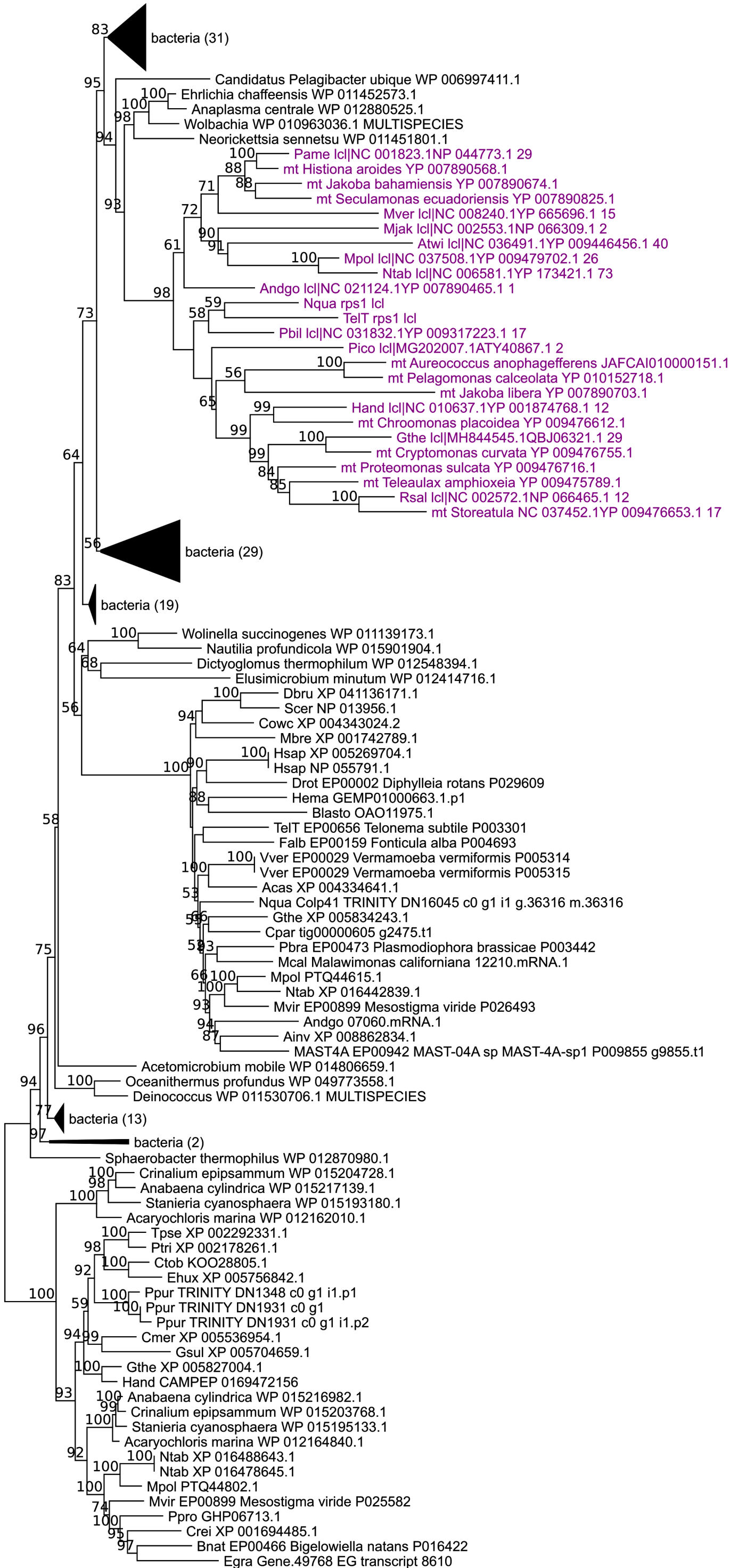
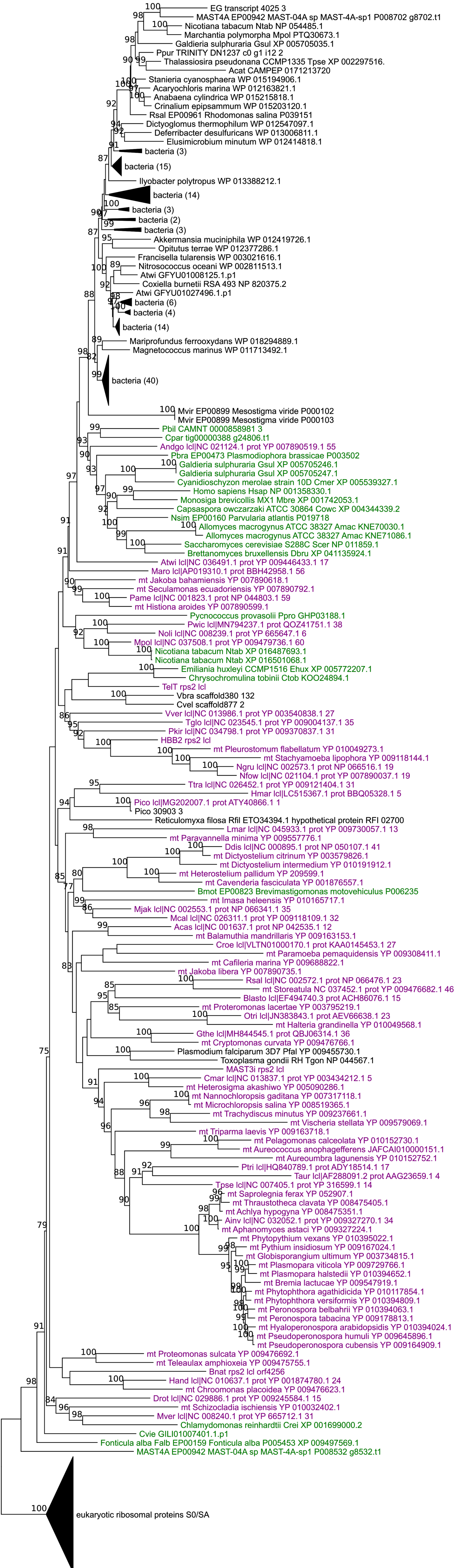


