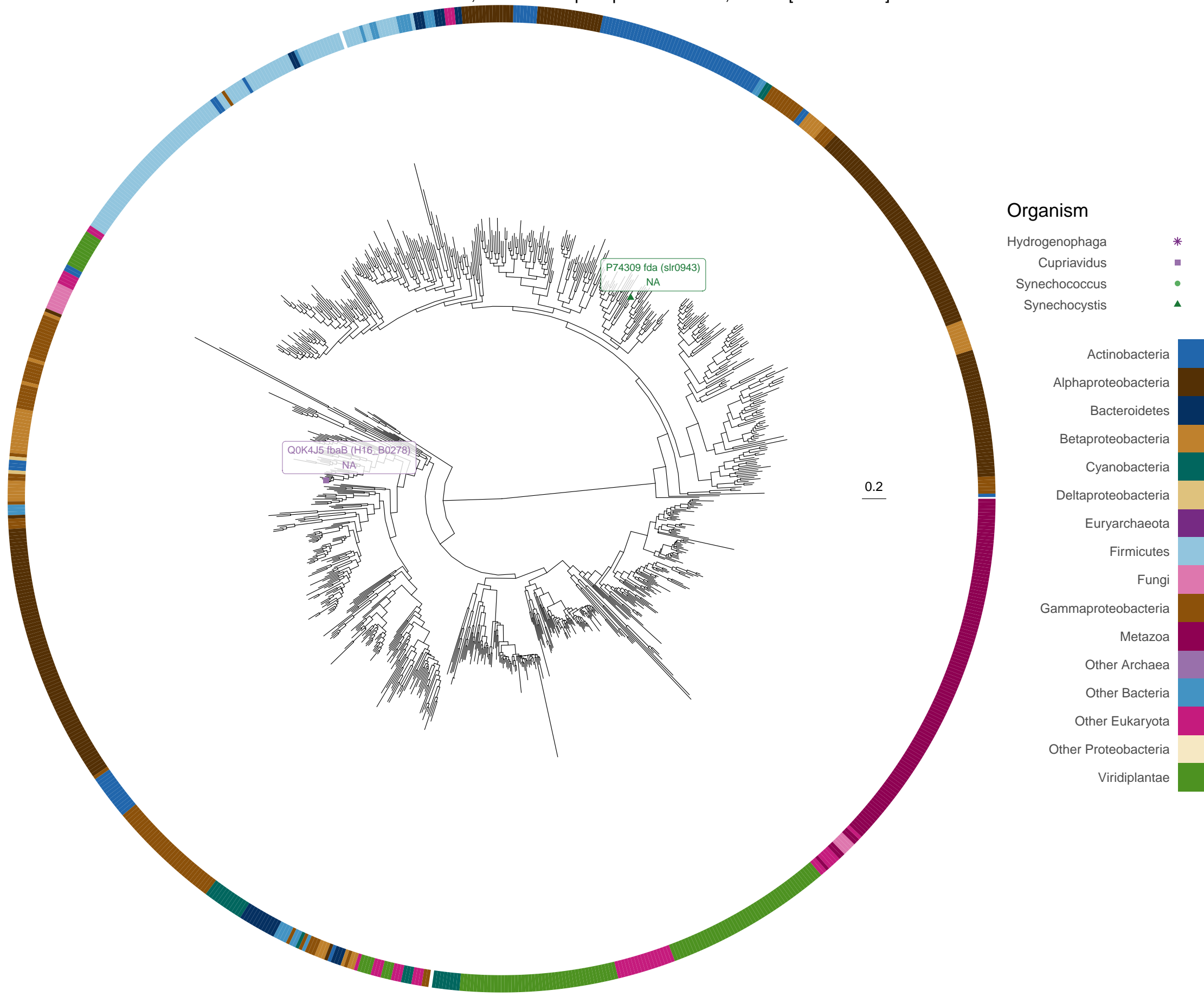
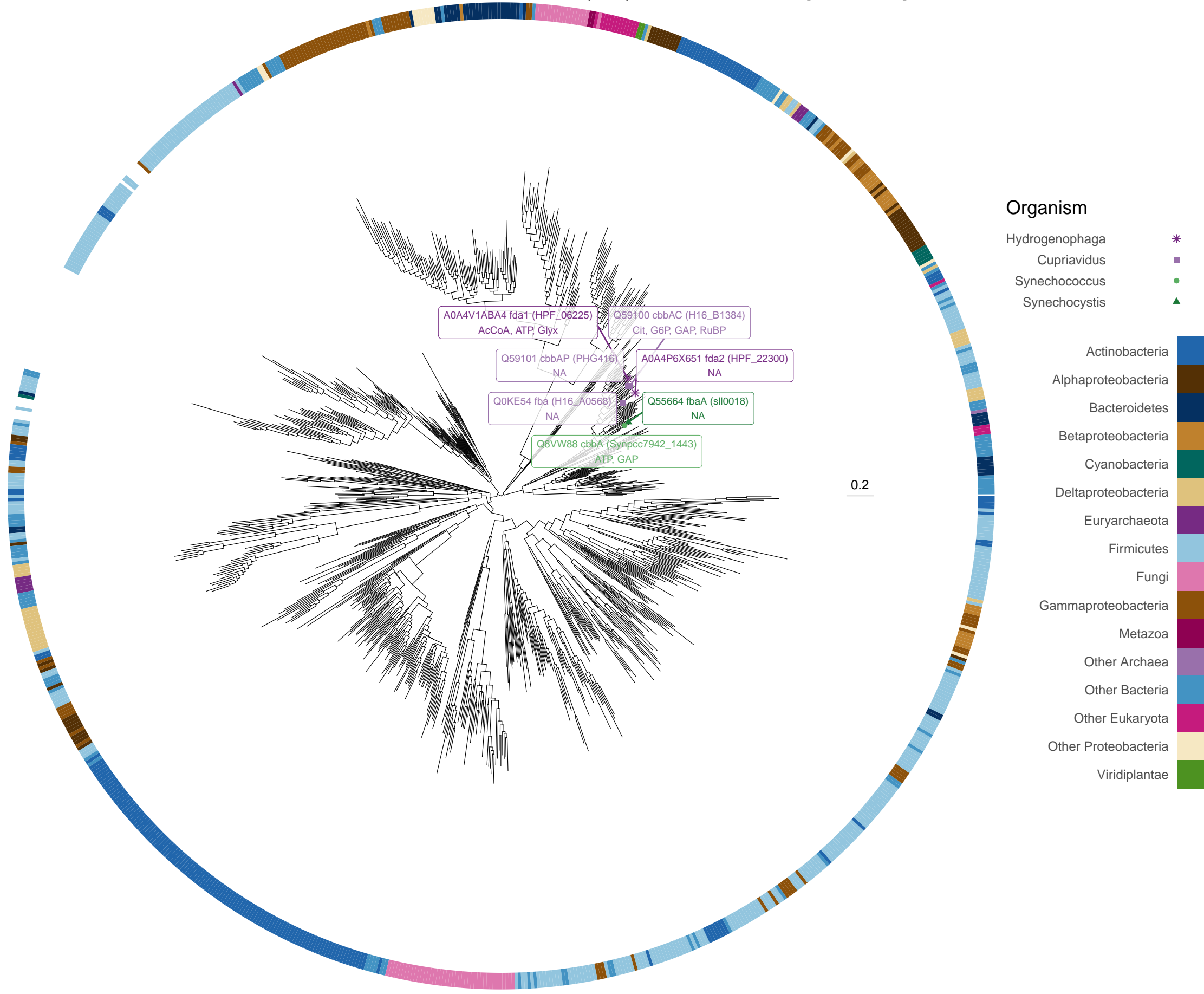


