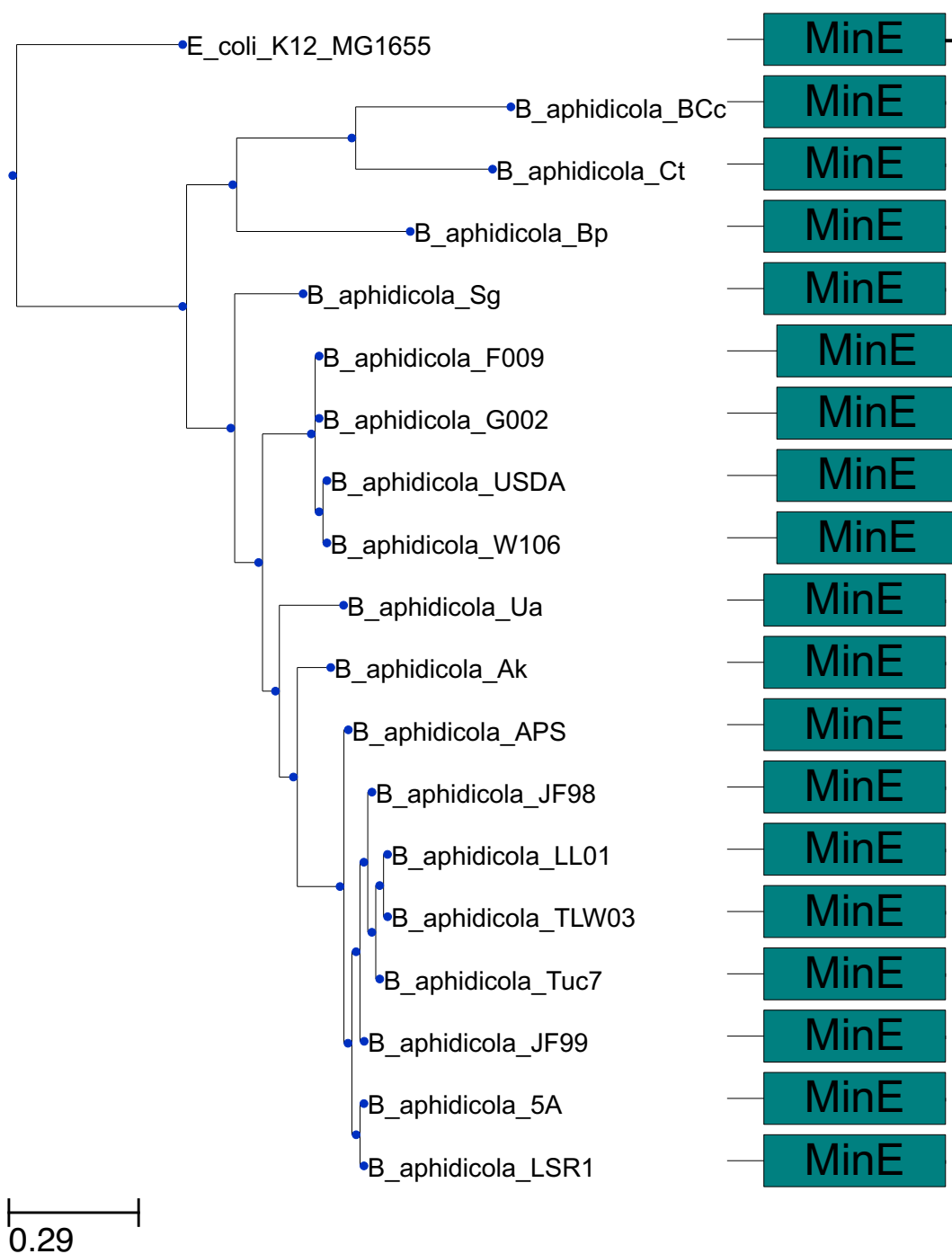
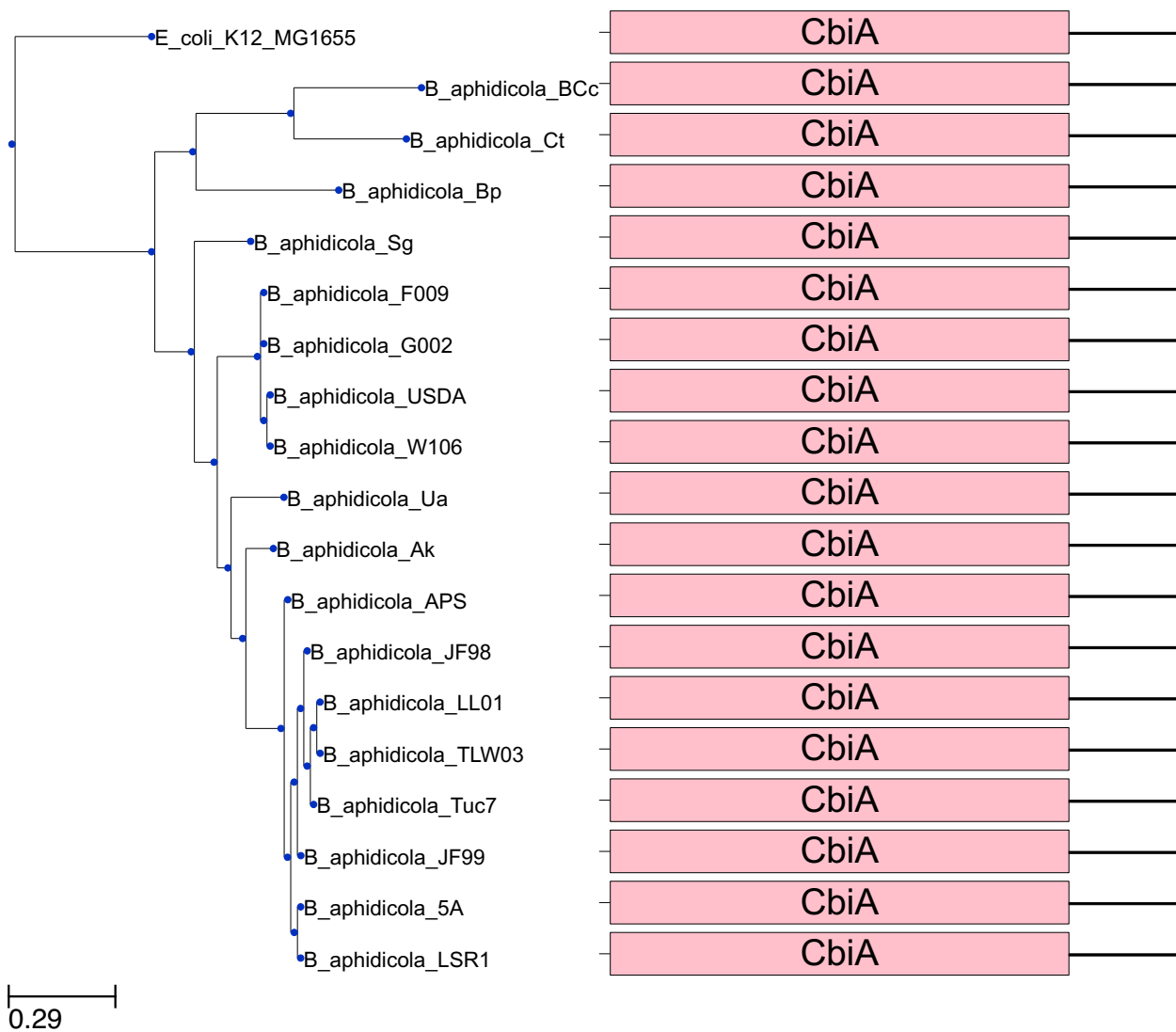


Phylogenetic tree of the *Buchnera*. The tree was reconstructed with MrBayes (see methods). Node numbers indicate posterior probabilities.



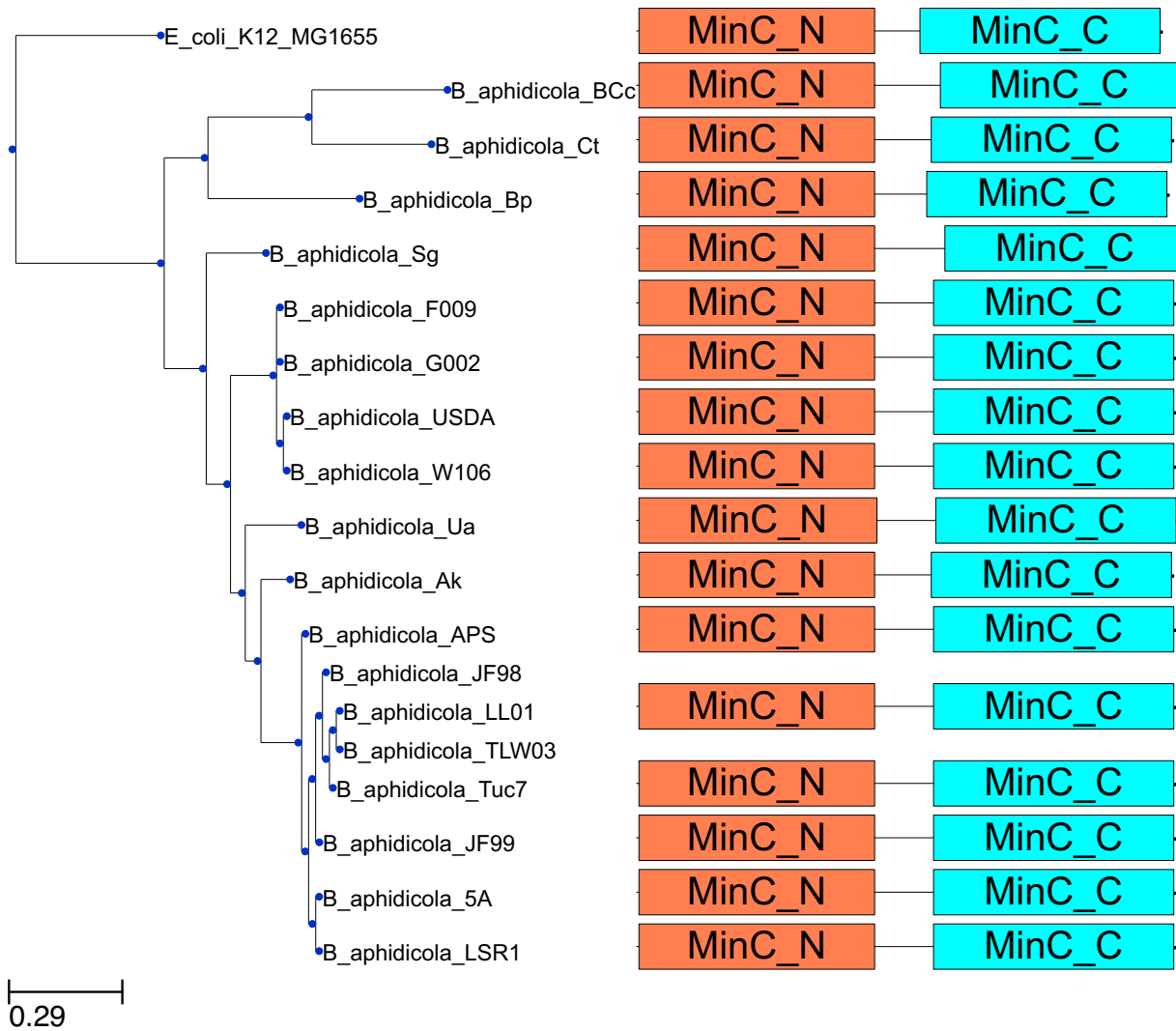
minE
NP_415692.1
cell division topological specificity factor.



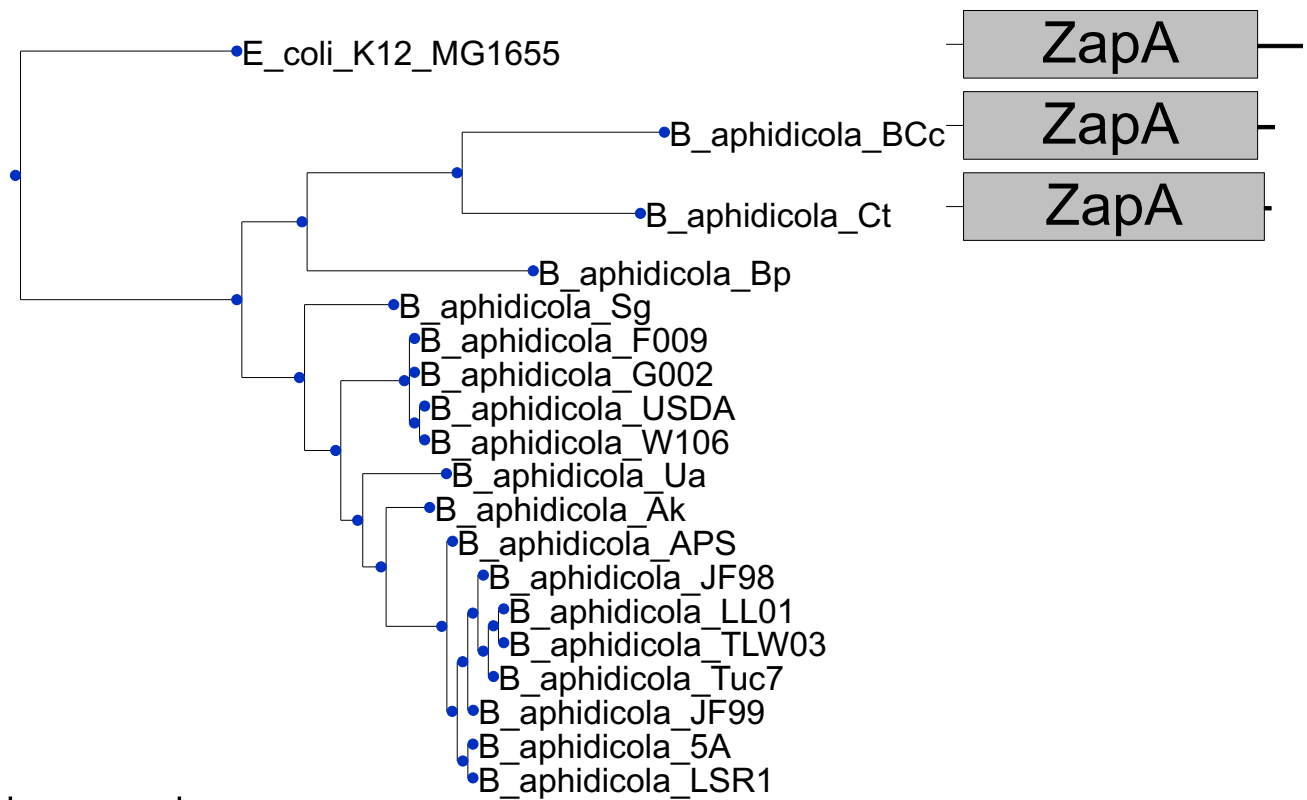
minD

NP_415693.1

inhibitor of FtsZ ring polymerization; chromosome-membrane tethering protein; membrane ATPase of the MinCDEE system

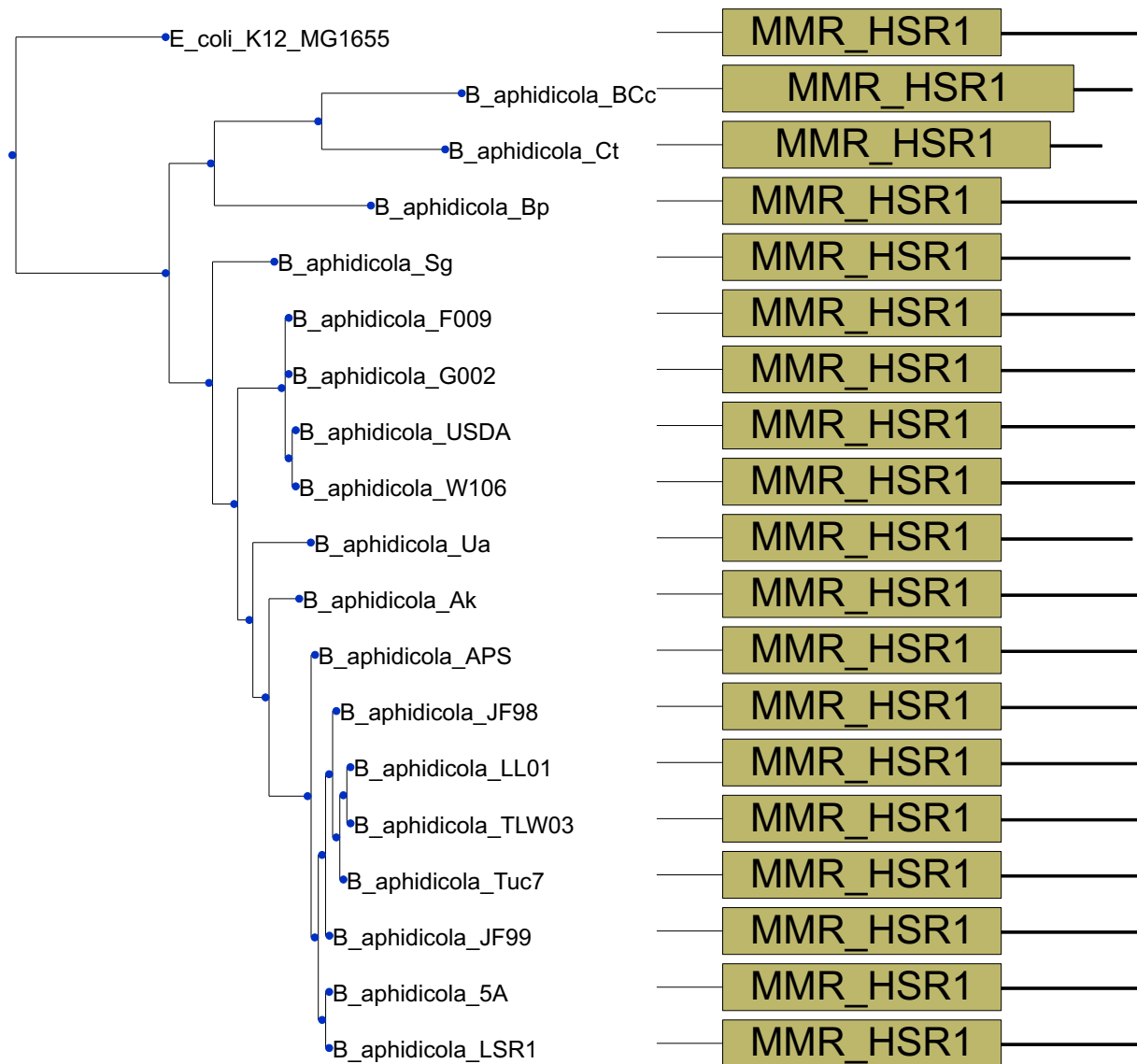


minC
NP_415694.1
inhibitor of FtsZ ring polymerization



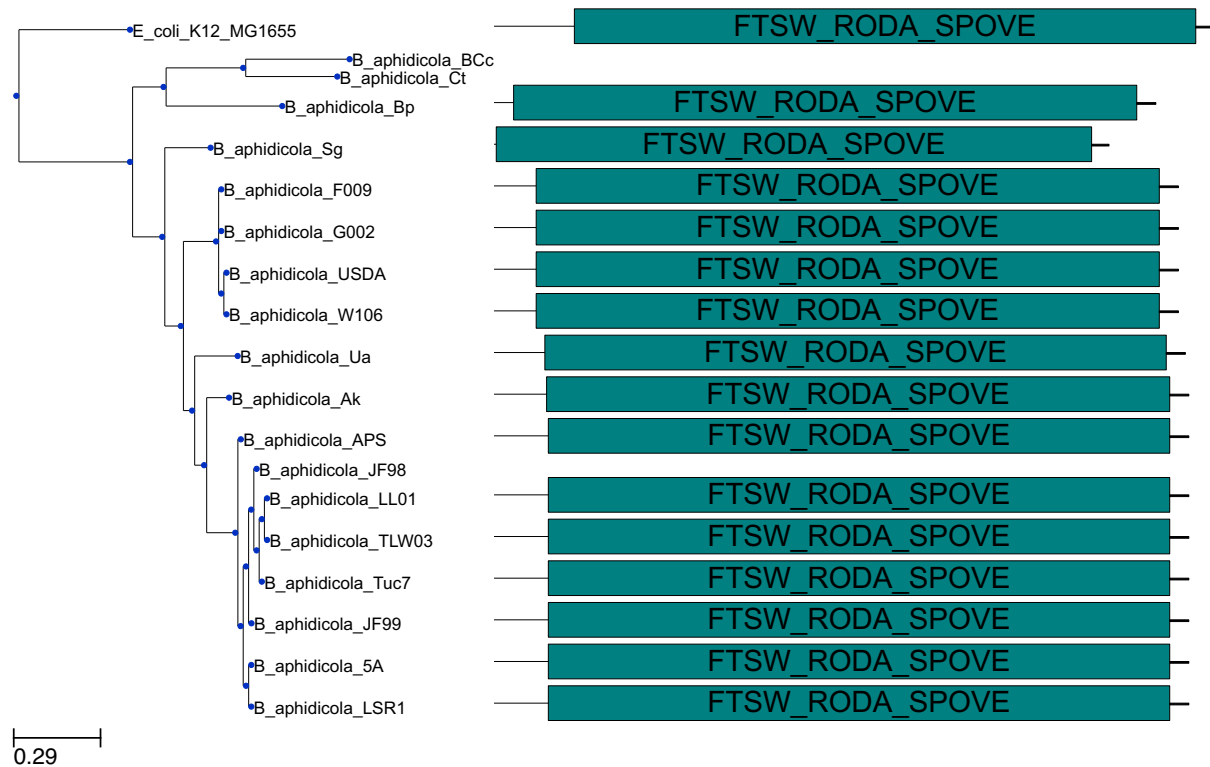
0.29

zapA
NP_417386.1
FtsZ stabilizer



0.29

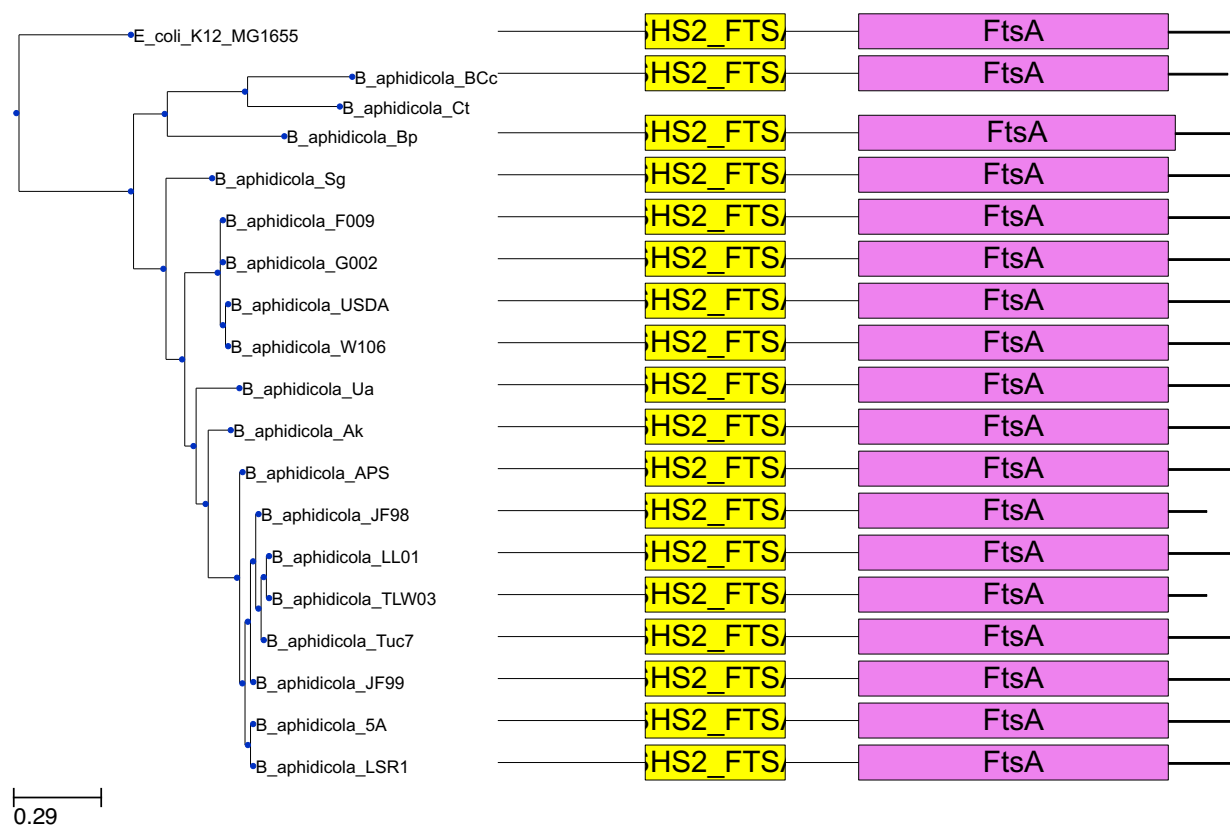
yihA
NP_418301.3
cell division GTP-binding protein



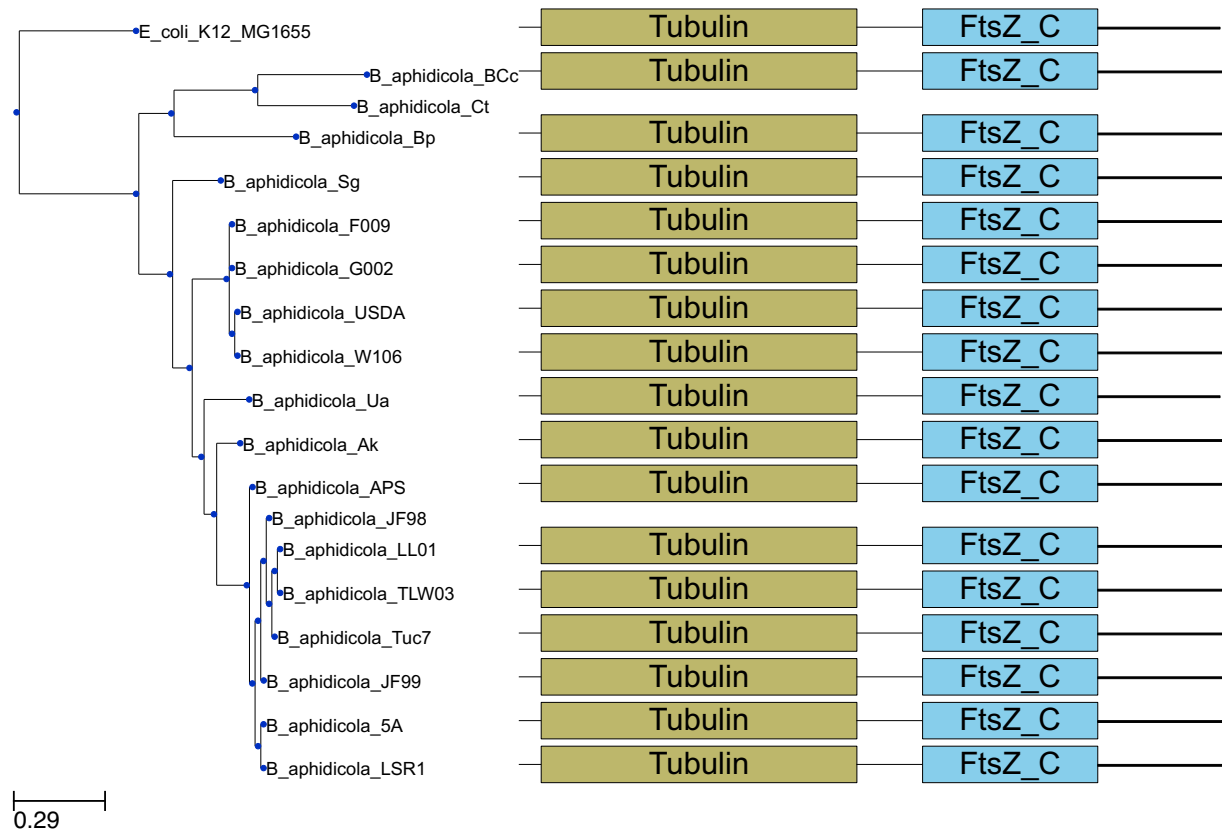
ftsW

NP_414631.1

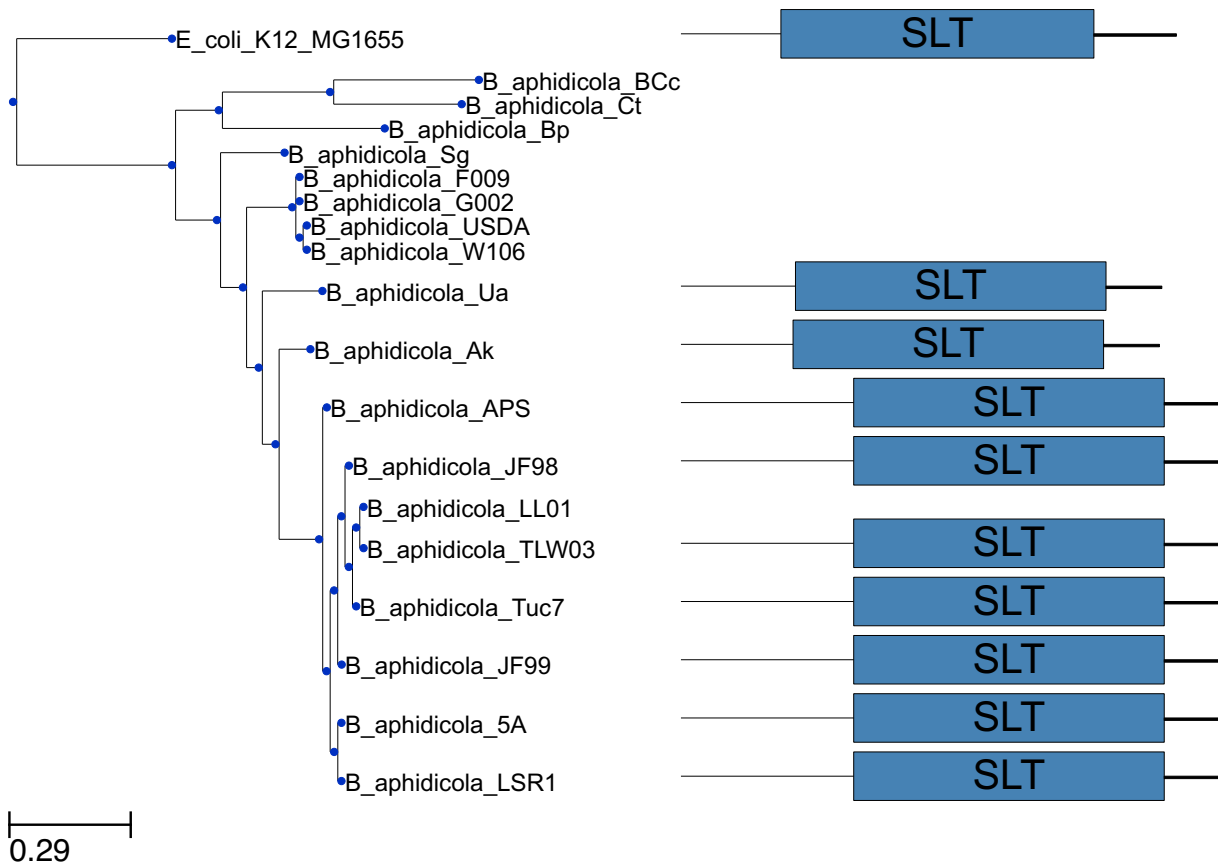
putative lipid II flippase; integral membrane protein; FtsZ ring stabilizer



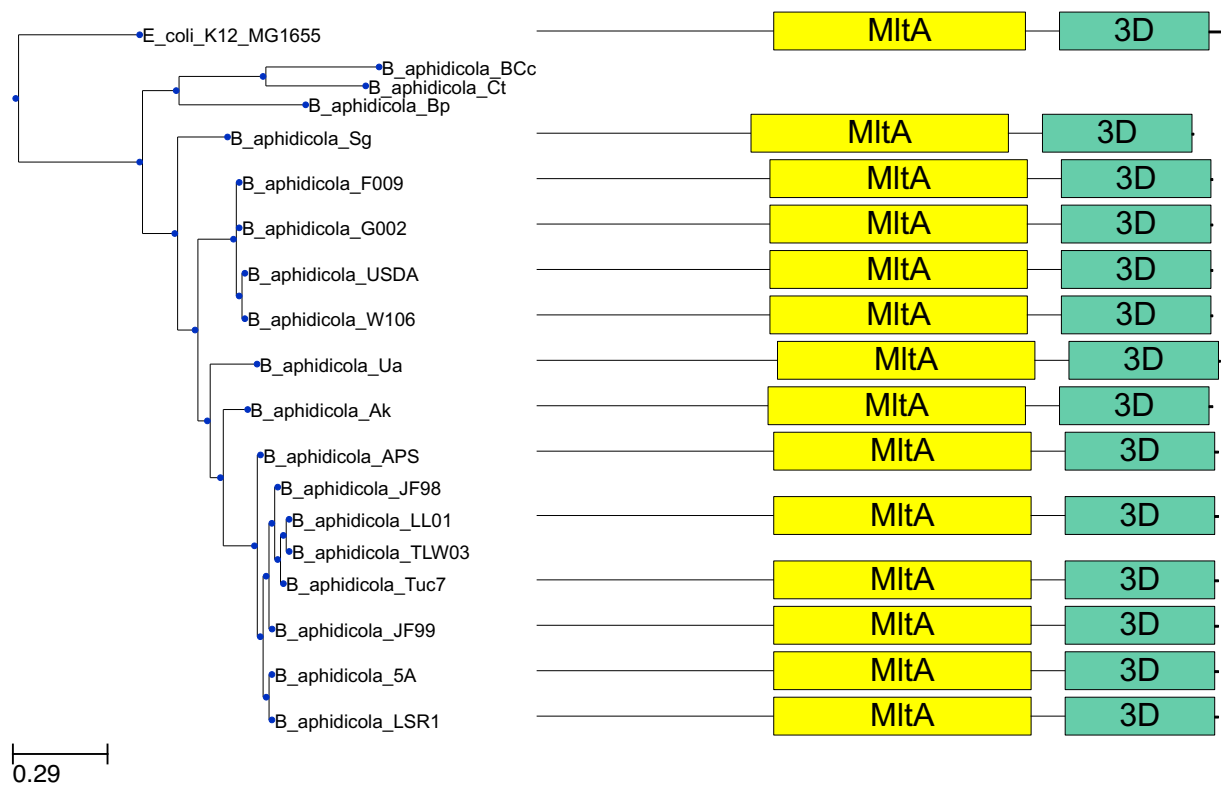
ftsA
NP_414636.1
ATP-binding cell division FtsK recruitment protein



ftsZ
NP_414637.1
GTP-binding tubulin-like cell division protein



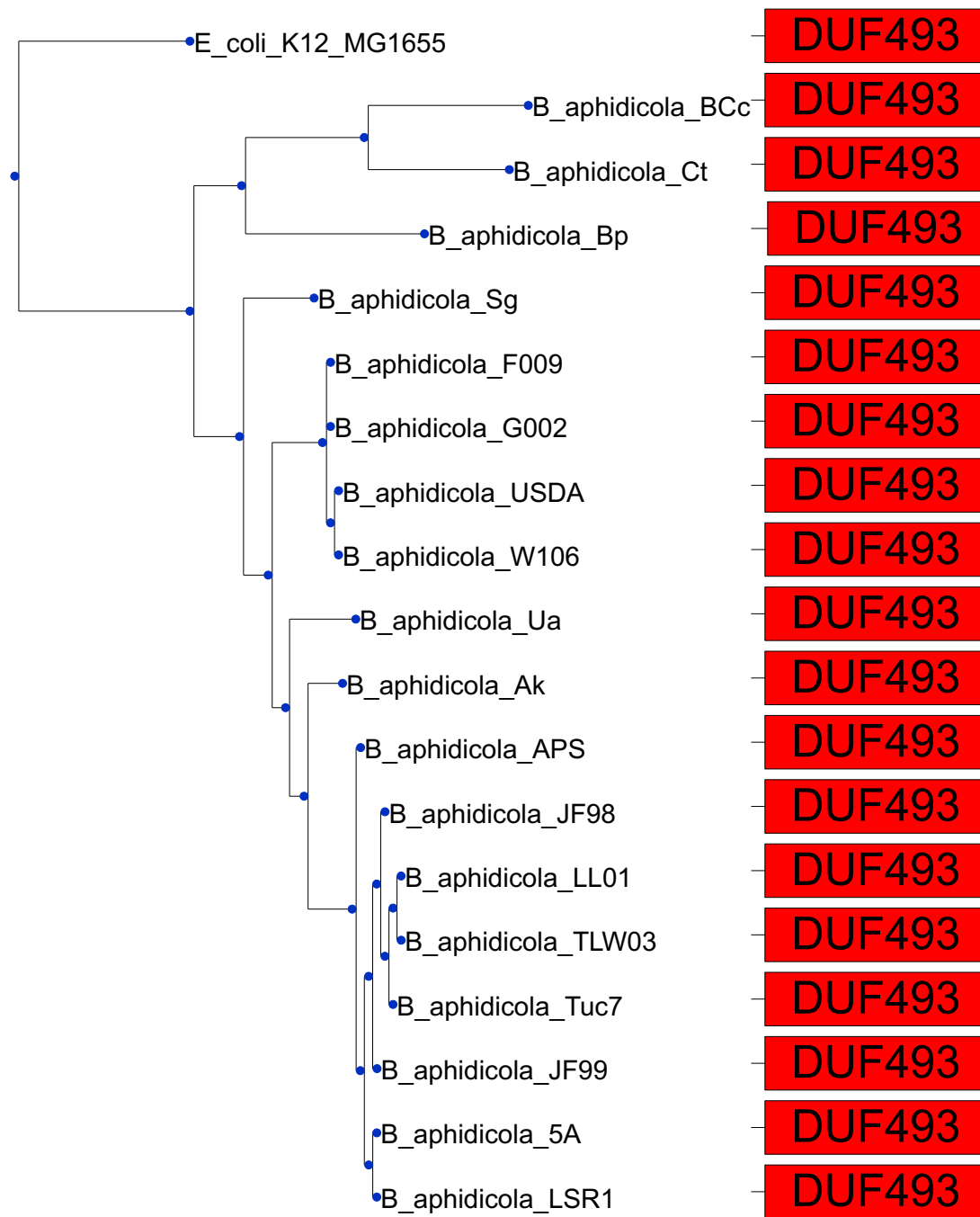
emtA
NP_415711.2
lytic murein endotransglycosylase E



mltA

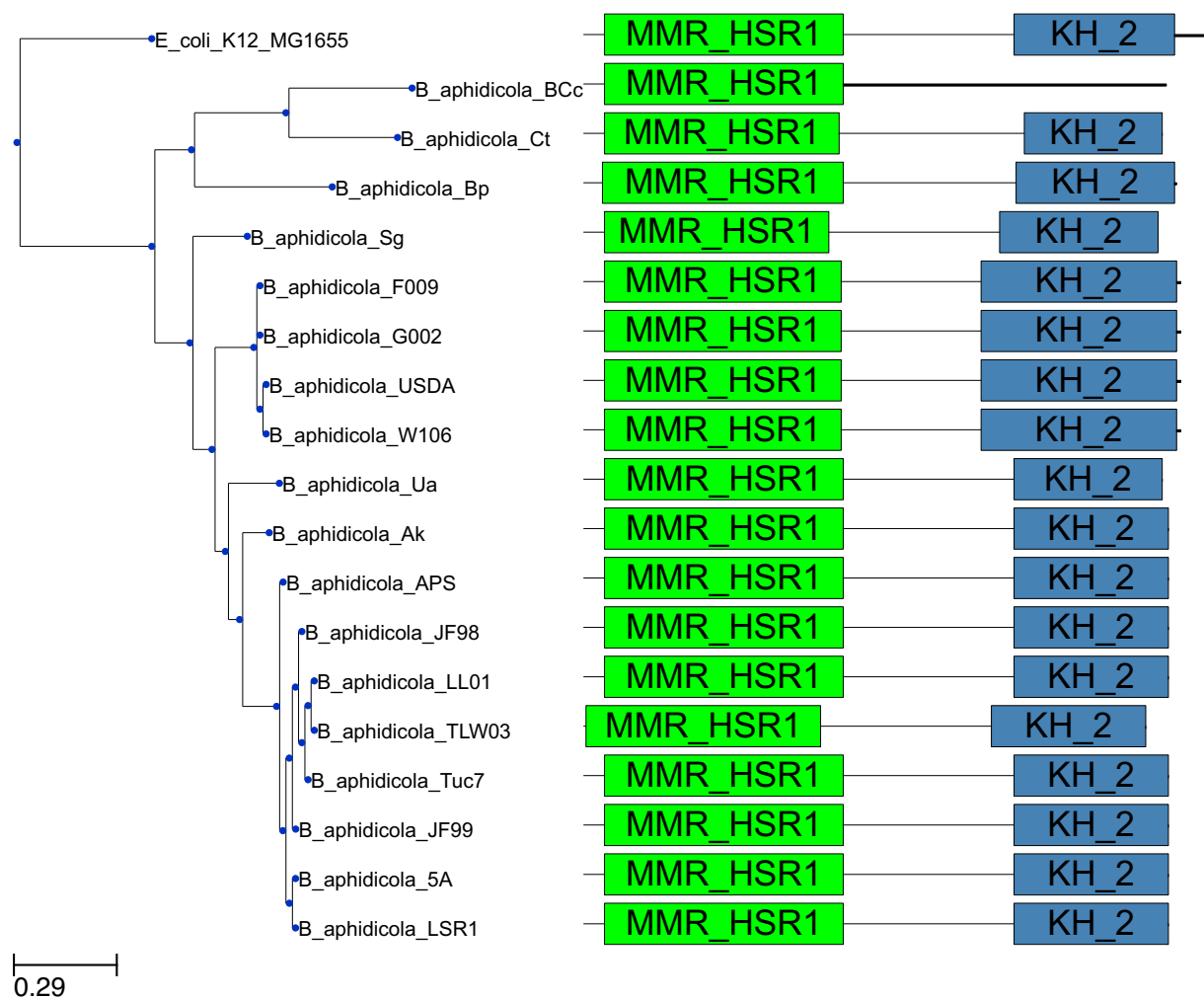
NP_417293.1

membrane-bound lytic murein transglycosylase A

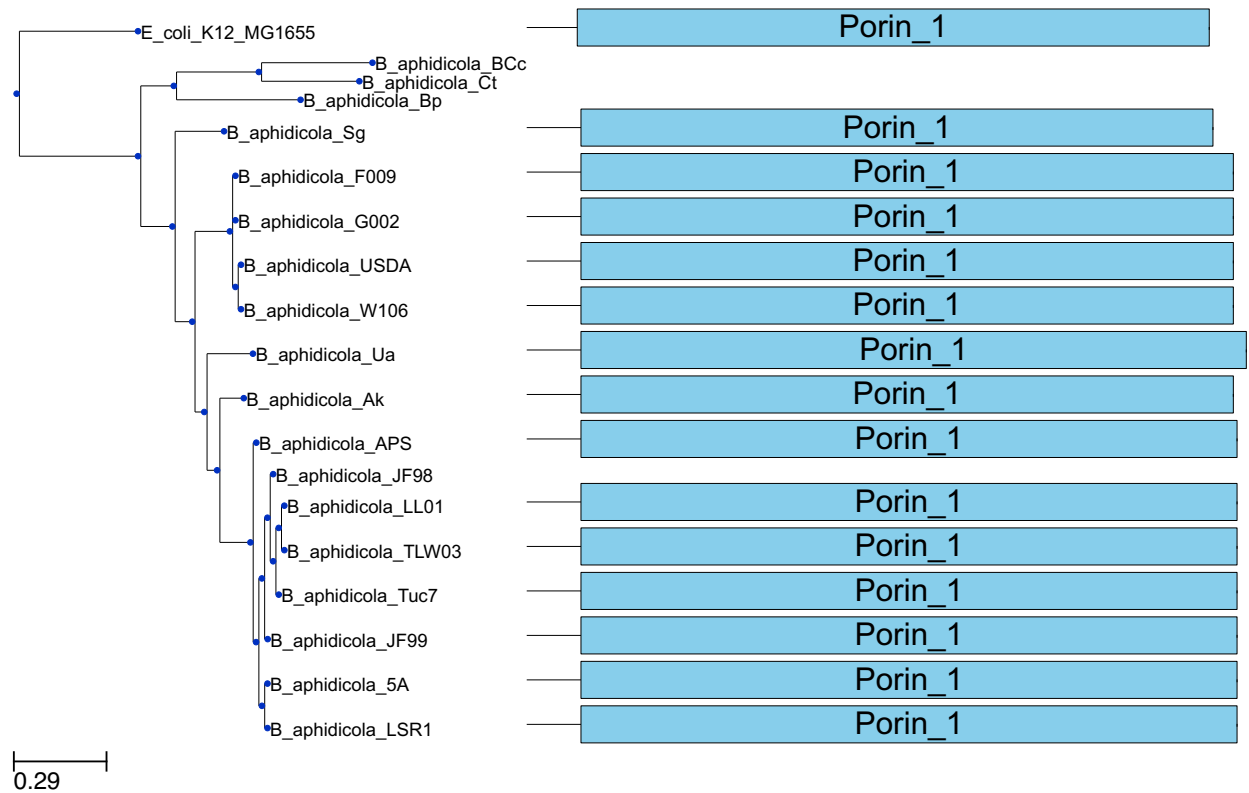


0.29

ybeD
NP_415164.1
UPF0250 family protein



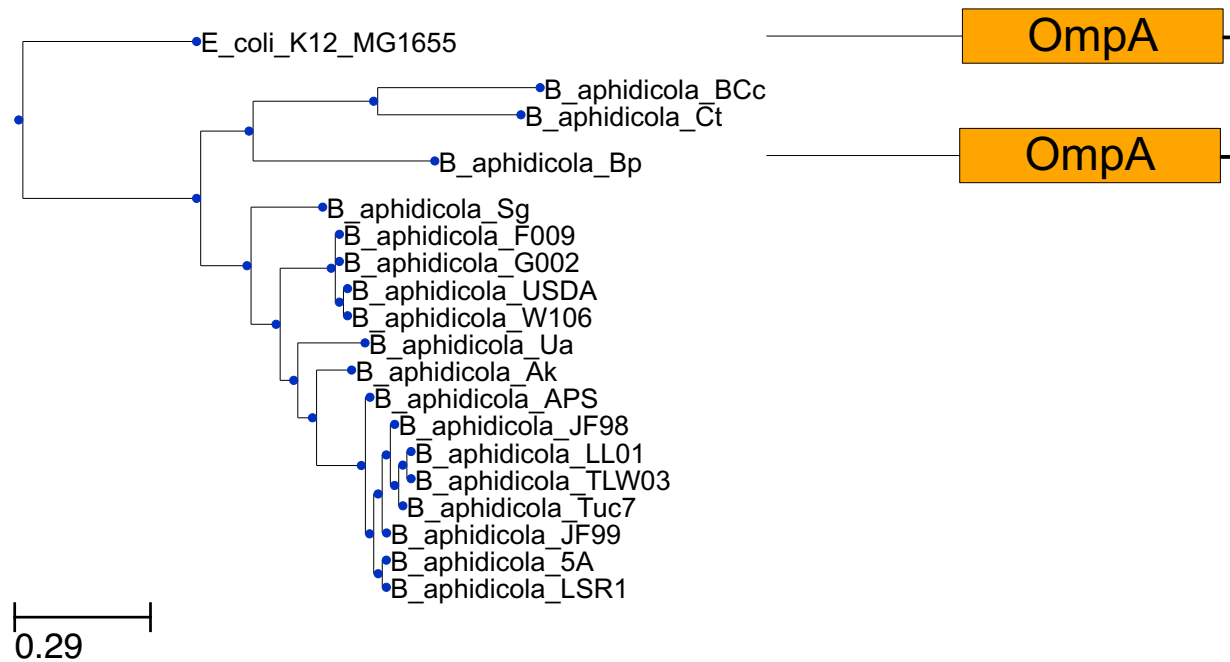
era
NP_417061.1
membrane-associated, 16S rRNA-binding GTPase