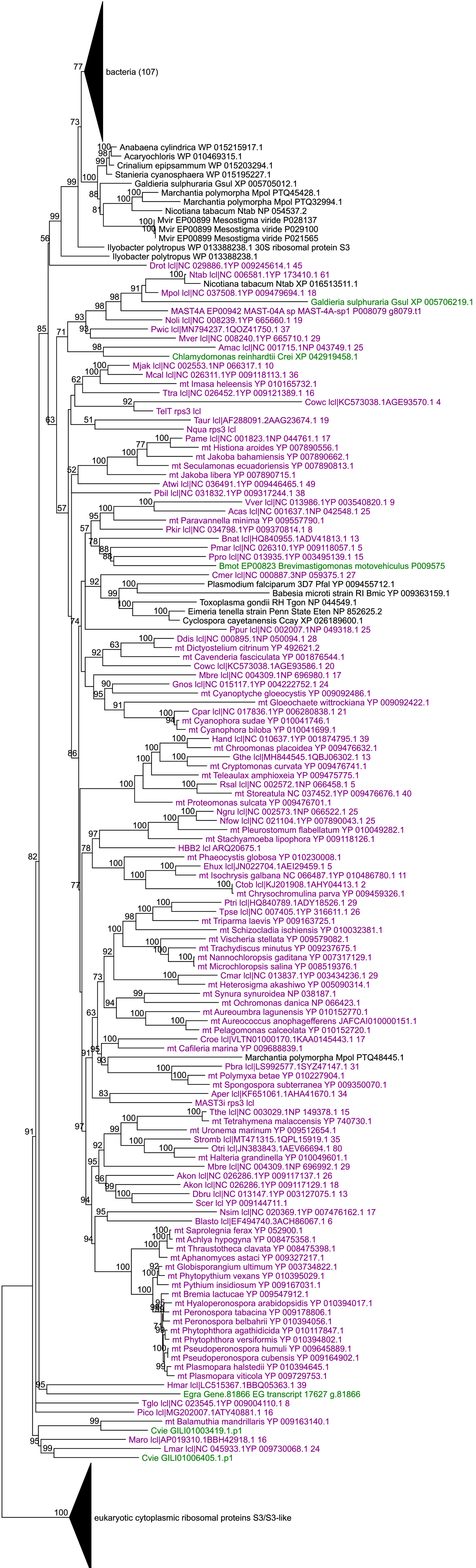


Protein: **rps1**; alignment timming: ClipKIT; IQ-TREE2 best-fit model: LG+R7

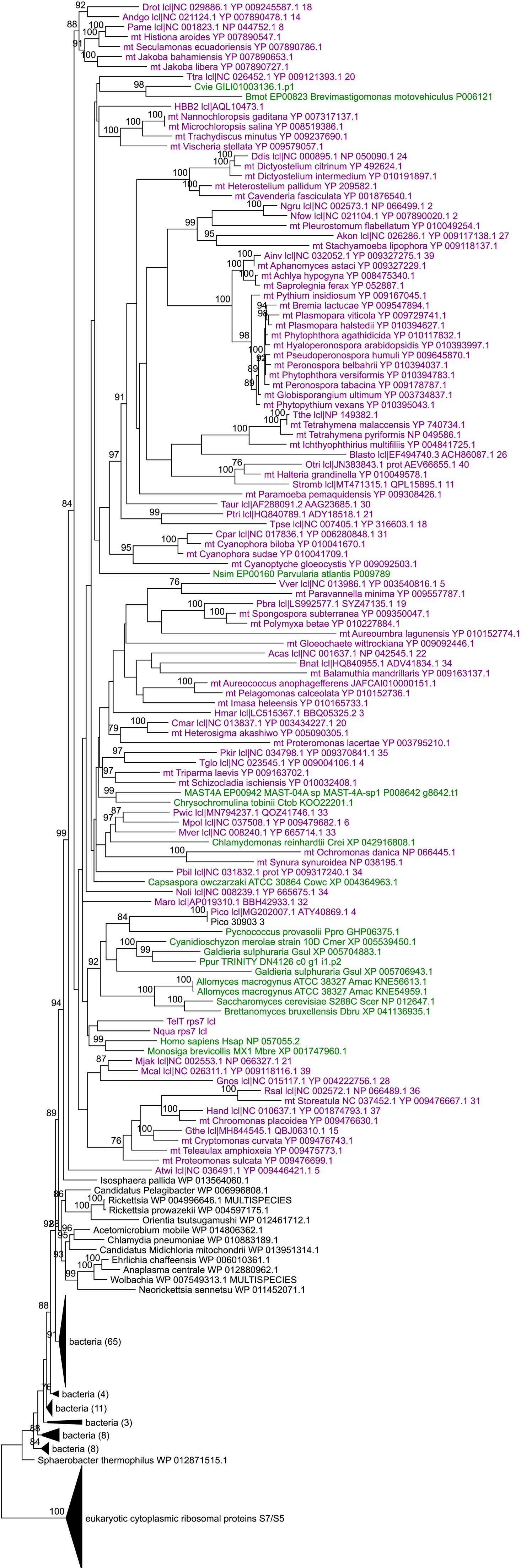
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Protein: **rps2**; alignment timming: ClipKIT; IQ-TREE2 best-fit model: LG+R8