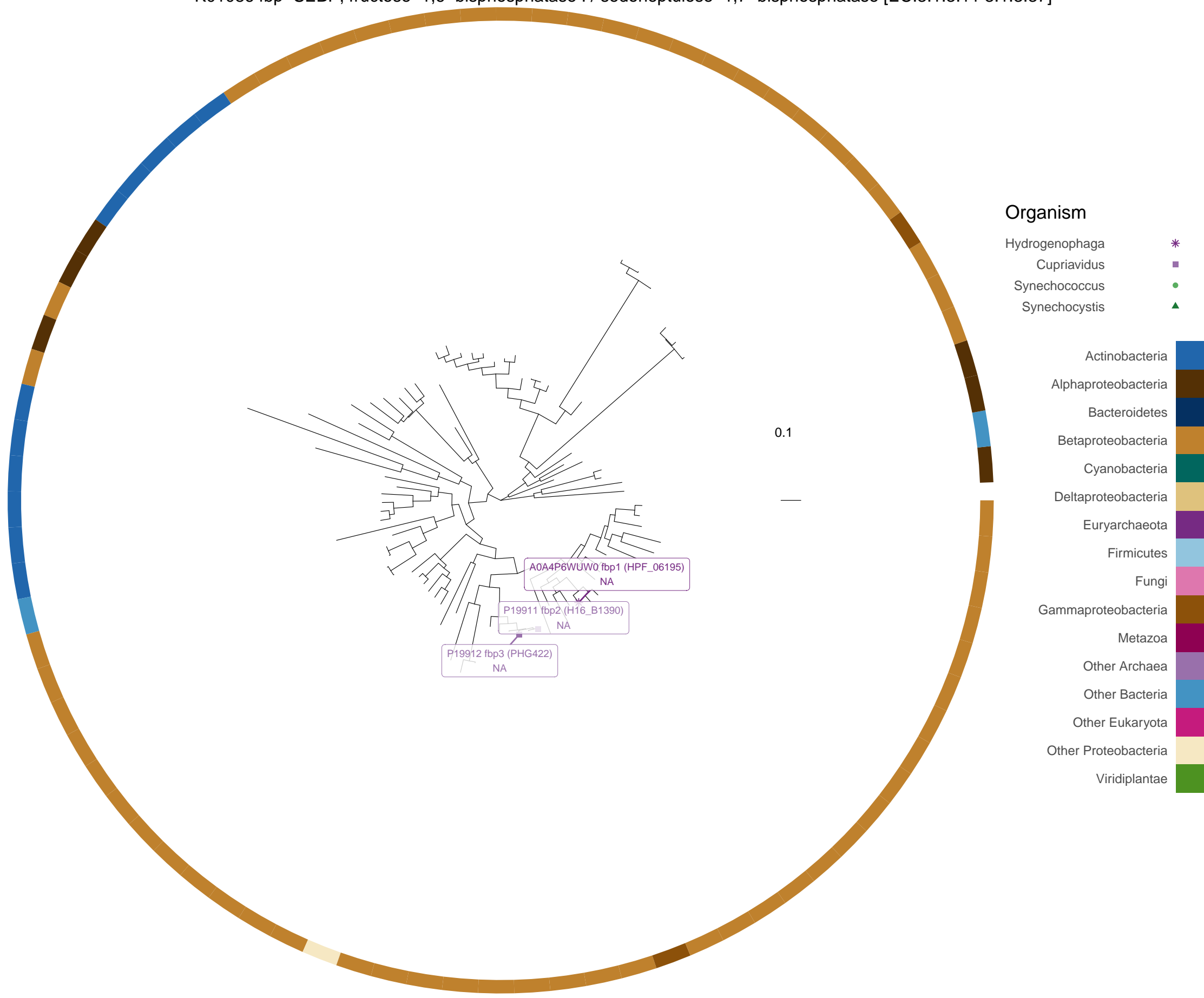
ALD
K01623 ALDO; fructose-bisphosphate aldolase, class I [EC:4.1.2.13]



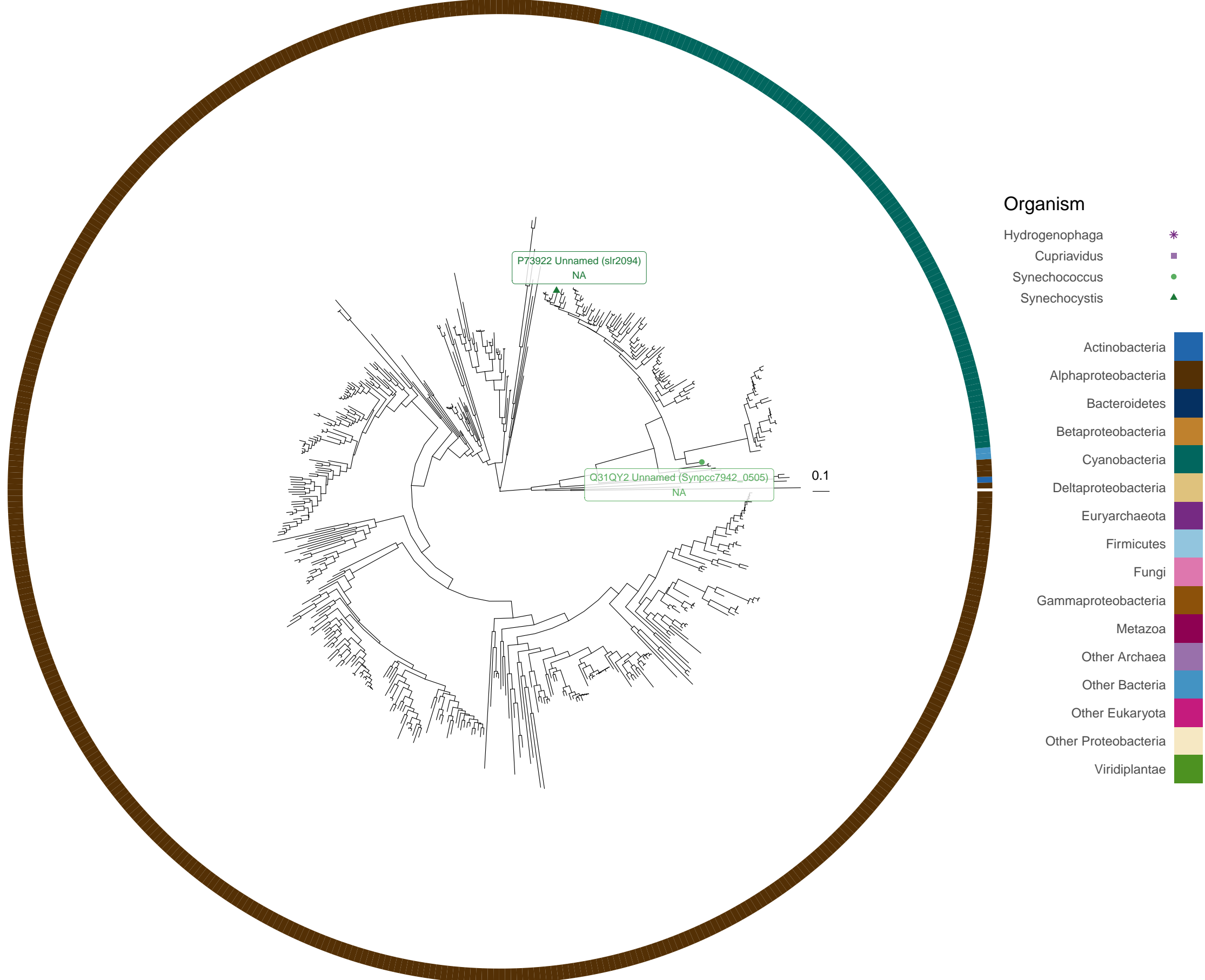
FBA
K01624 FBA, fbaA; fructose-bisphosphate aldolase, class II [EC:4.1.2.13]