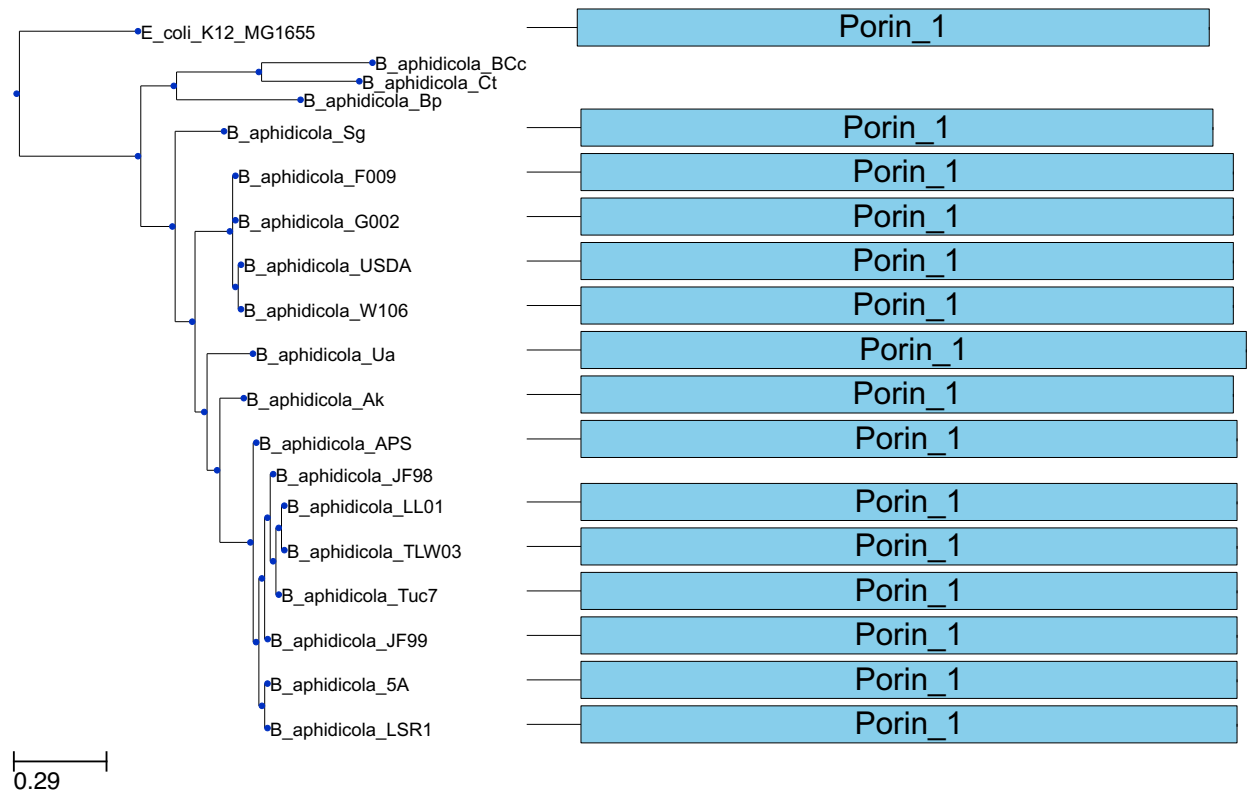
phoE

NP_414776.1

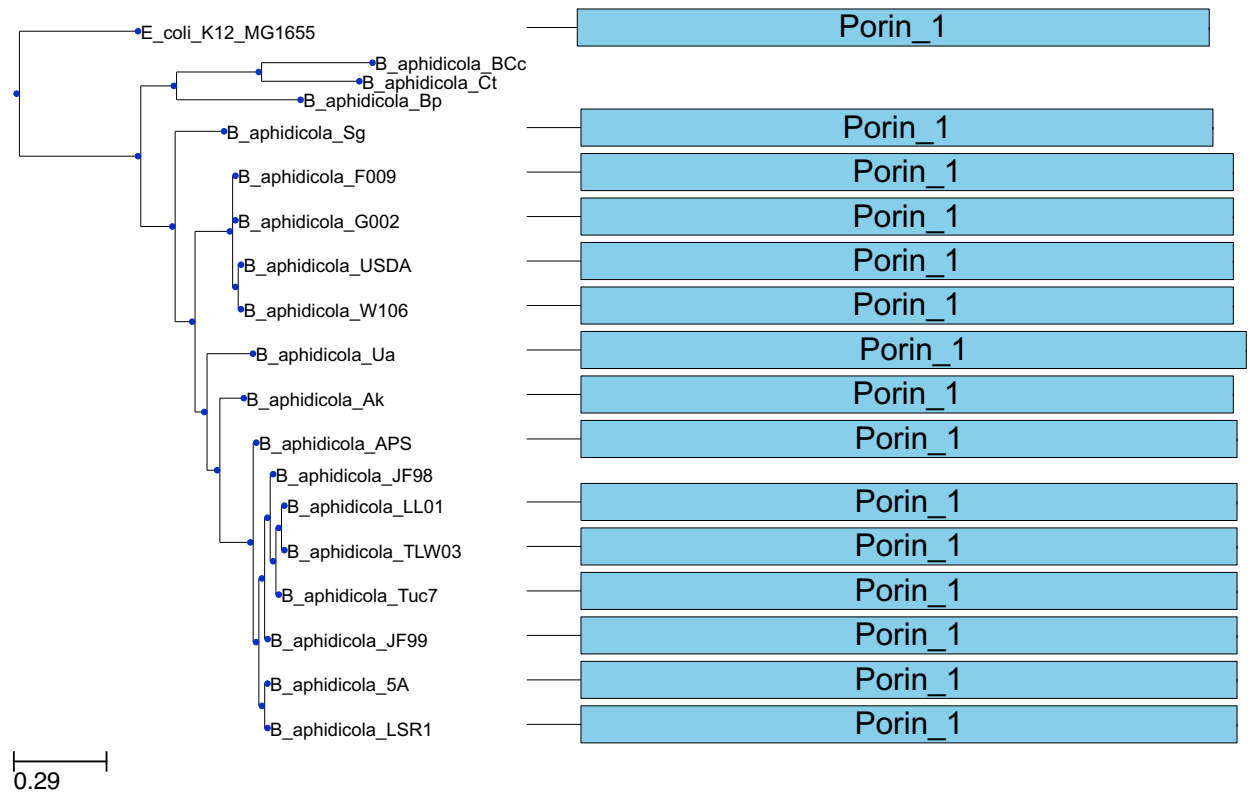
outer membrane phosphoporin protein E



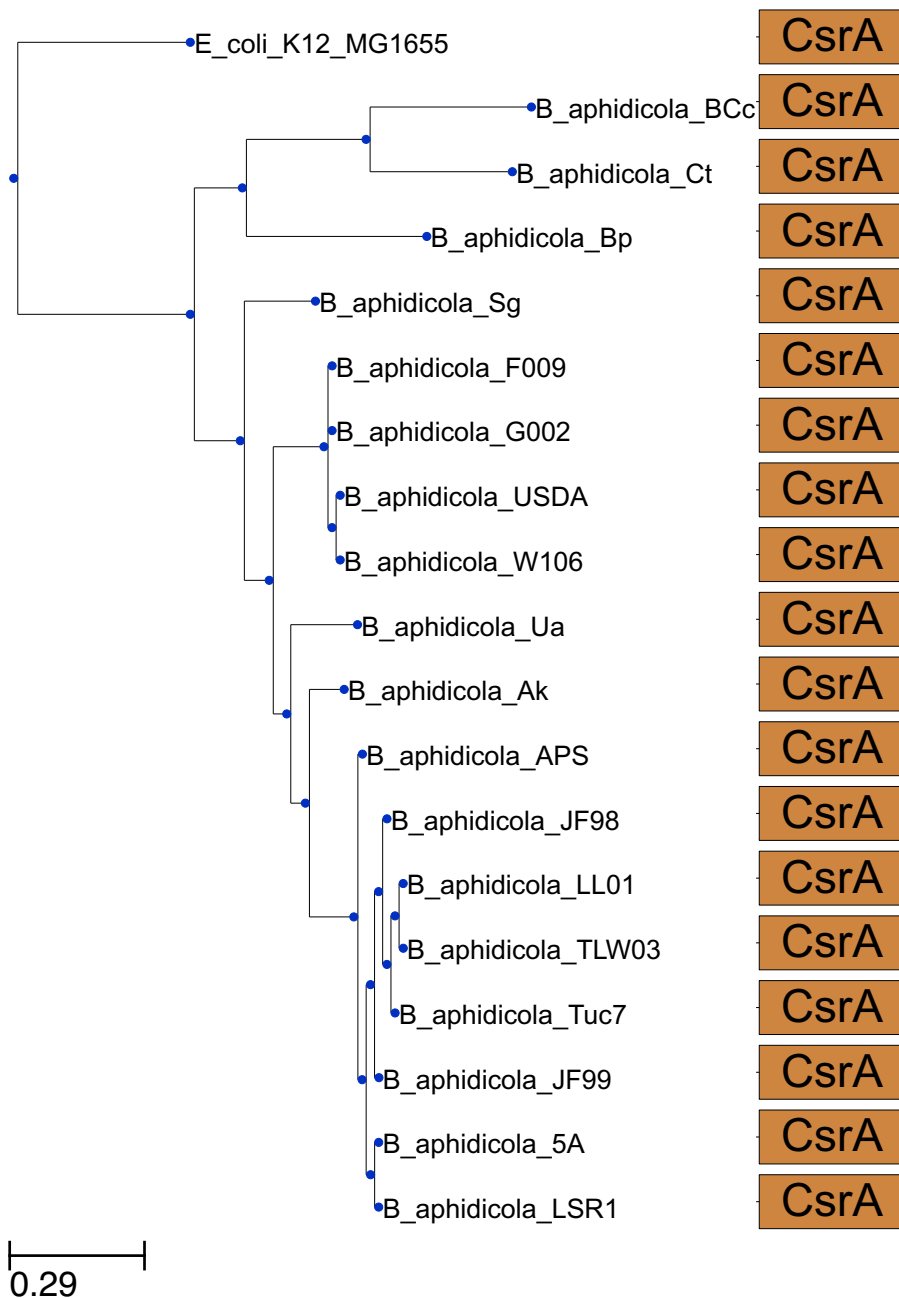
pal
 NP_415269.1
 peptidoglycan-associated outer membrane lipoprotein



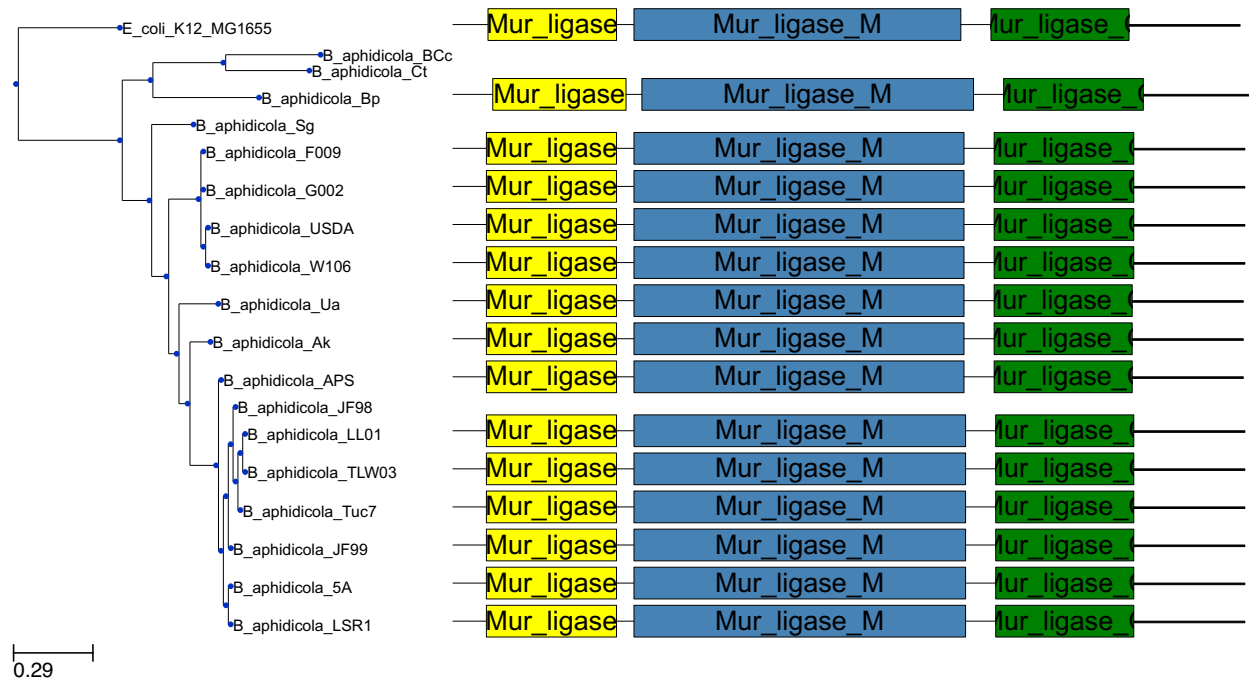
ompF
 NP_415449.1
 outer membrane porin 1a (Ia;b;F)



ompC
NP_416719.1
outer membrane porin protein C



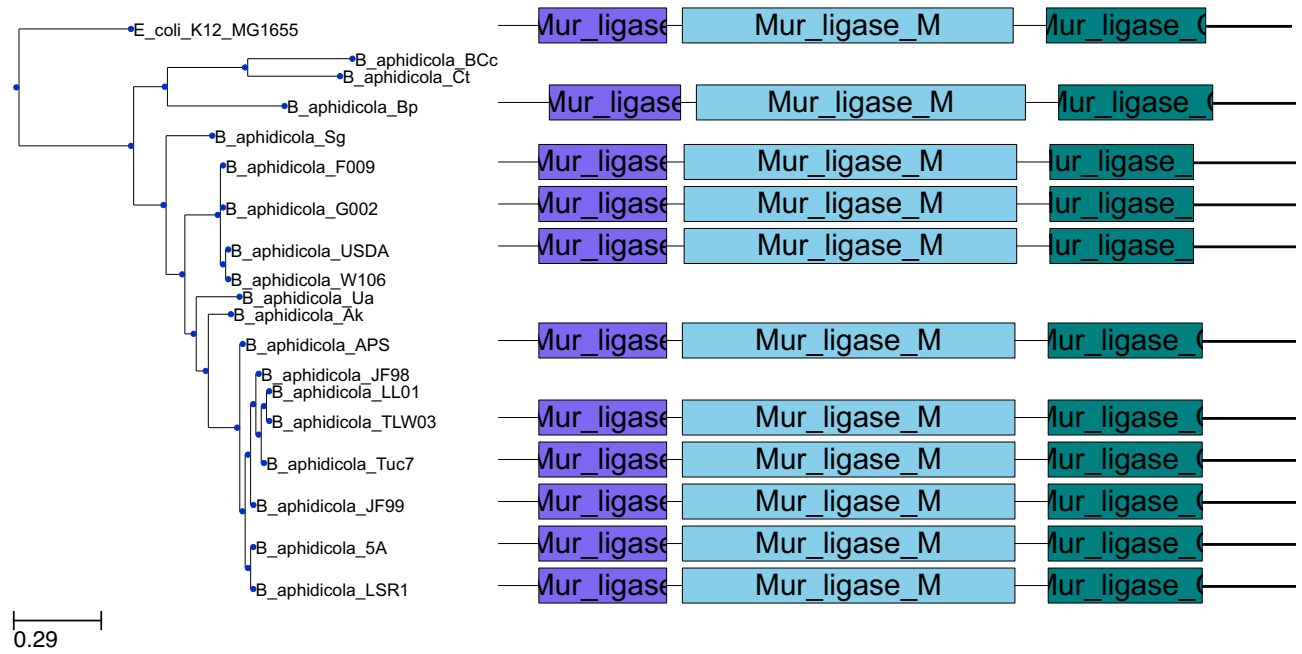
csrA
NP_417176.1
pleiotropic regulatory protein for carbon source metabolism



murE

NP_414627.1

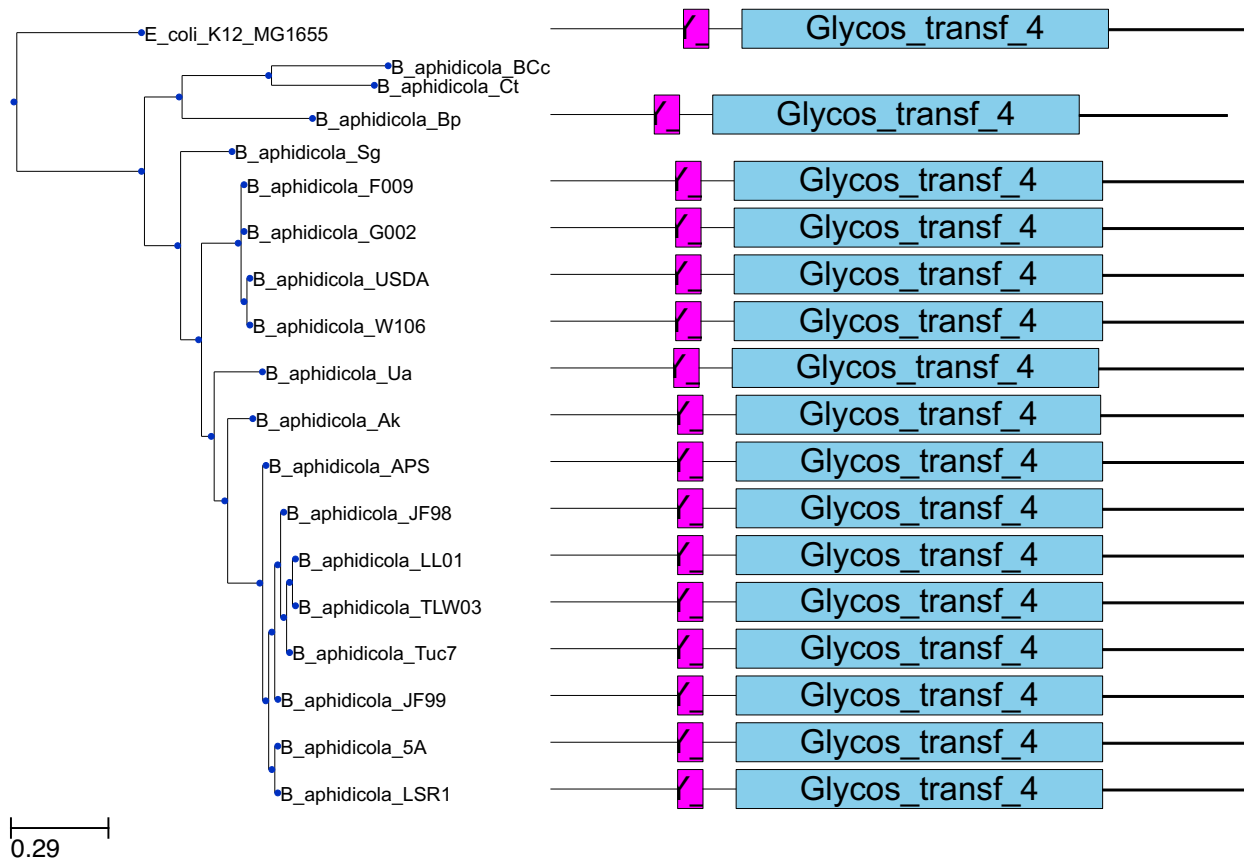
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate:meso- diaminopimelate ligase



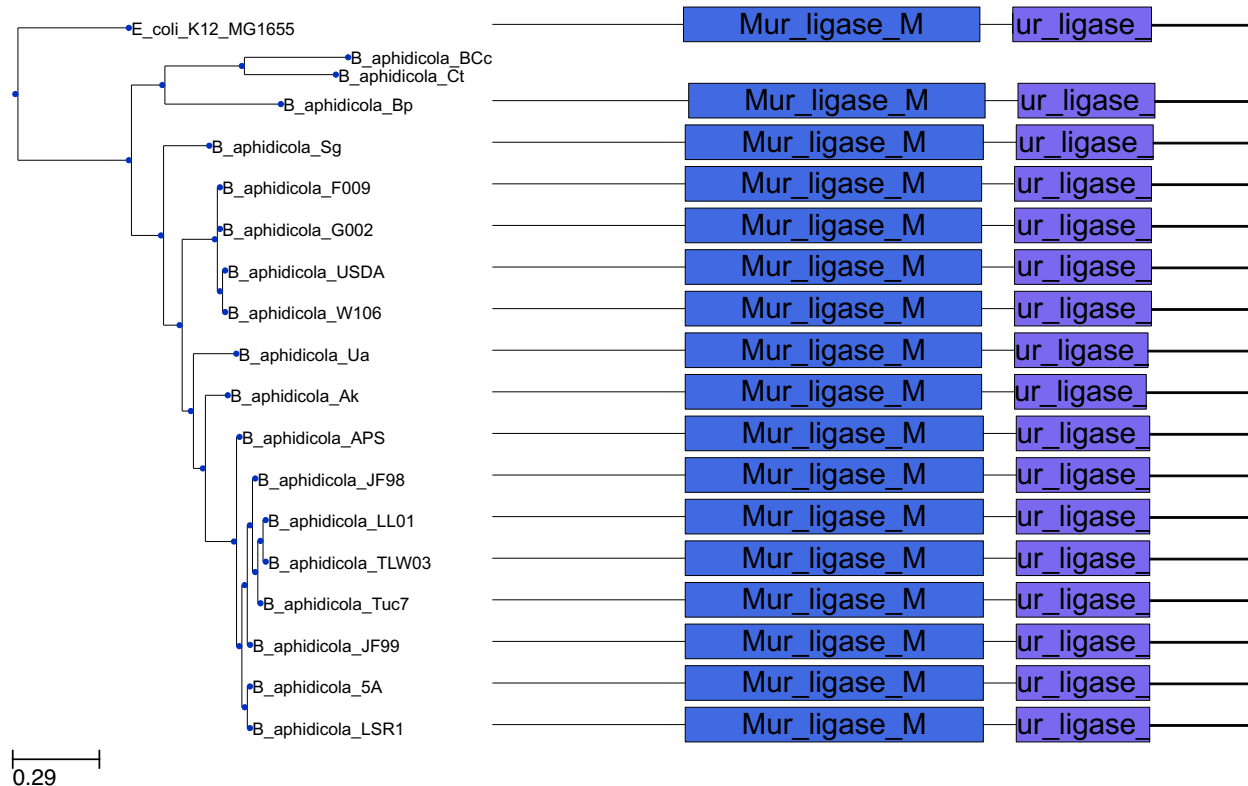
murF

NP_414628.1

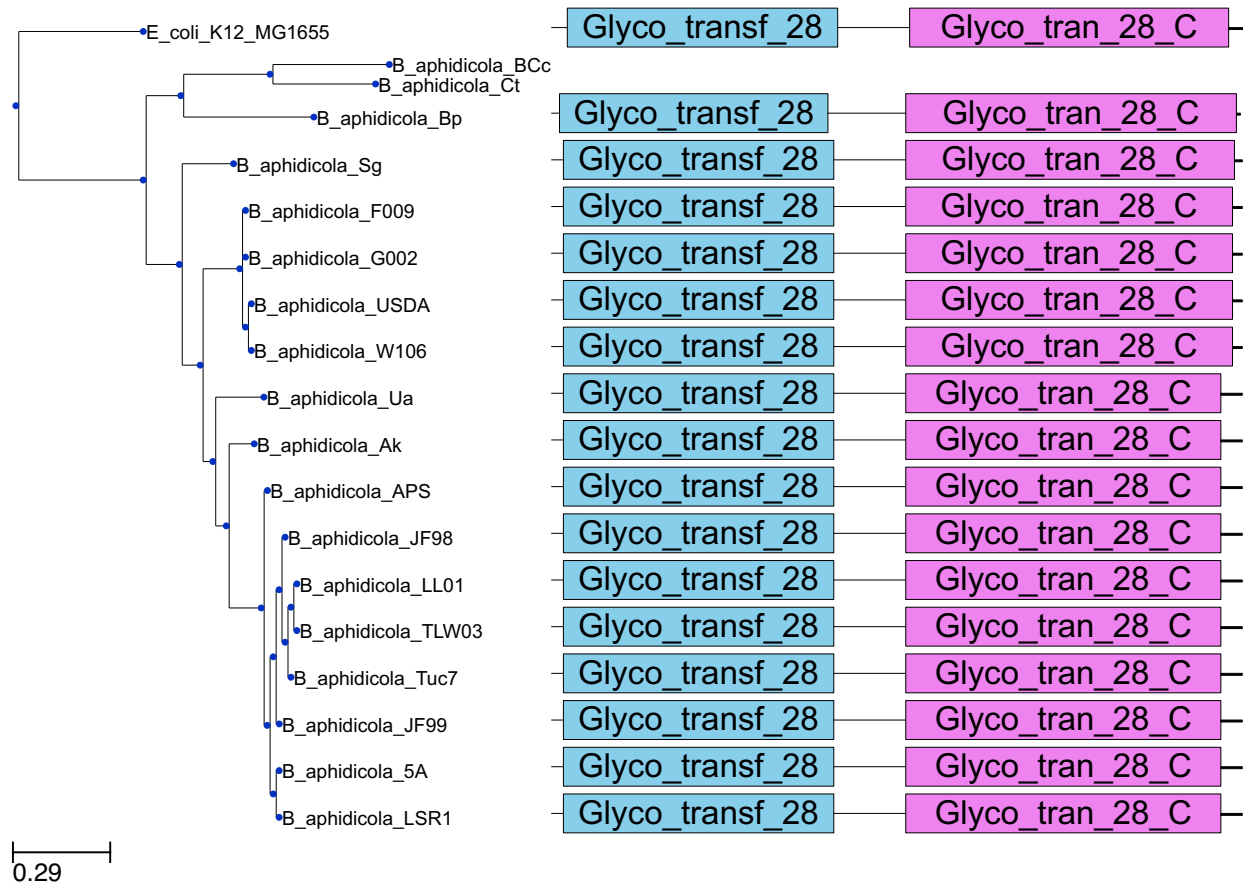
UDP-N-acetylmuramoyl-tripeptide:D-alanyl-D- alanine ligase



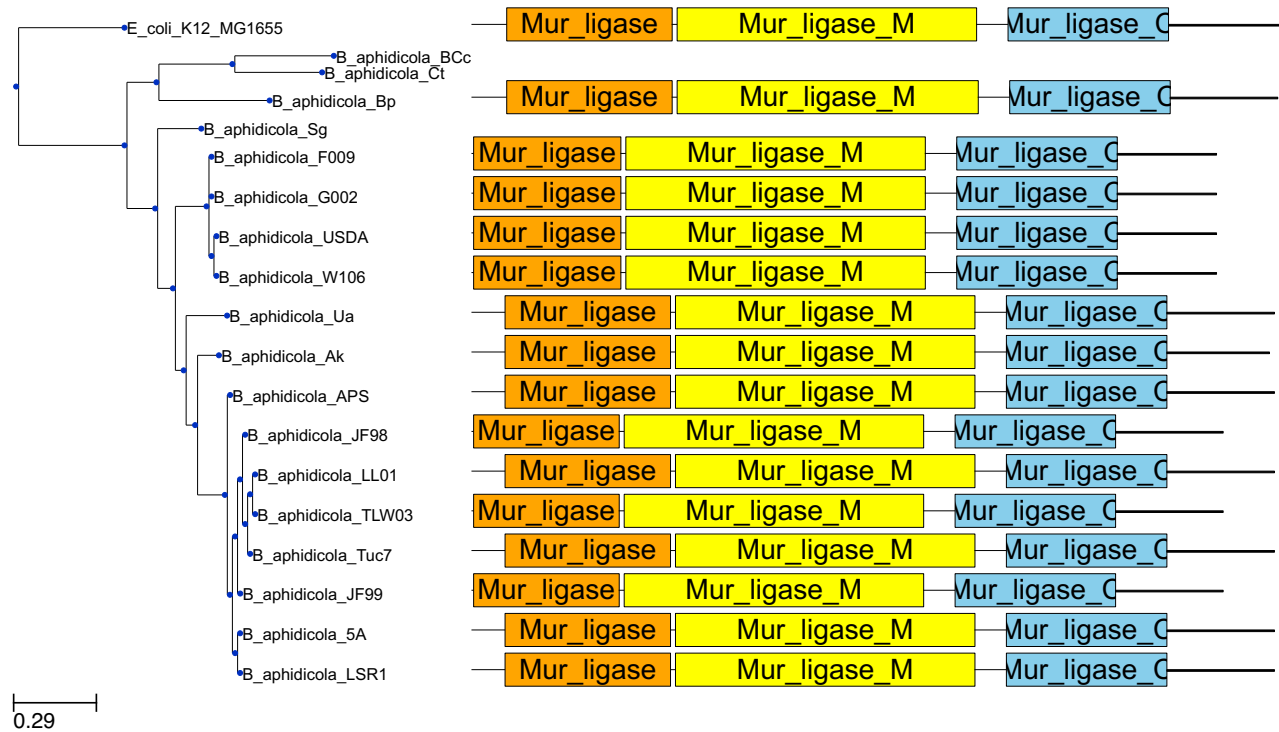
mraY
NP_414629.1
phospho-N-acetylmuramoyl-pentapeptide transferase



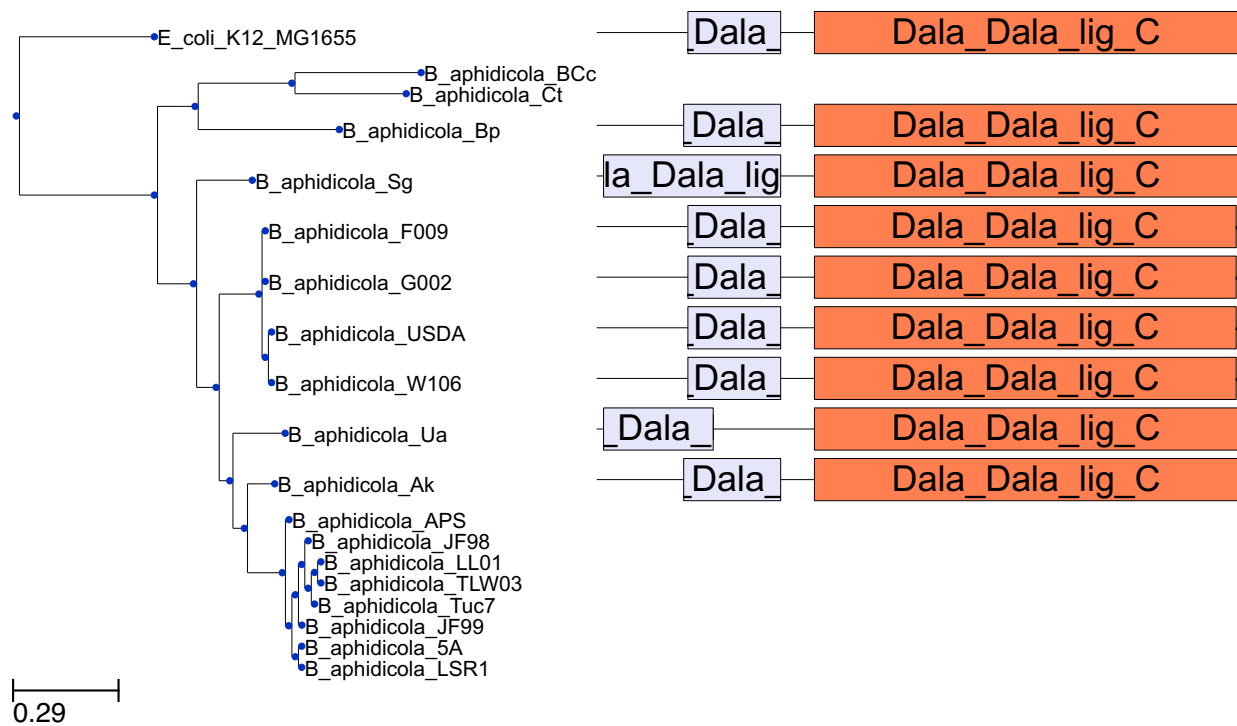
murD
 NP_414630.1
 UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase



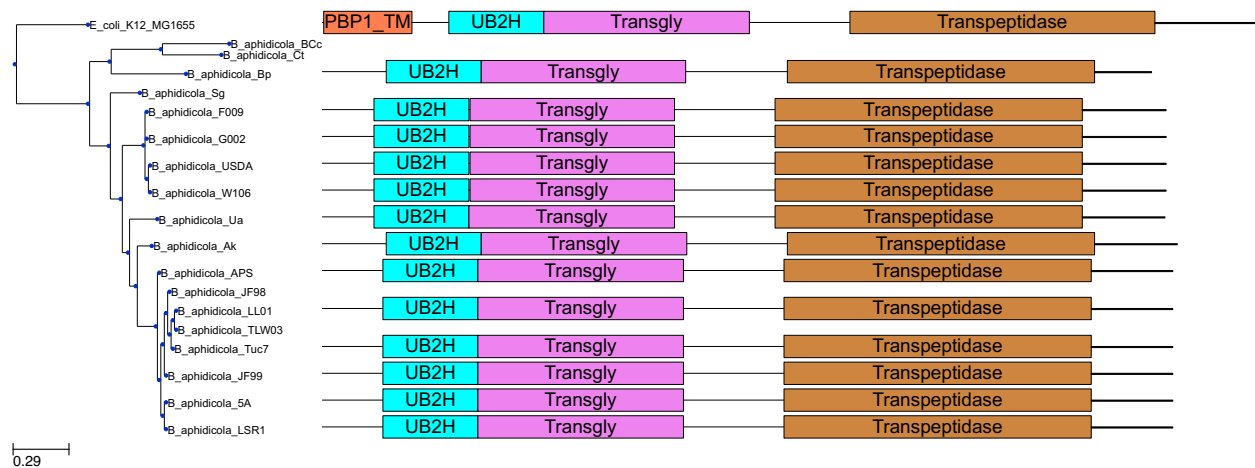
murG
NP_414632.1
N-acetylglucosaminyl transferase



murC
NP_414633.1
UDP-N-acetylmuramate:L-alanine ligase



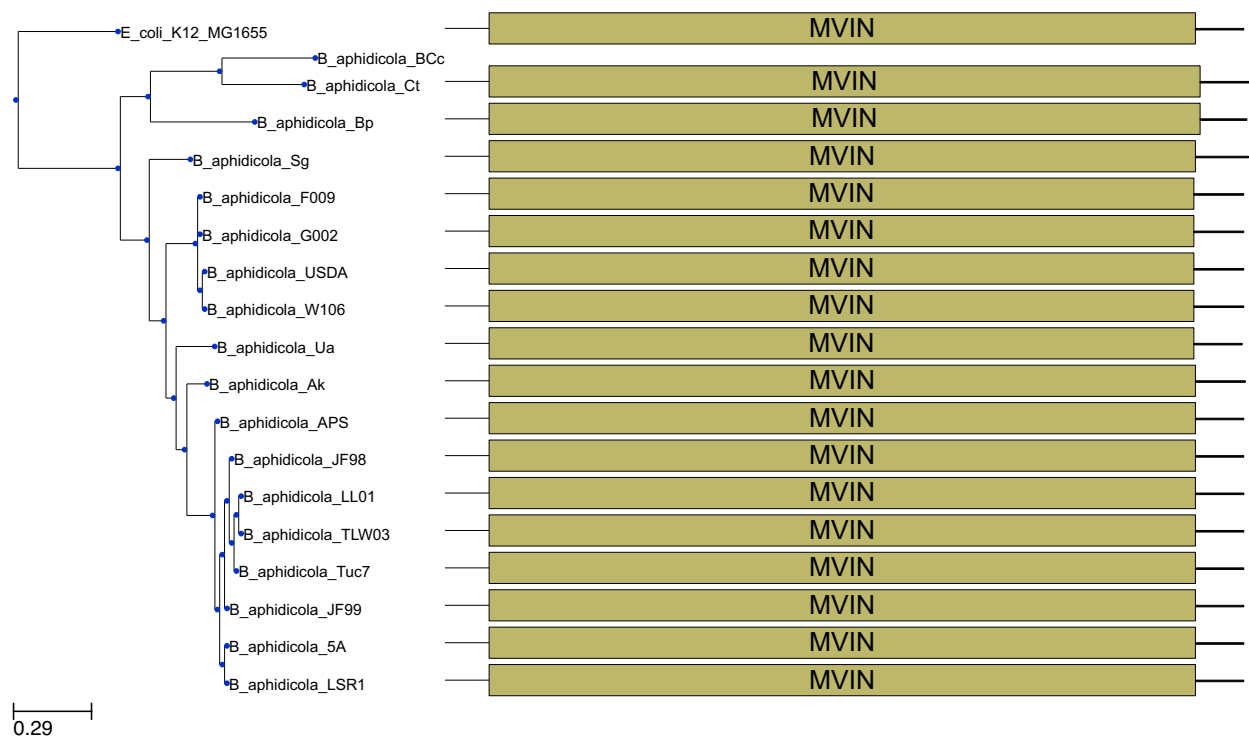
ddlB
NP_414634.1
D-alanine:D-alanine ligase



mrcB

NP_414691.1

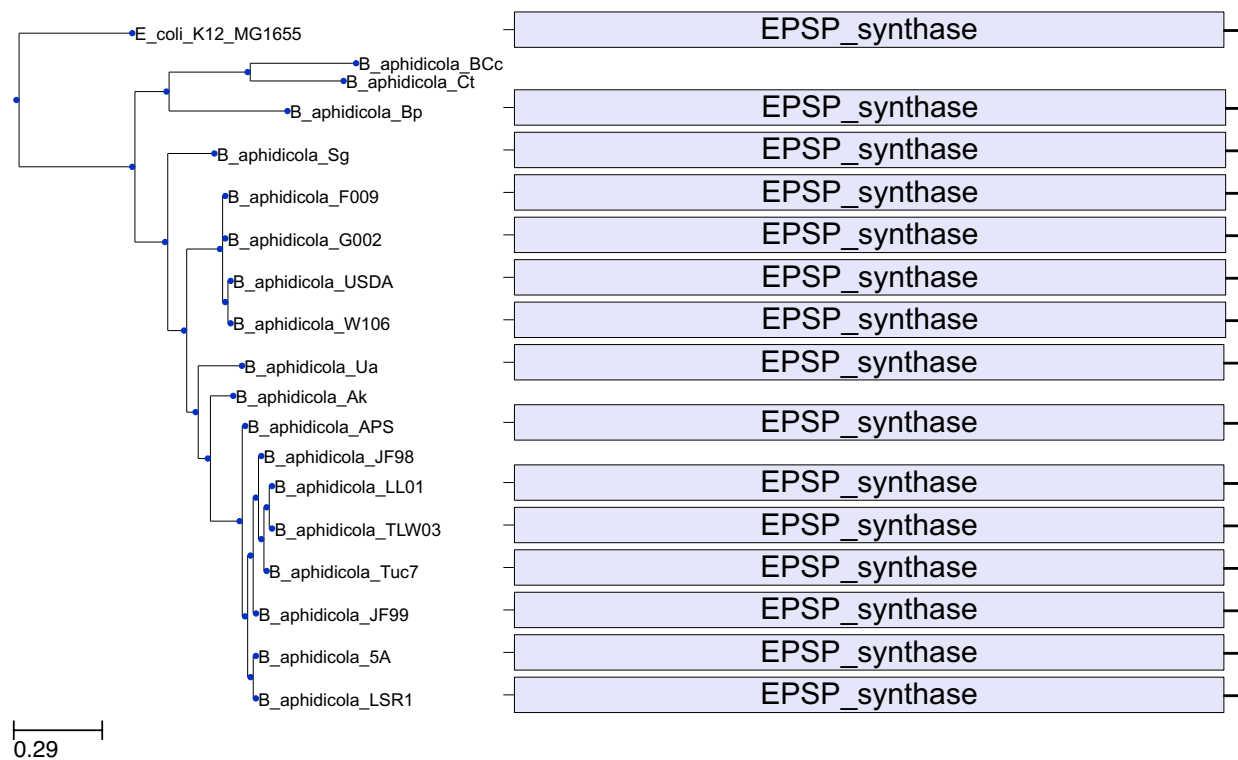
fused glycosyl transferase and transpeptidase