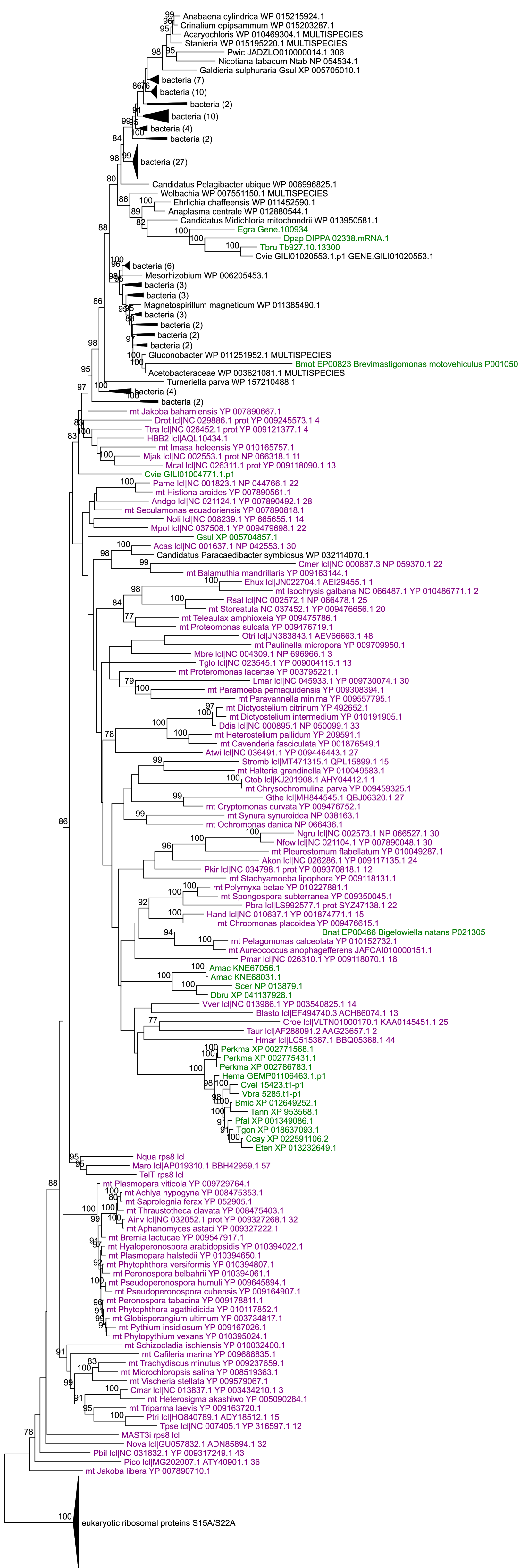


Protein: **rps3**; alignment timing: ClipKIT; IQ-TREE2 best-fit model: Q.yeast+R7



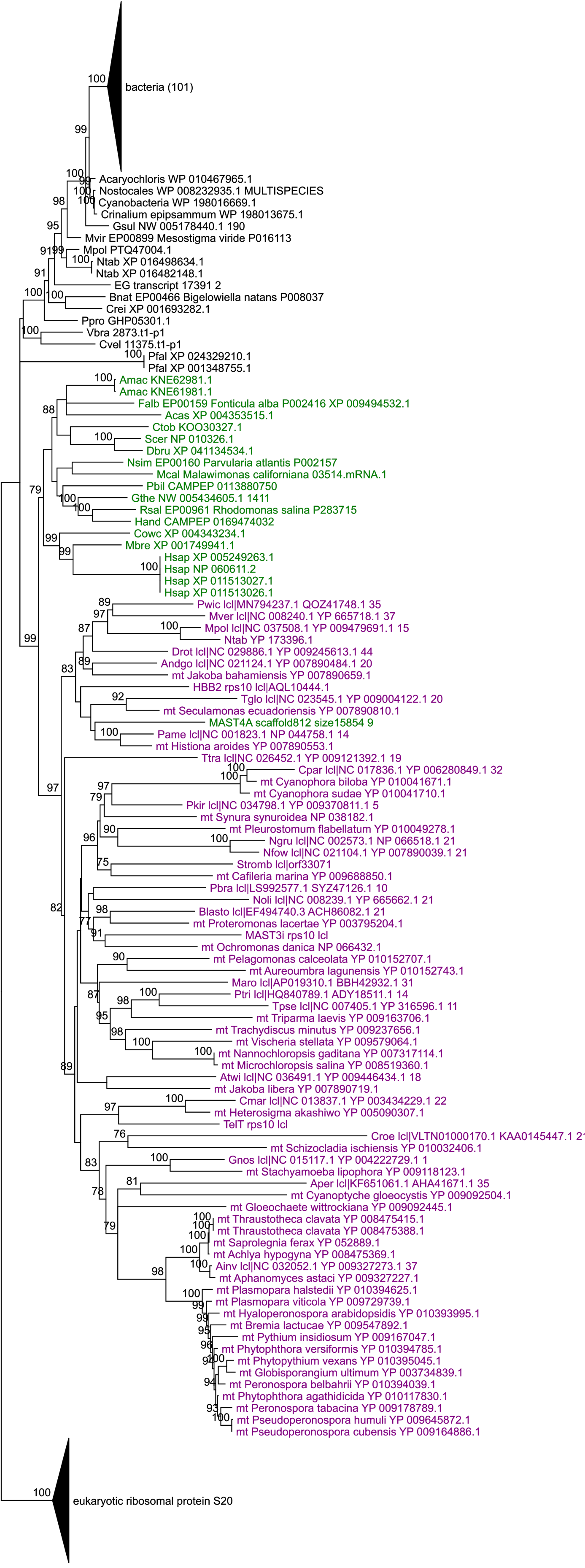
Protein: **rps7**; alignment timming: trimAl; IQ-TREE2 best-fit model: Q.yeast+R9