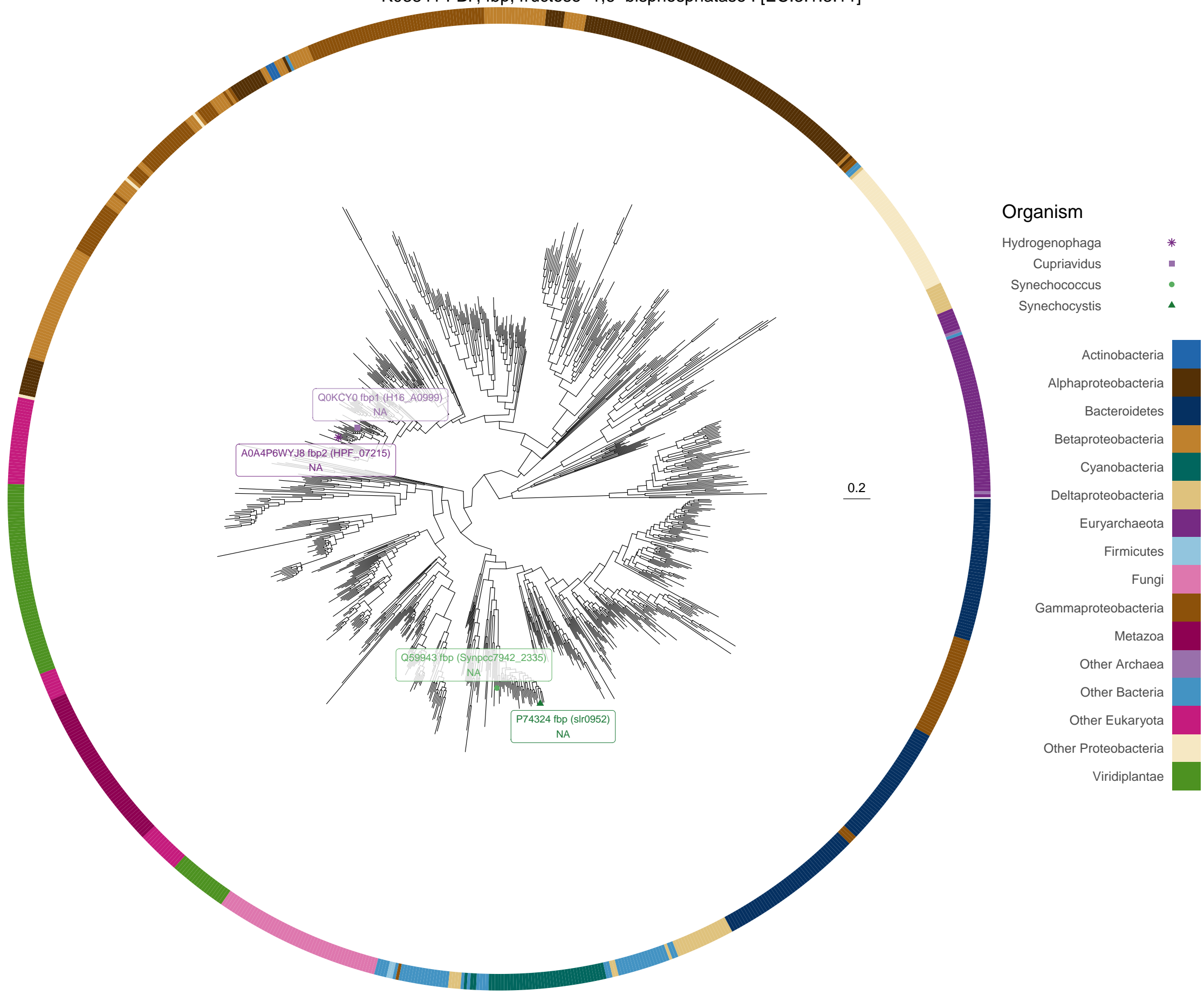
FBP-SBPase_I
K01086 fbp-SEBP; fructose-1,6-bisphosphatase I / sedoheptulose-1,7-bisphosphatase [EC:3.1.3.11 3.1.3.37]



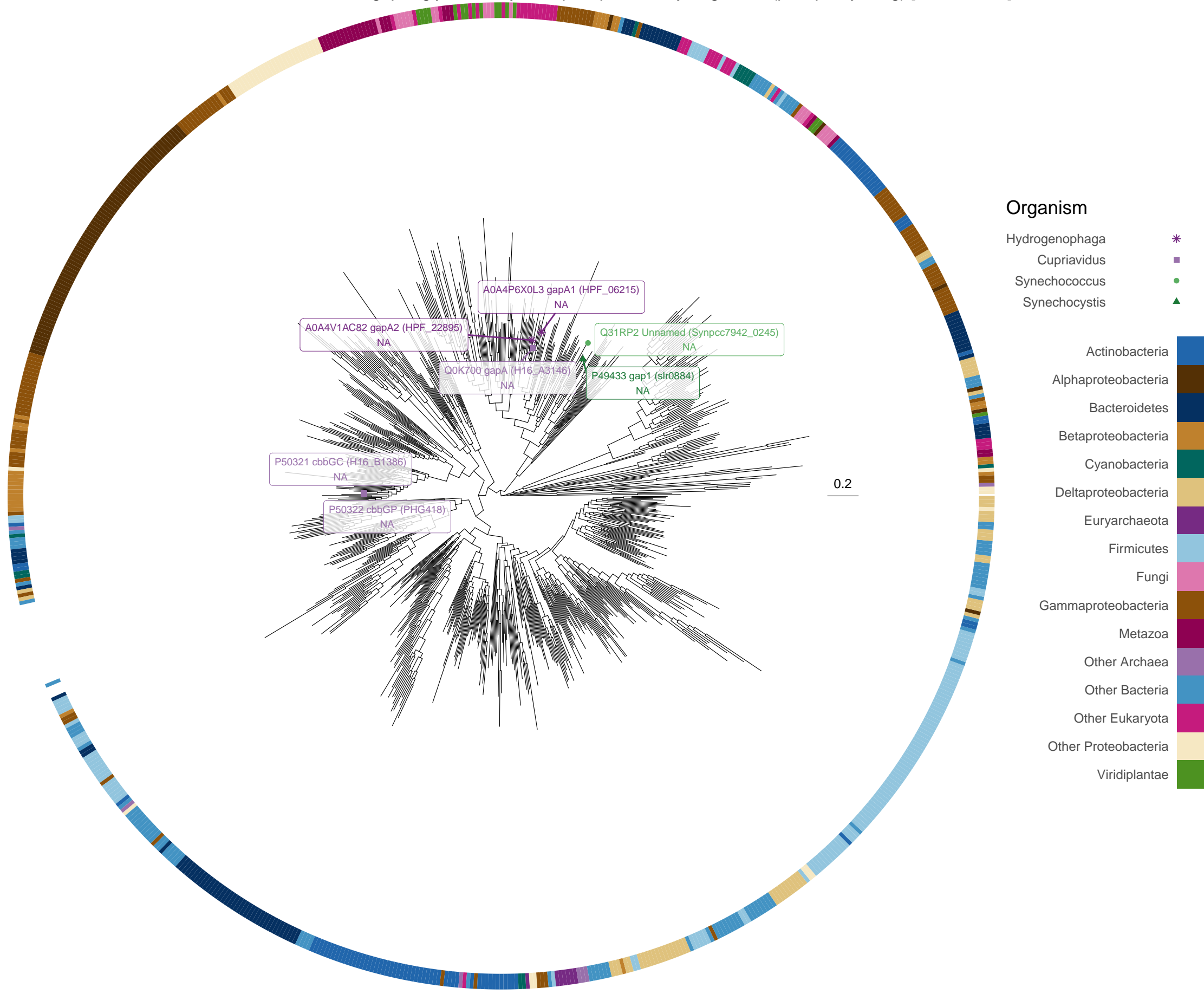
FBP-SBPase_II_glpX
K11532 glpX-SEBP; fructose-1,6-bisphosphatase II / sedoheptulose-1,7-bisphosphatase [EC:3.1.3.11 3.1.3.37]