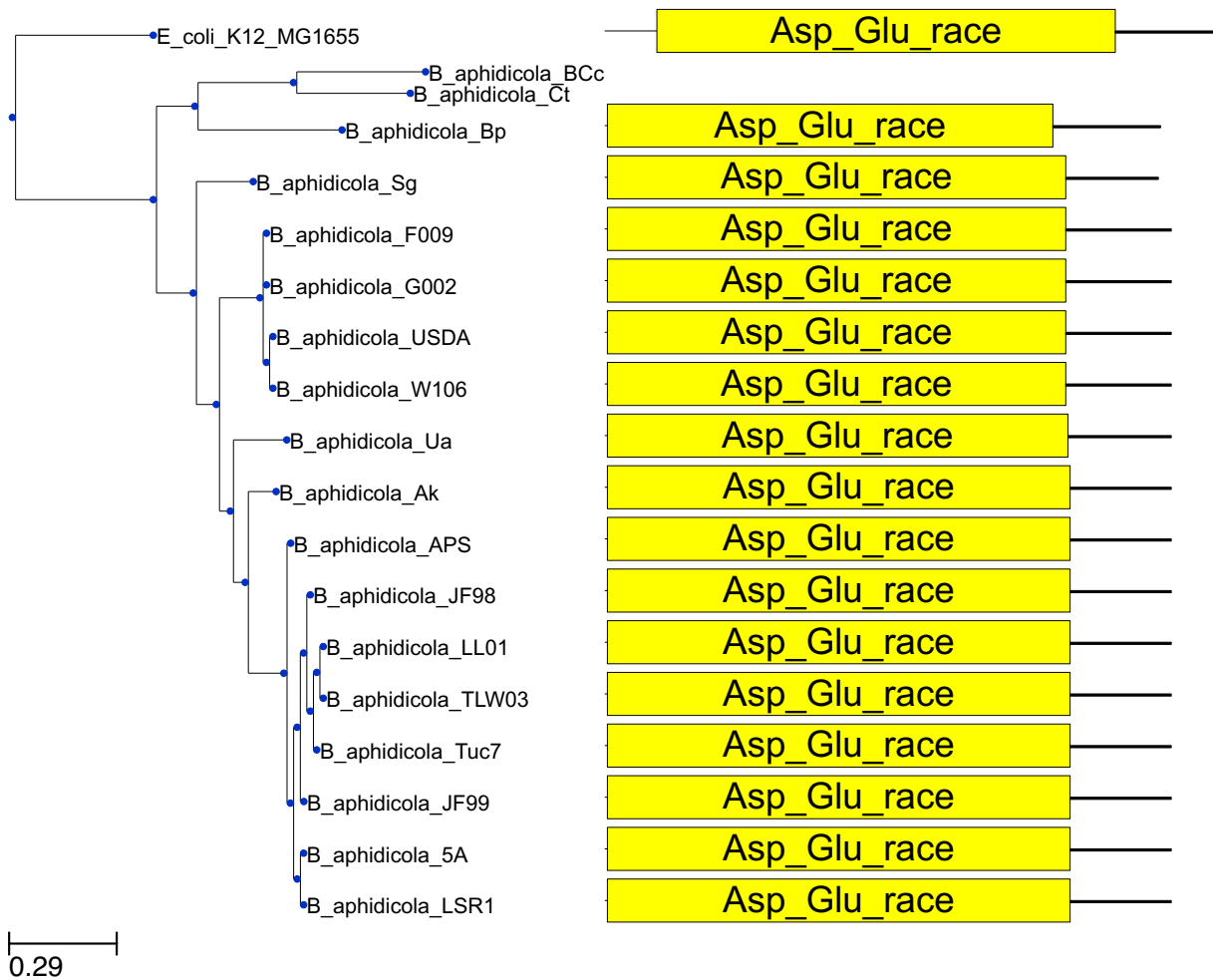
mviN

NP_415587.1

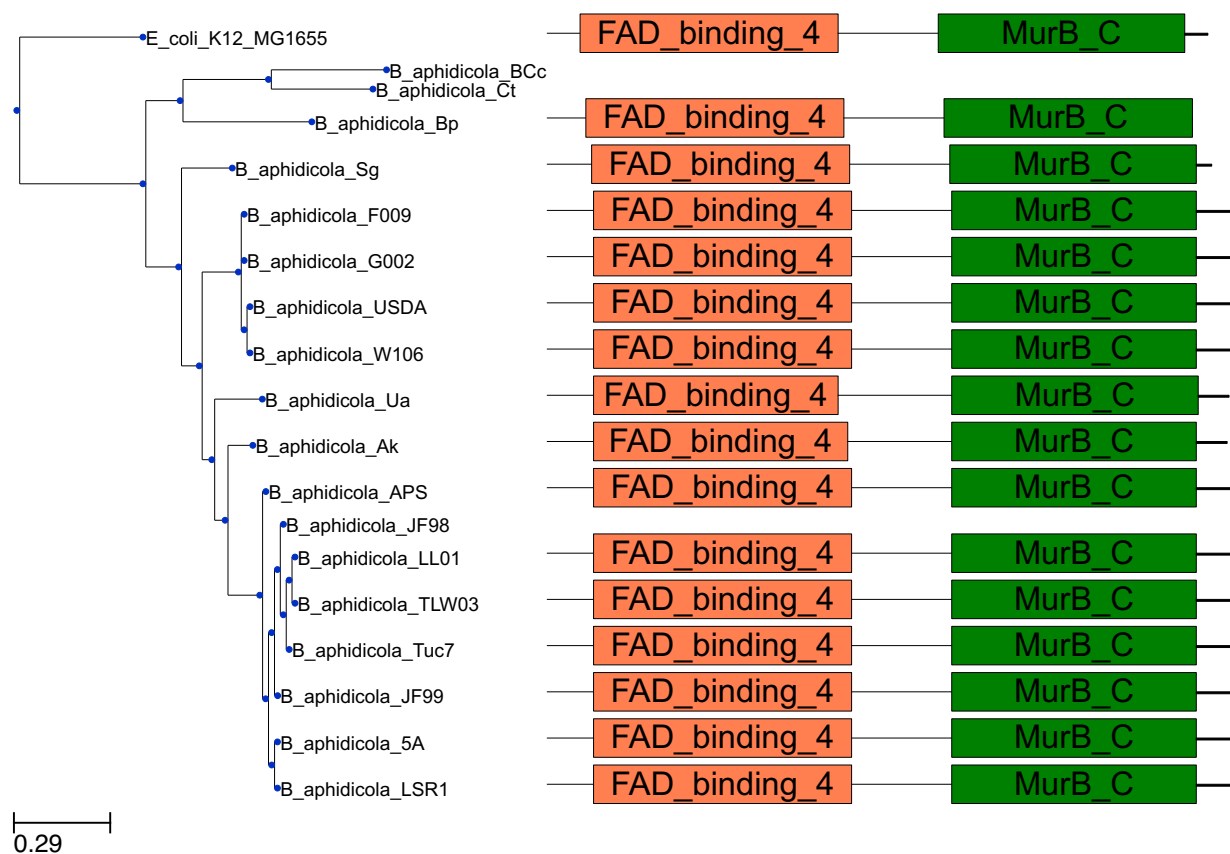
putative lipid II flippase



murA
NP_417656.1
UDP-N-acetylglucosamine 1-carboxyvinyltransferase



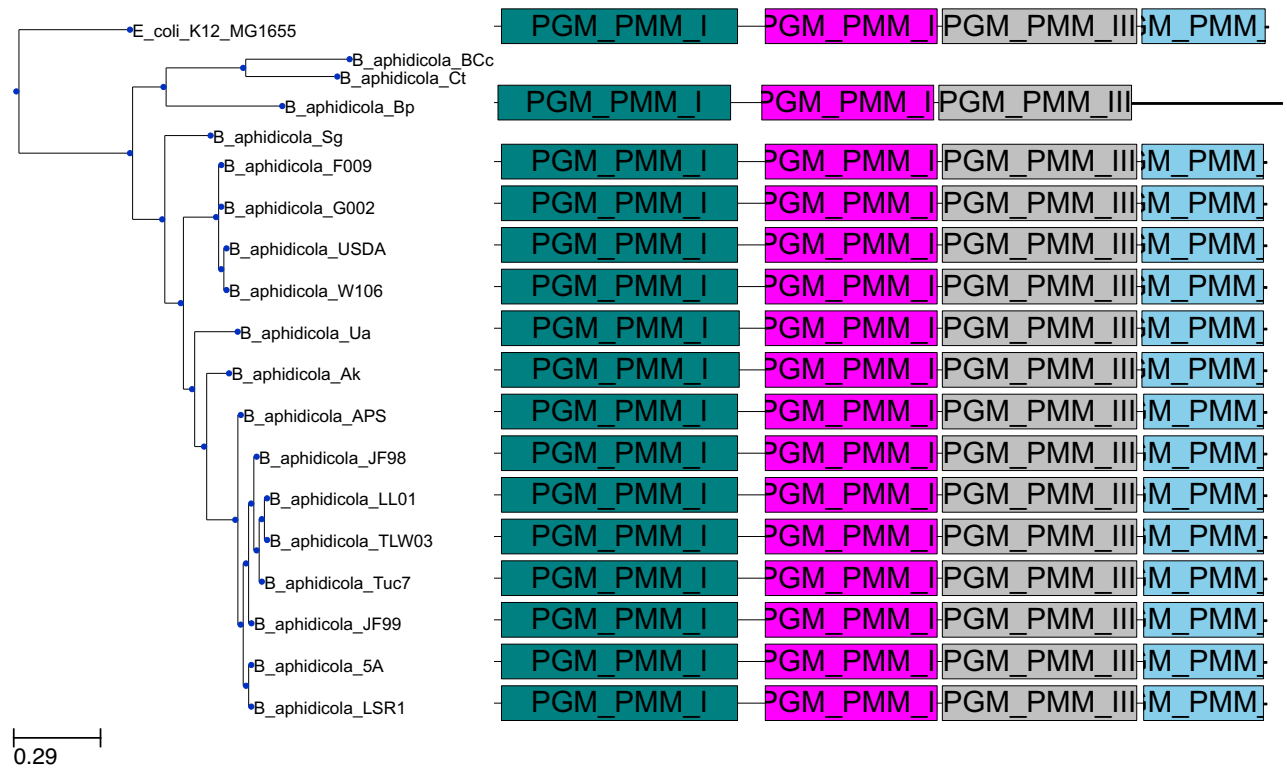
murl
NP_418402.2
glutamate racemase



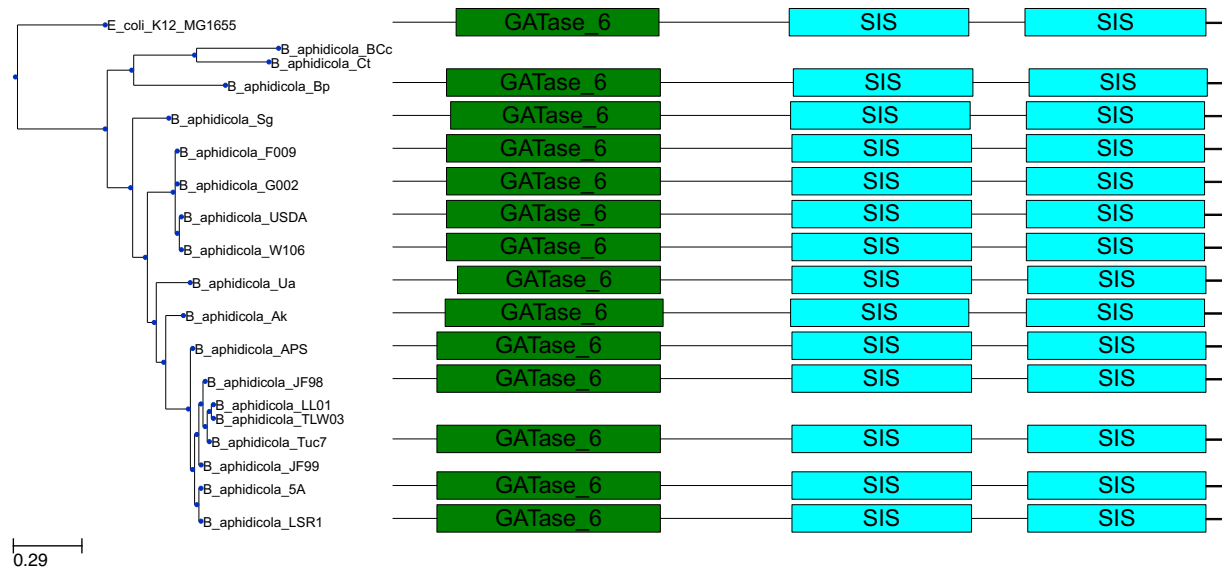
murB

NP_418403.1

"UDP-N-acetylenolpyruvoylglucosamine reductase, FAD-binding"



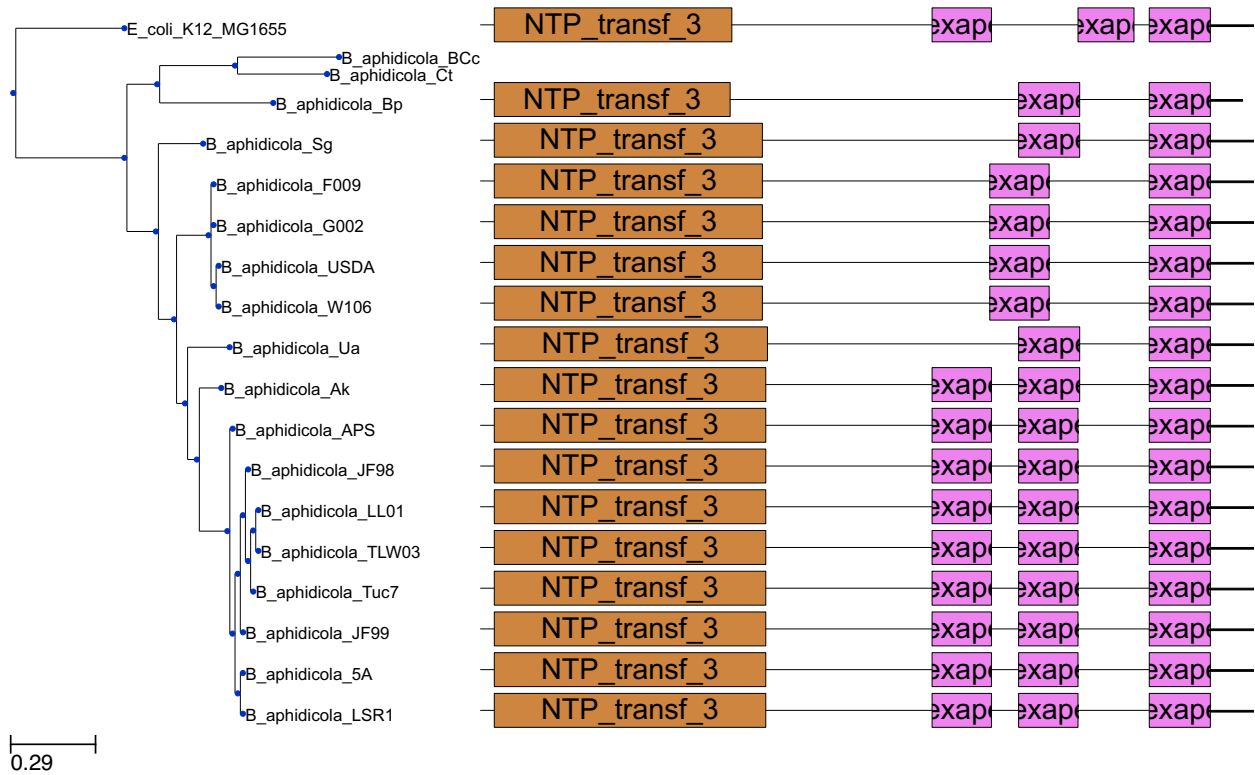
glmM
NP_417643.1
phosphoglucosamine mutase



glms

NP_418185.1

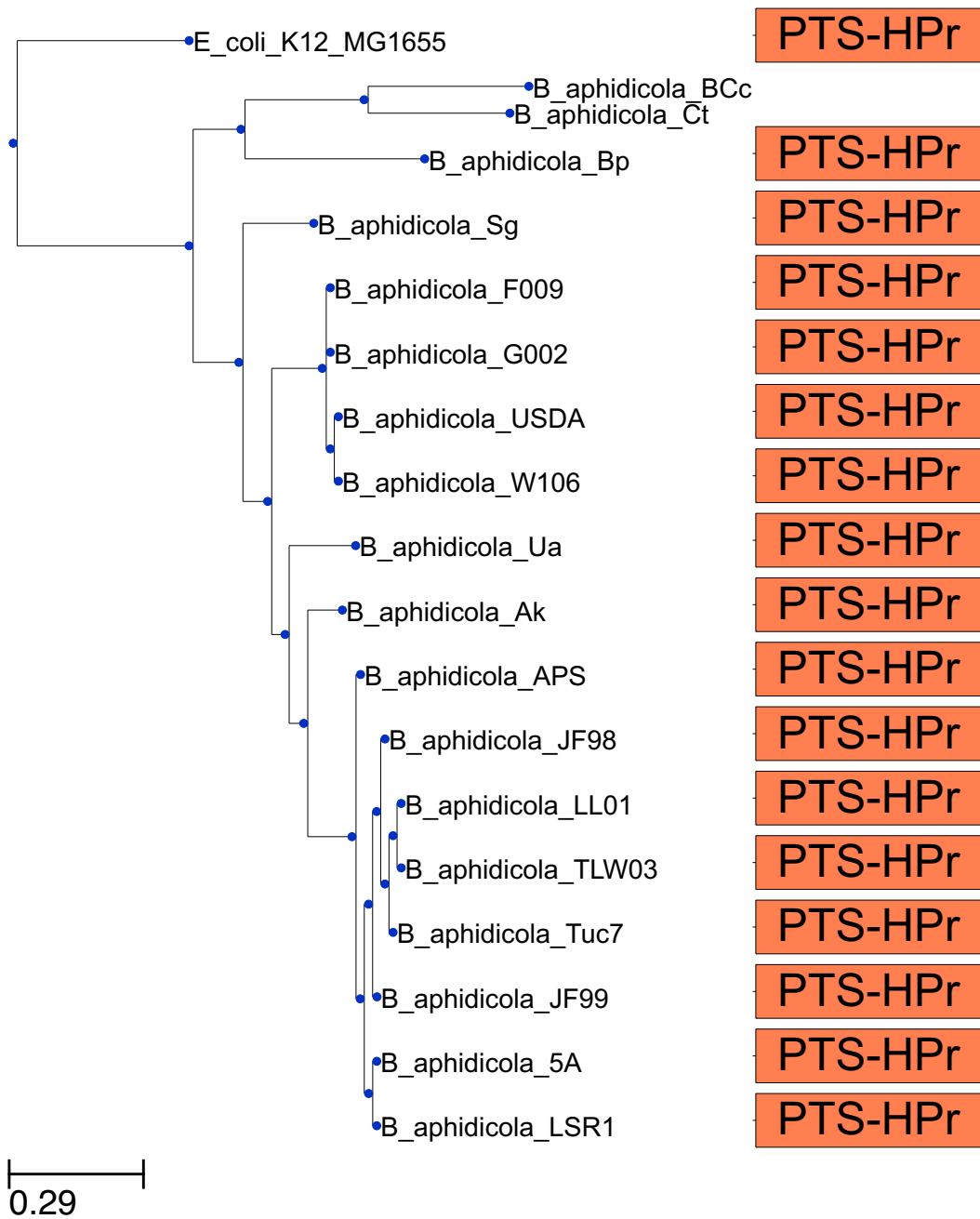
L-glutamine:D-fructose-6-phosphate aminotransferase



glmU

NP_418186.1

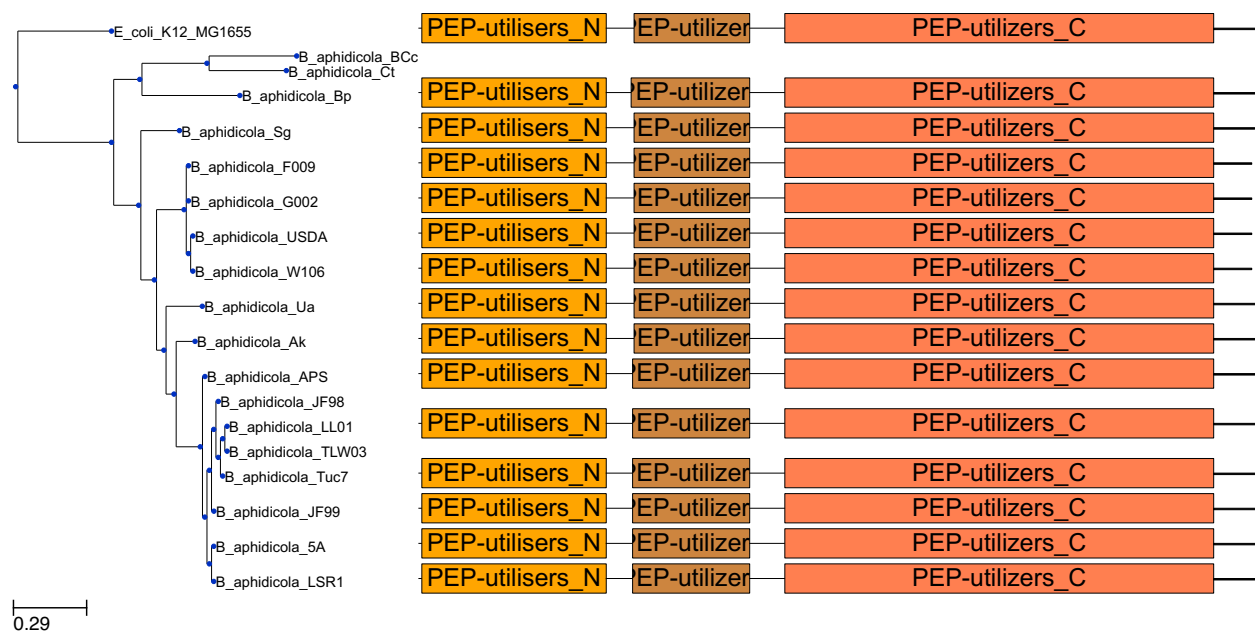
fused N-acetyl glucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyl transferase



ptsH

NP_416910.1

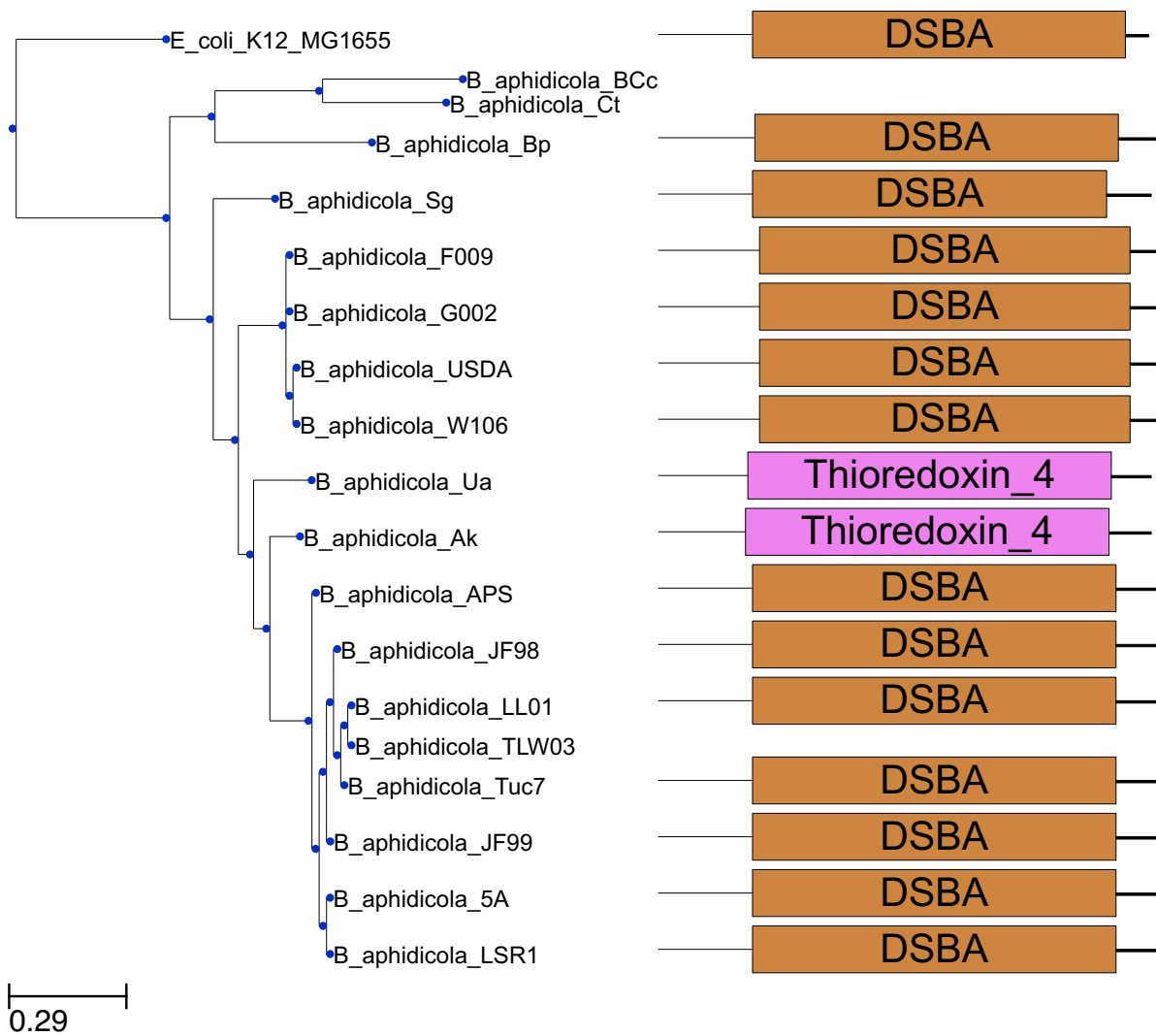
phosphohistidinoprotein-hexose phosphotransferase component of PTS system (Hpr)



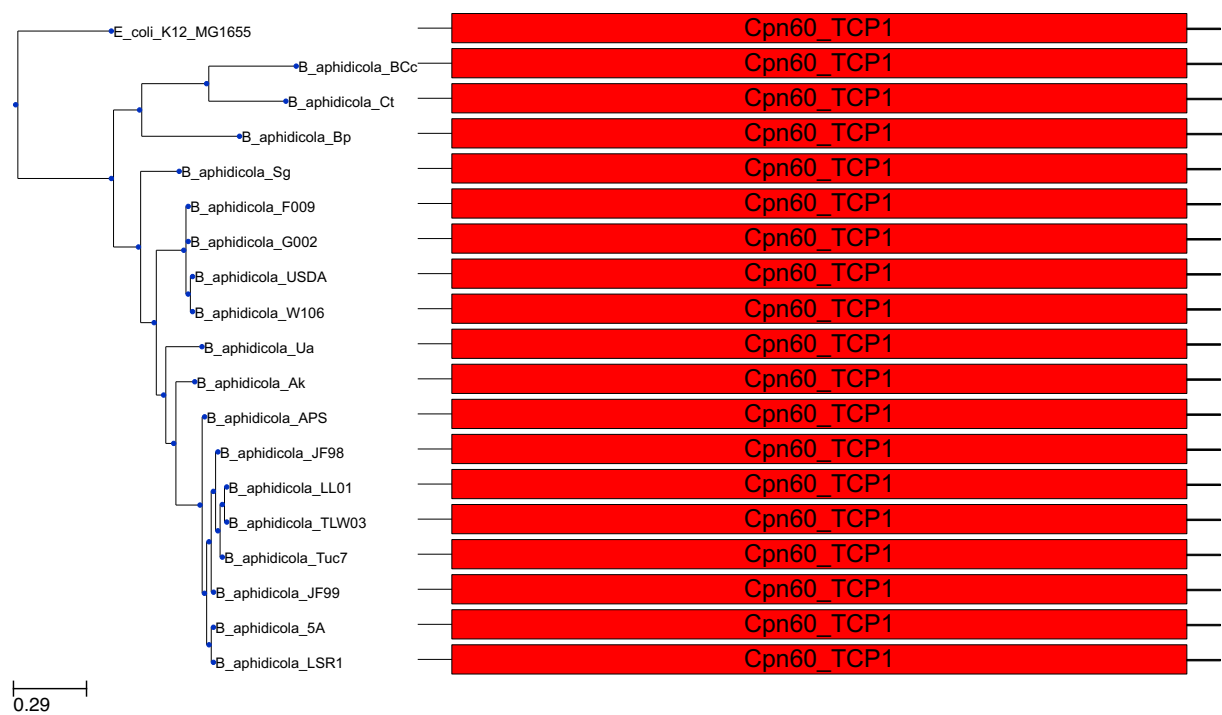
ptsI

NP_416911.1

PEP-protein phosphotransferase of PTS system (enzyme I)



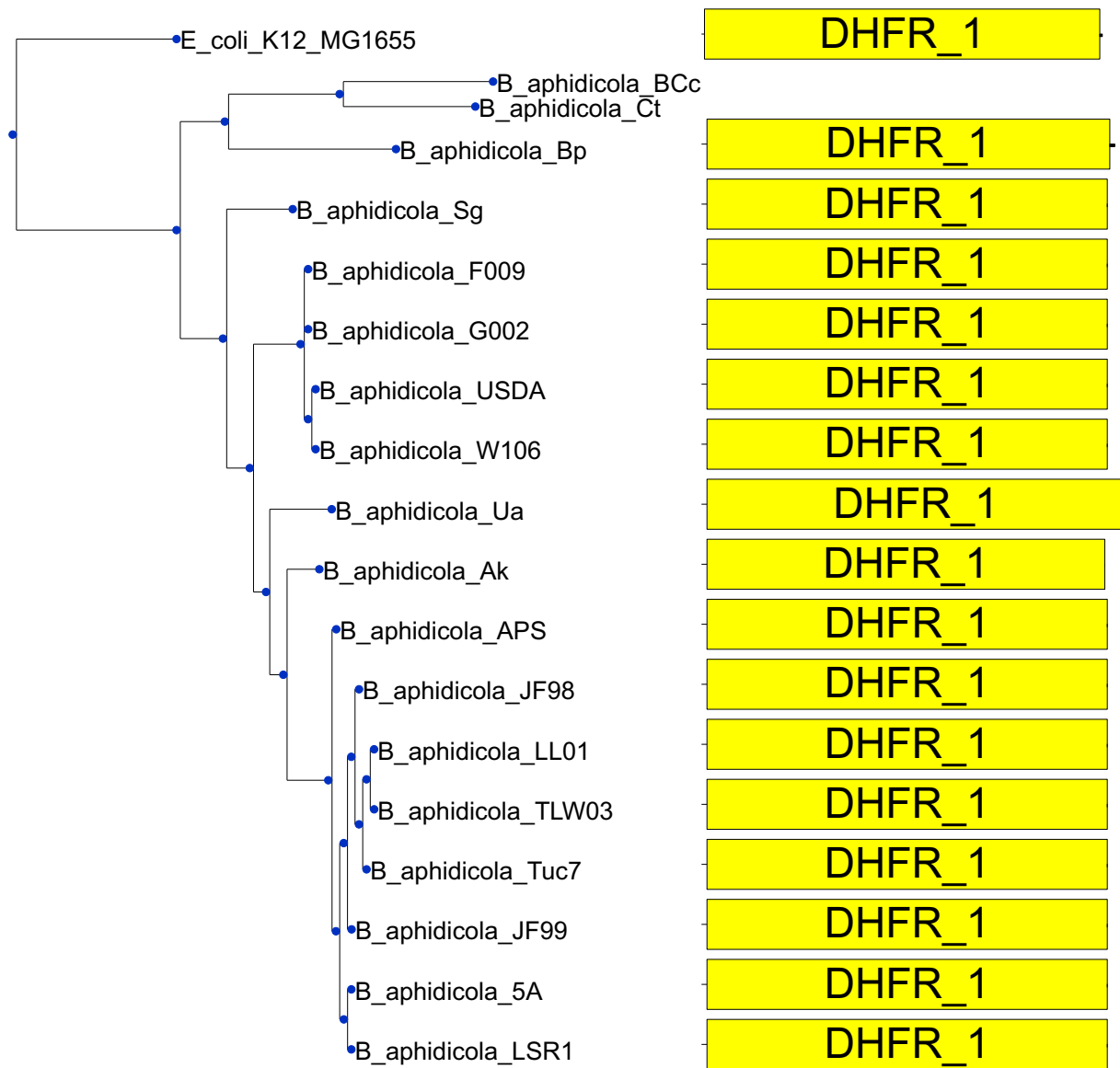
dsbA
NP_418297.1
periplasmic protein disulfide isomerase I



groL

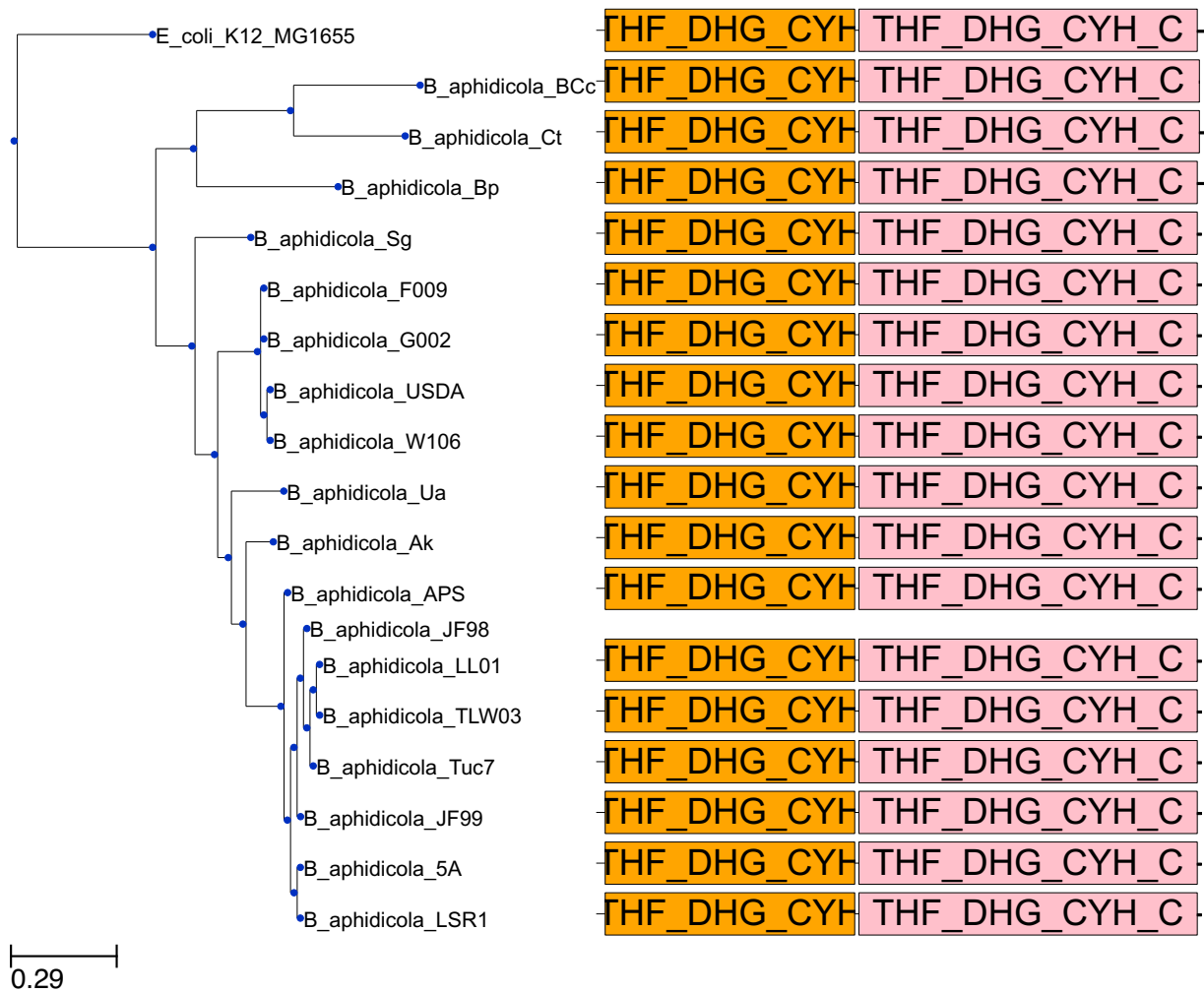
NP_418567.1

"Cpn60 chaperonin GroEL, large subunit of GroESL"



0.29

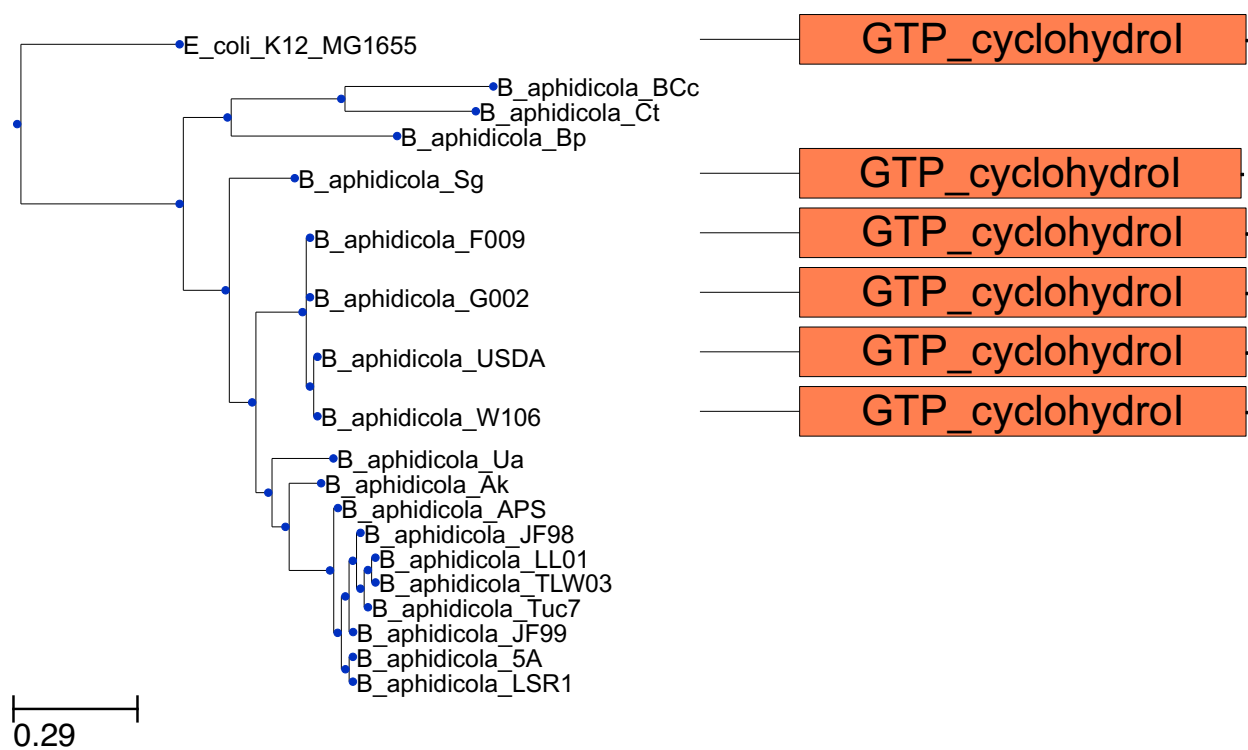
folA
NP_414590.1
dihydrofolate reductase