0.50



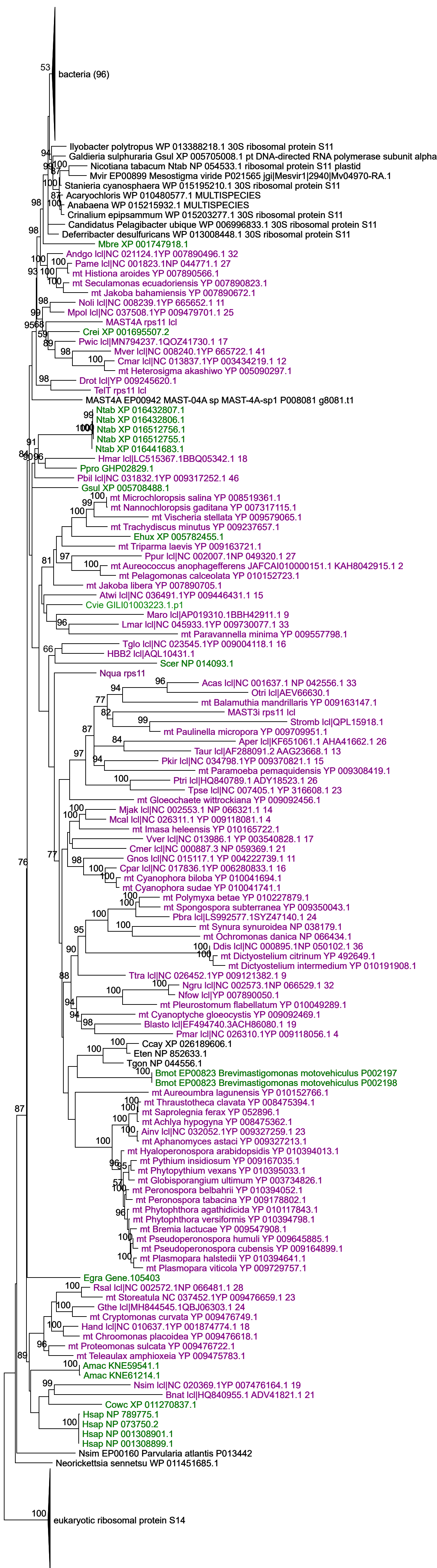
Protein: **rps8**; alignment timming: trimAl; IQ-TREE2 best-fit model: LG+F+R7

0.50

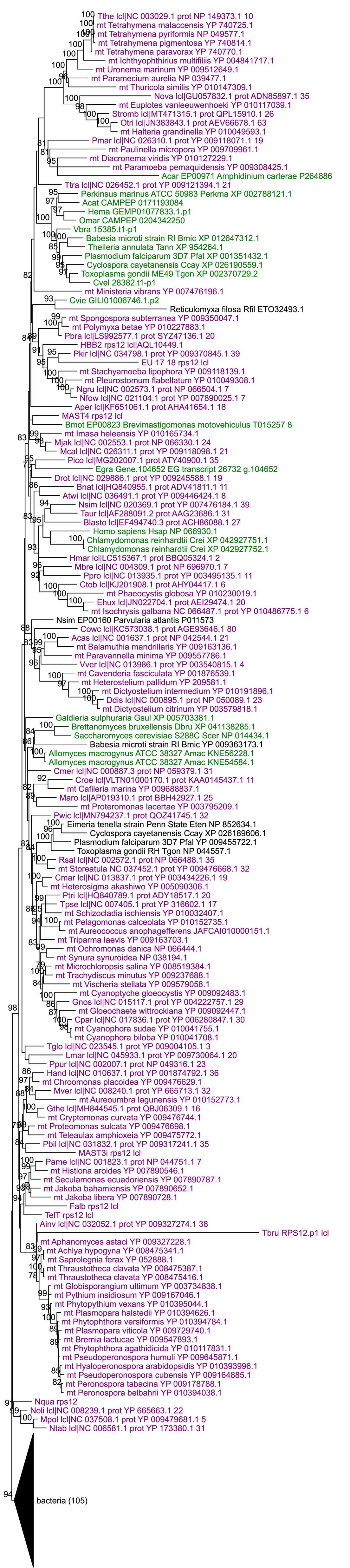


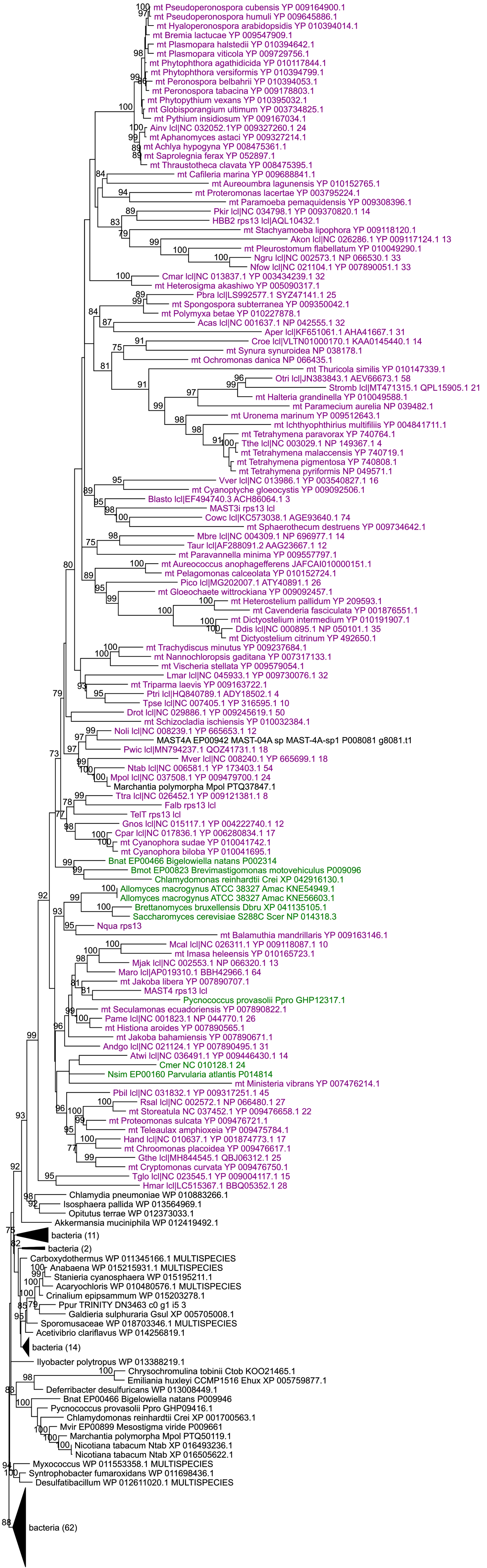
Protein: **rps10**; alignment timming: ClipKIT; IQ-TREE2 best-fit model: Q.yeast+R7