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

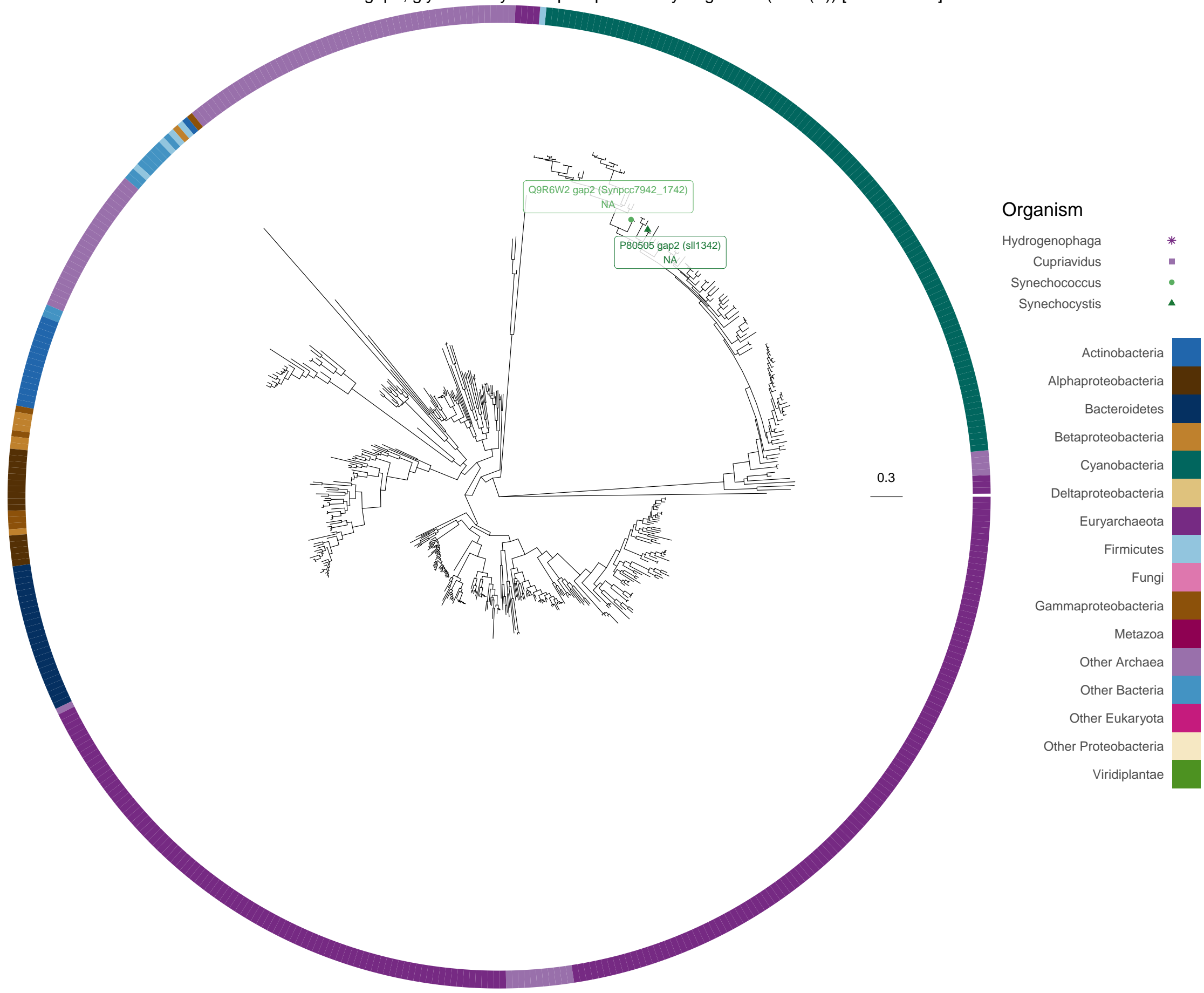


GAPDH
K00134 GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [EC:1.2.1.12]