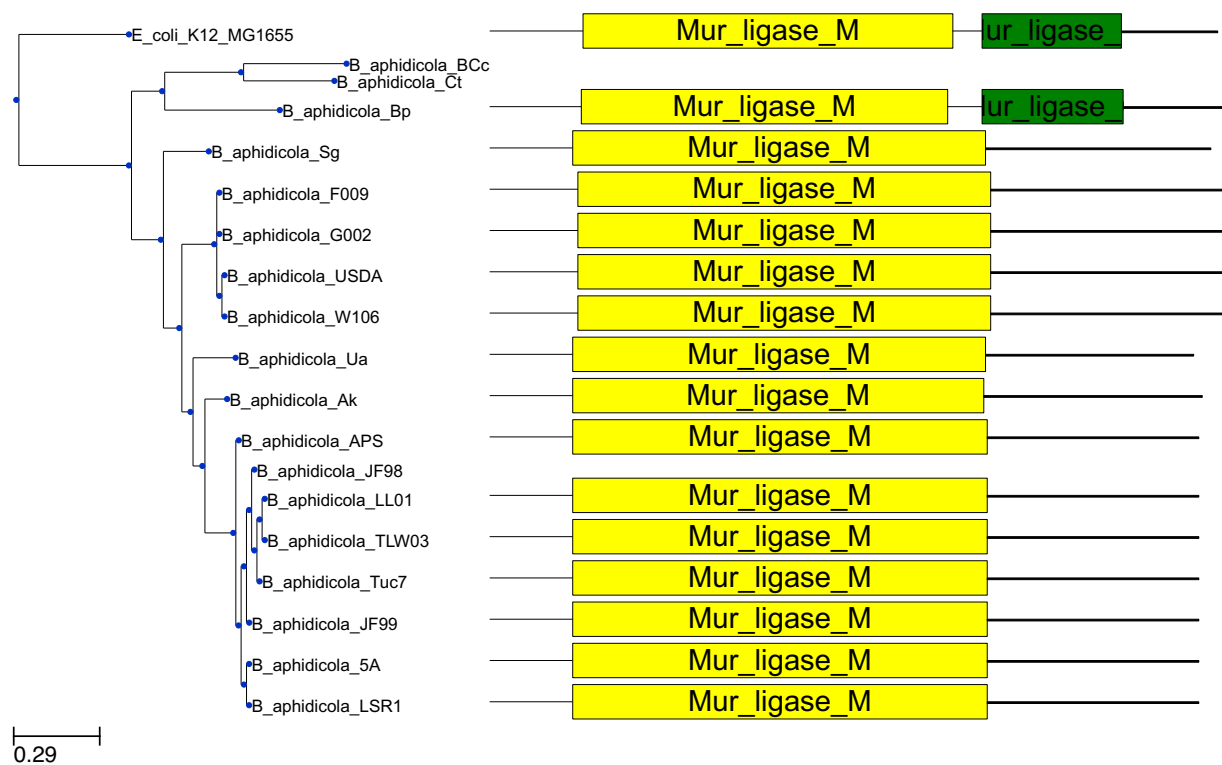
fold

NP_415062.1

"bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase"



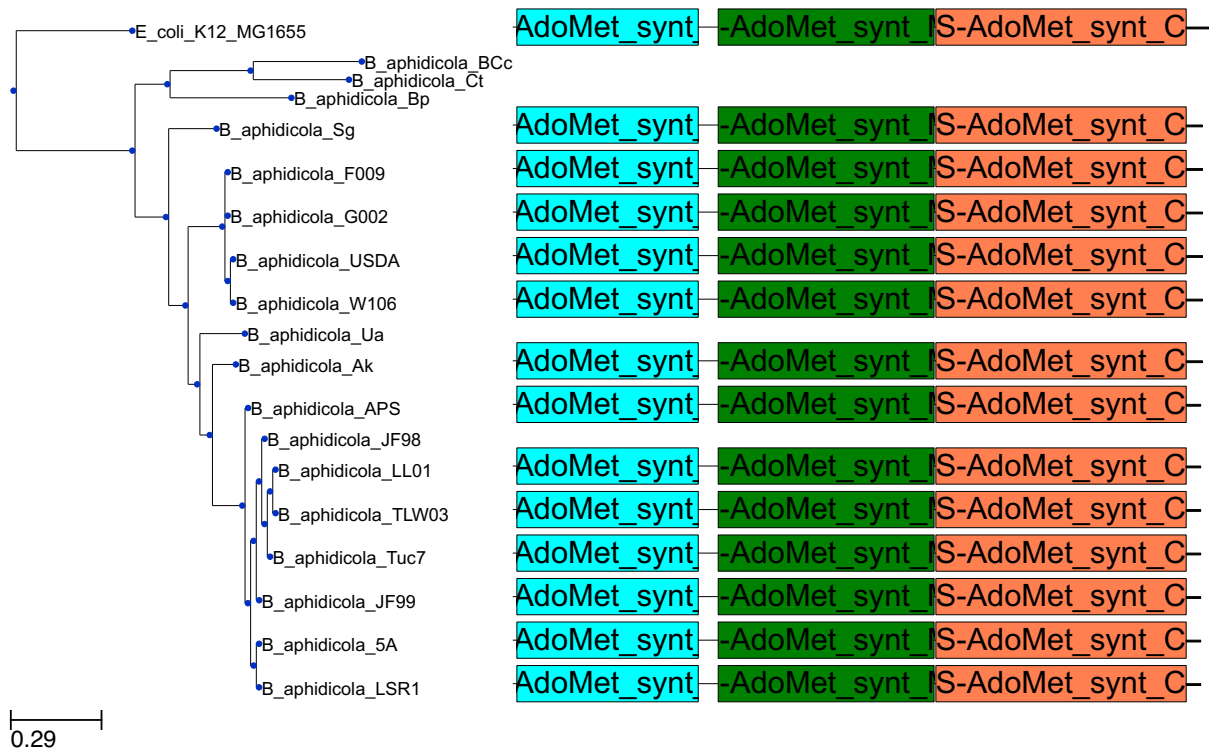
foIE
 NP_416658.1
 GTP cyclohydrolase I



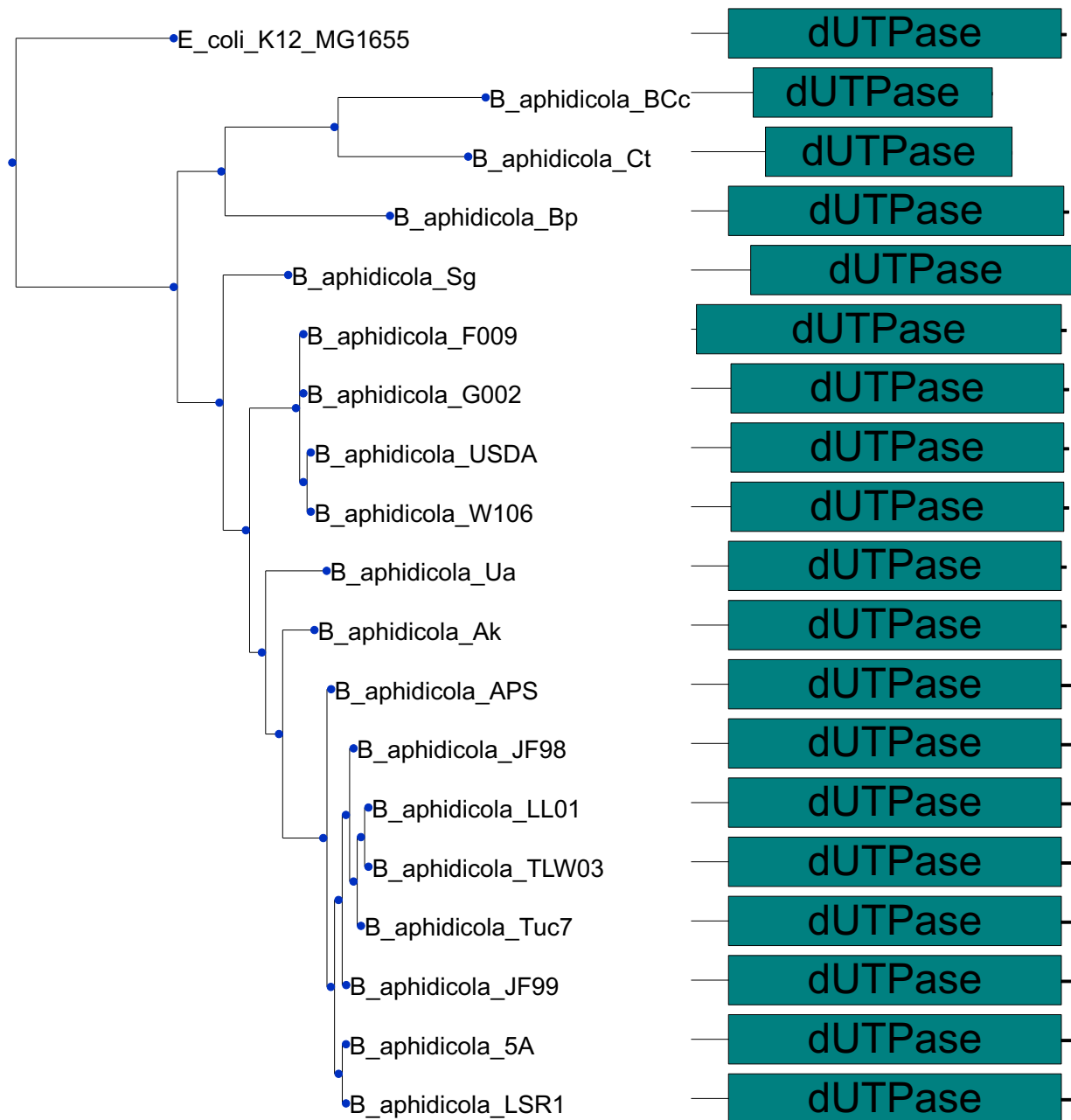
folC

NP_416818.1

bifunctional folylpolyglutamate synthase/ dihydrofolate synthase

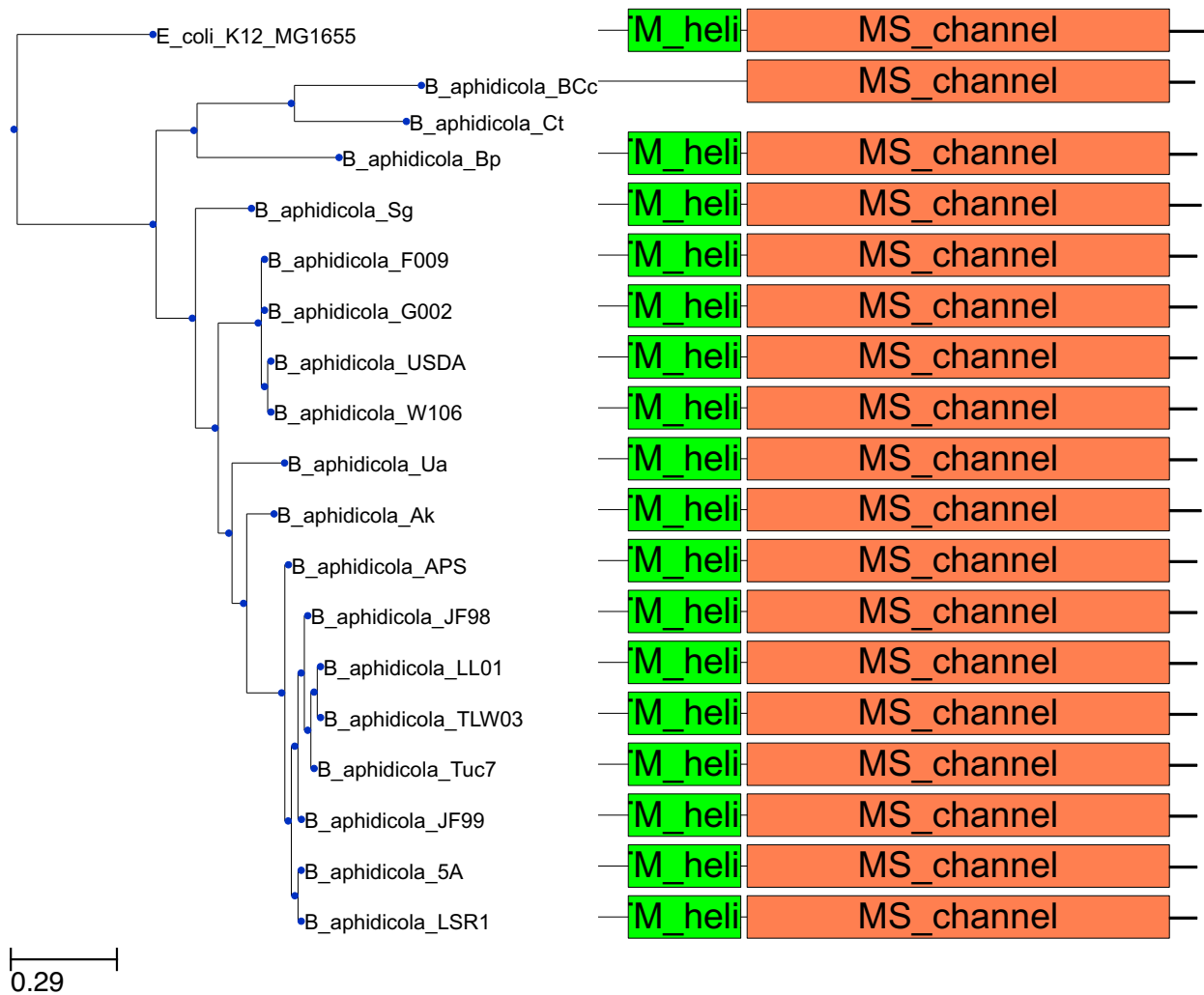


metK
NP_417417.1
S-adenosylmethionine synthetase

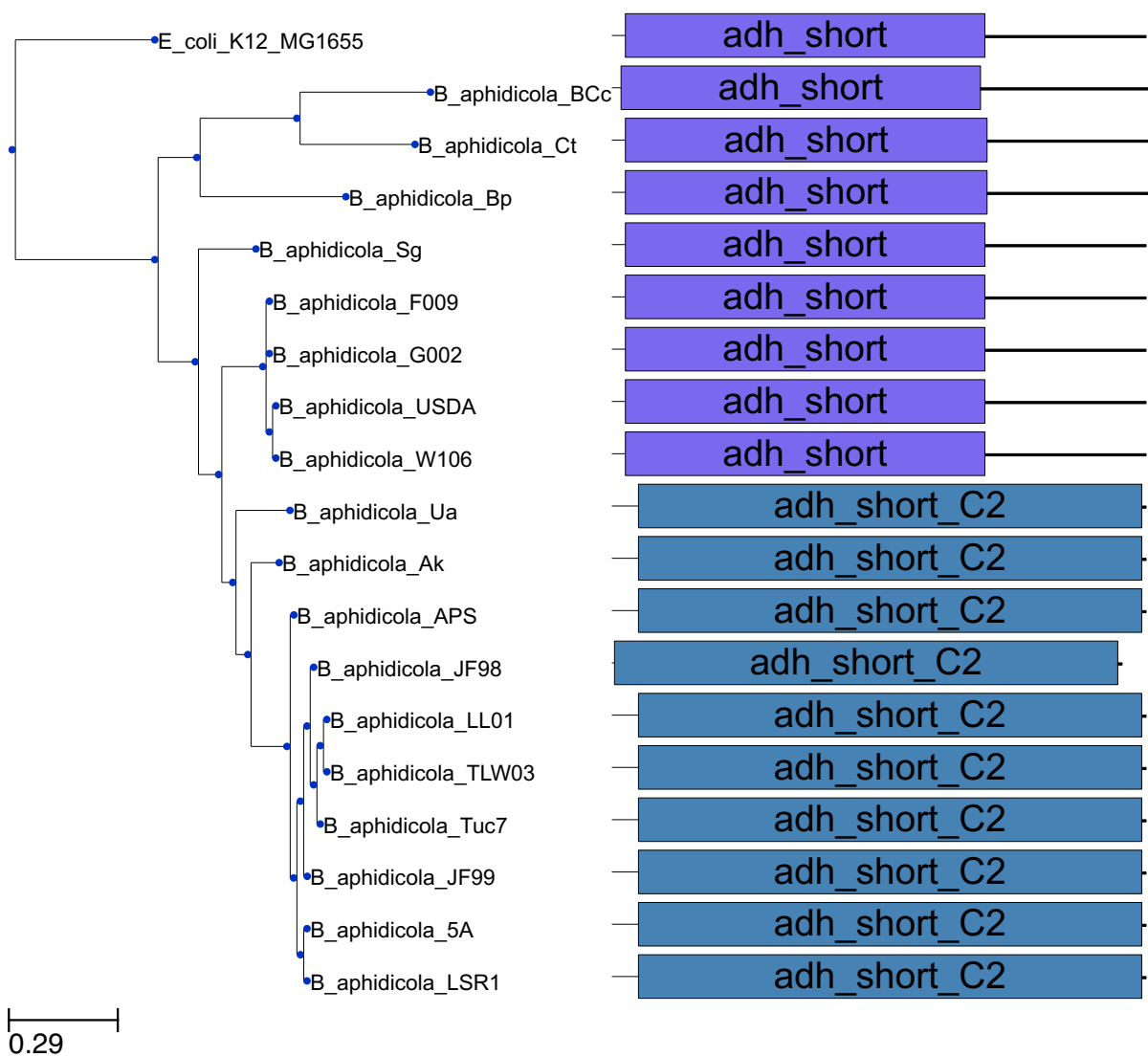


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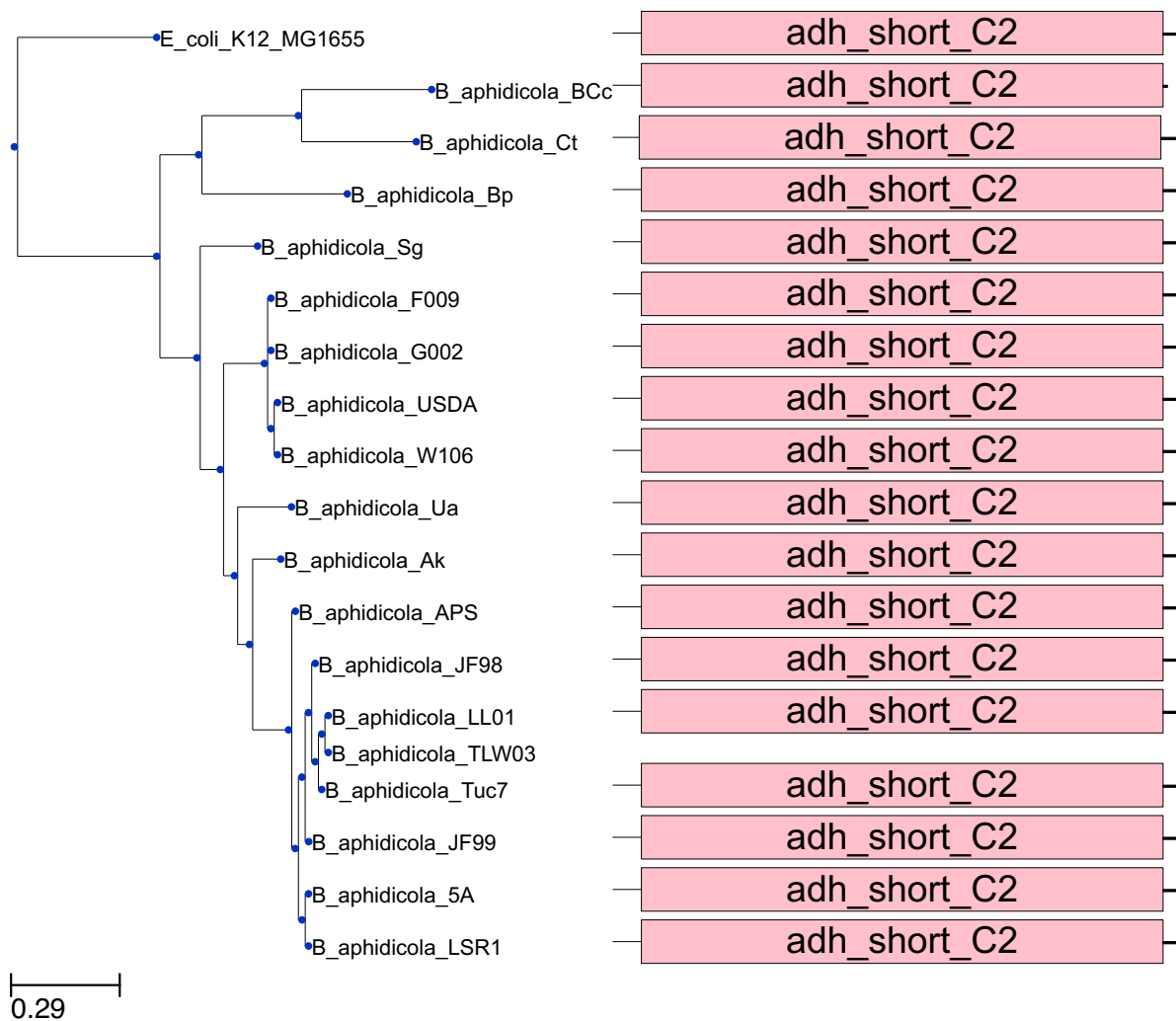
dut
NP_418097.1
deoxyuridinetriphosphatase



mscS
NP_417399.1
"mechanosensitive channel protein, small conductance"



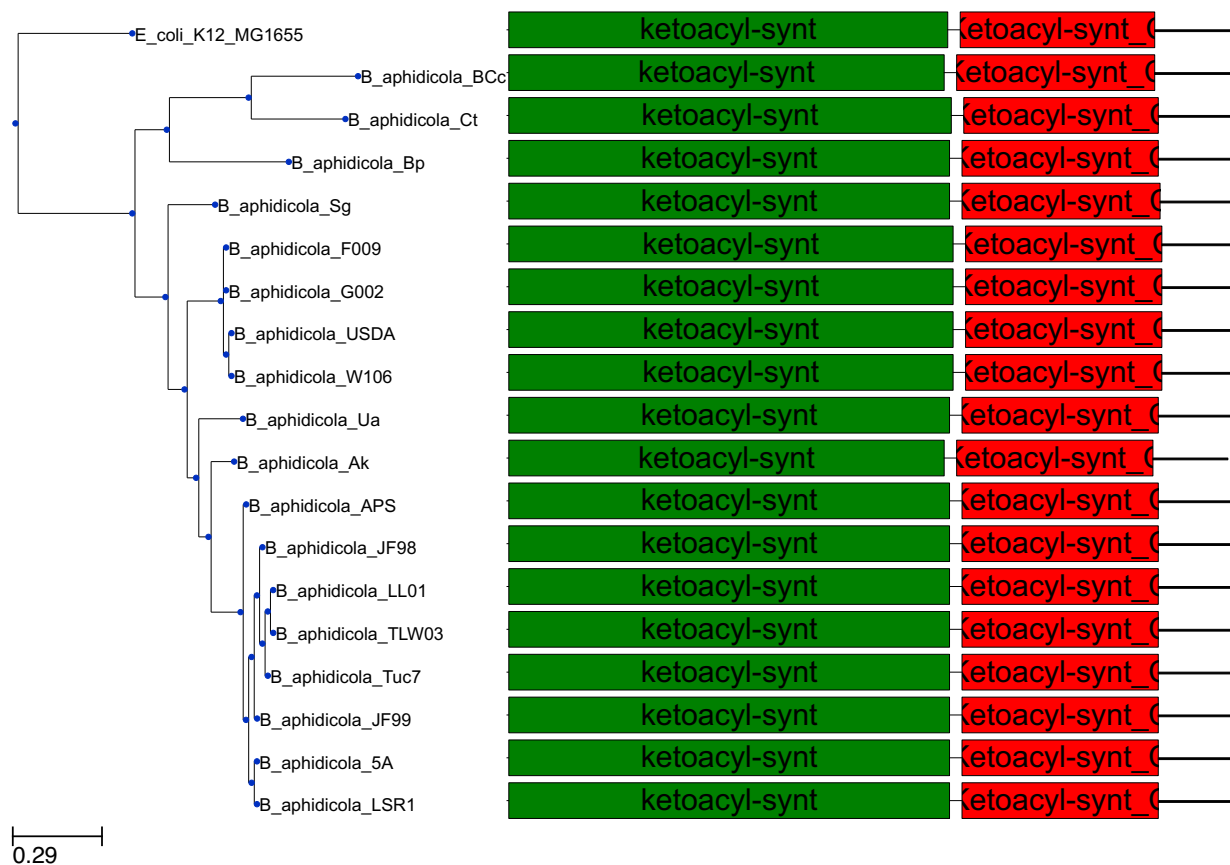
fabG
NP_415611.1
3-oxoacyl-[acyl-carrier-protein] reductase



fabI

NP_415804.1

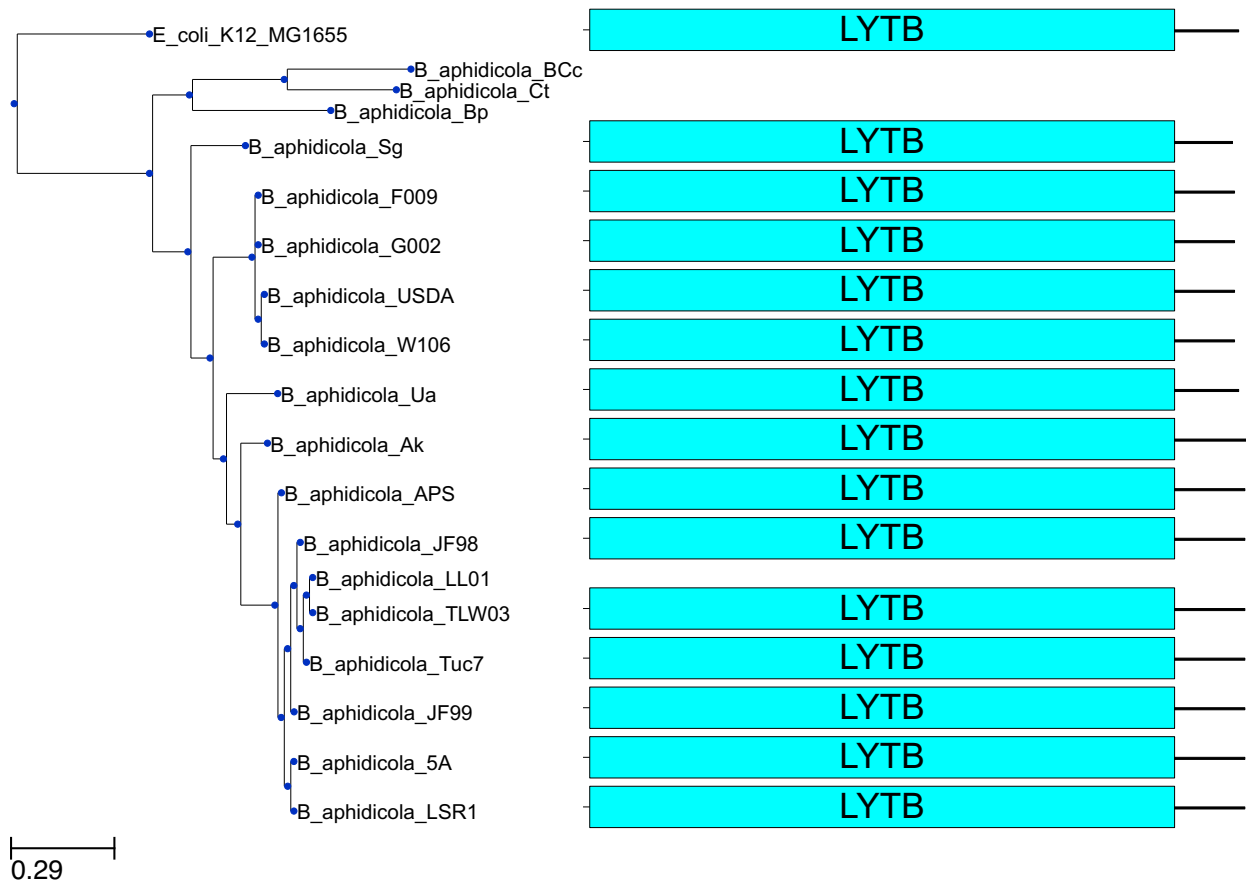
"enoyl-[acyl-carrier-protein] reductase, NADH-dependent"



fabB

NP_416826.1

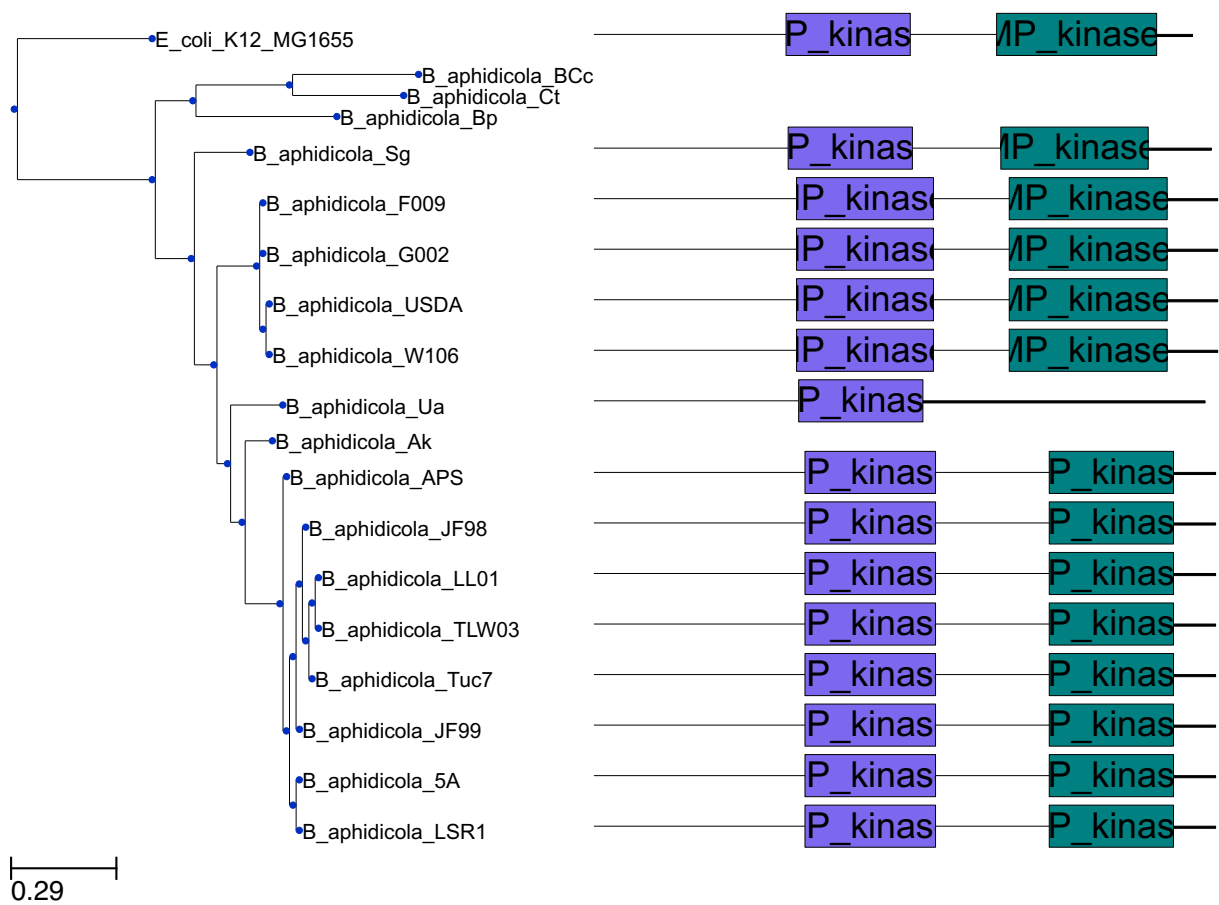
3-oxoacyl-[acyl-carrier-protein] synthase I



ispH

NP_414570.1

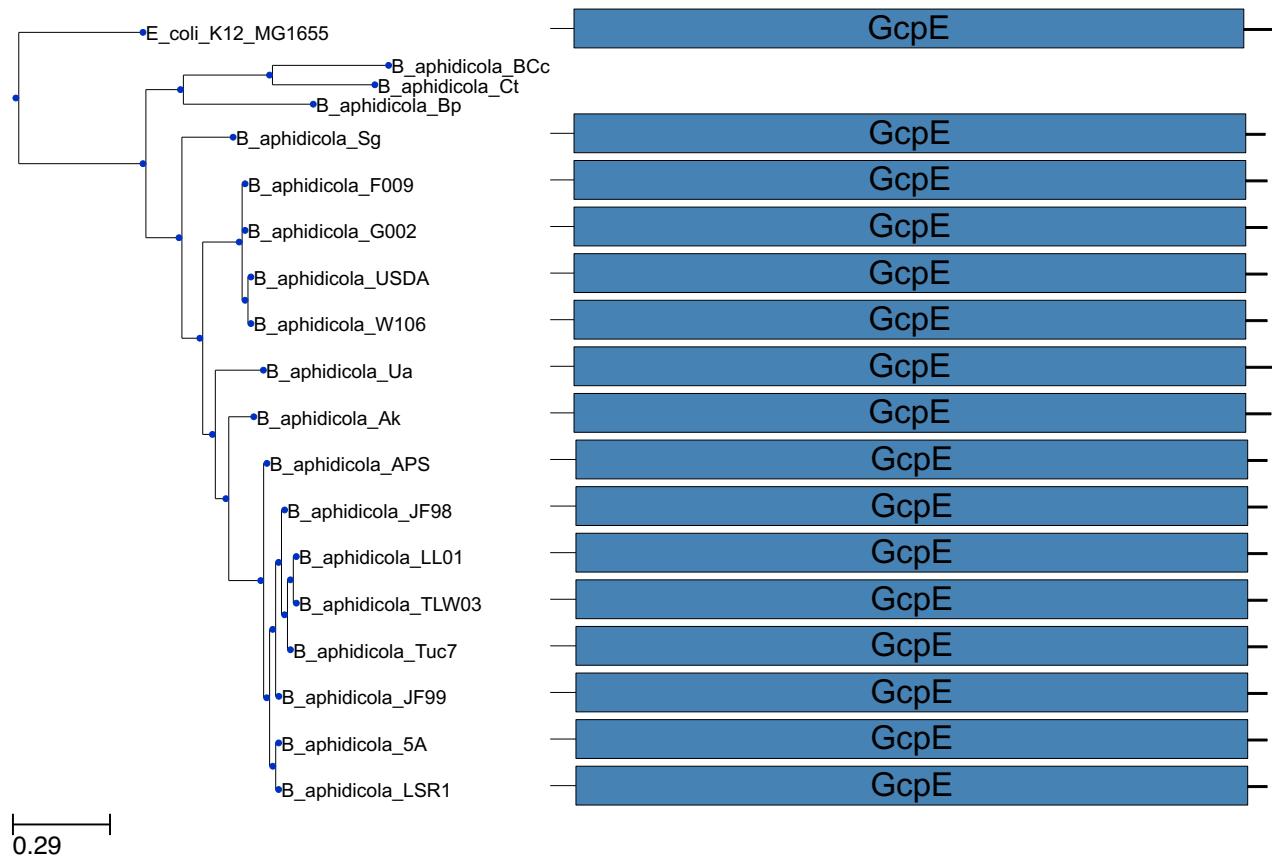
"4-hydroxy-3-methylbut-2-enyl diphosphate reductase, 4Fe-4S protein"



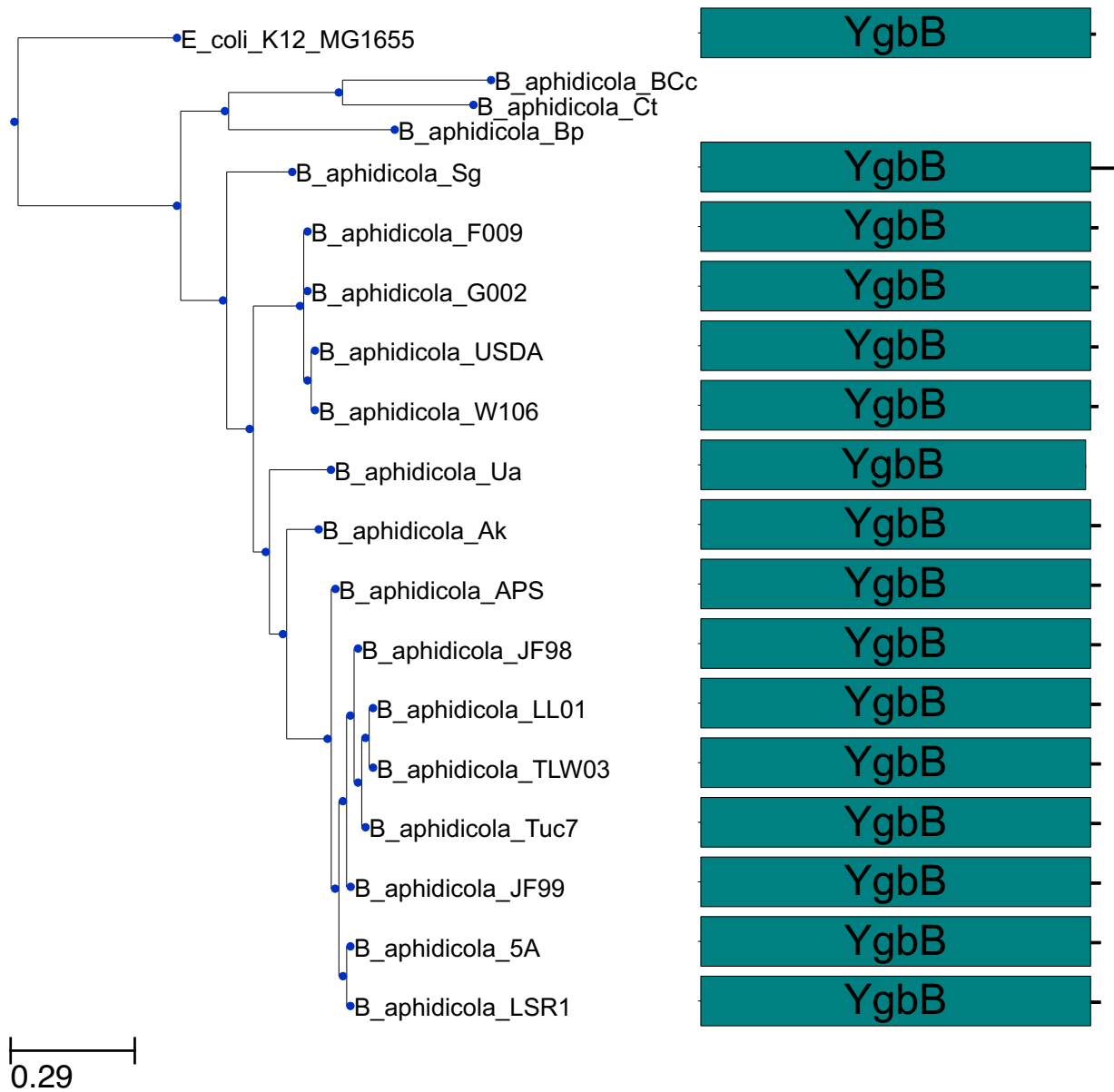
ispE

NP_415726.1

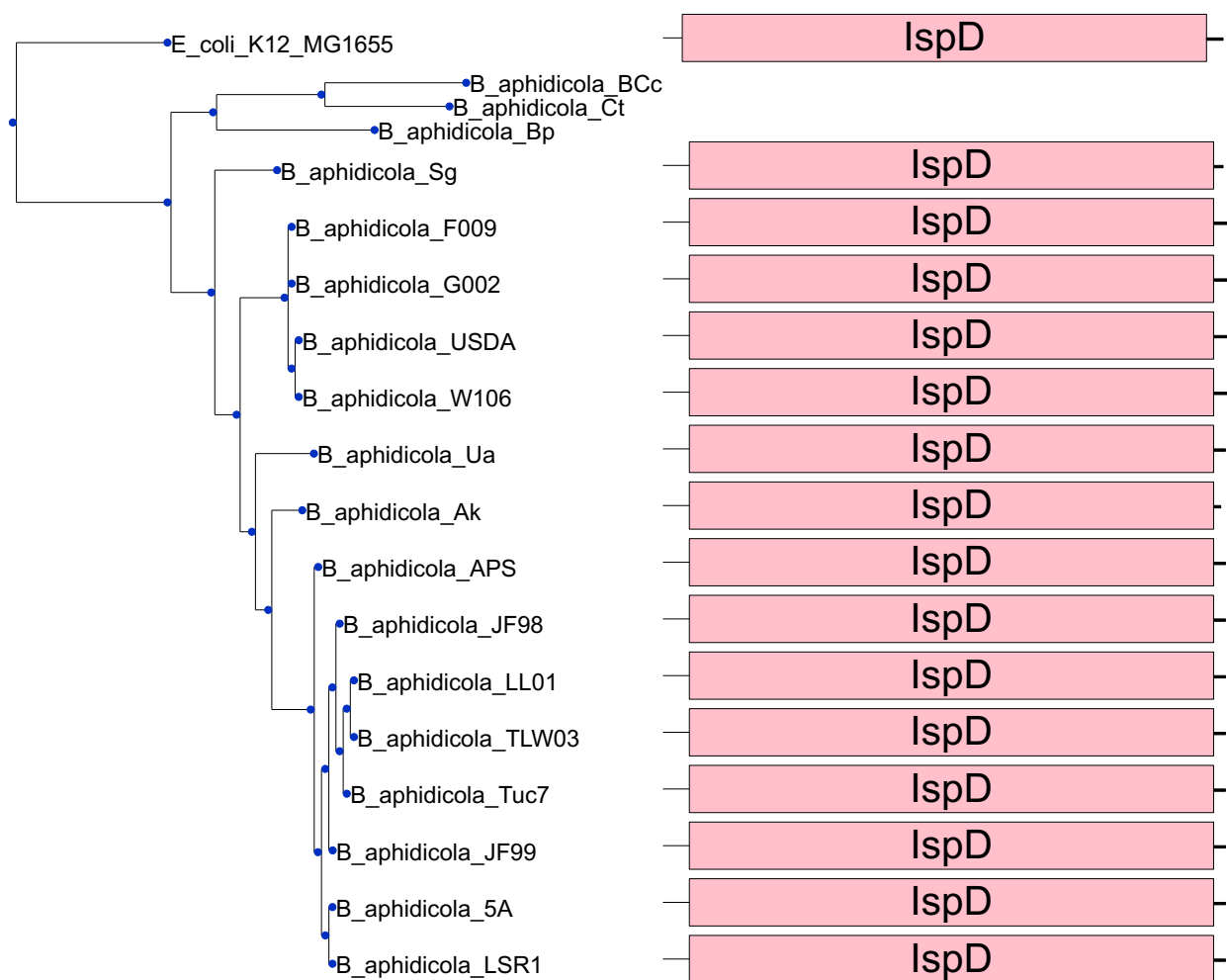
4-diphosphocytidyl-2-C-methylerythritol kinase



ispG
NP_417010.1
1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase

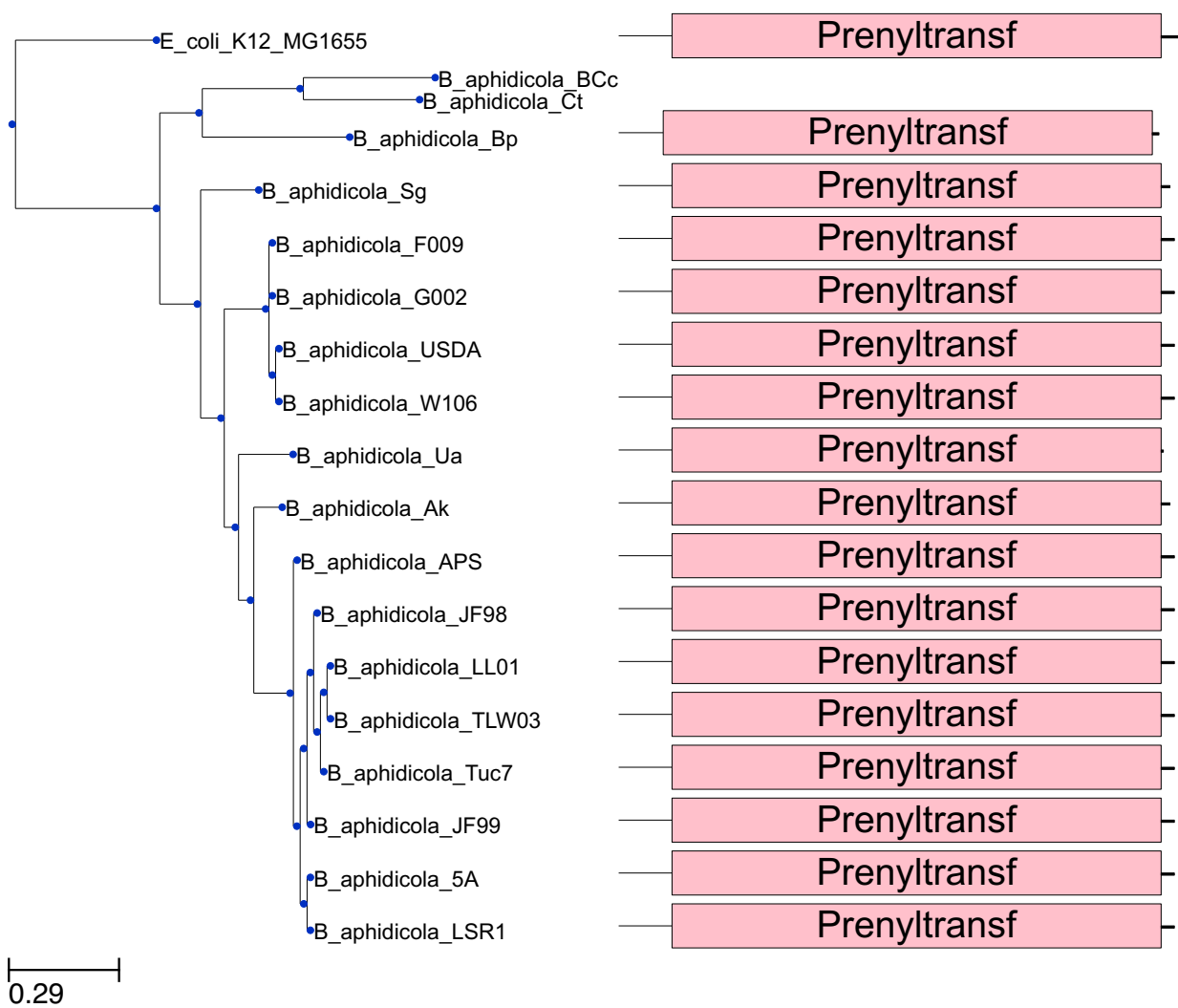


ispF
NP_417226.1
"2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase"