0.50



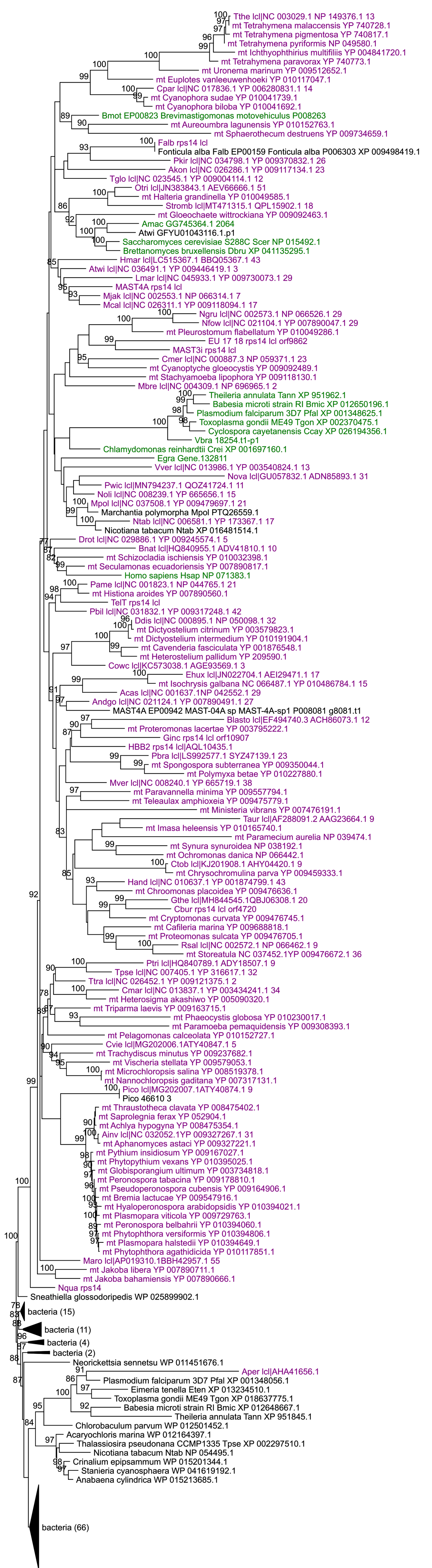
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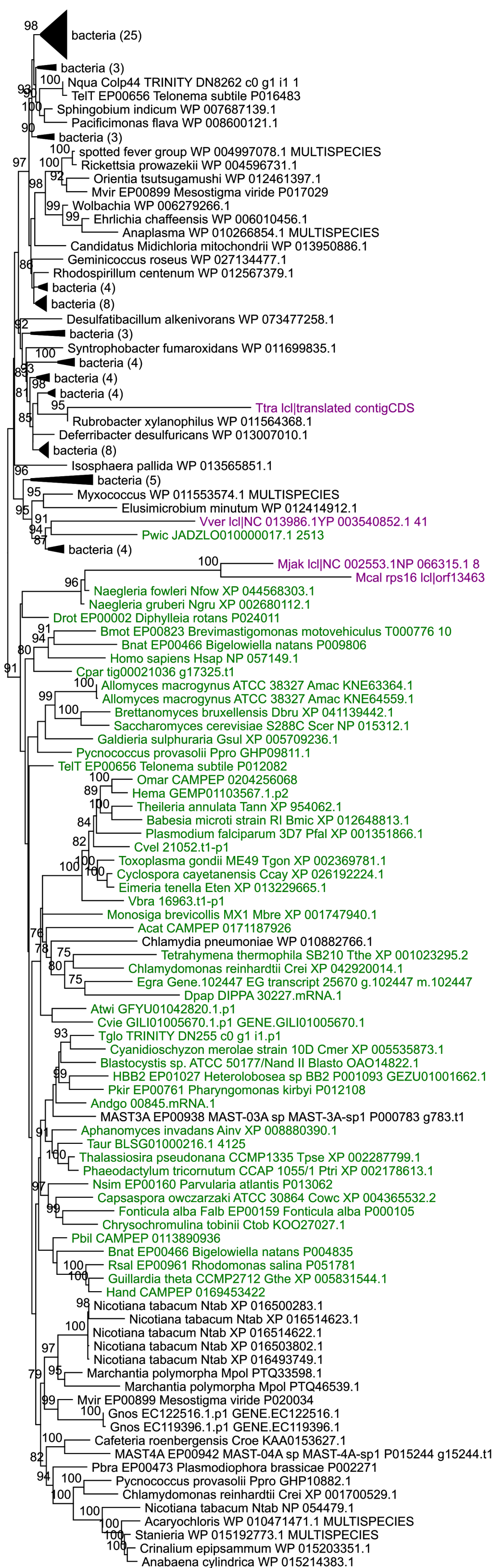
Protein: **rps13**; alignment timming: trimAl; IQ-TREE2 best-fit model: Q.yeast+R7