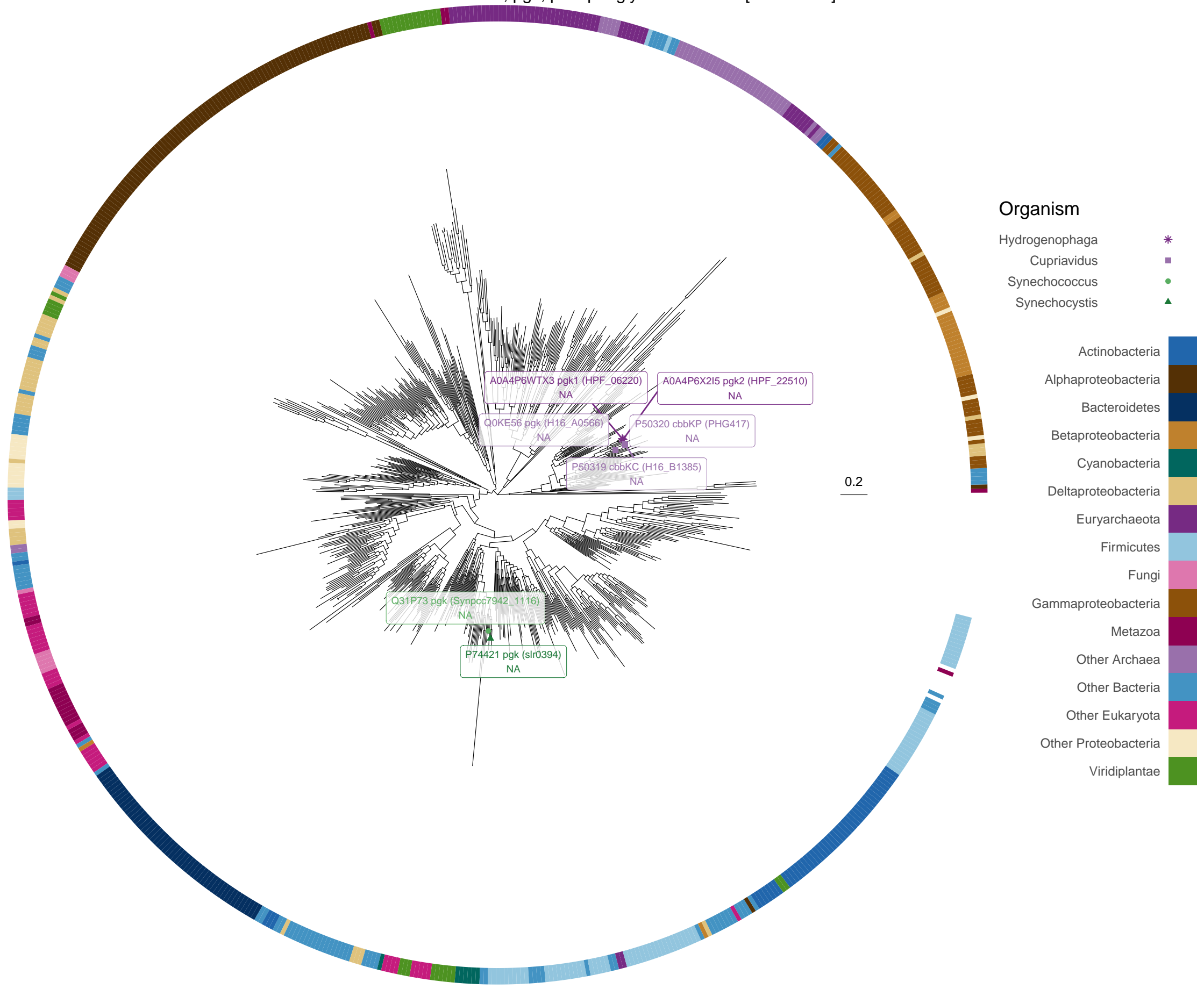


GAPDH2

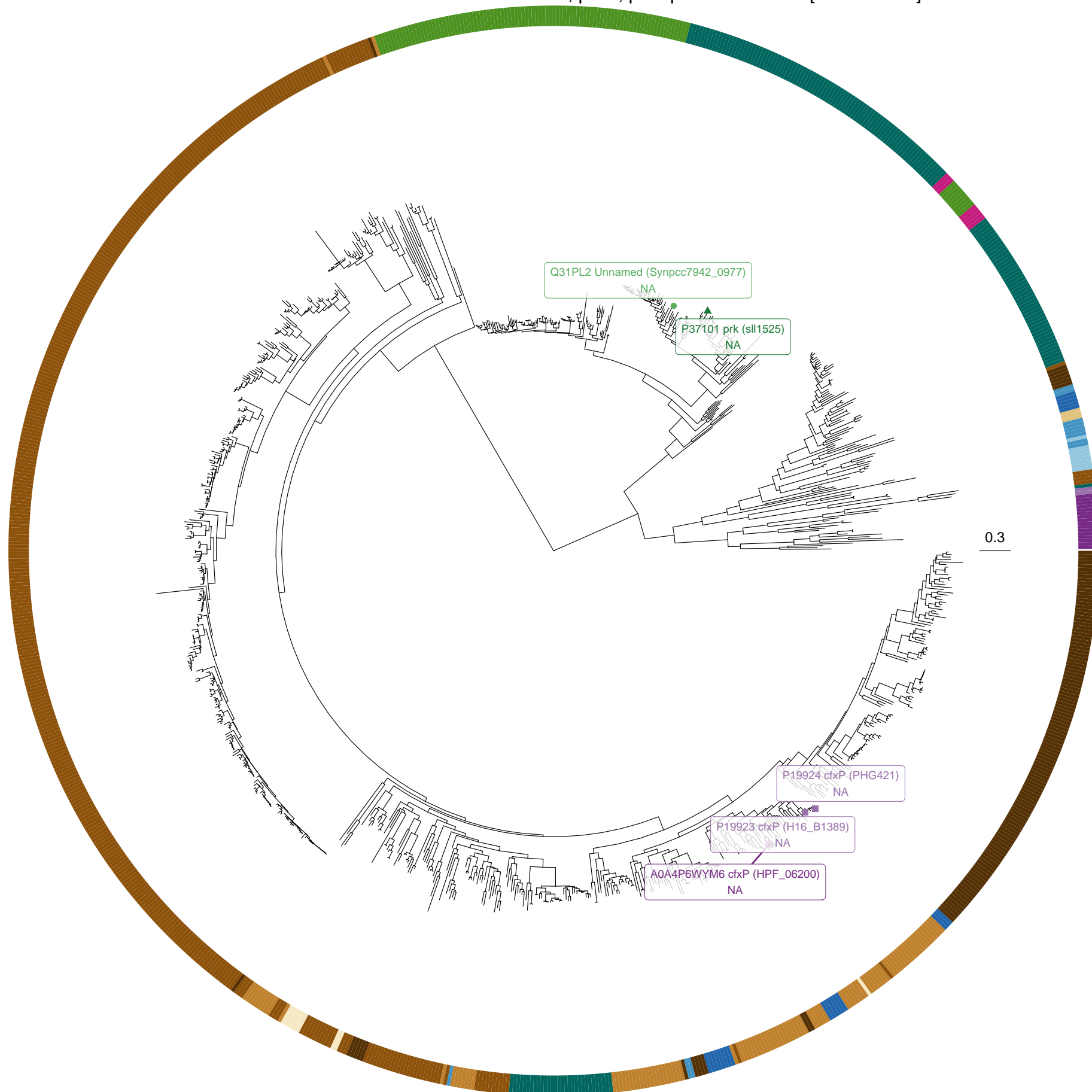
K00150 gap2; glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) [EC:1.2.1.59]