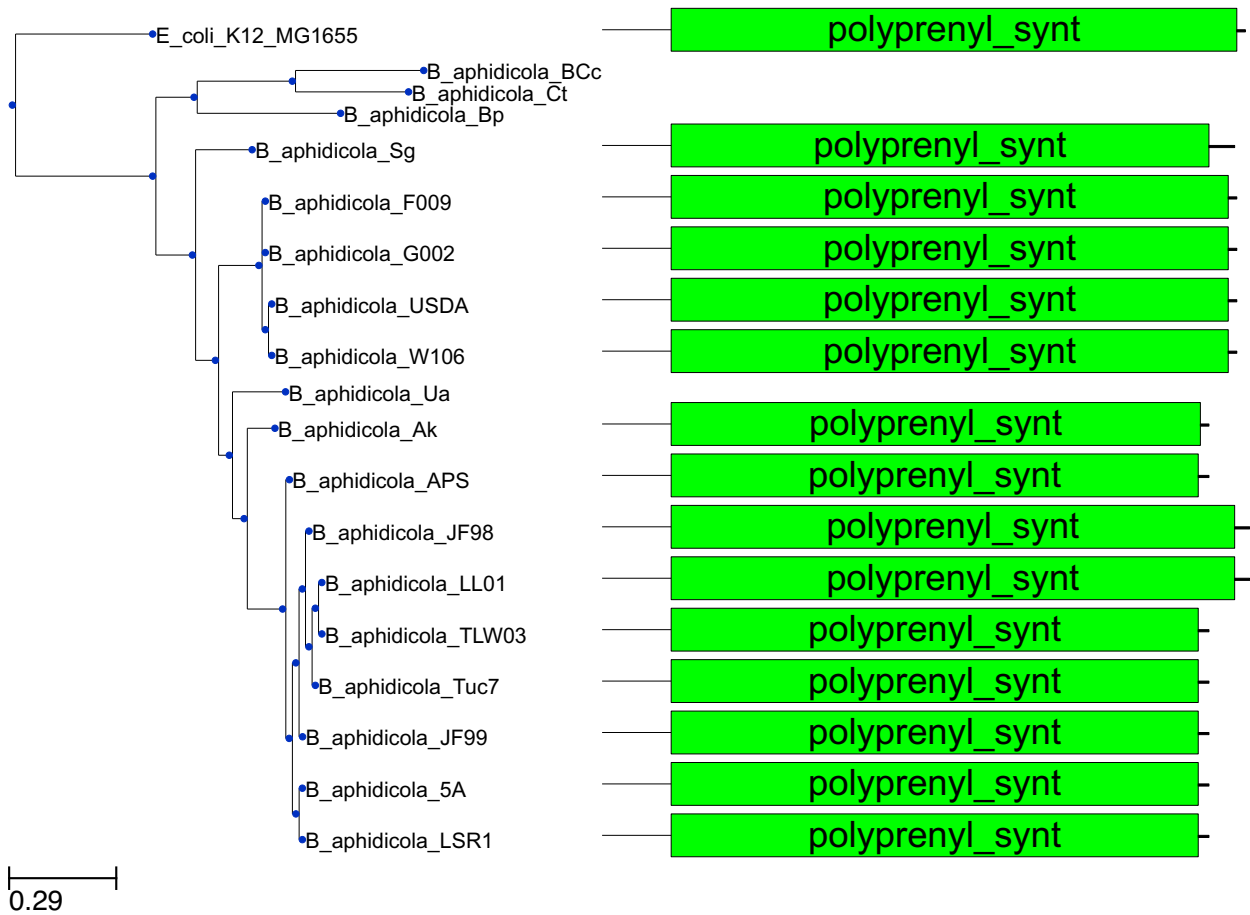


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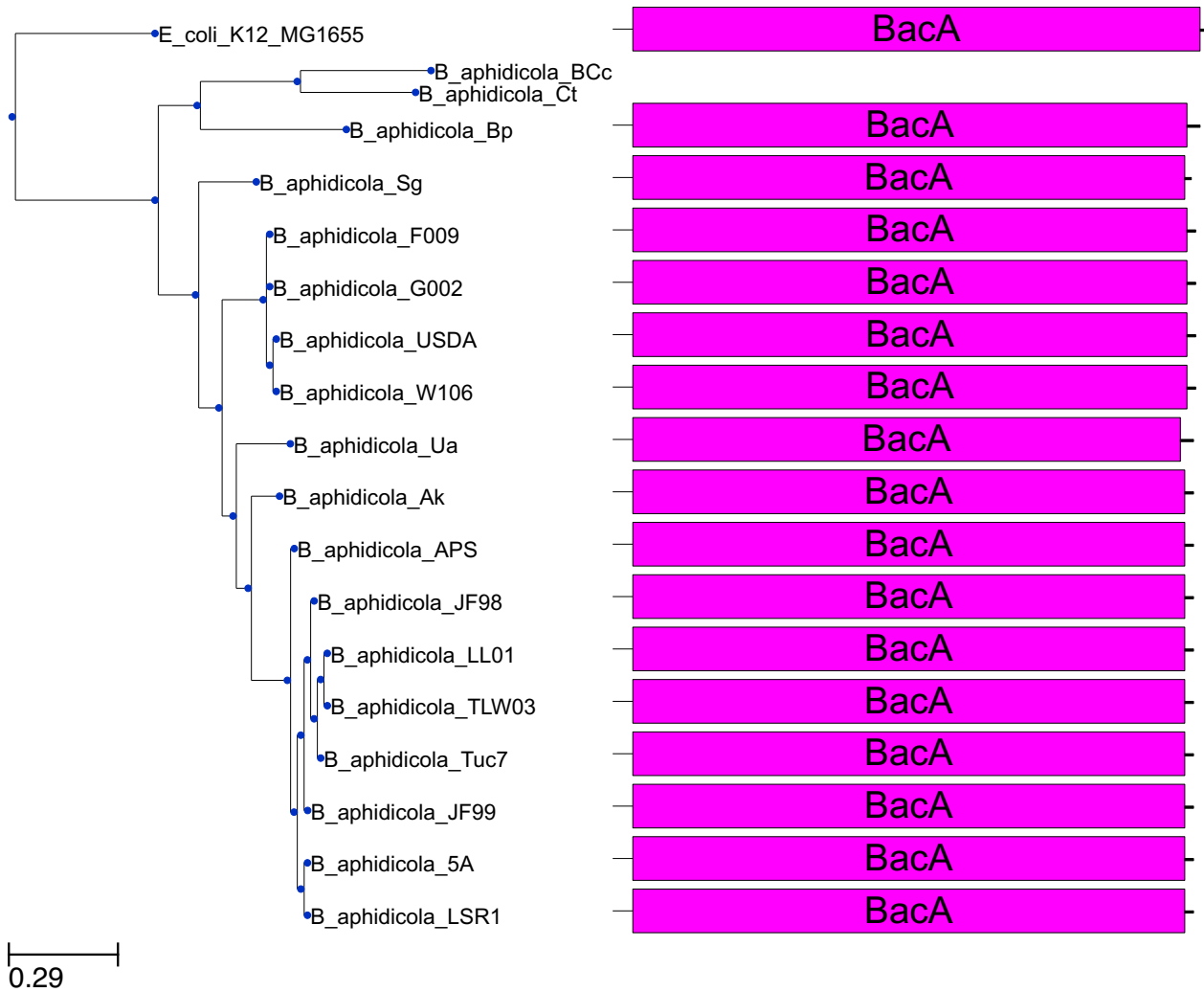
ispD
NP_417227.1
4-diphosphocytidyl-2C-methyl-D-erythritol synthase



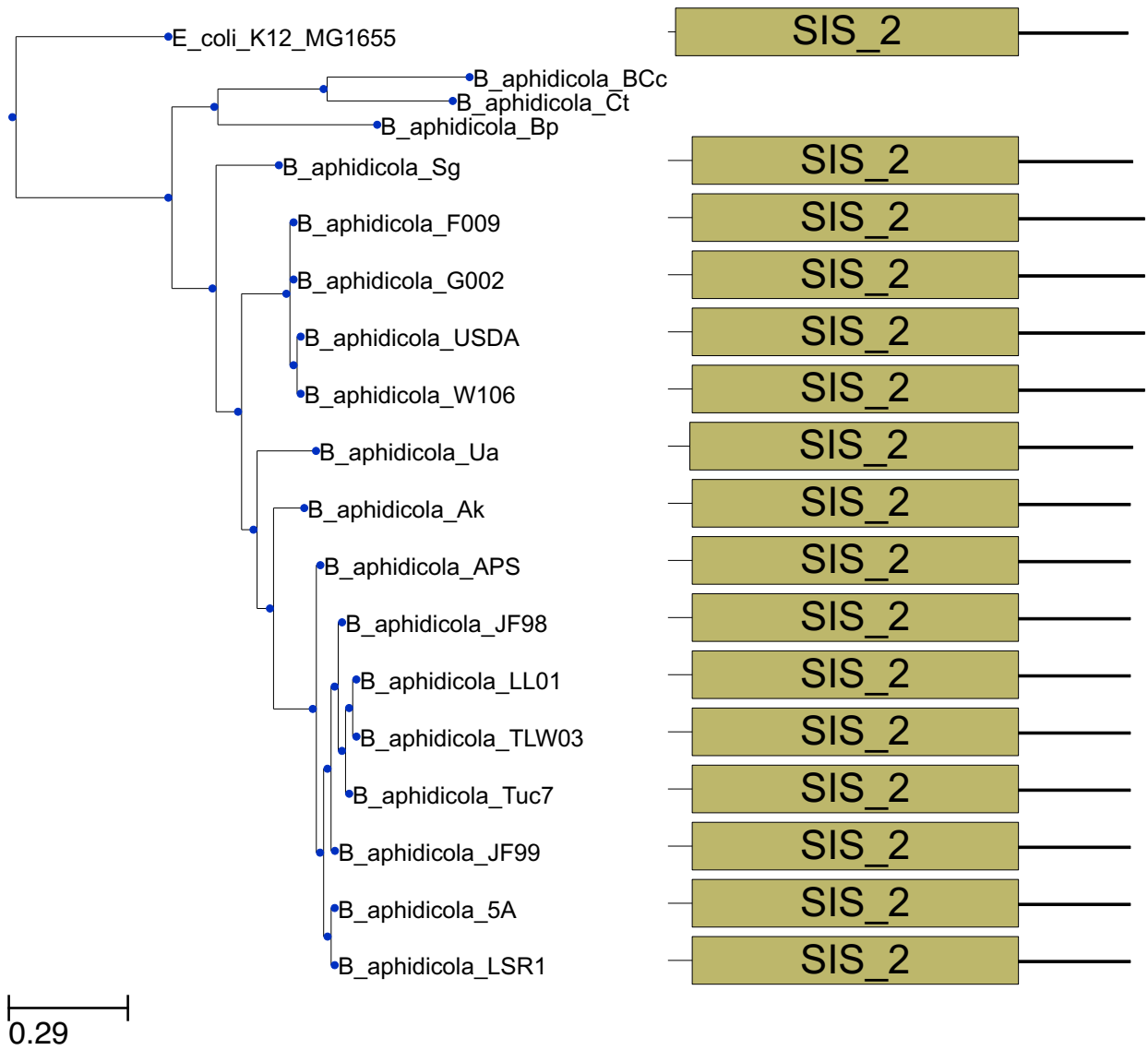
ispU
NP_414716.1
undecaprenyl pyrophosphate synthase



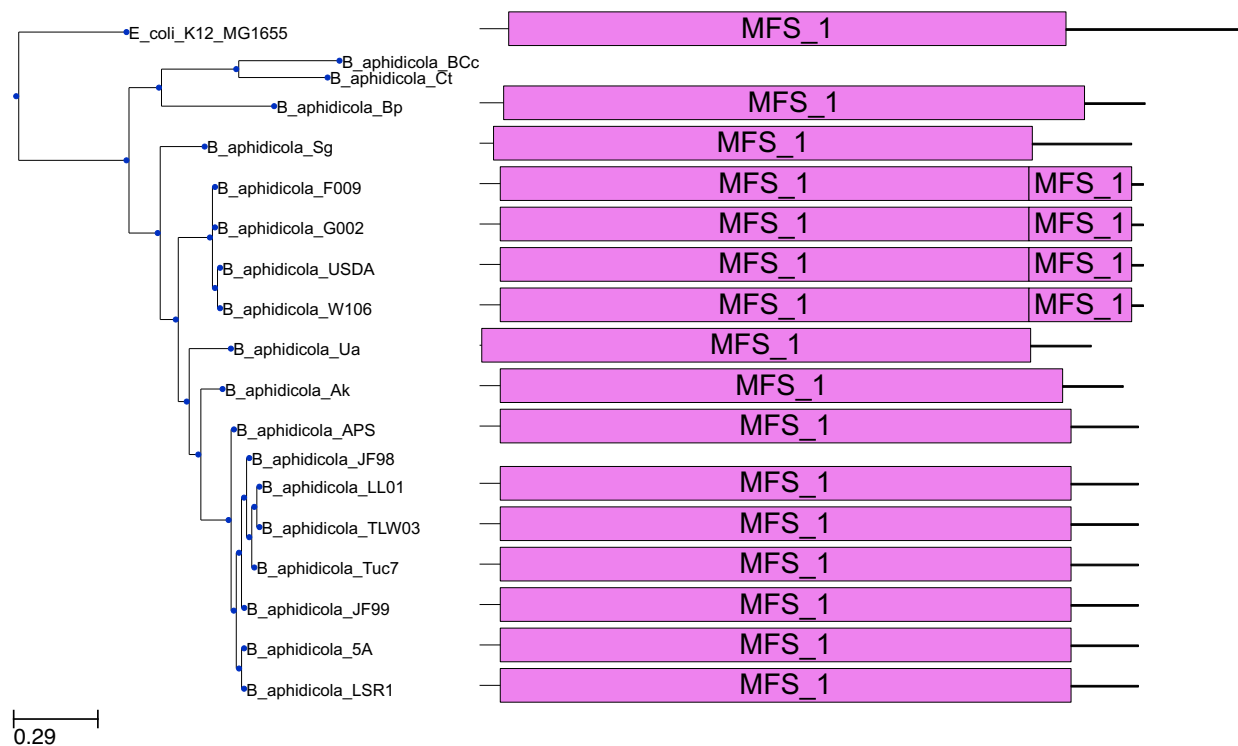
ispA
NP_414955.1
geranyltranstransferase



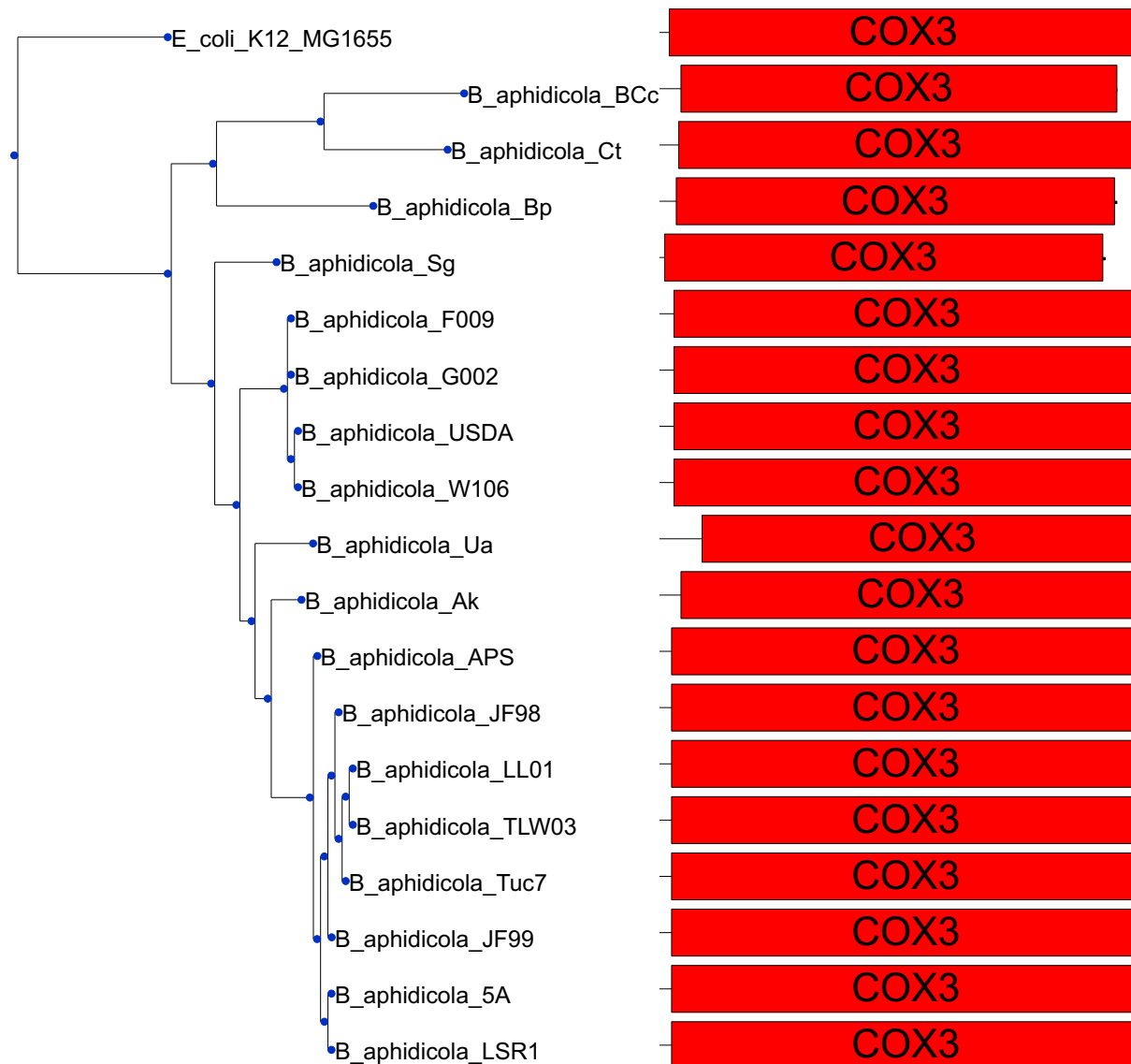
bacA
NP_417529.1
undecaprenyl pyrophosphate phosphatase



lpcA
NP_414757.1
D-sedoheptulose 7-phosphate isomerase

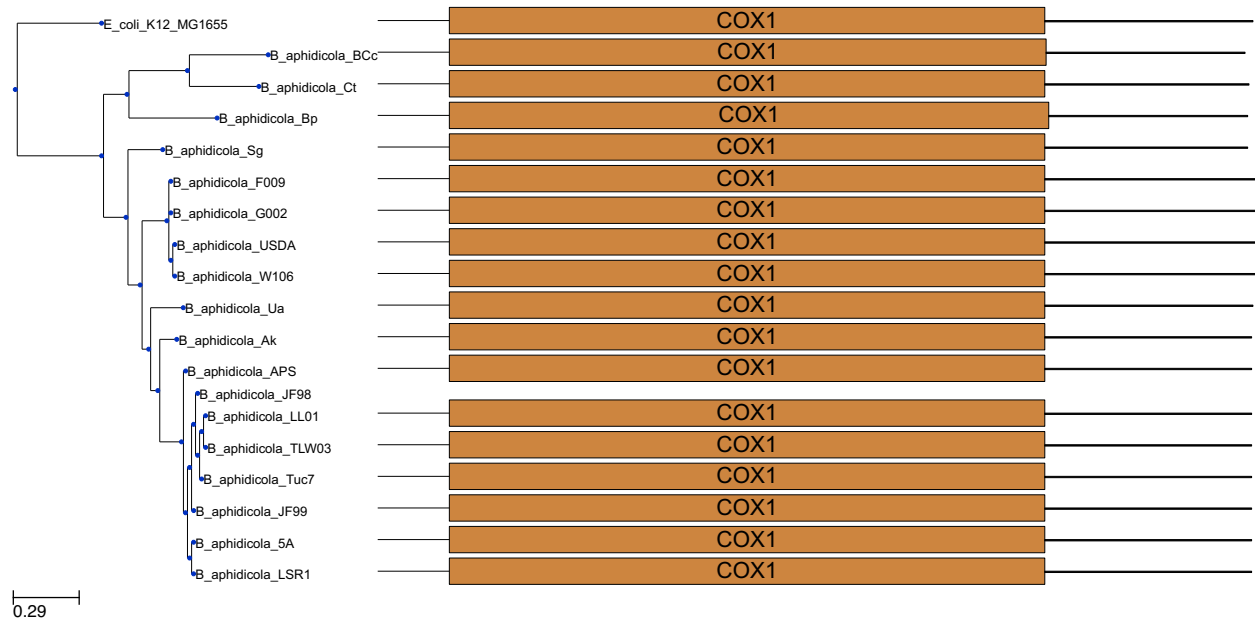


yajR
NP_414961.4
putative transporter



0.29

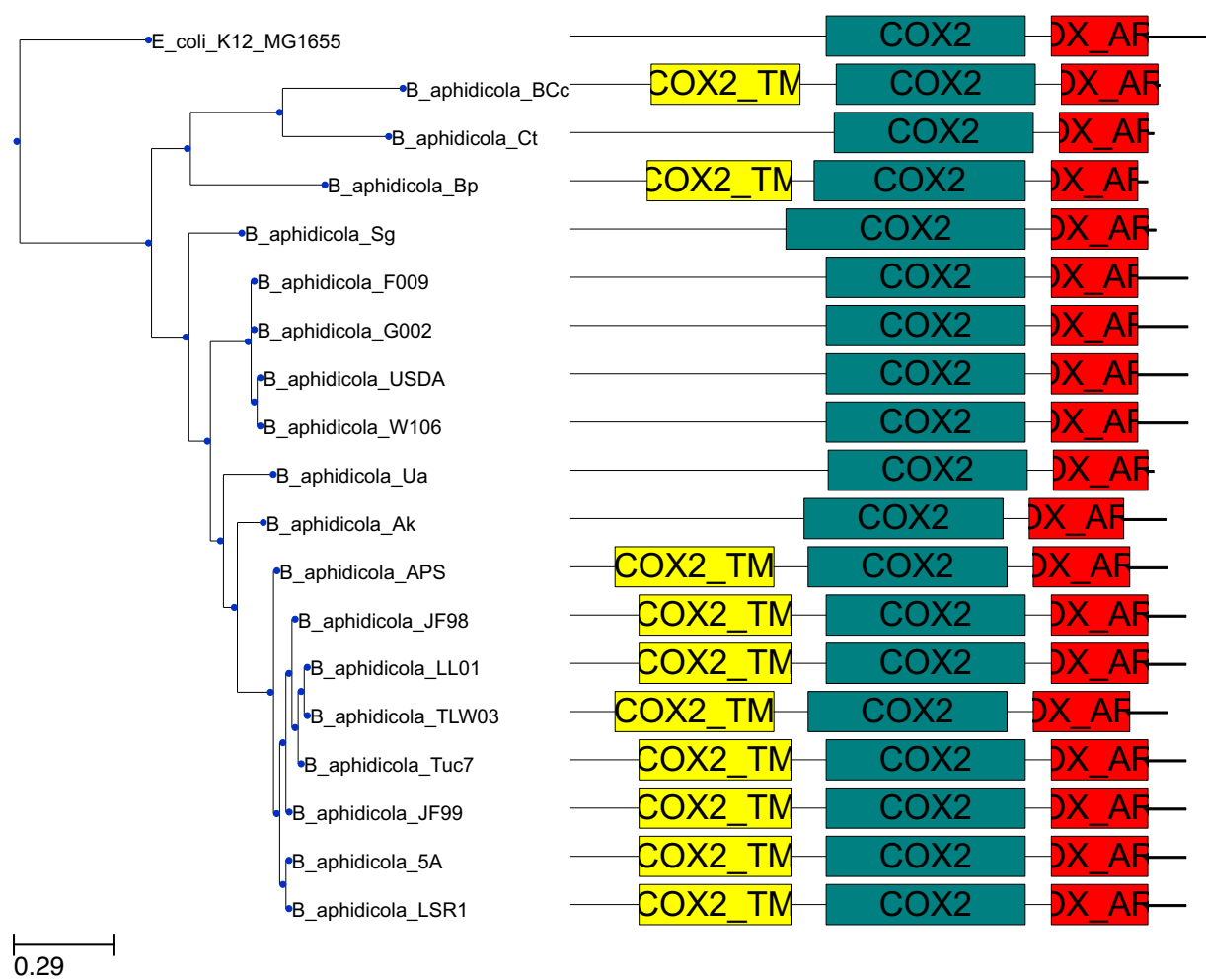
cyoC
NP_414964.1
cytochrome o ubiquinol oxidase subunit III



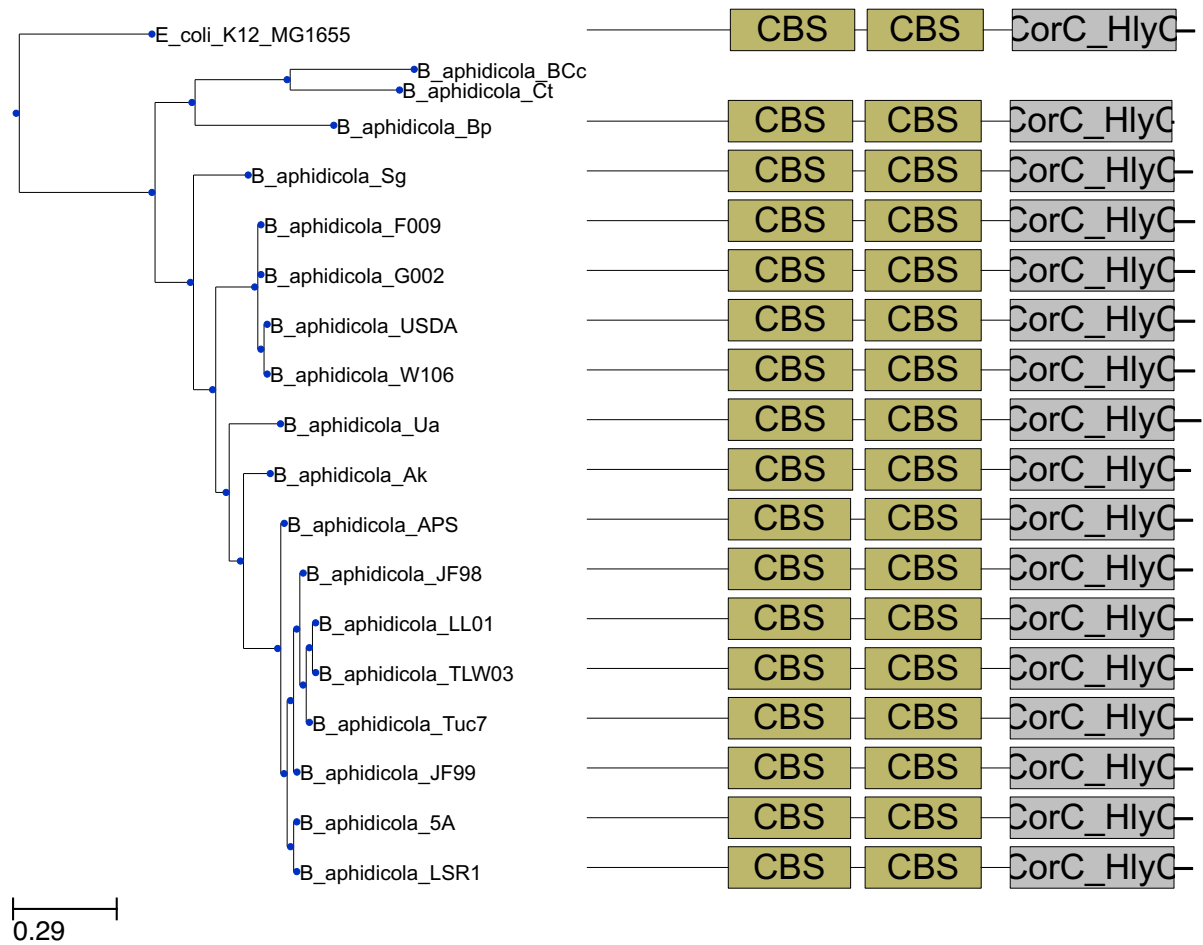
cyoB

NP_414965.1

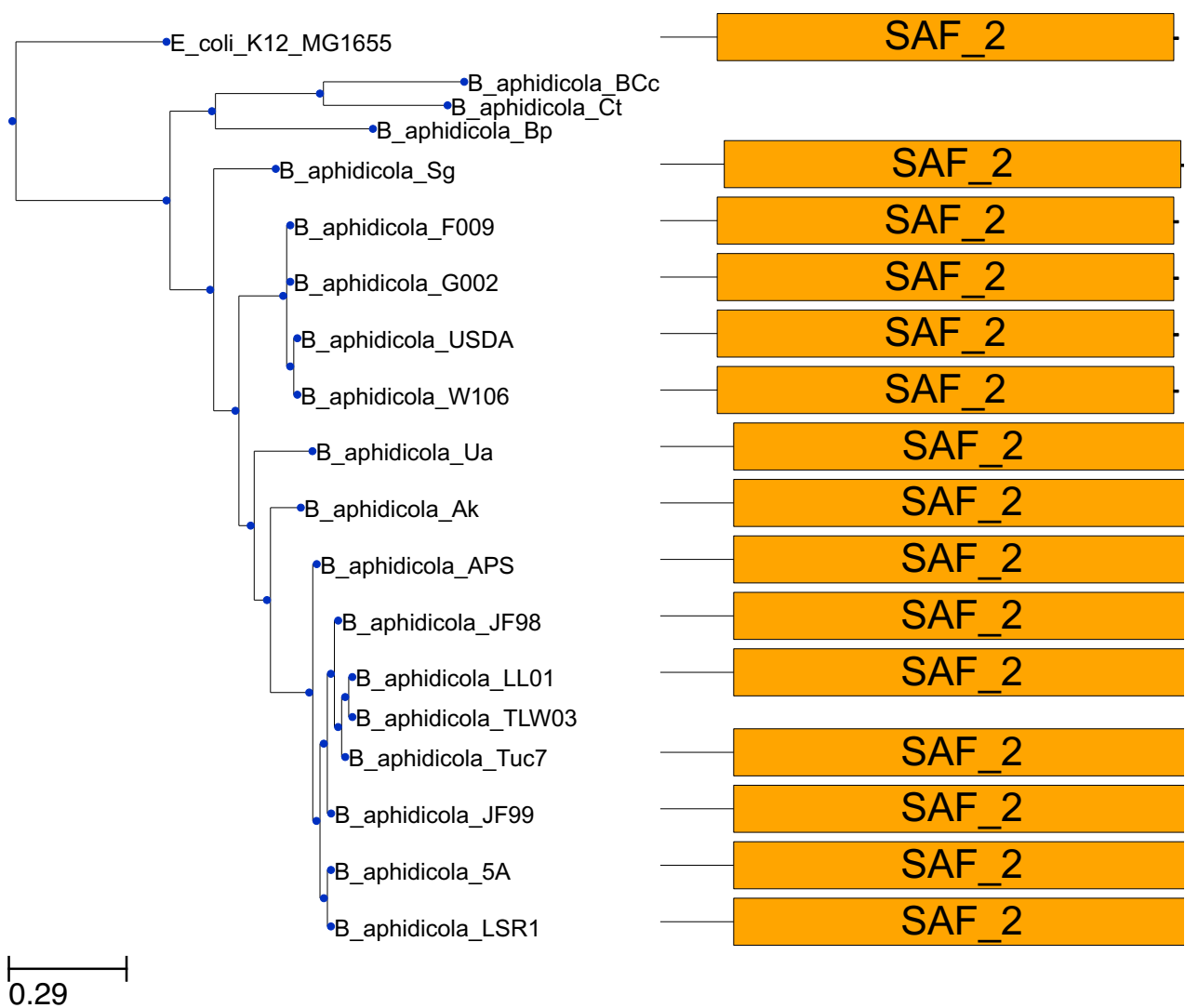
cytochrome o ubiquinol oxidase subunit I



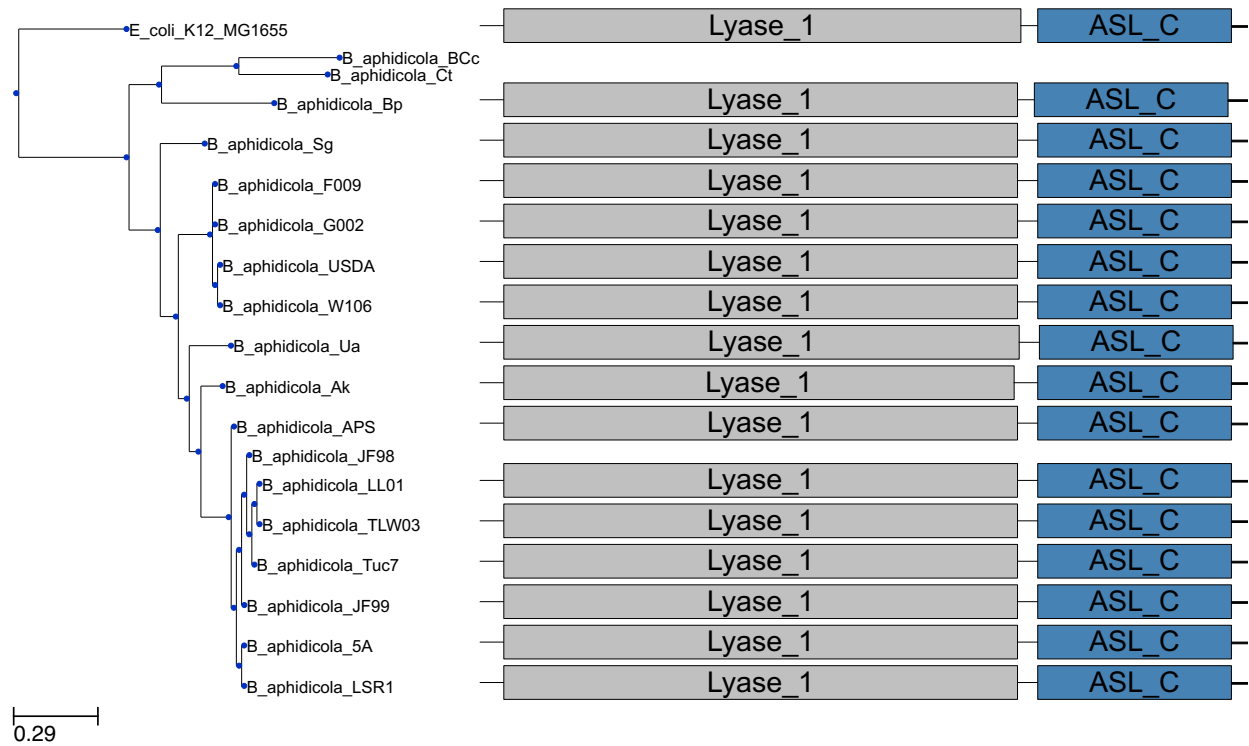
cyoA
NP_414966.1
cytochrome o ubiquinol oxidase subunit II