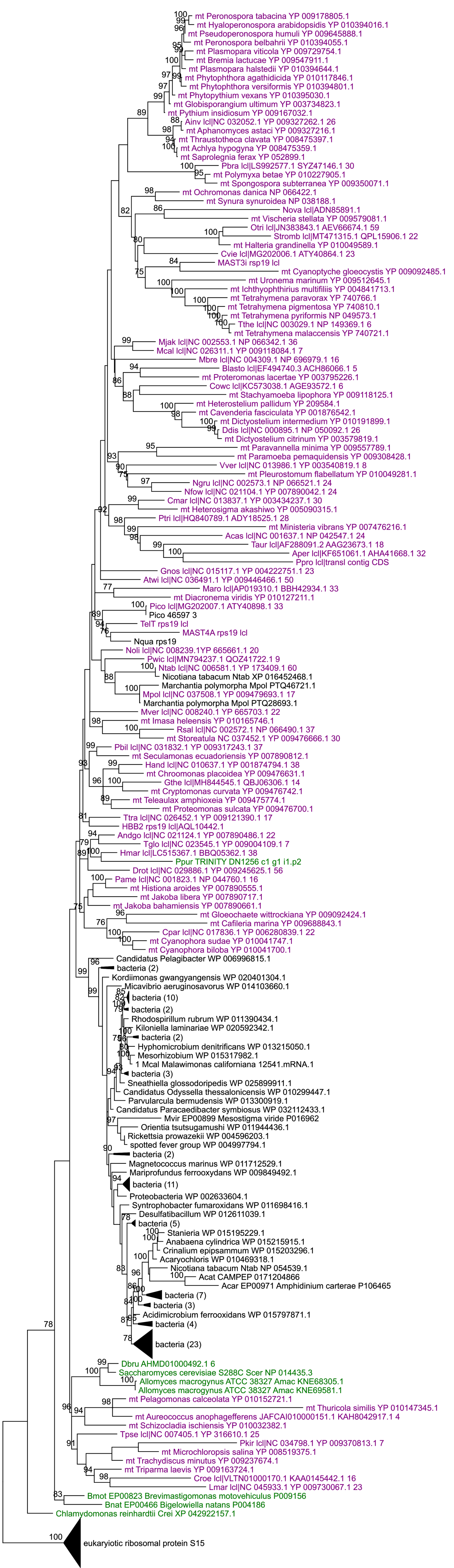
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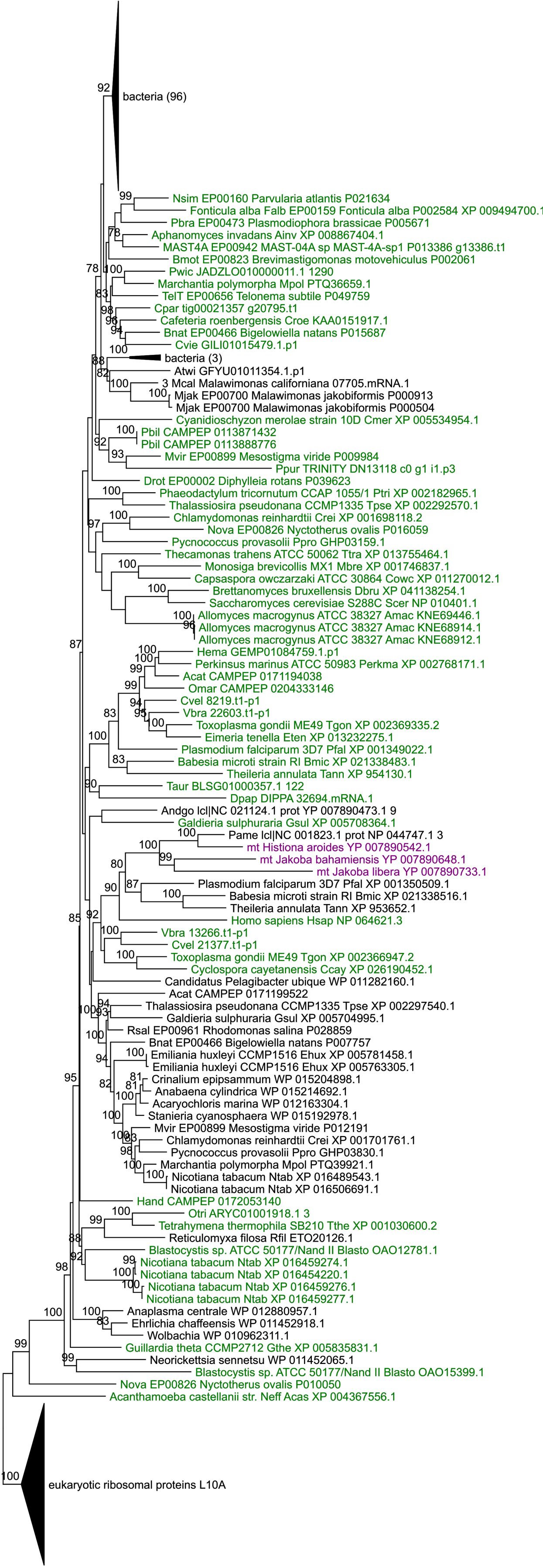


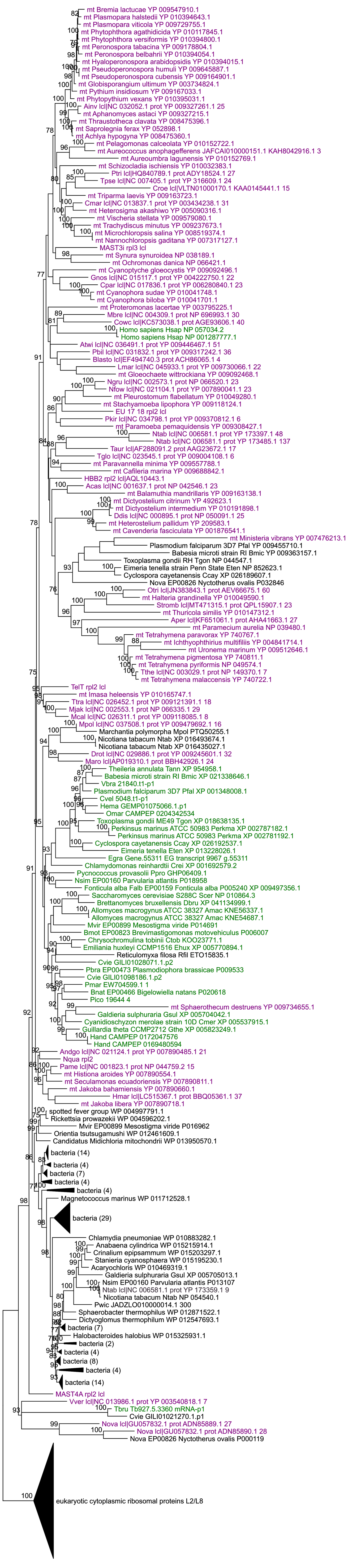
Protein: **rps14**; alignment timing: trimAl; IQ-TREE2 best-fit model: Q,yeast+R7