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



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

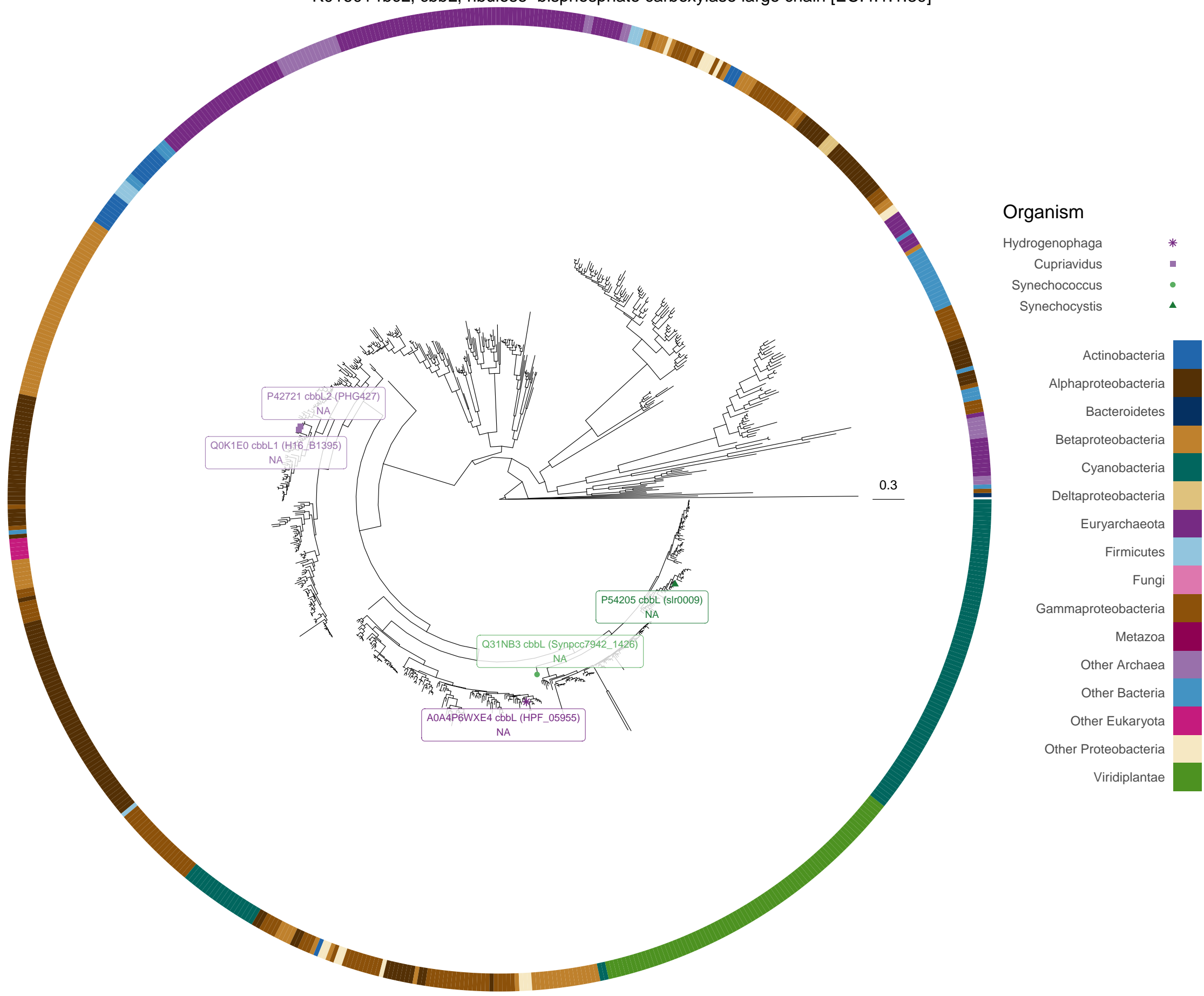


Organism

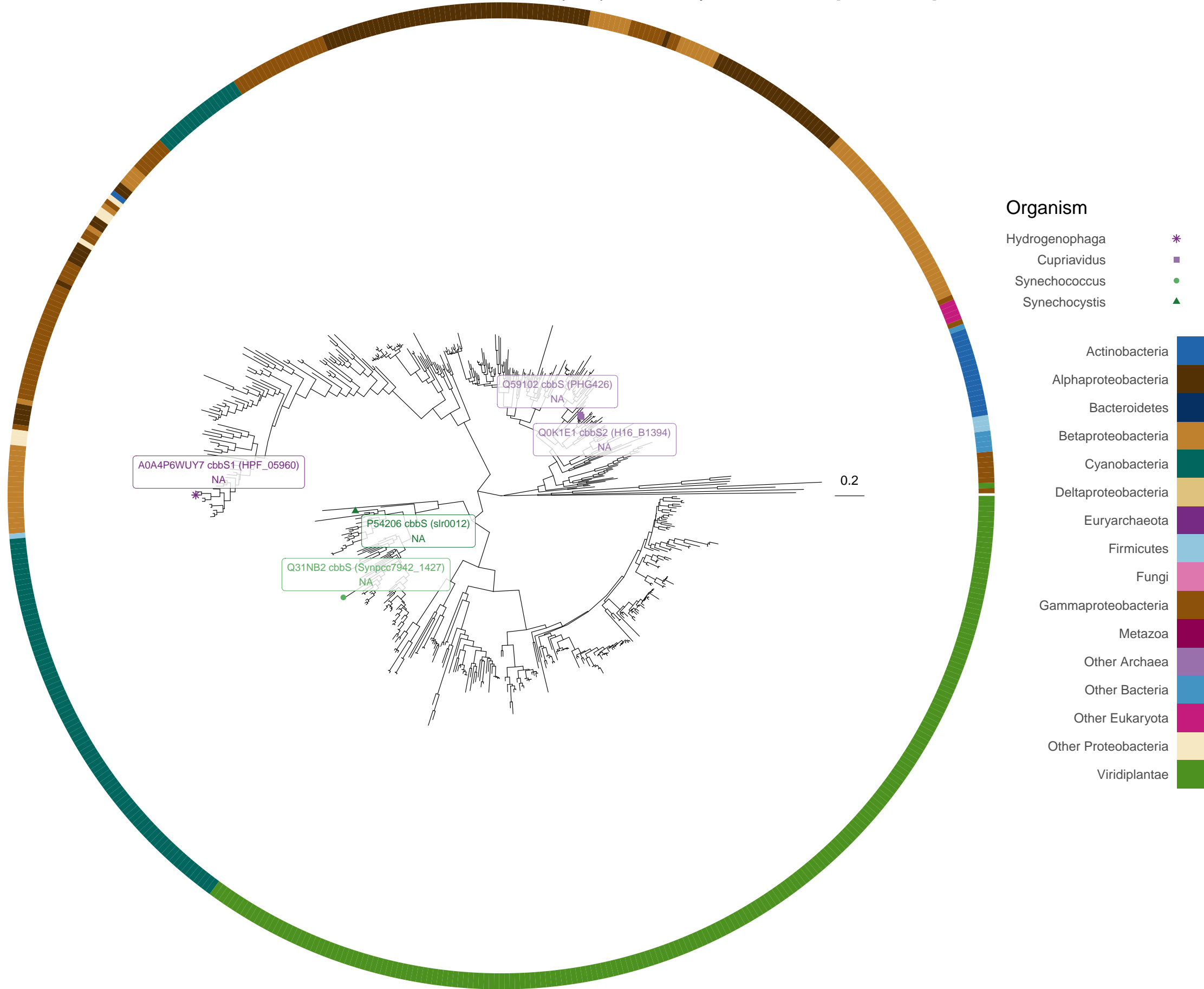
- Hydrogenophaga *
- Cupriavidus *
- Synechococcus •
- Synechocystis ▲

- Actinobacteria
- Alphaproteobacteria
- Bacteroidetes
- Betaproteobacteria
- Cyanobacteria
- Deltaproteobacteria
- Euryarchaeota
- Firmicutes
- Fungi
- Gamma proteobacteria
- Metazoa
- Other Archaea
- Other Bacteria
- Other Eukaryota
- Other Proteobacteria
- Viridiplantae

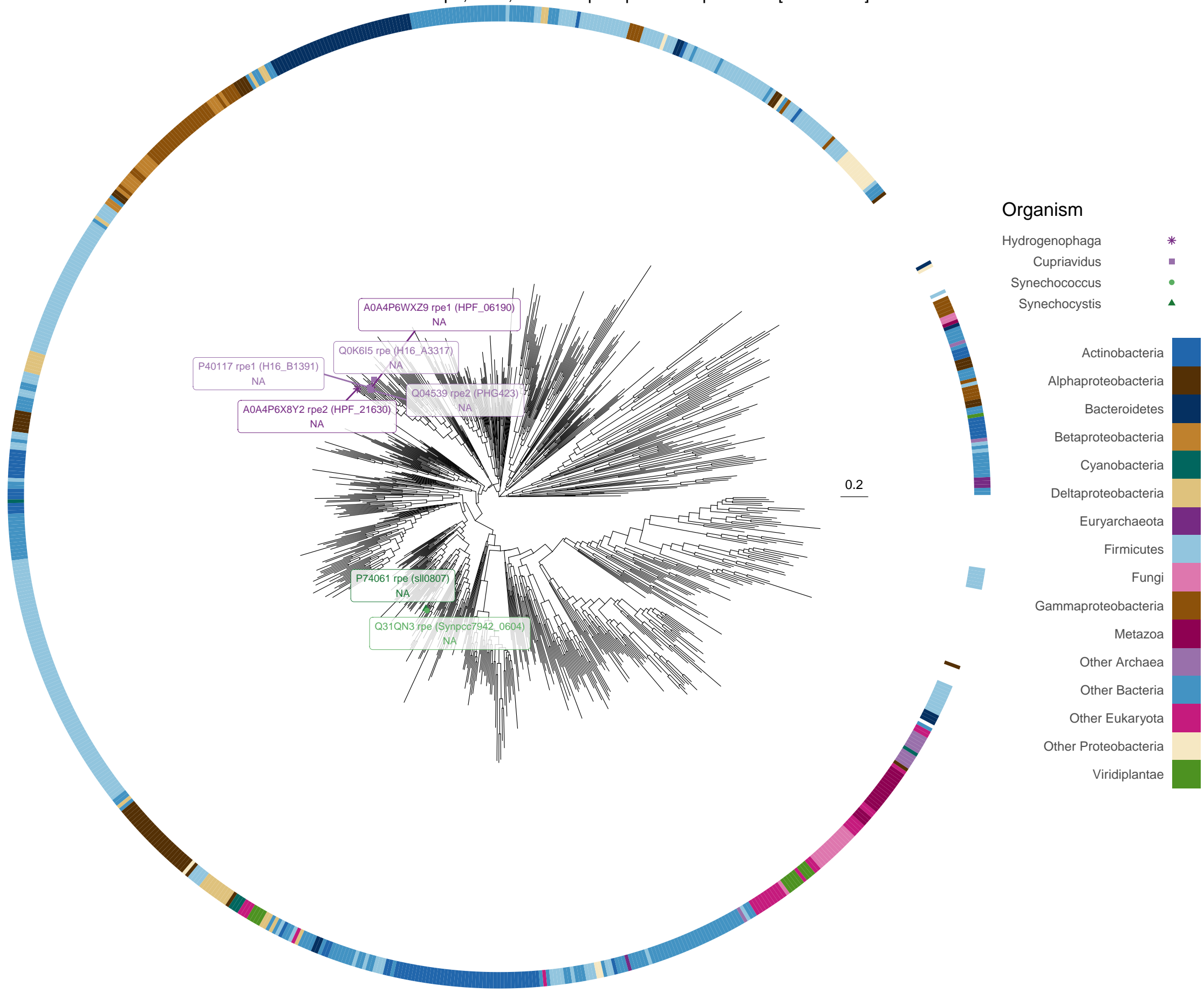
rbcL
K01601 rbcL, cbbL; ribulose-bisphosphate carboxylase large chain [EC:4.1.1.39]