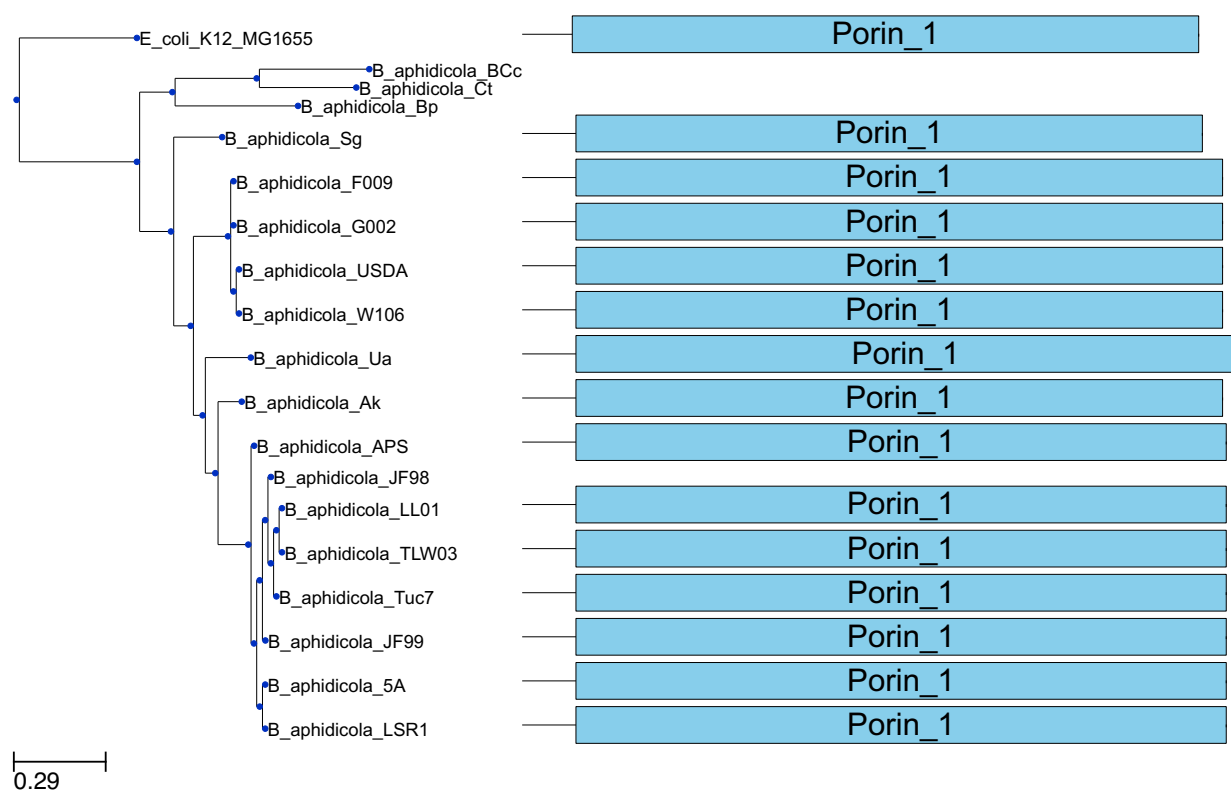
ybeX
NP_415191.1
putative ion transport



flgA
NP_415590.1
assembly protein for flagellar basal-body periplasmic P ring



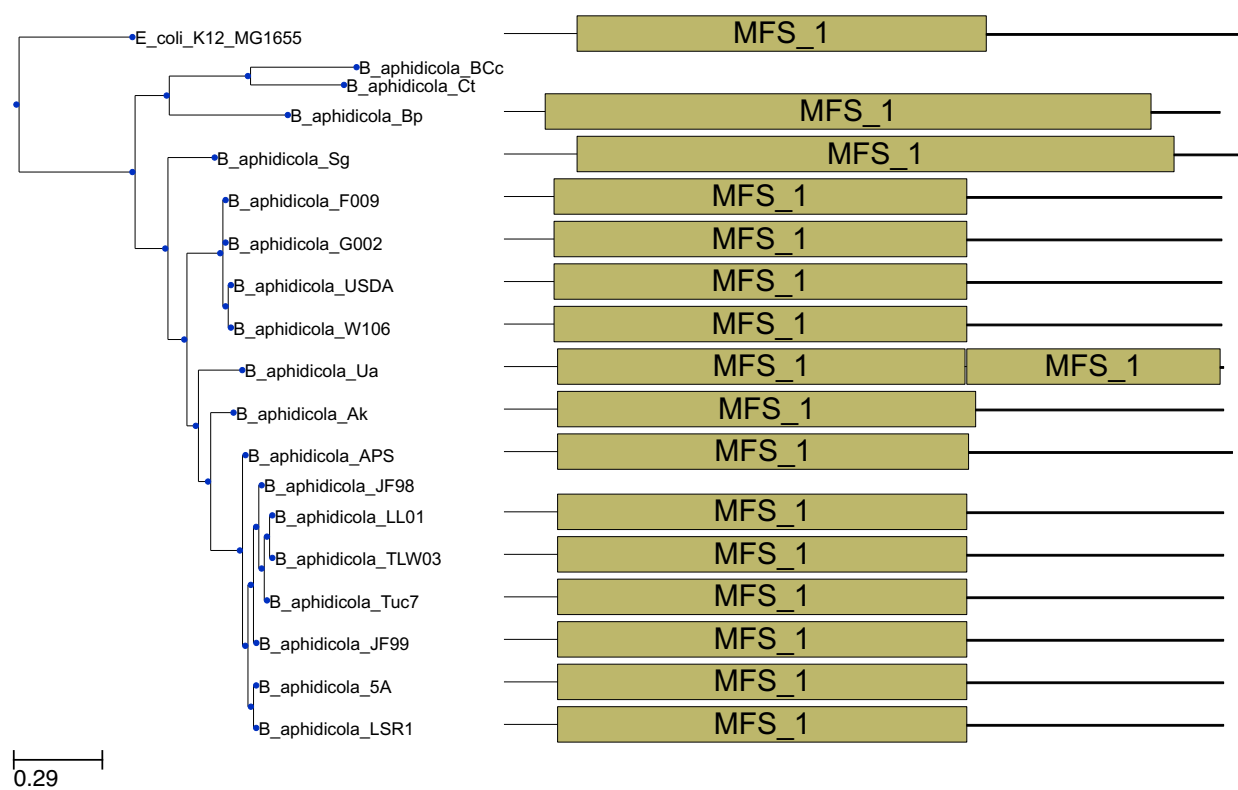
purB
NP_415649.1
adenylosuccinate lyase



ompN

NP_415895.1

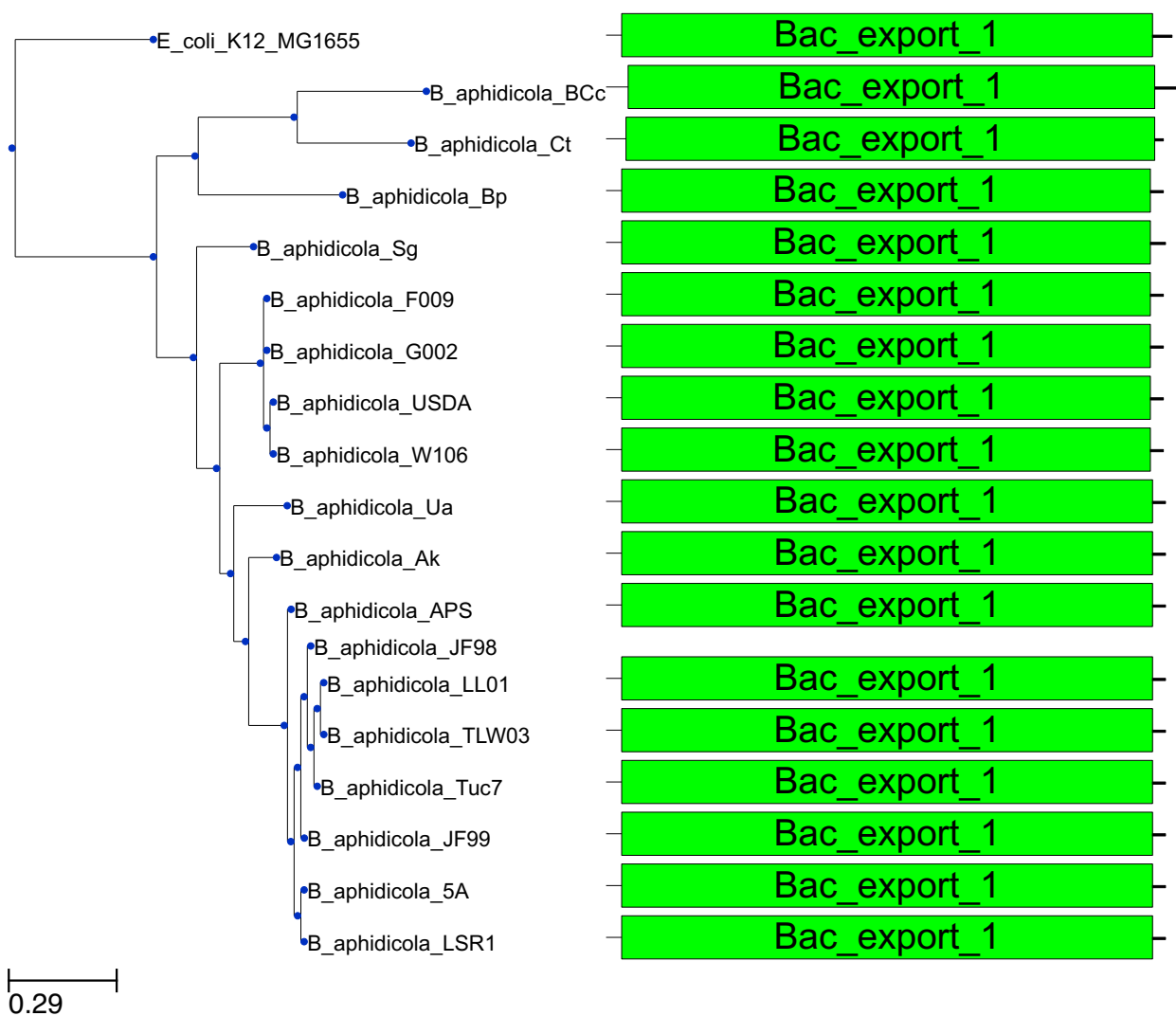
"outer membrane pore protein N, non-specific"



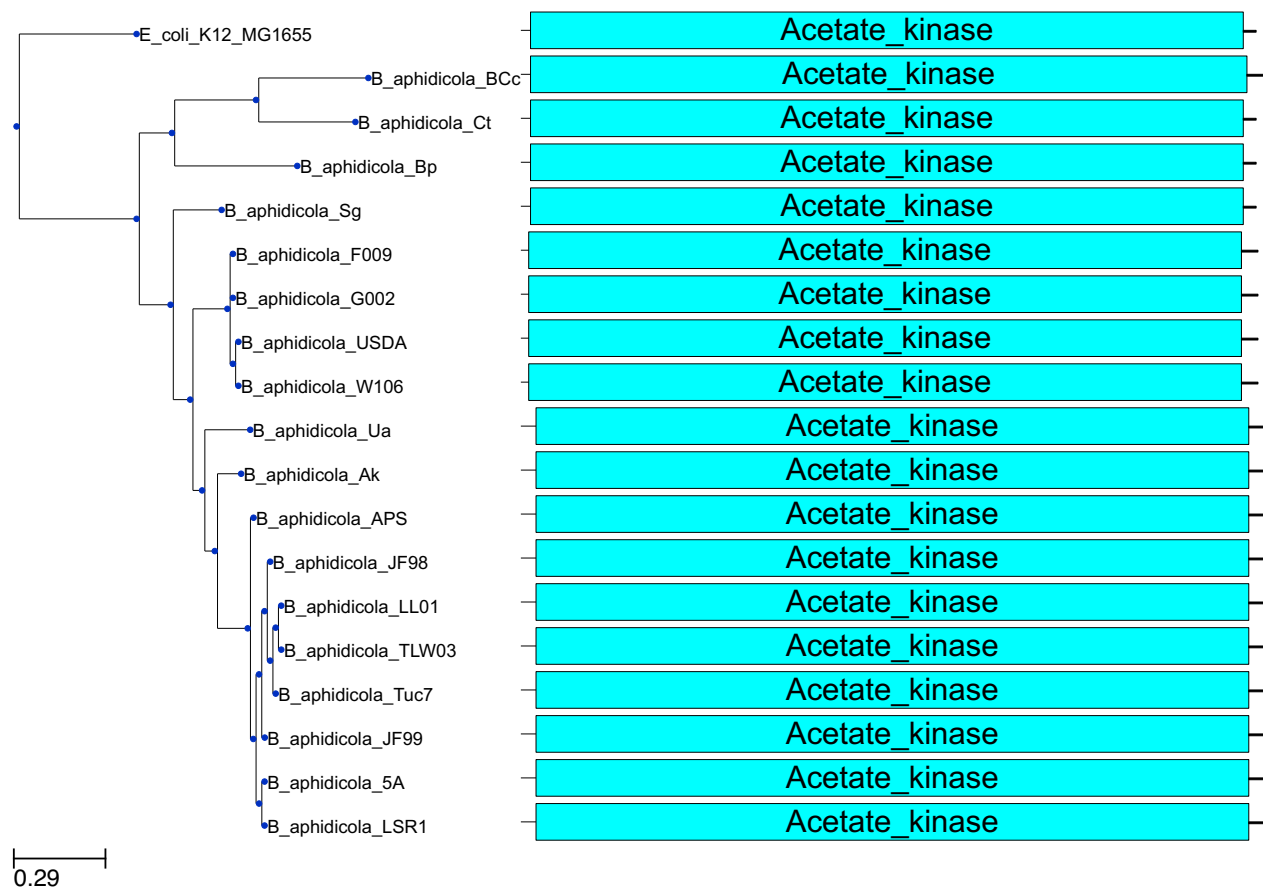
ynfM

NP_416113.1

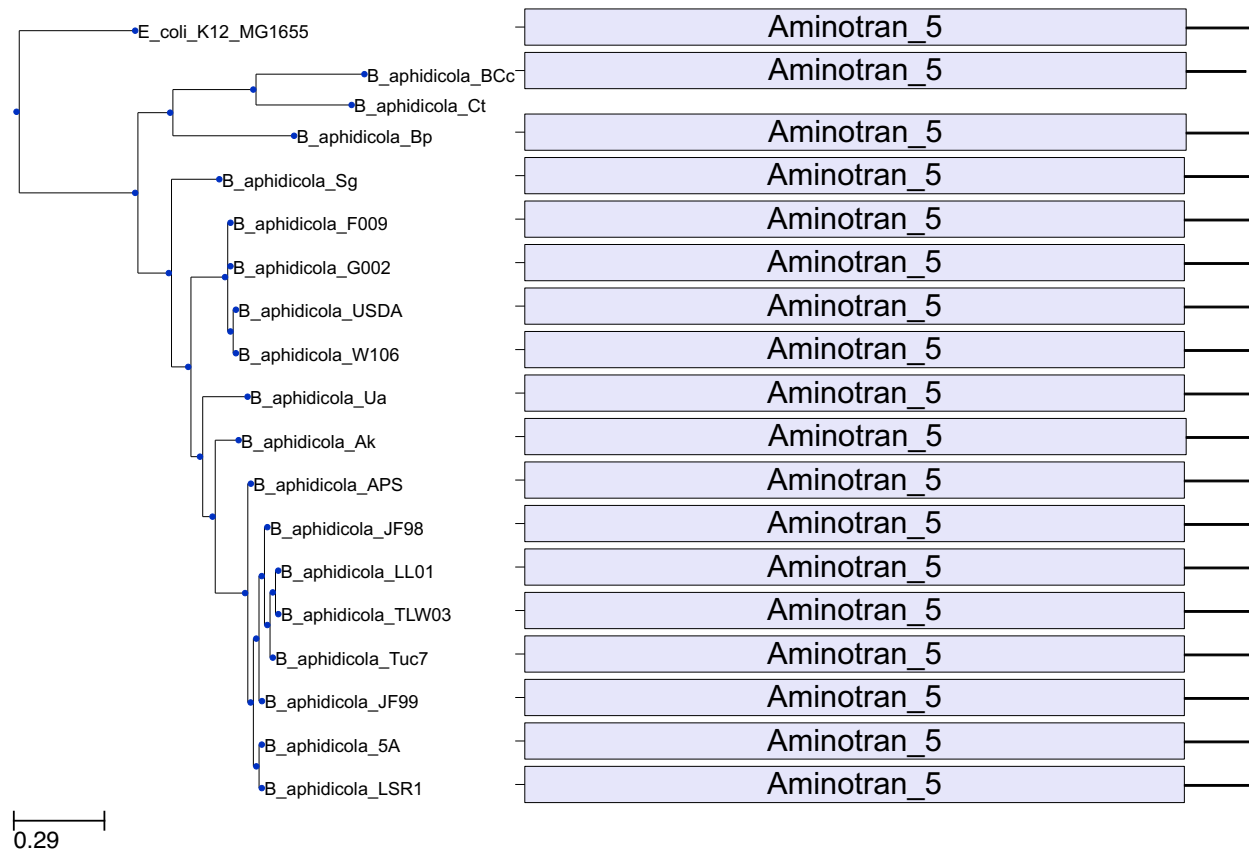
putative arabinose efflux transporter



fliR
NP_416460.1
flagellar export pore protein



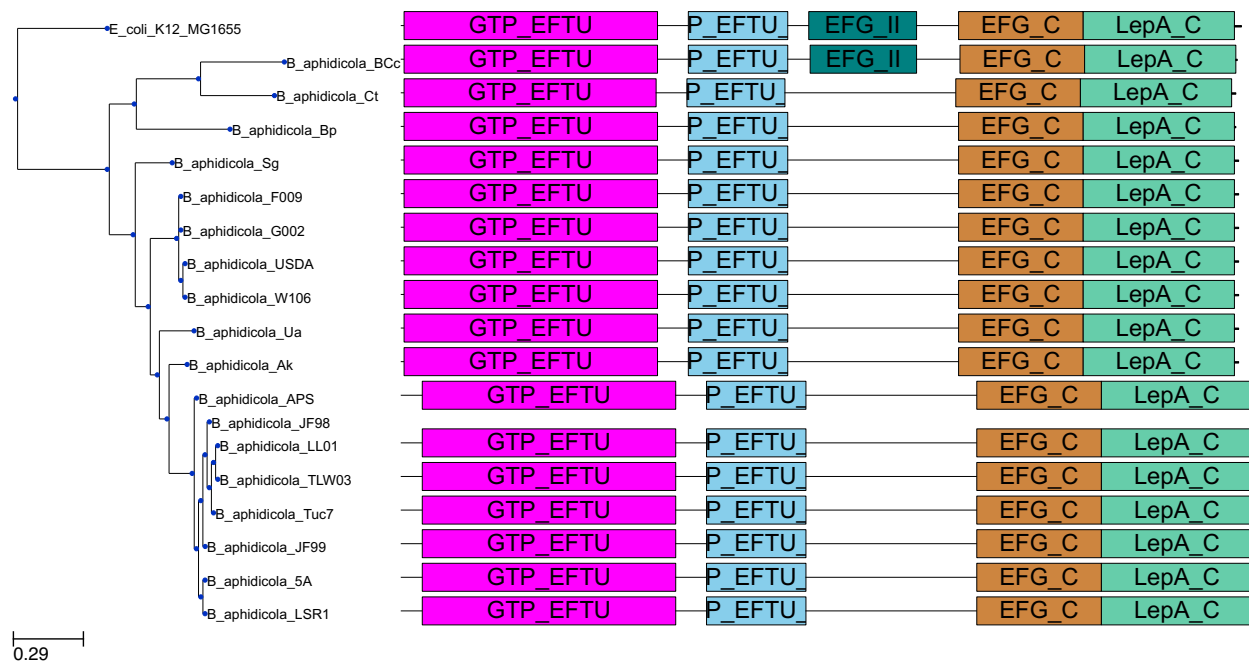
ackA
 NP_416799.1
 acetate kinase A and propionate kinase 2



iscS

YP_026169.1

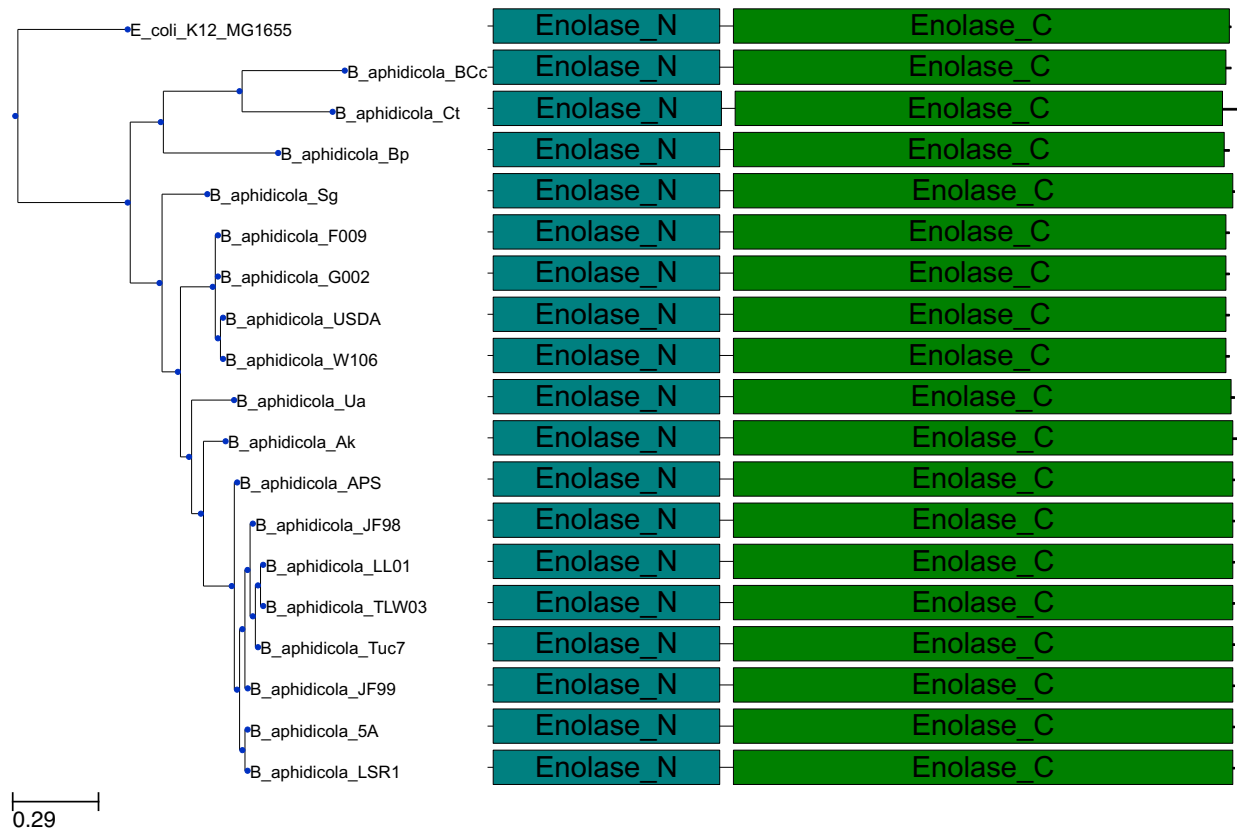
"cysteine desulfurase (tRNA sulfurtransferase), PLP-dependent"



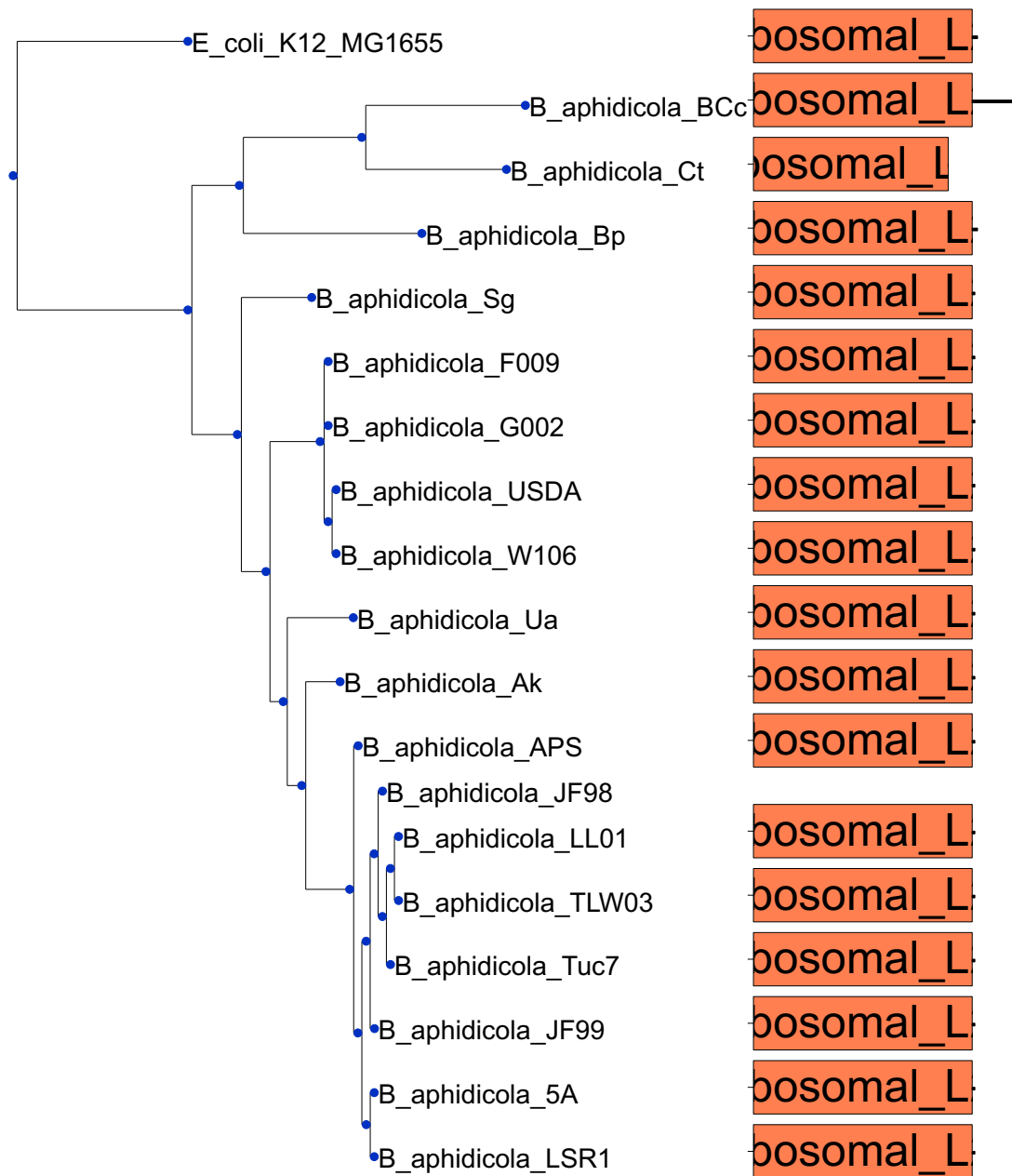
lepA

NP_417064.1

"back-translocating elongation factor EF4, GTPase"