0.50



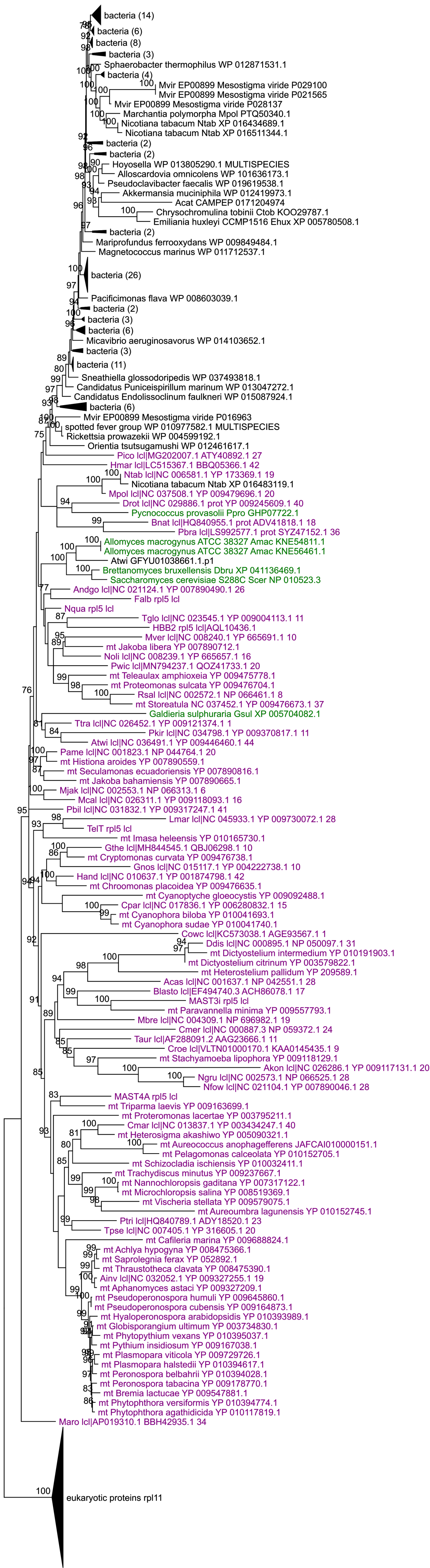


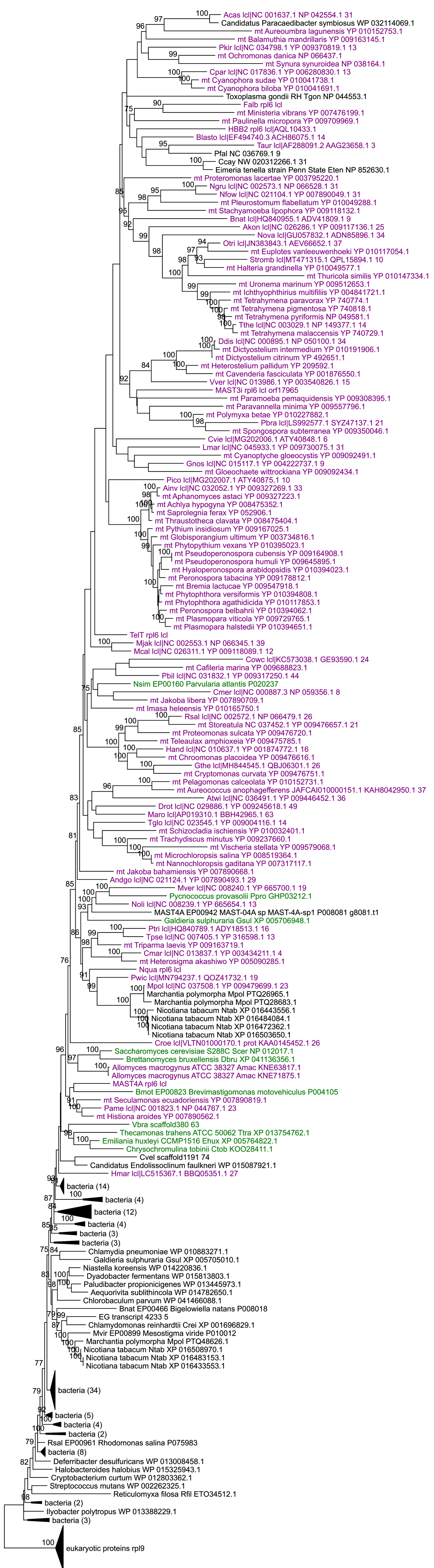




Protein: rpl2; alignment timing: ClipKIT; IQ-TREE2 best-fit model: Q.insect+R10

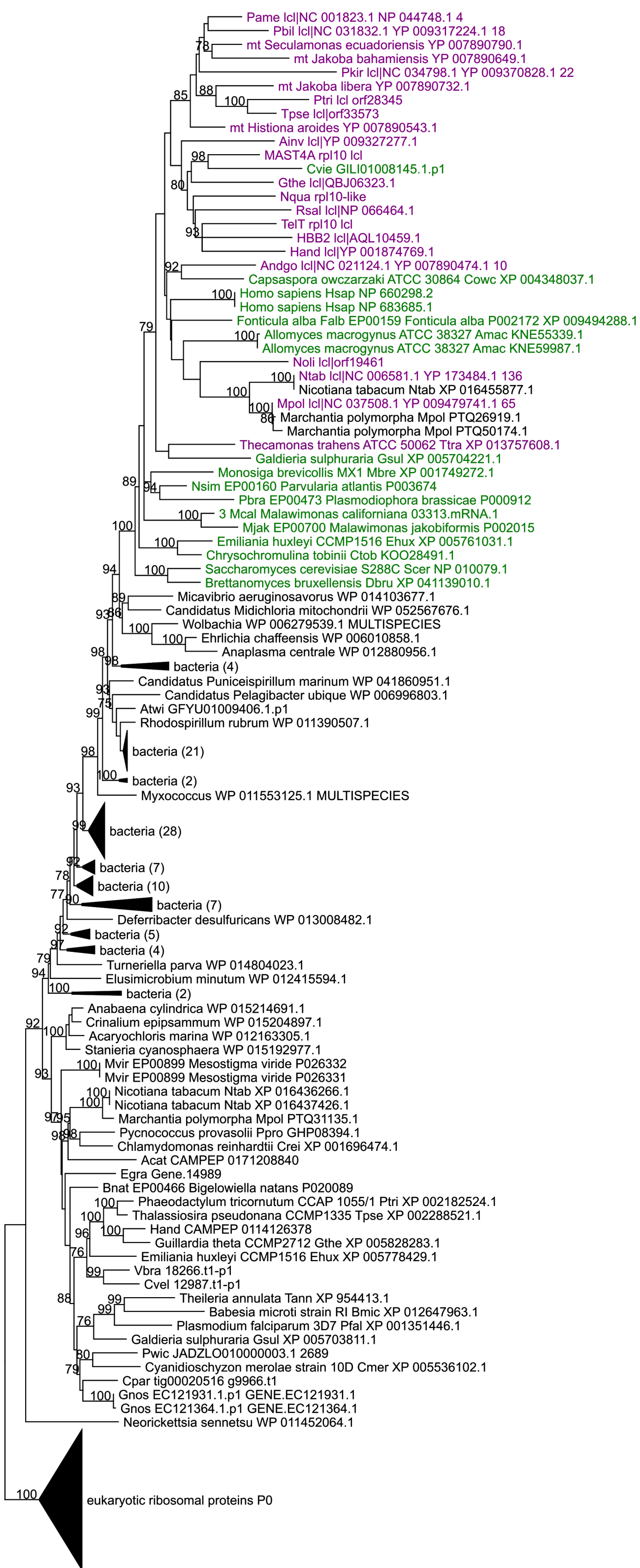