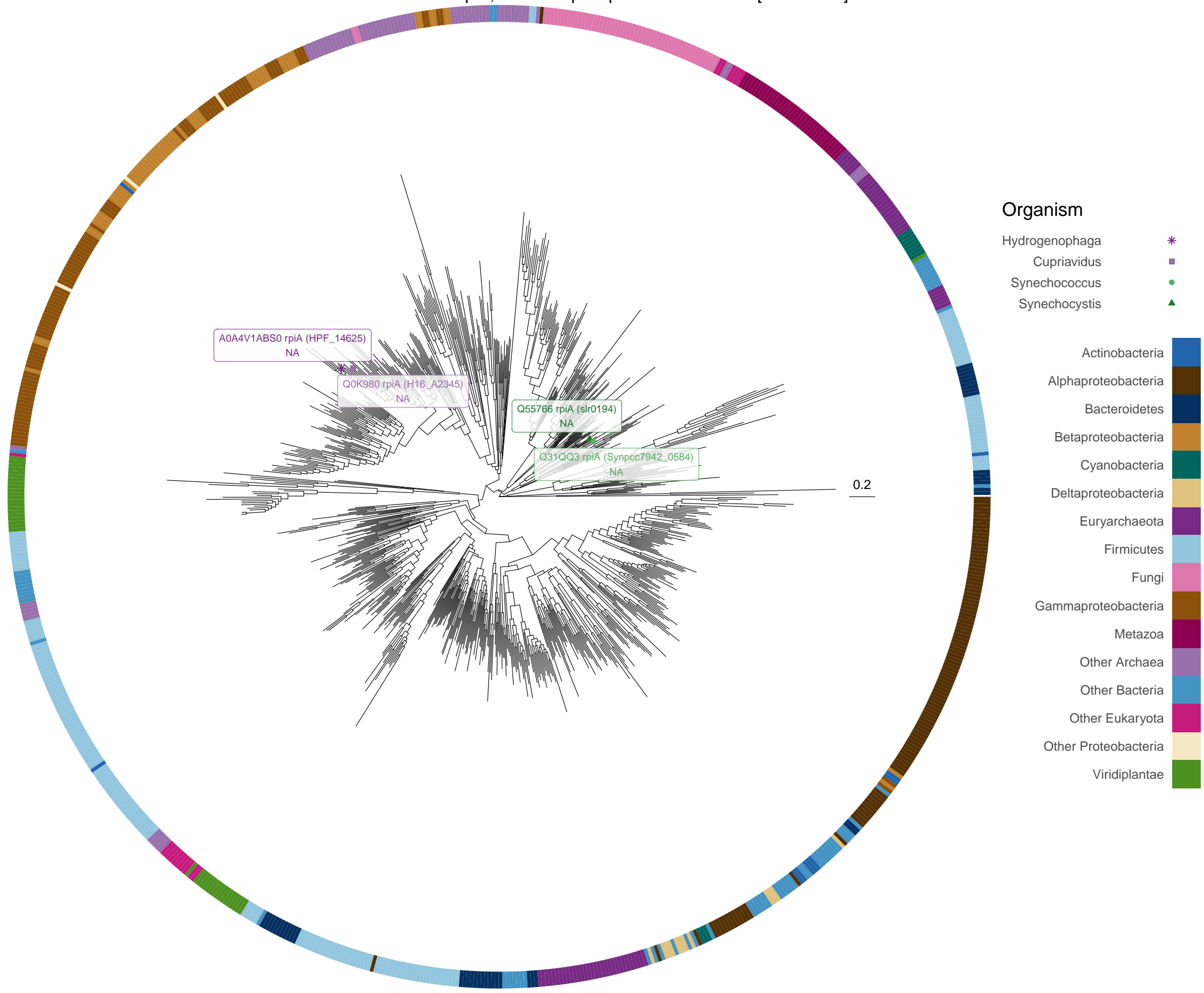
rbcS
K01602 rbcS, cbbS; ribulose-bisphosphate carboxylase small chain [EC:4.1.1.39]



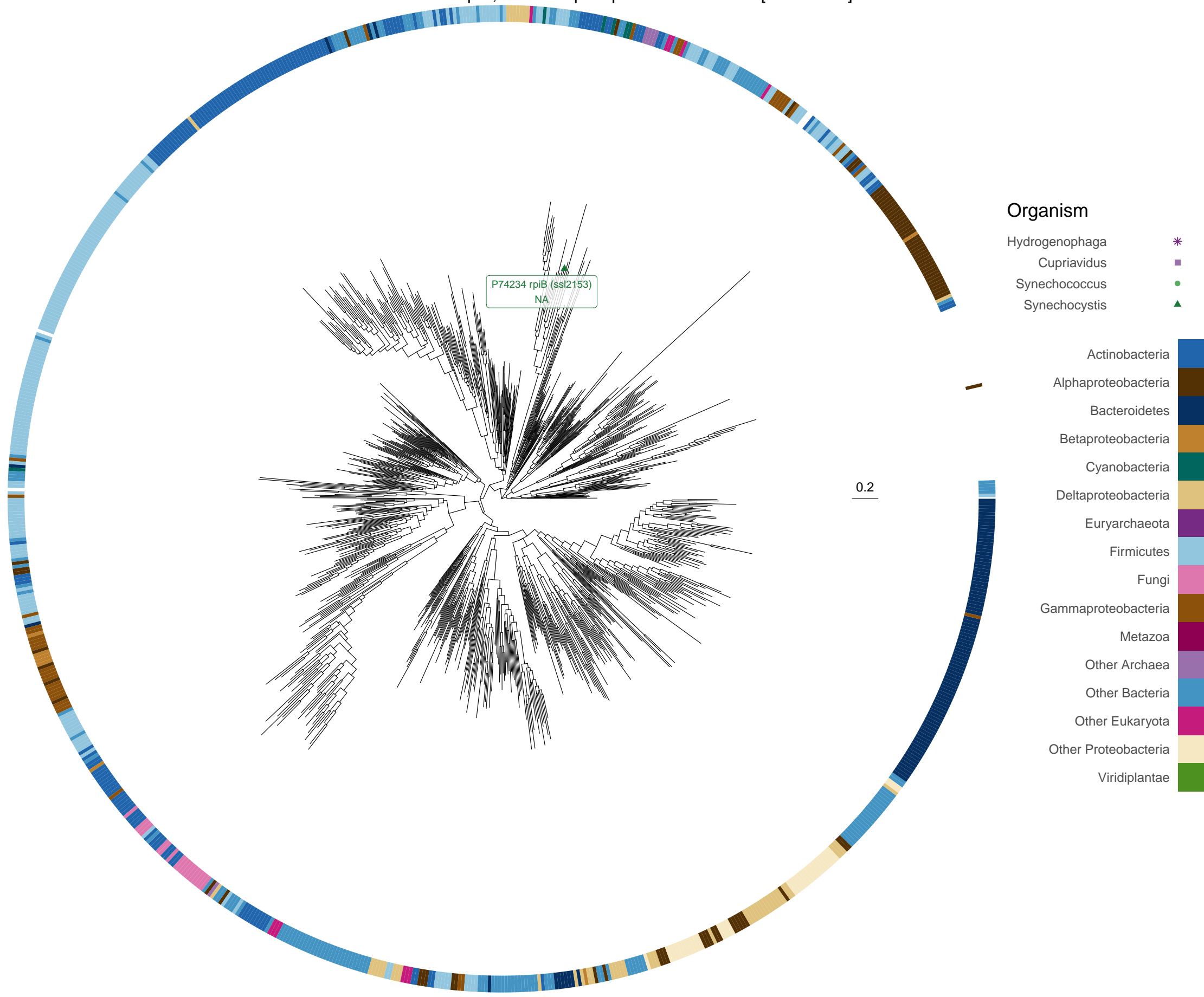
RPE
K01783 rpe, RPE; ribulose-phosphate 3-epimerase [EC:5.1.3.1]