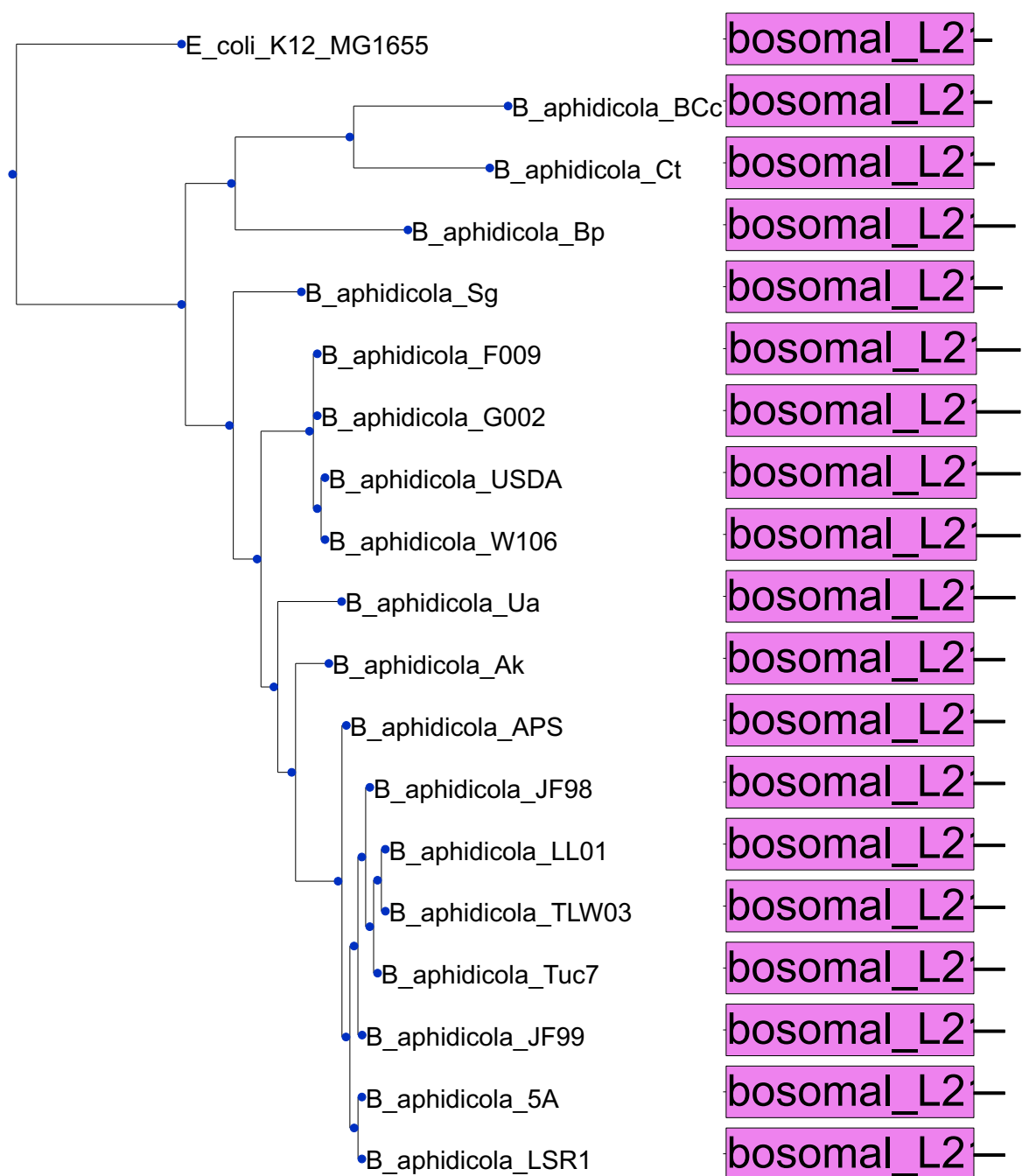


eno
NP_417259.1
enolase



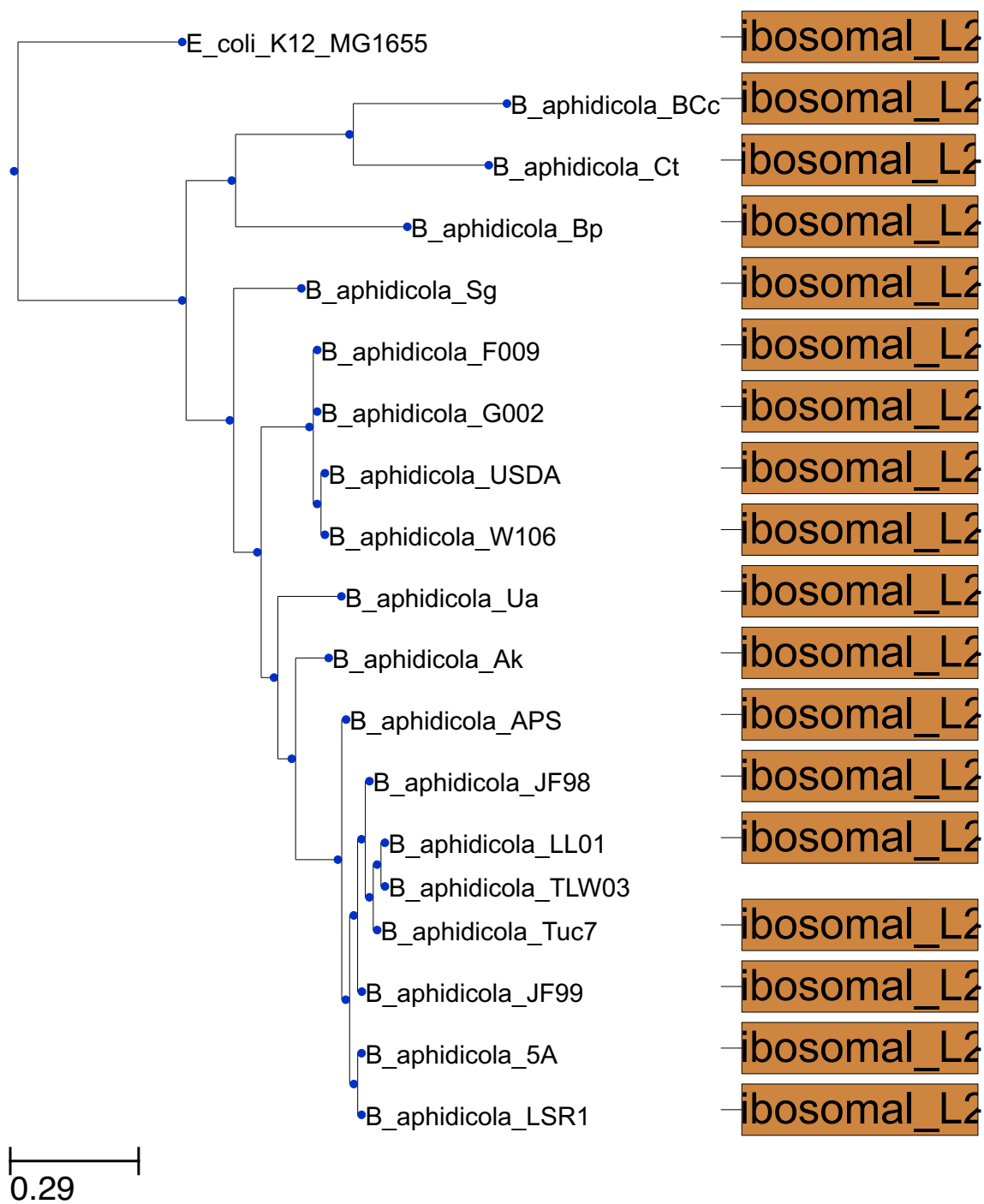
0.29

rpmA
 NP_417652.1
 50S ribosomal subunit protein L27



0.29

rplU
 NP_417653.1
 50S ribosomal subunit protein L21

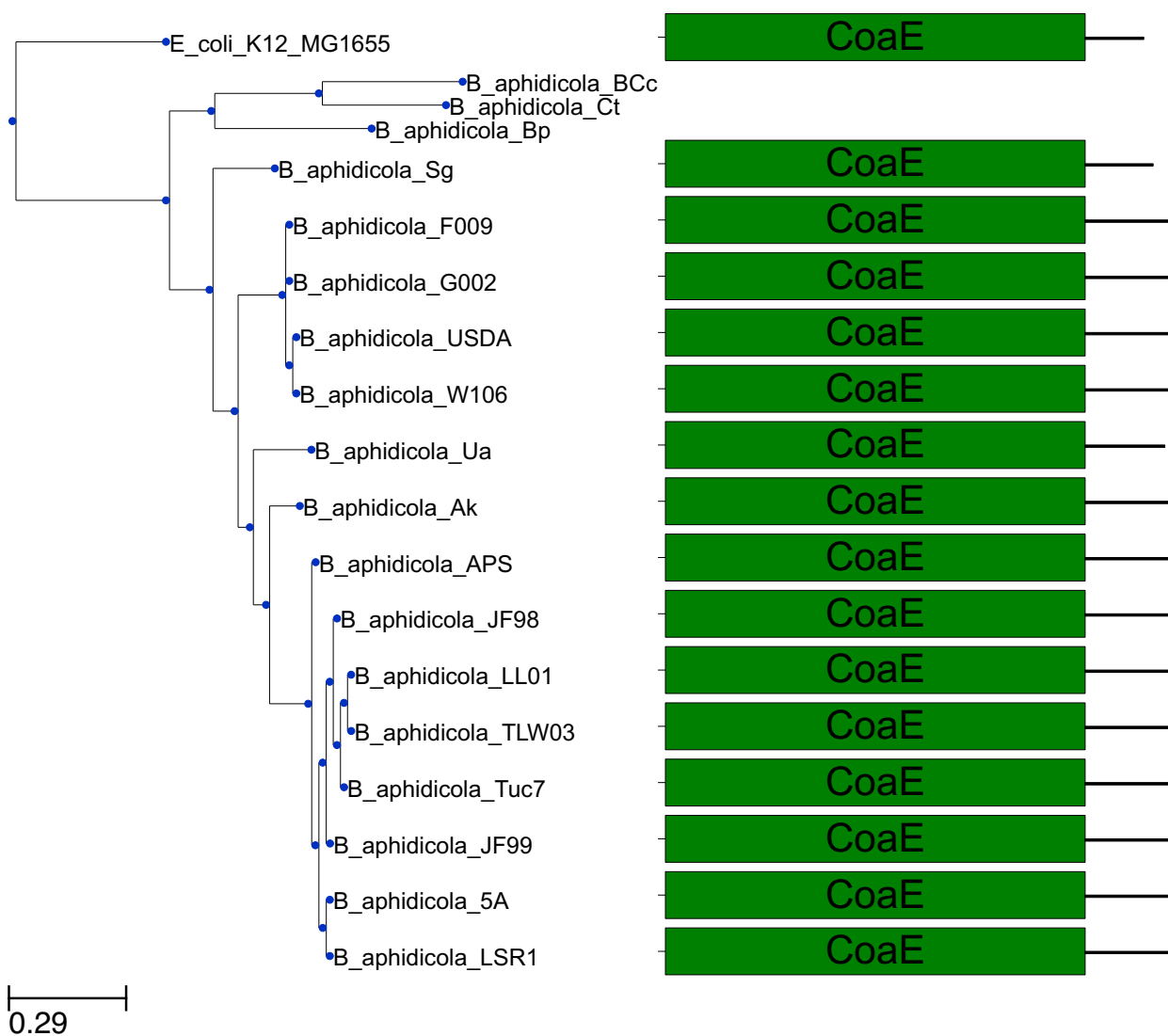


rplW
NP_417777.1
50S ribosomal subunit protein L23

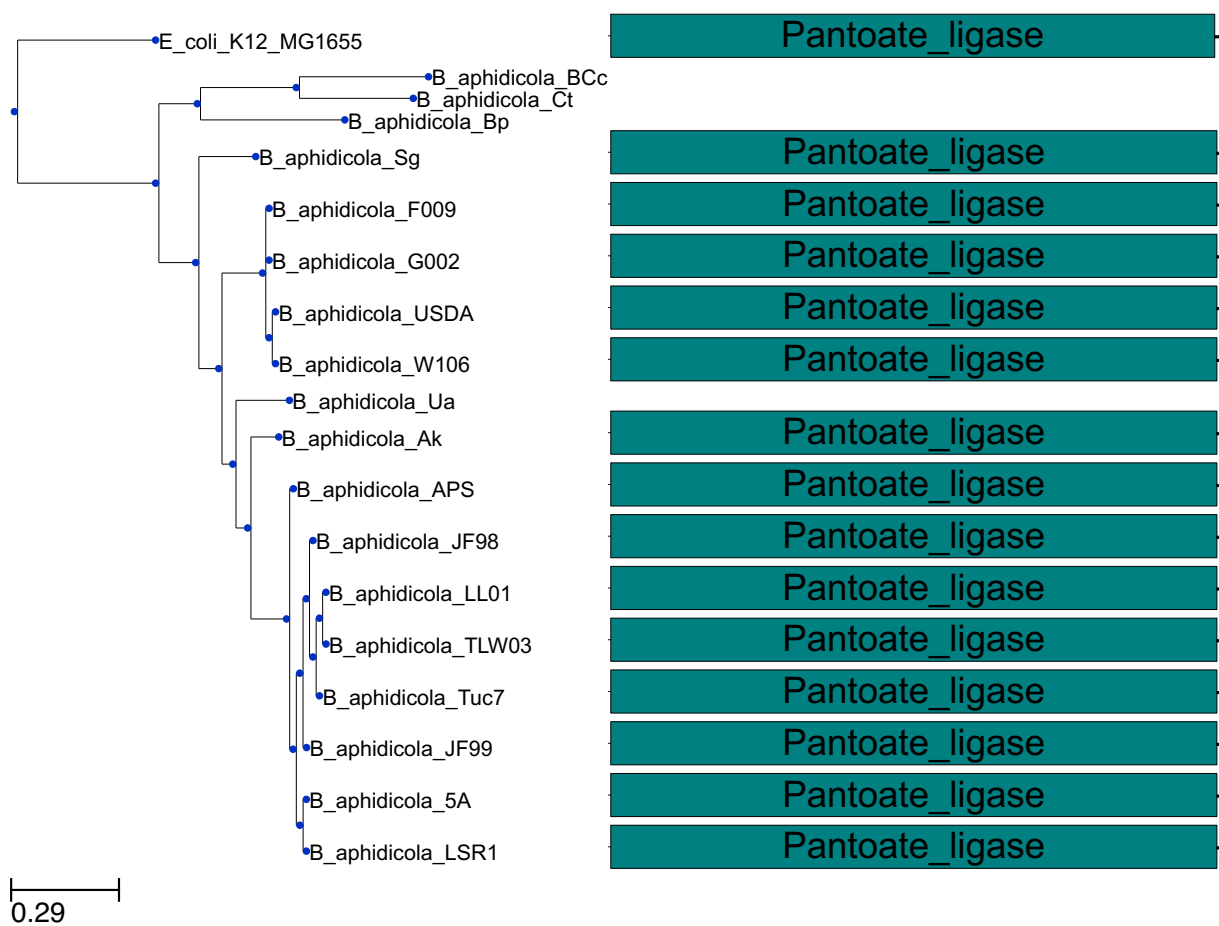


0.29

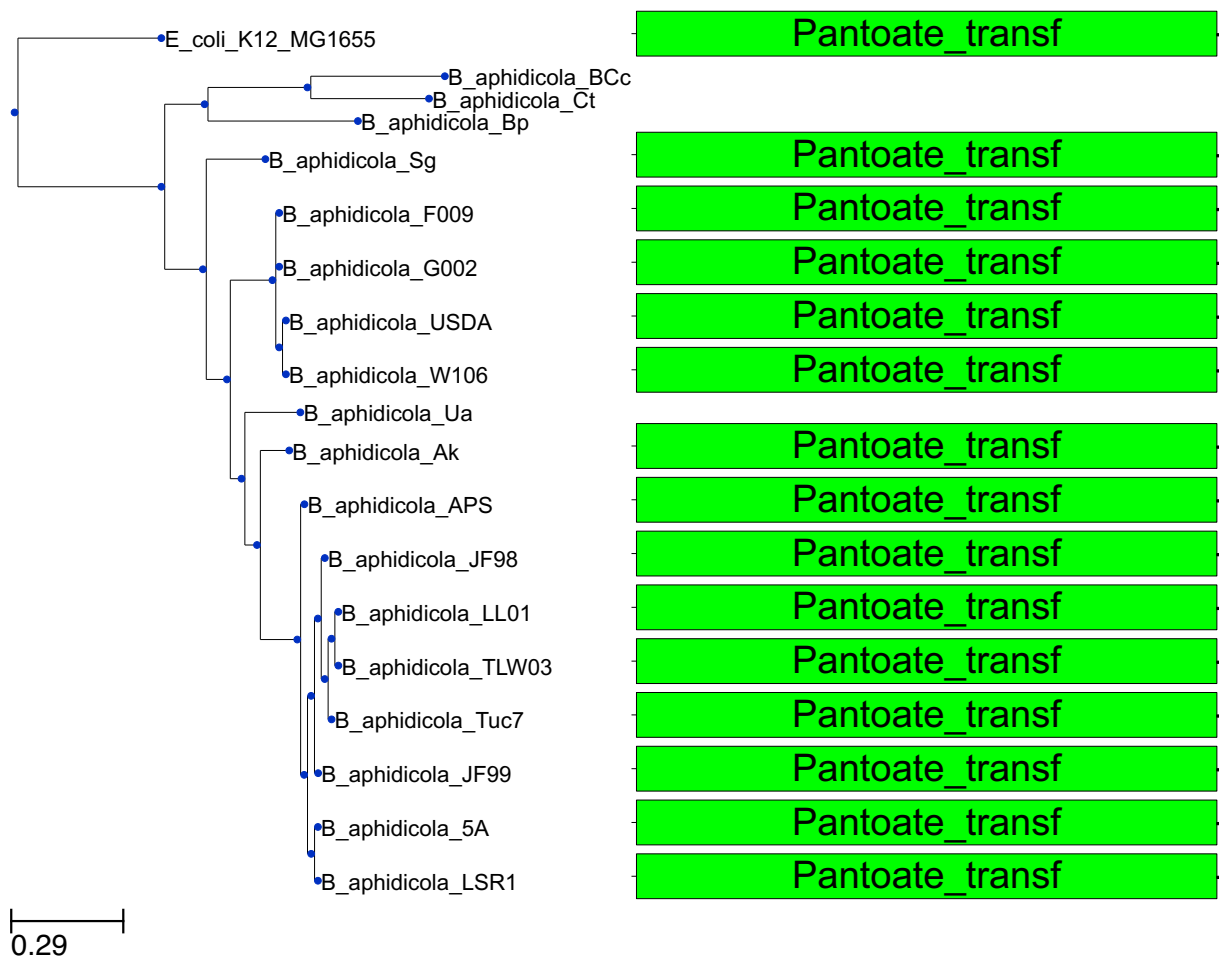
trxA
NP_418228.2
thioredoxin 1



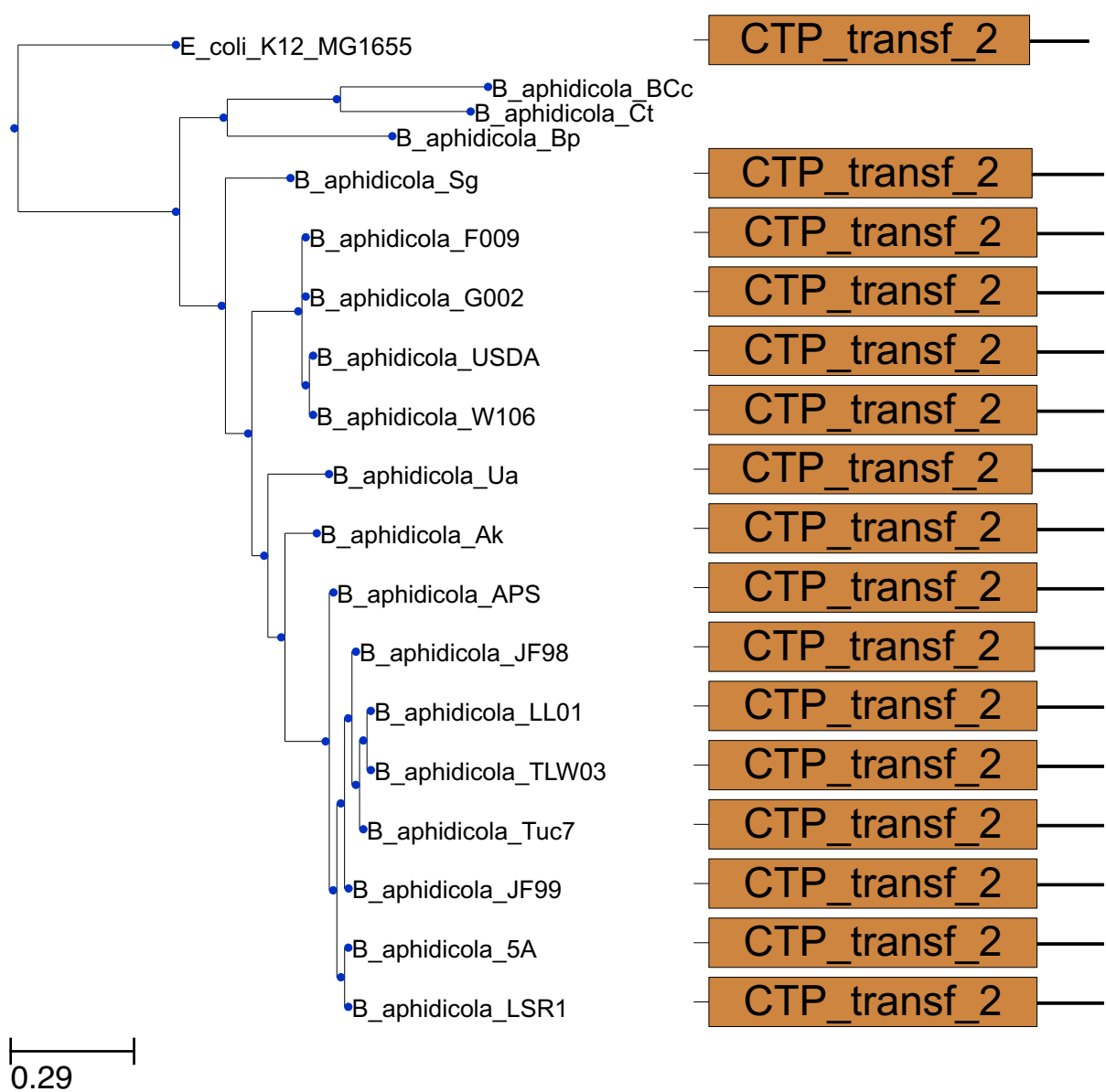
coaE
NP_414645.1
dephospho-CoA kinase



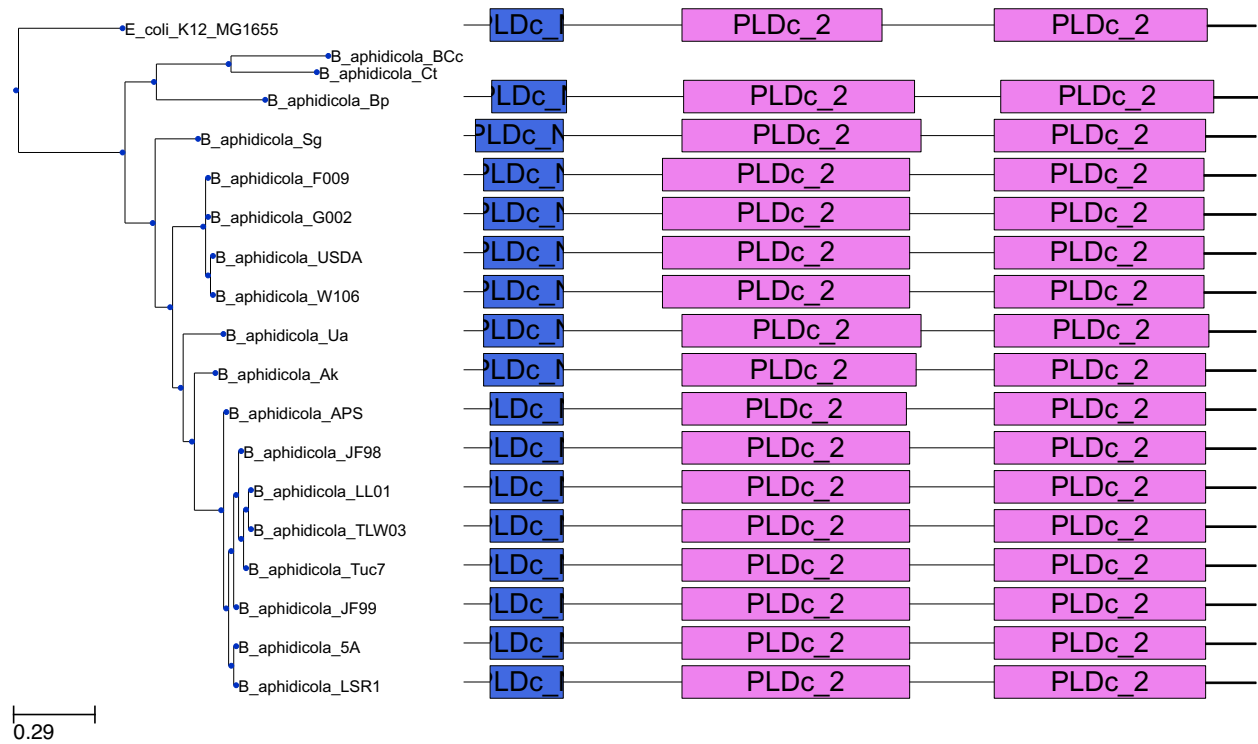
panC
NP_414675.1
pantothenate synthetase



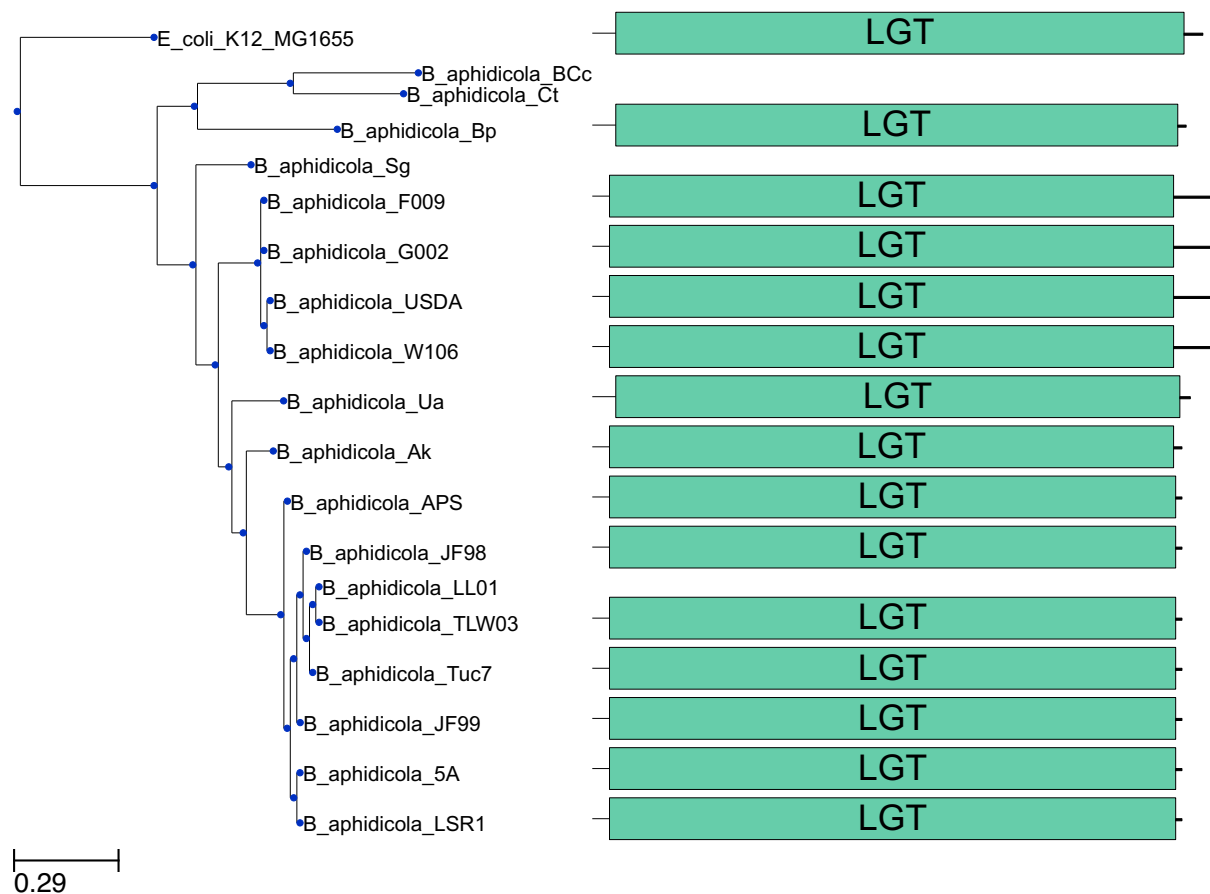
panB
 NP_414676.1
 3-methyl-2-oxobutanoate hydroxymethyltransferase



coaD
NP_418091.1
pantetheine-phosphate adenylyltransferase



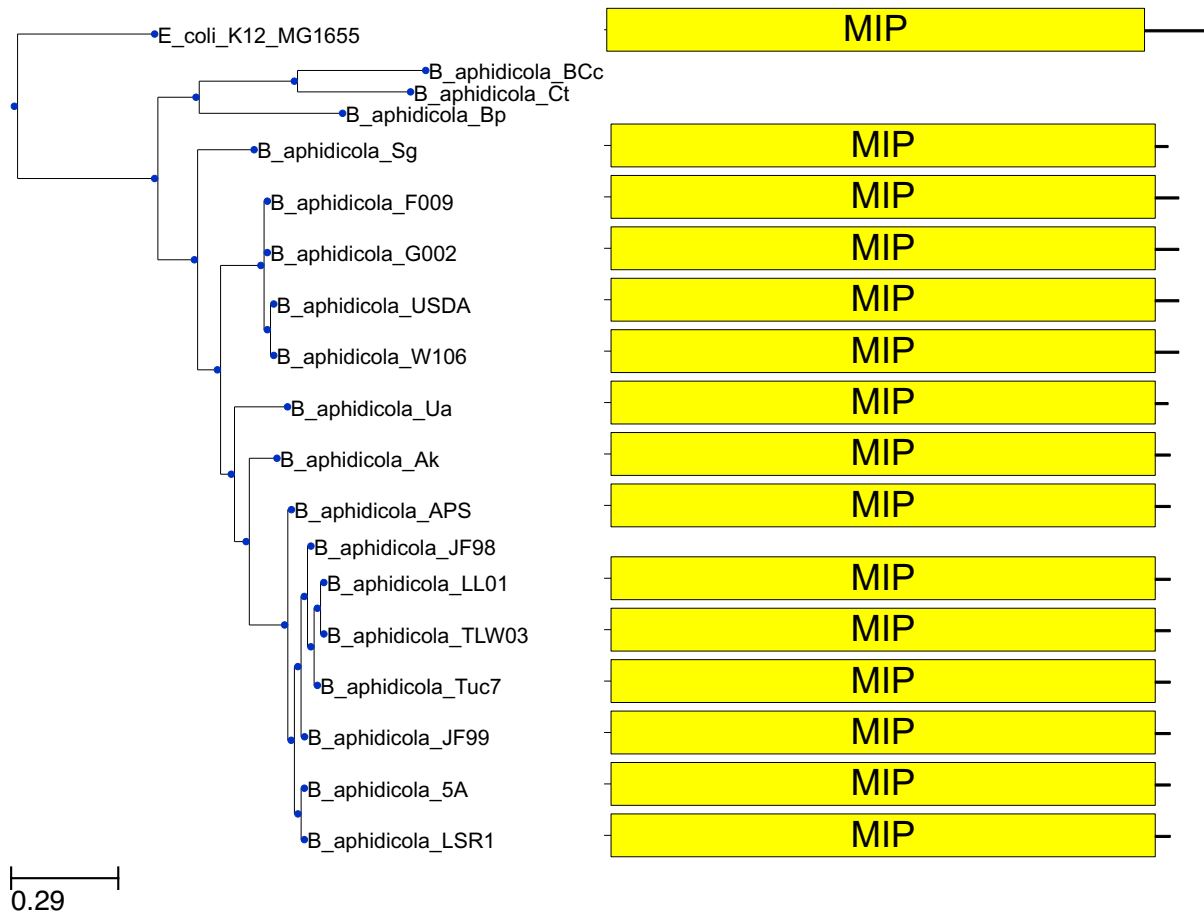
cls
NP_415765.1
cardiolipin synthase 1



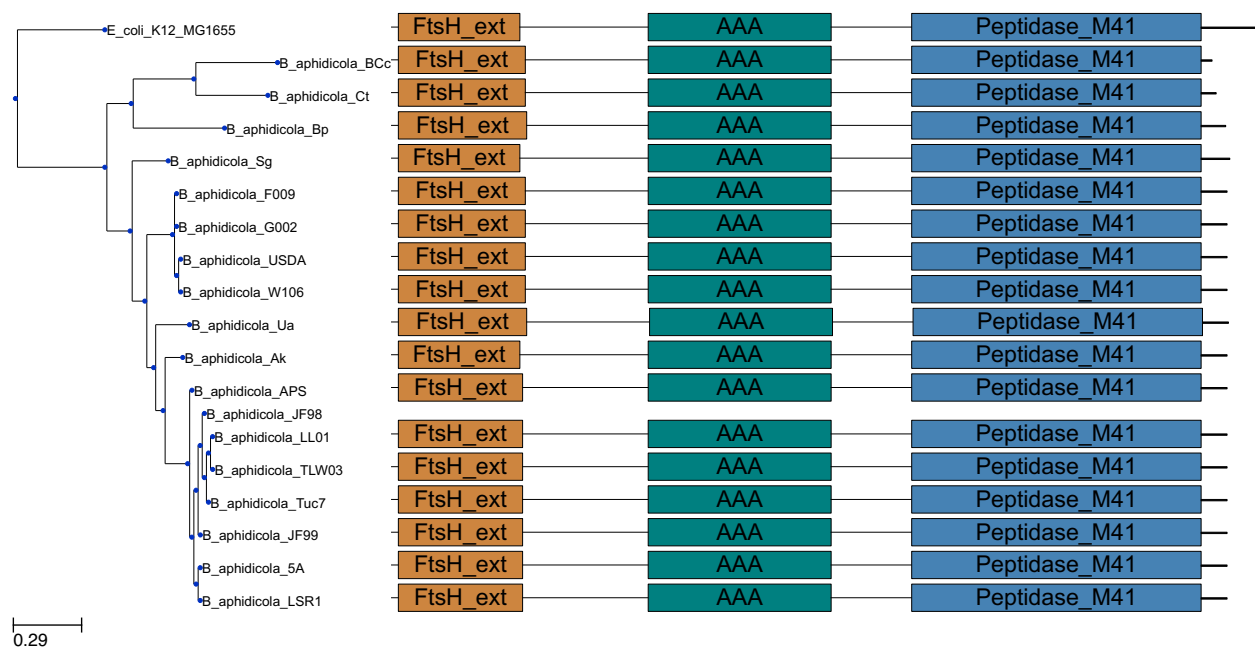
lgt

NP_417305.1

phosphatidylglycerol-prolipoprotein diacylglyceryl transferase



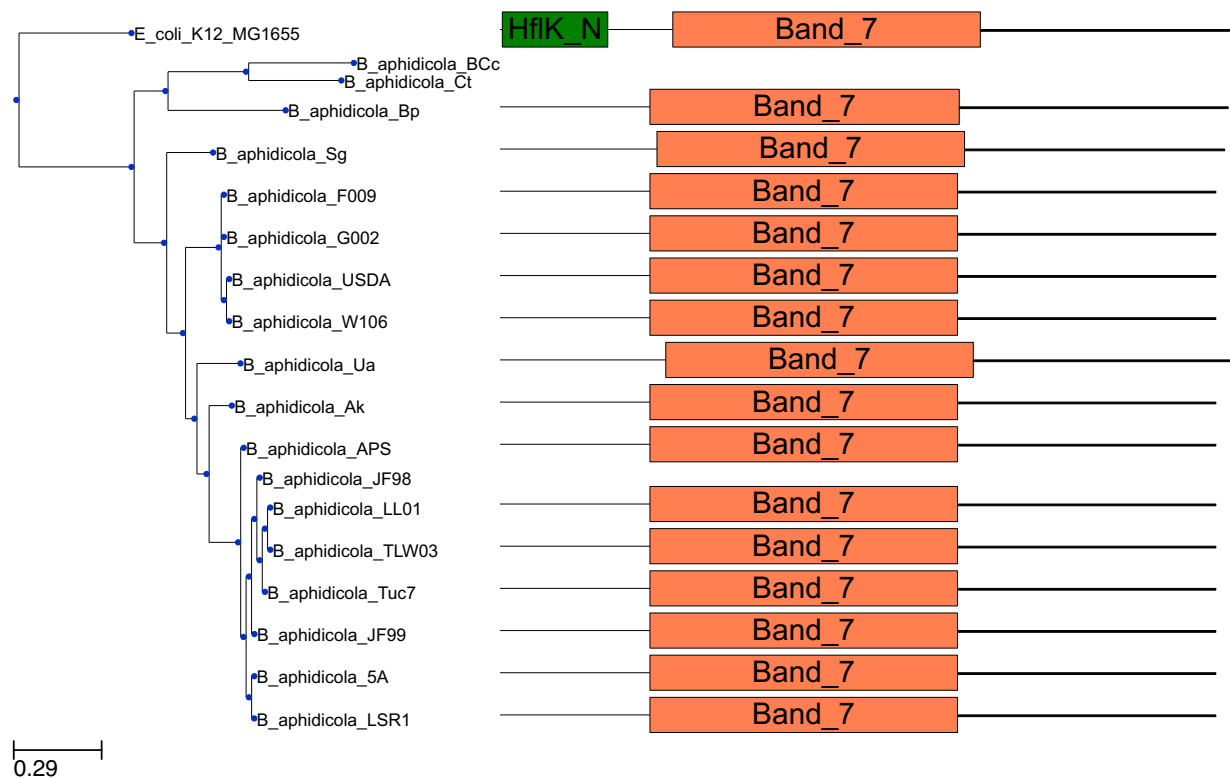
glpF
NP_418362.1
glycerol facilitator



ftsH

NP_417645.1

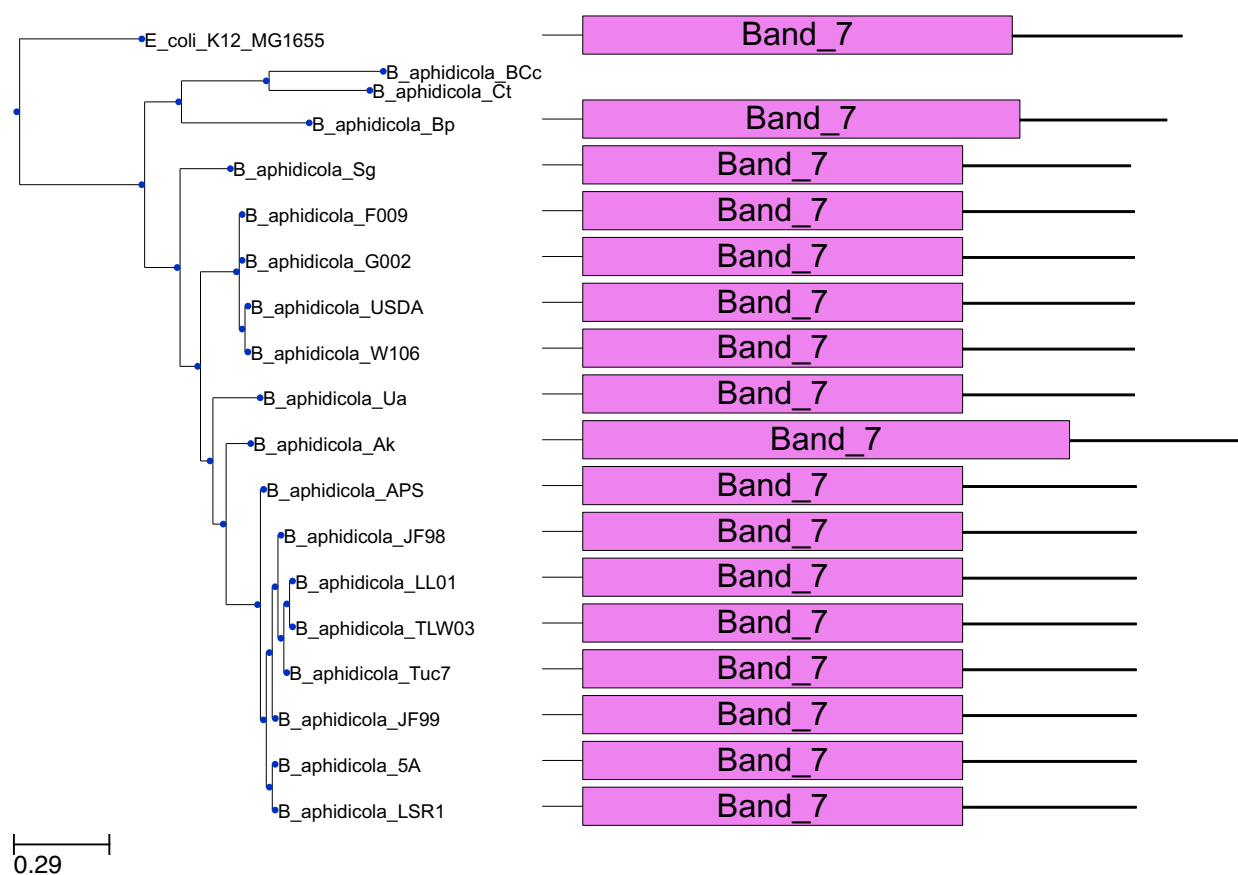
"protease, ATP-dependent zinc-metallo"



hflK

NP_418595.1

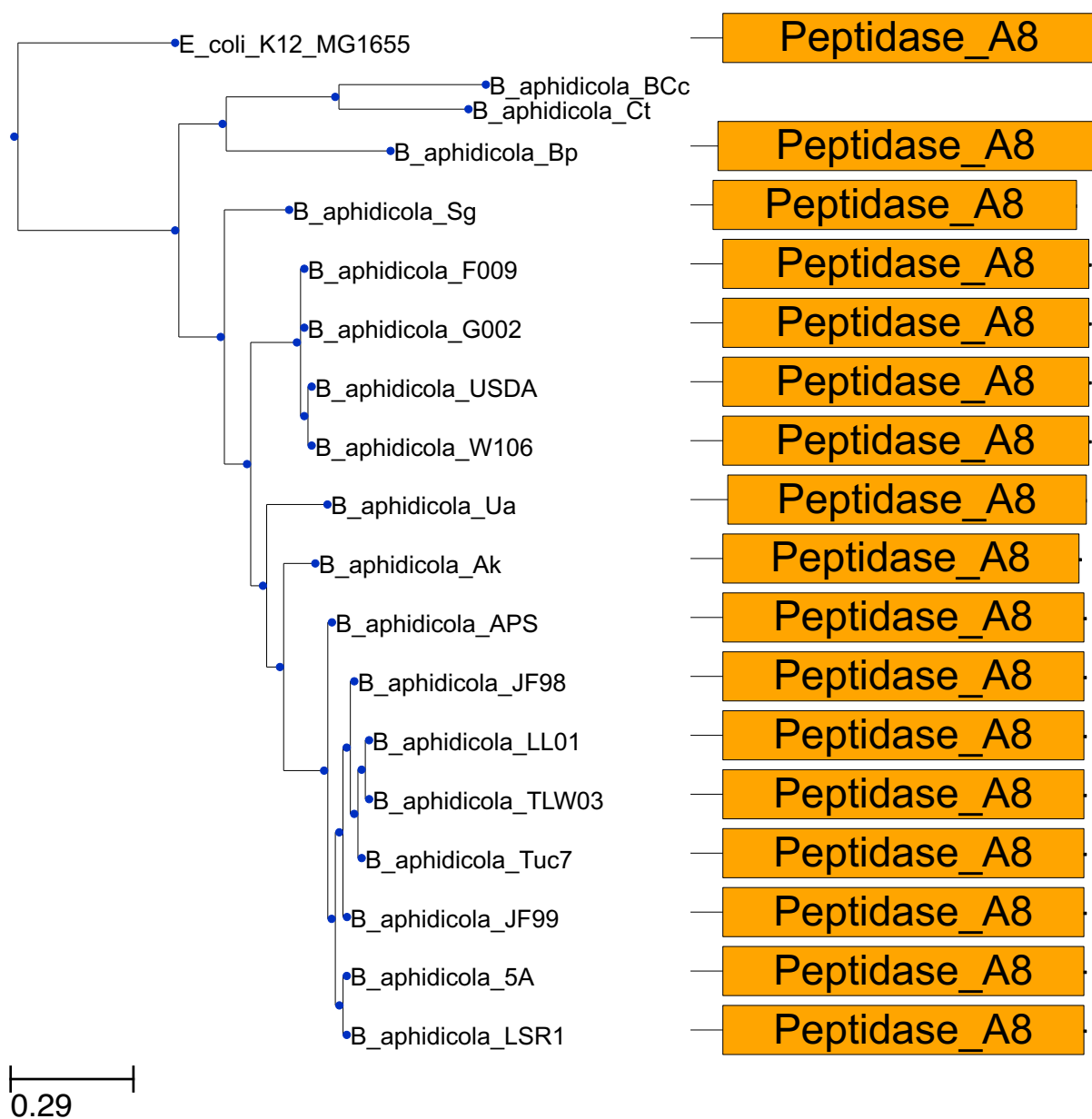
modulator for HflB protease specific for phage lambda cII repressor



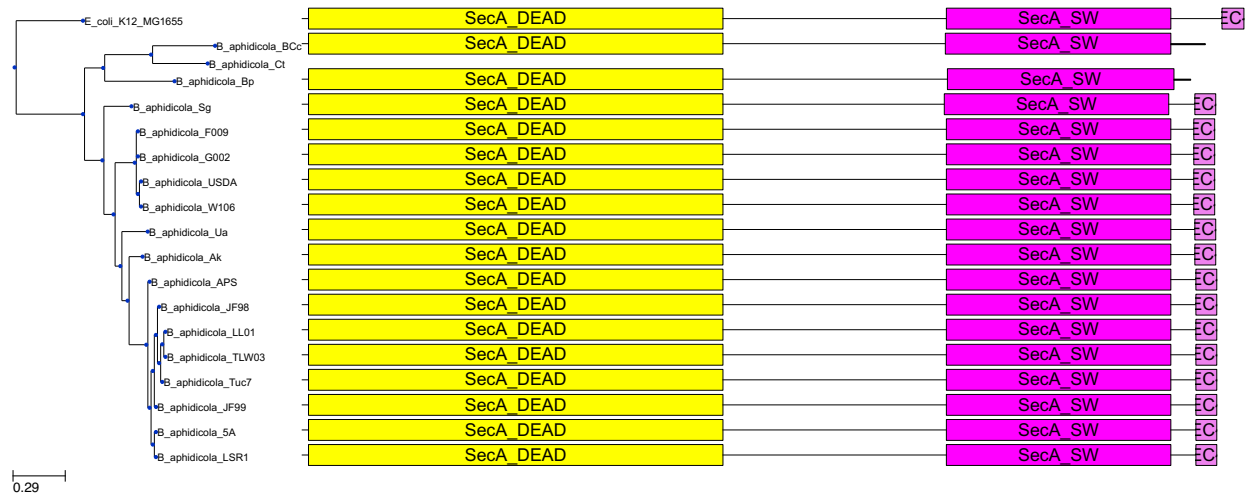
hflC

NP_418596.1

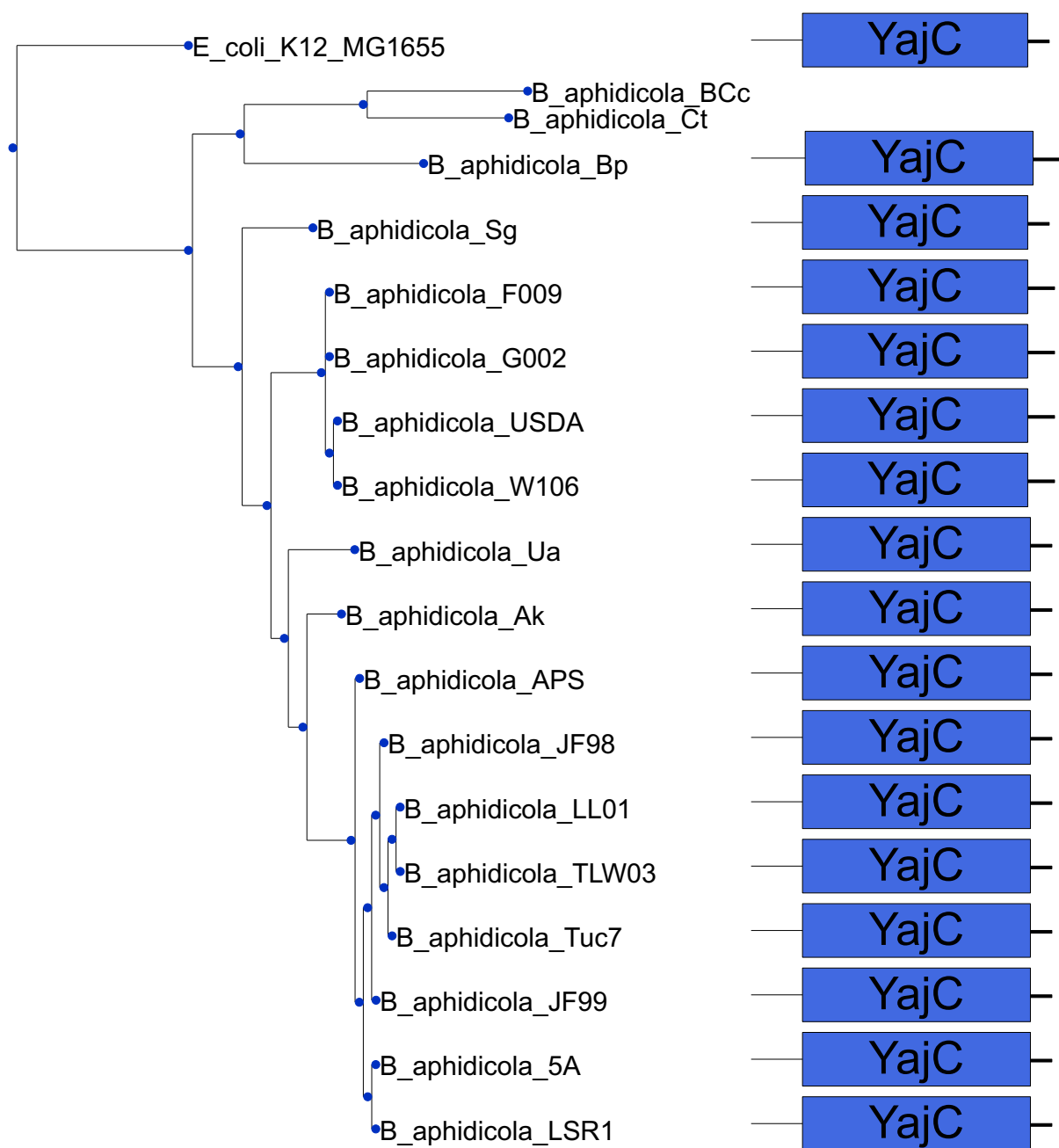
HflB protease modulator specific for phage lambda cII repressor



LspA
NP_414568.1
prolipoprotein signal peptidase (signal peptidase II)

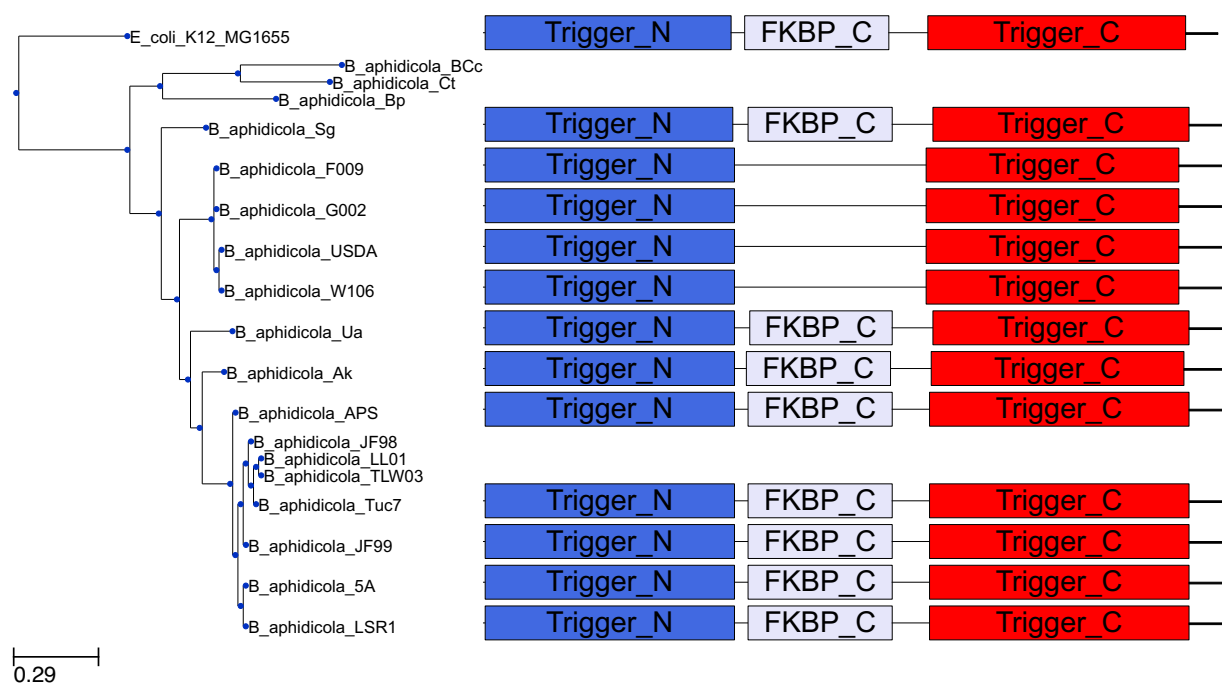


secA
NP_414640.1
"preprotein translocase subunit, ATPase"

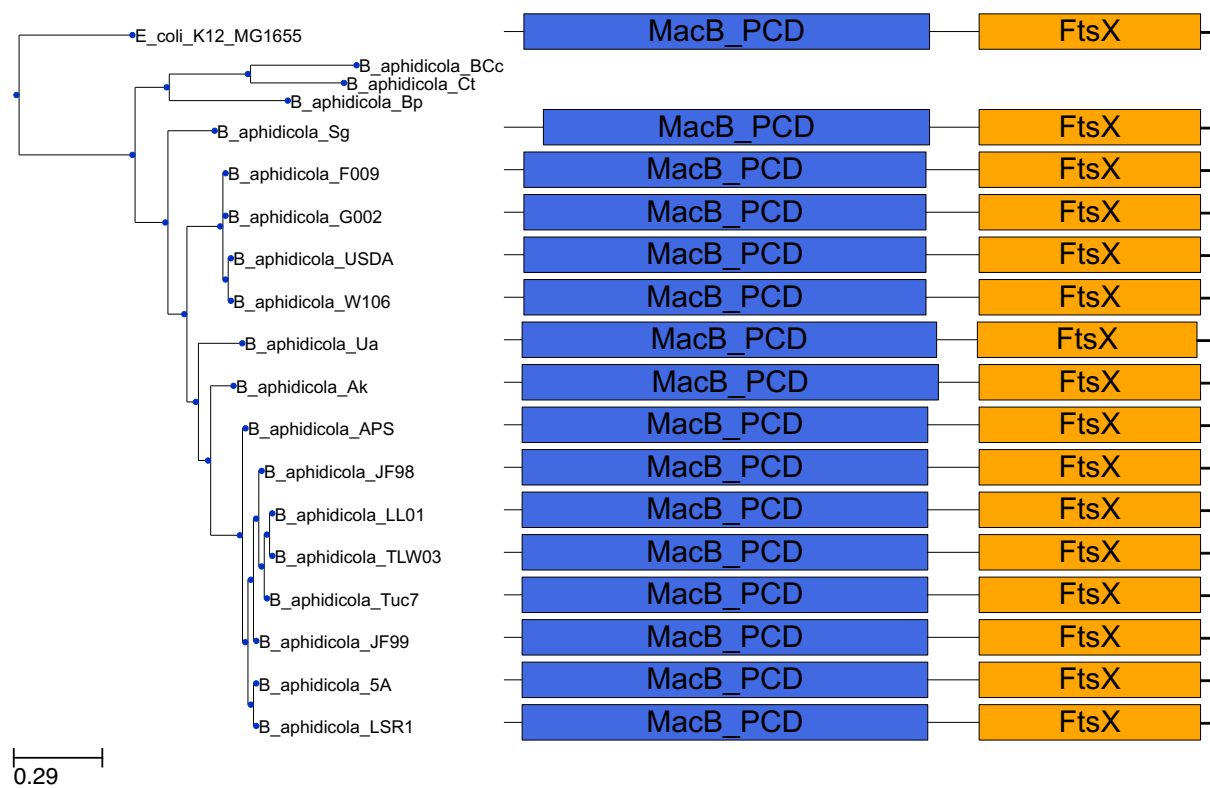


0.29

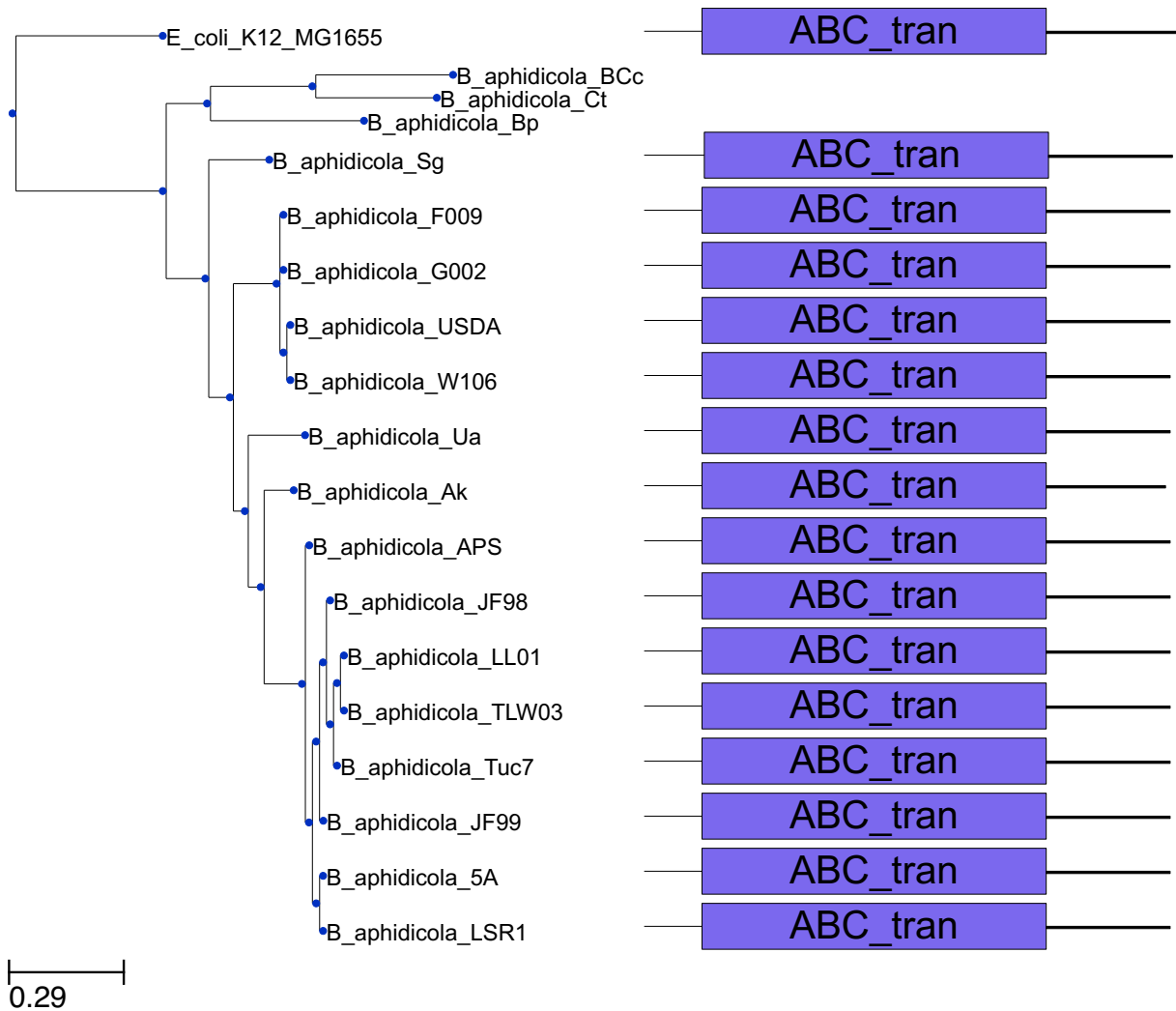
yajC
NP_414941.1
SecYEG protein translocase auxillary subunit



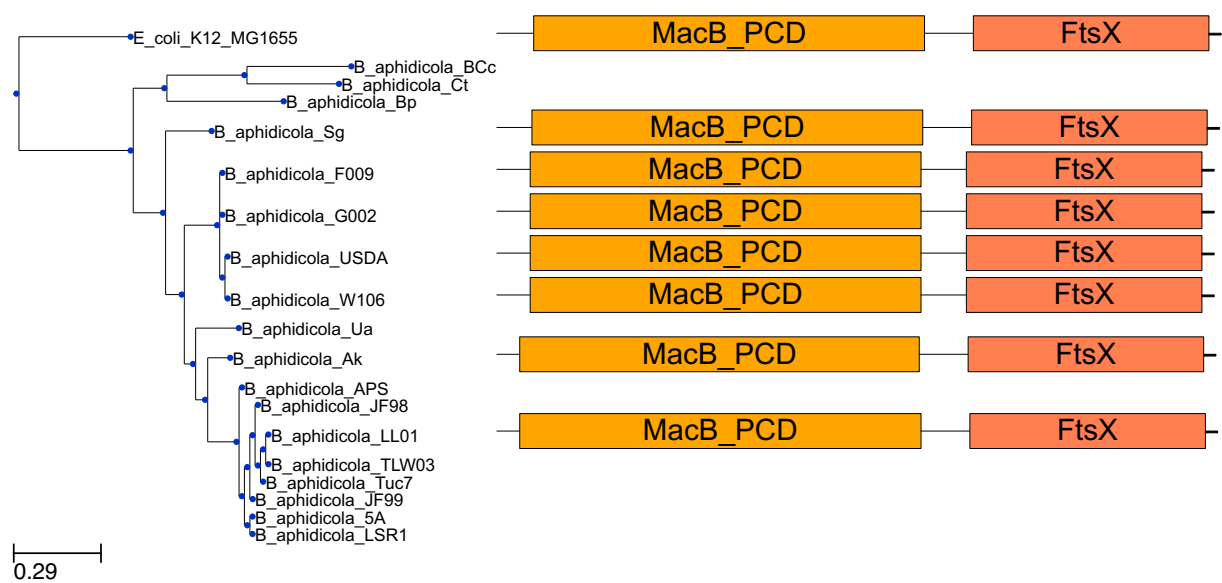
tig
NP_414970.1
peptidyl-prolyl cis/trans isomerase (trigger factor)



loIC
NP_415634.1
lipoprotein-releasing system transmembrane protein



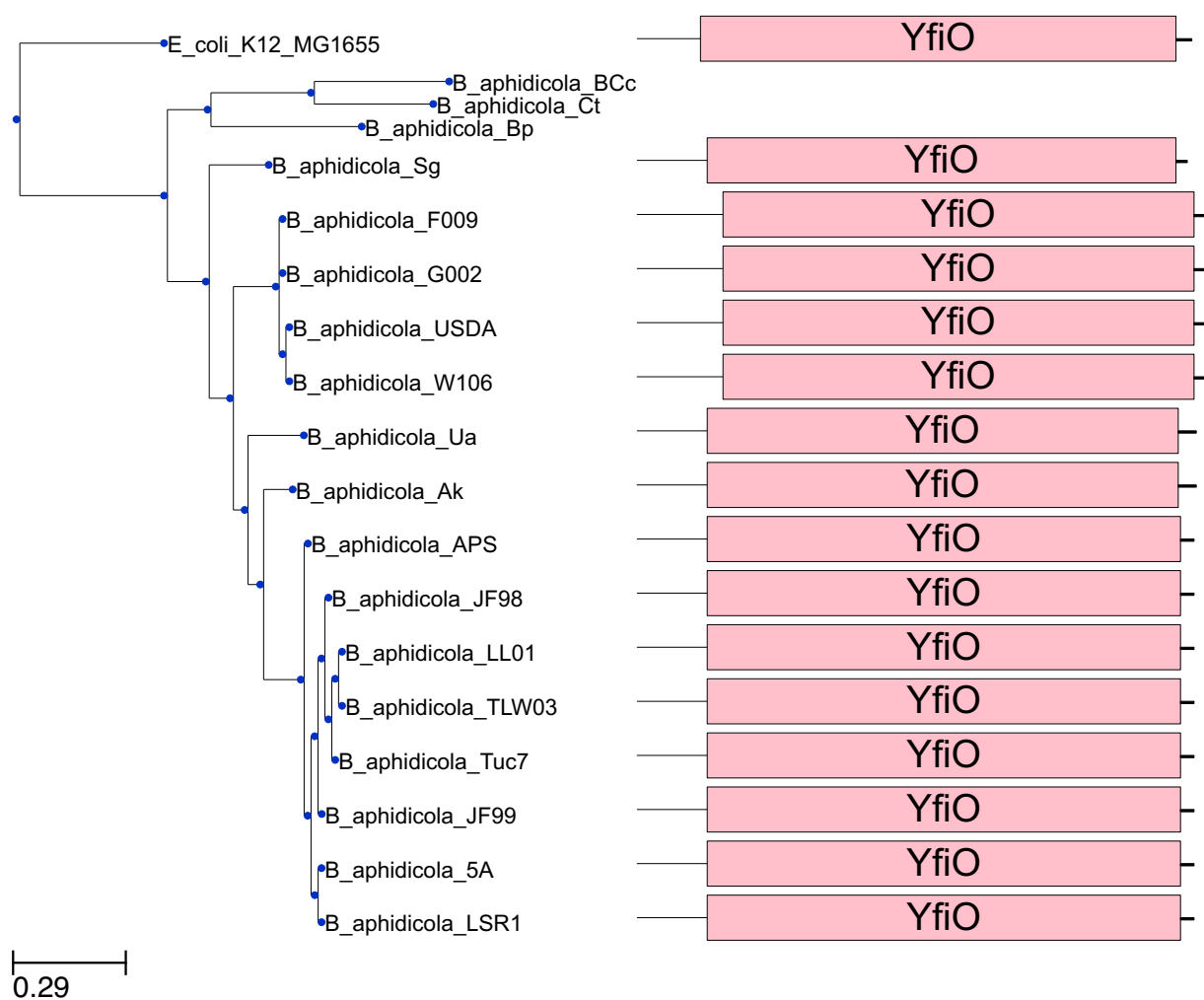
loID
NP_415635.4
outer membrane-specific lipoprotein transporter subunit



loIE

NP_415636.1

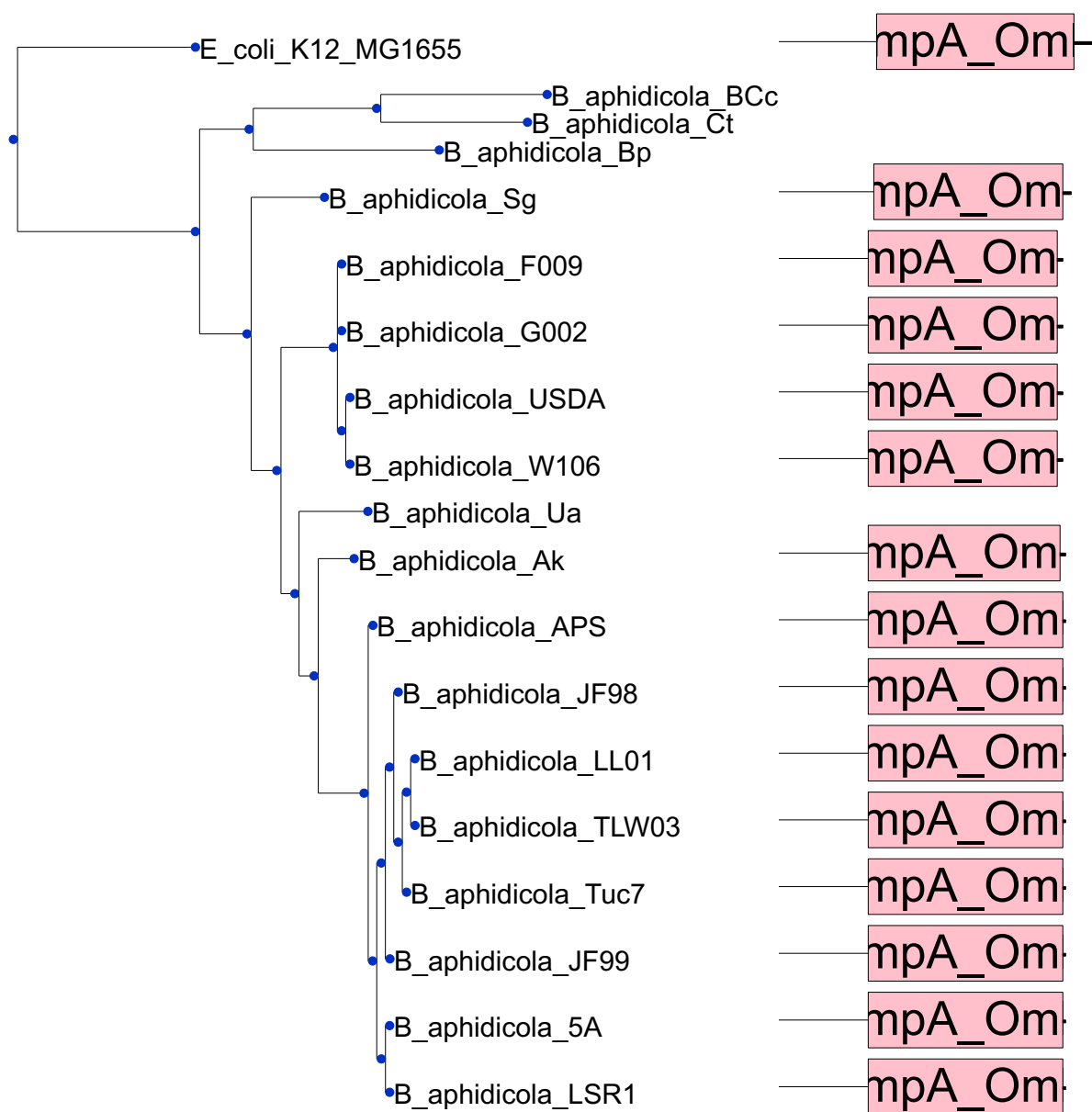
lipoprotein-releasing system transmembrane protein



yfiO

NP_417086.1

BamABCDE complex OM biogenesis lipoprotein

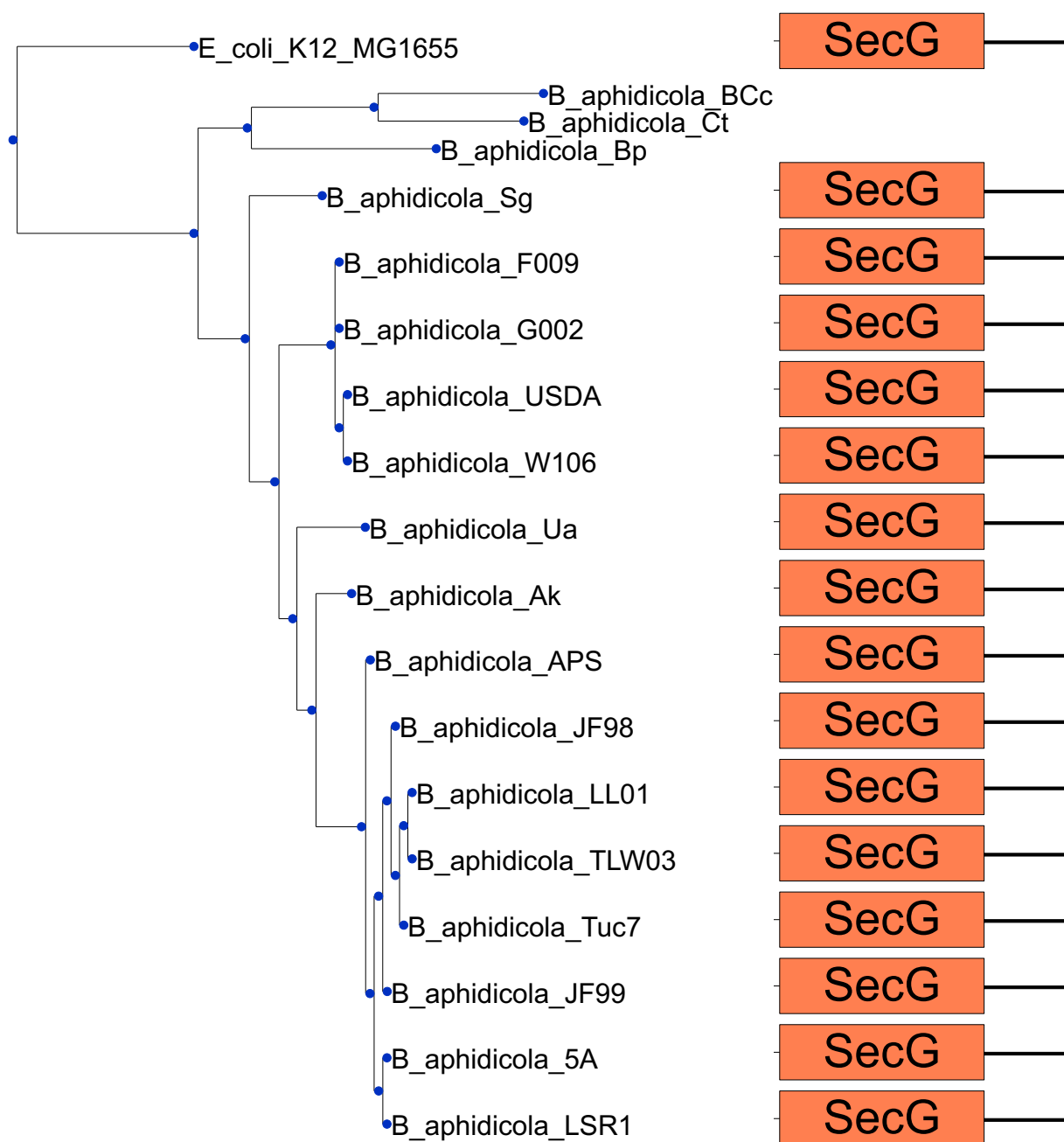


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smpA

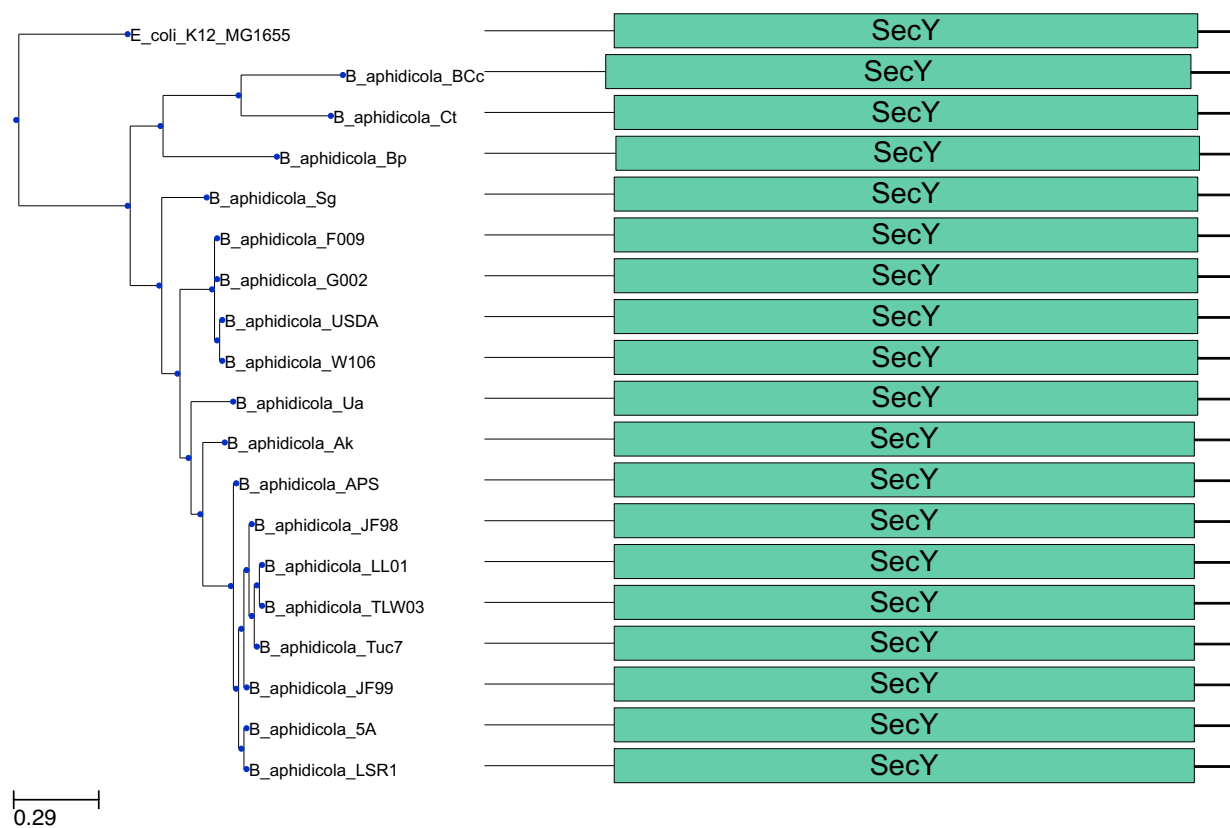
NP_417107.2

lipoprotein component of BamABCDE OM biogenesis complex

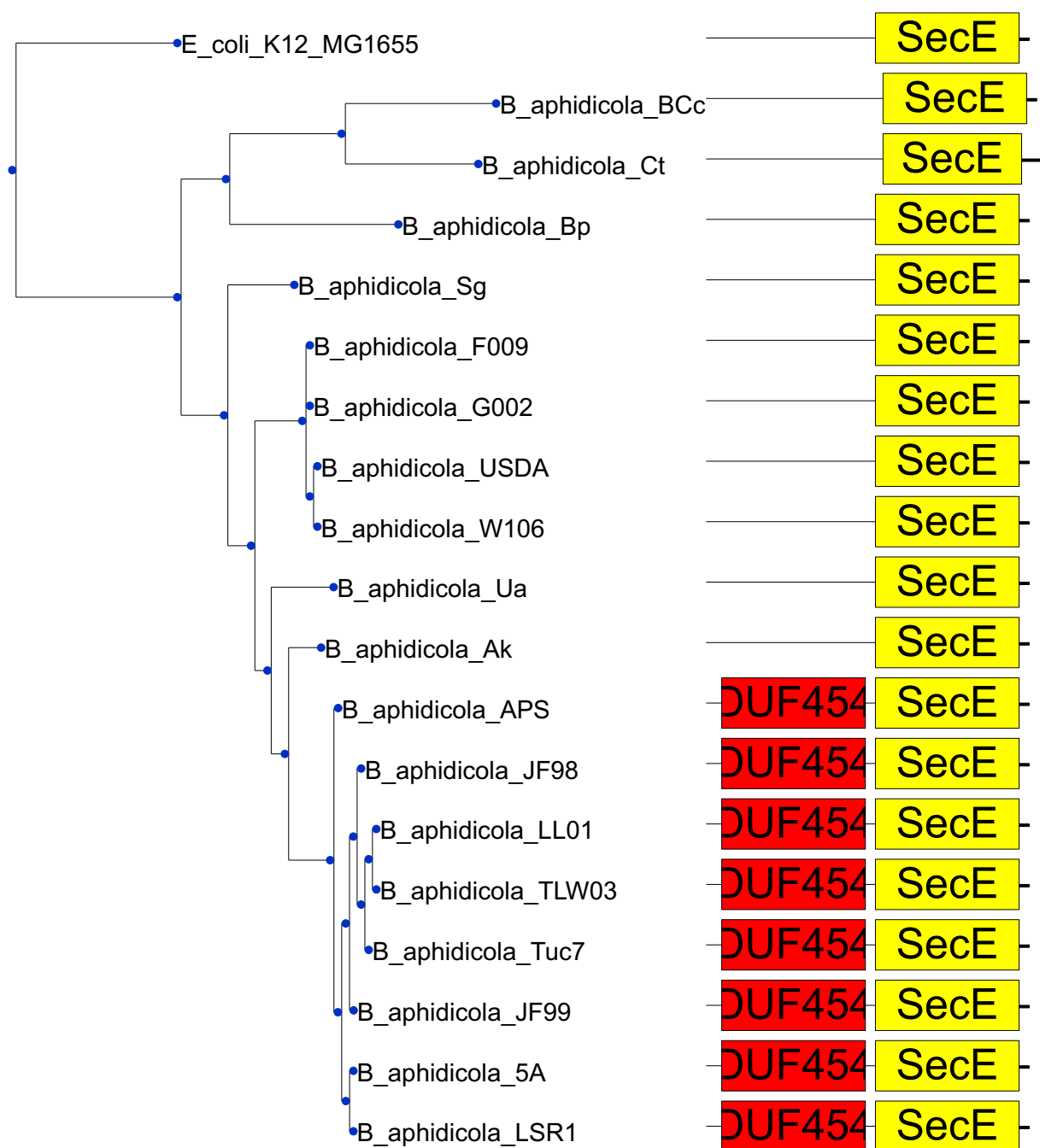


0.29

secG
 NP_417642.1
 preprotein translocase membrane subunit

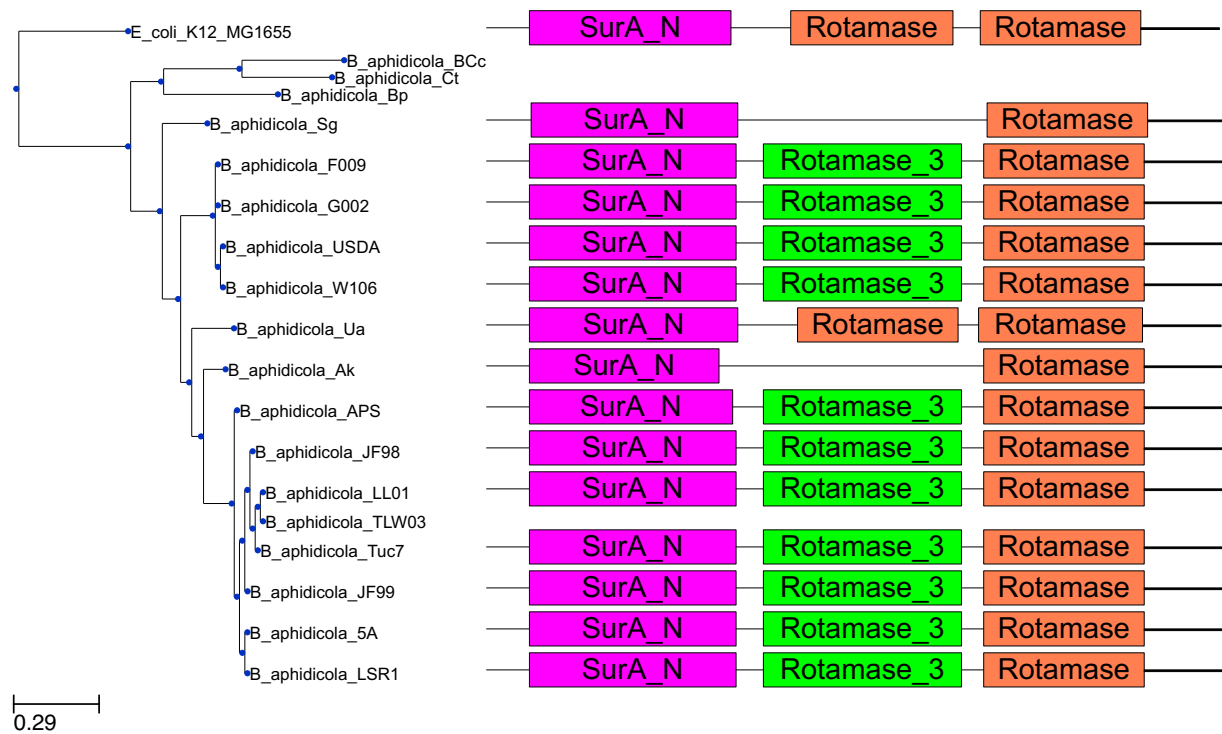


secY
NP_417759.1
preprotein translocase membrane subunit

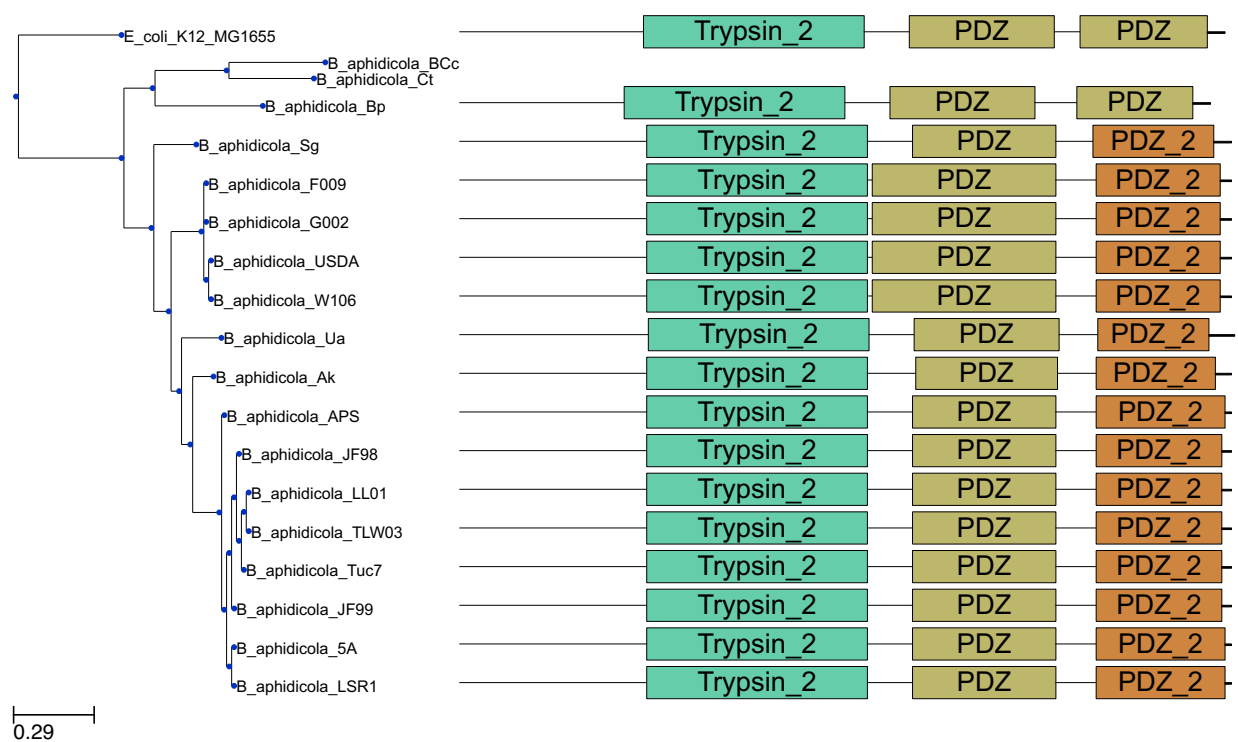


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secE
NP_418408.1
preprotein translocase membrane subunit



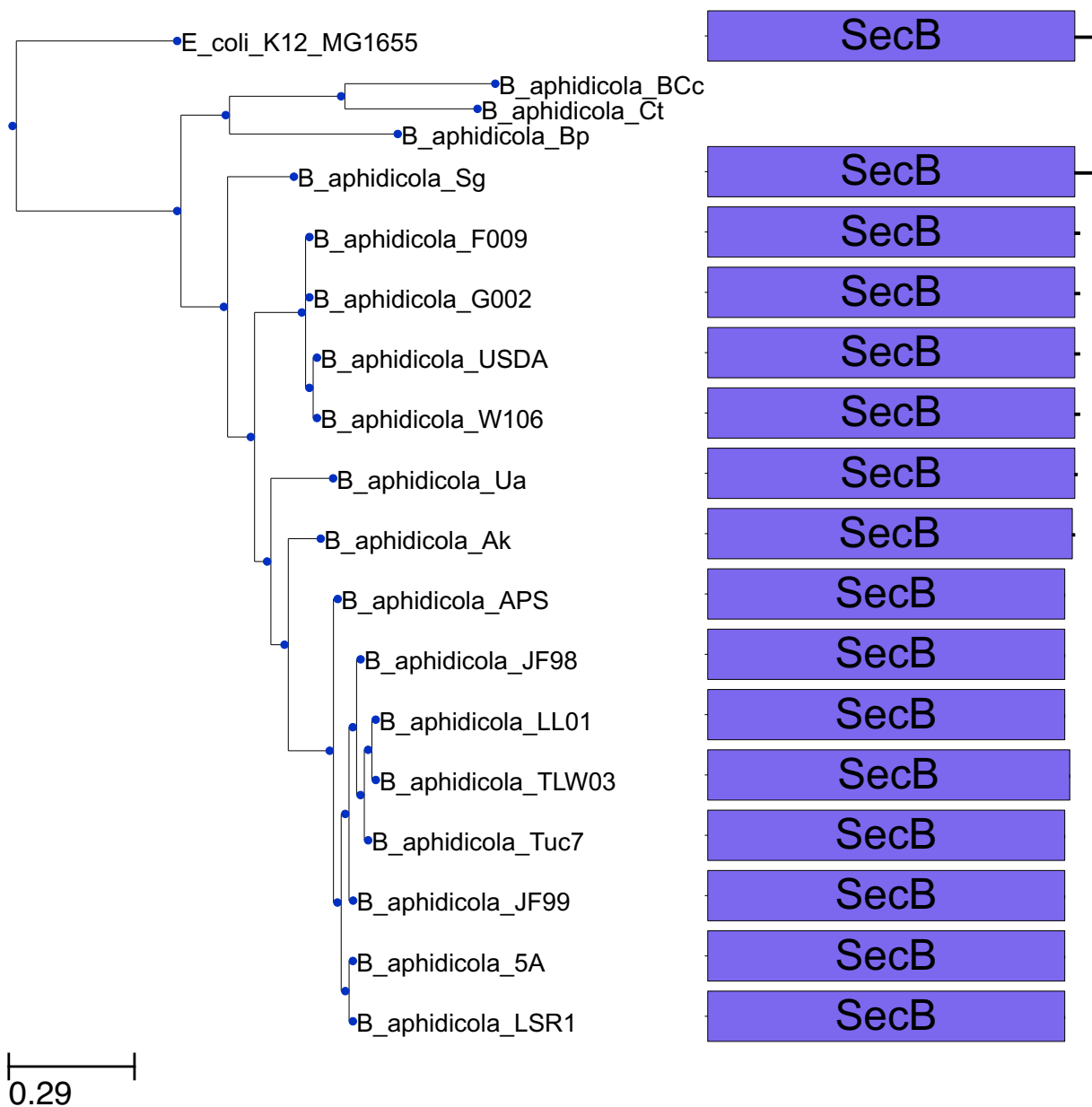
surA
NP_414595.1
peptidyl-prolyl cis-trans isomerase (PPIase)



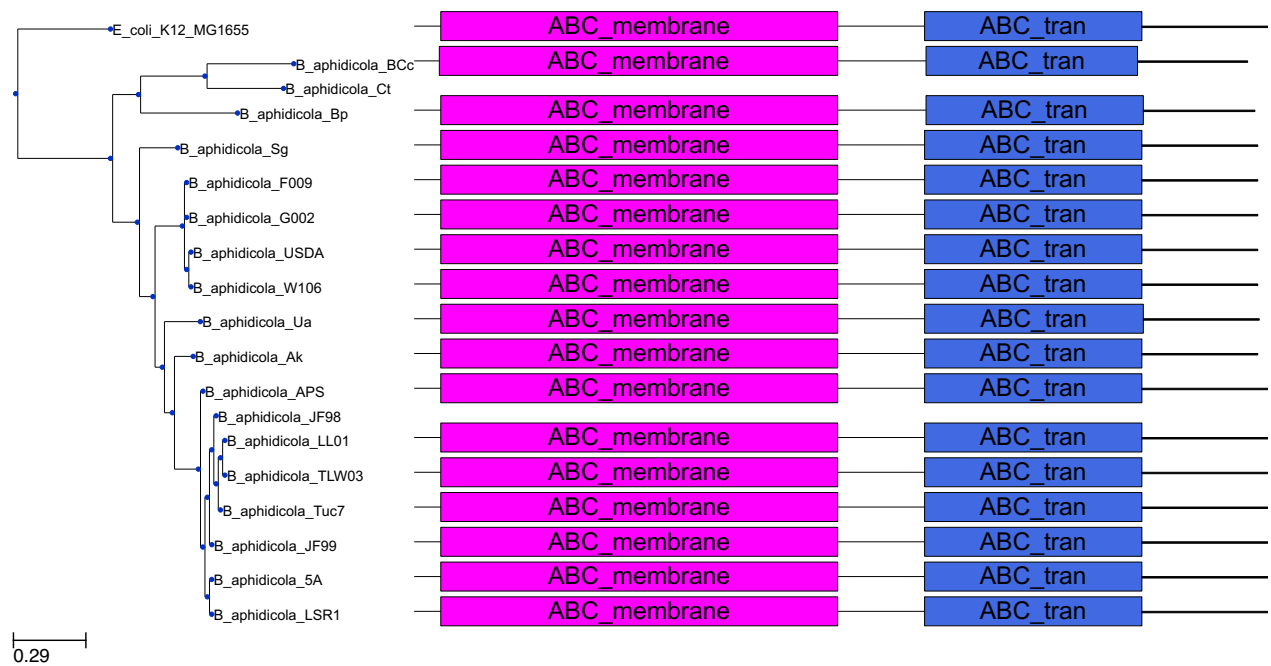
degP

NP_414703.1

"serine endoprotease (protease Do), membrane-associated"



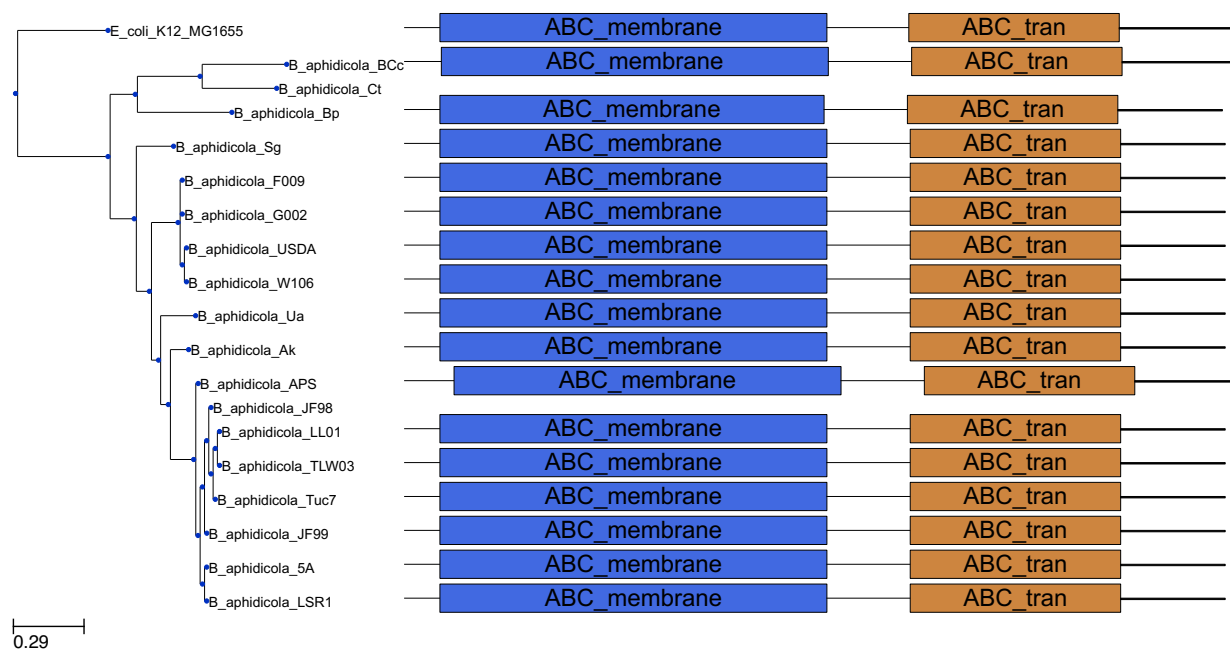
secB
 NP_418066.1
 protein export chaperone



mdIA

NP_414982.1

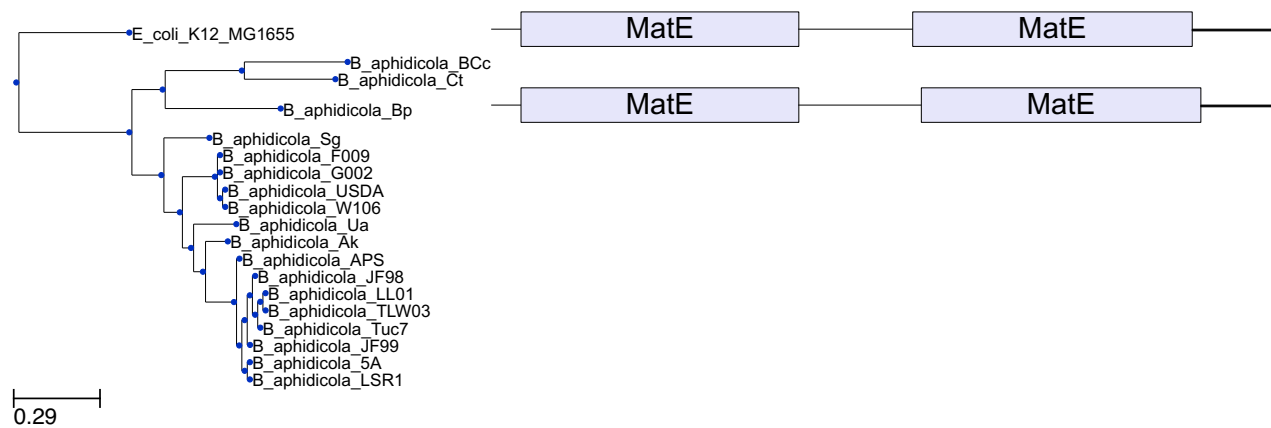
putative multidrug ABC transporter ATPase



mdlB

NP_414983.1

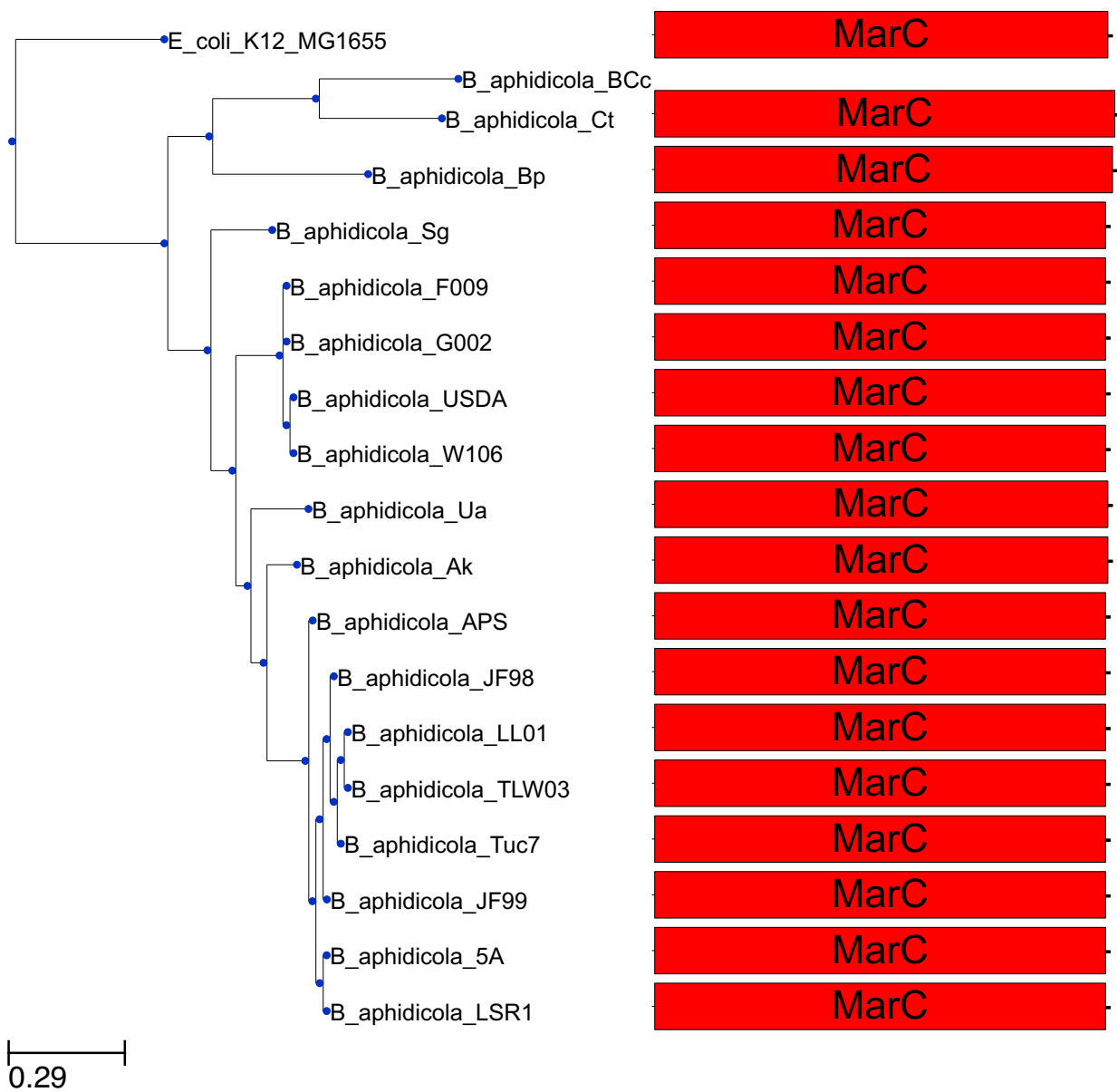
putative multidrug ABC transporter ATPase



mdtK

YP_025307.1

multidrug efflux system transporter



yhgN
NP_417892.1
UPF0056 family inner membrane protein