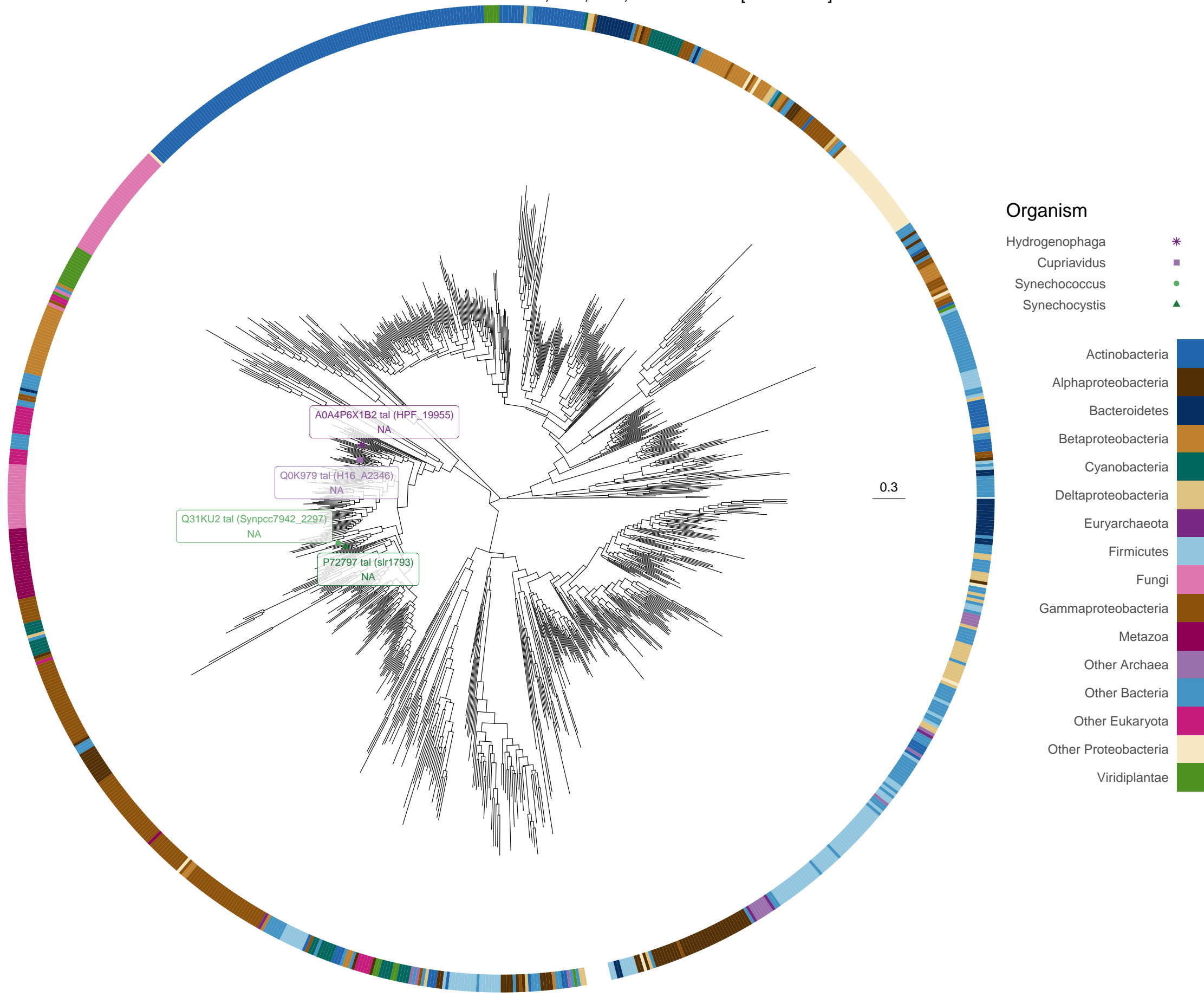
rpiA
K01807 rpiA; ribose 5-phosphate isomerase A [EC:5.3.1.6]



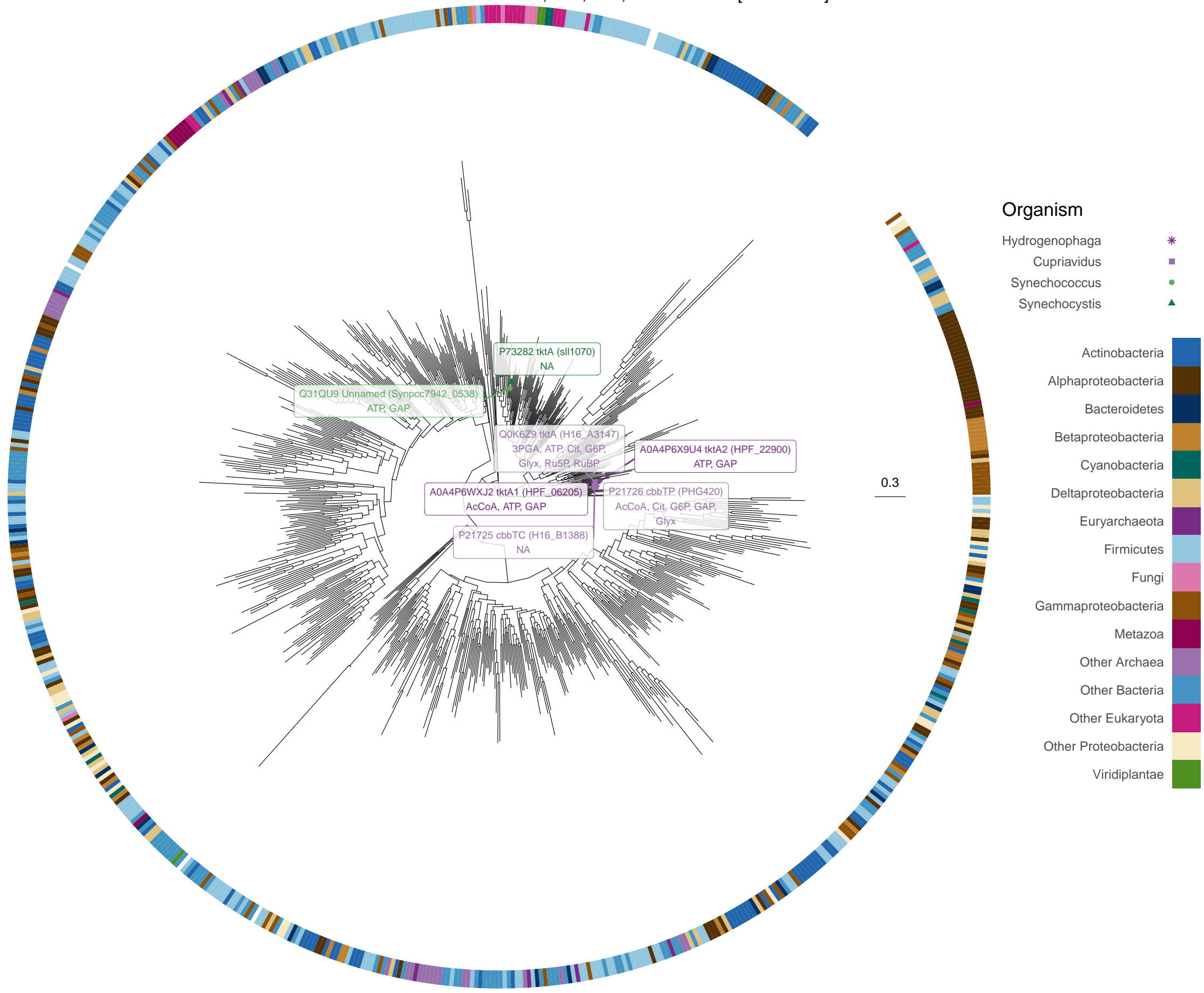
rpiB
K01808 rpiB; ribose 5-phosphate isomerase B [EC:5.3.1.6]



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



TKT
K00615 E2.2.1.1, tktA, tktB; transketolase [EC:2.2.1.1]



TPI
K01803 TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]