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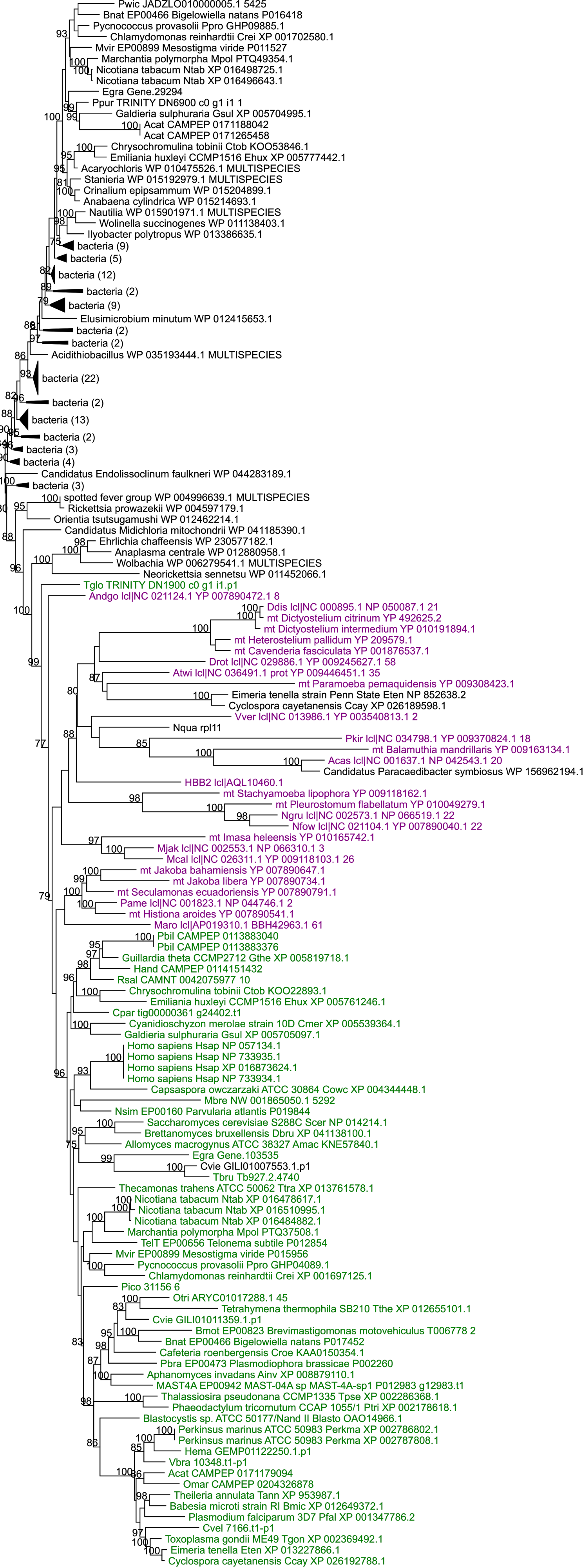




Protein: **rpl6**; alignment timing: trimAl; IQ-TREE2 best-fit model: Q.pfam+F+R8

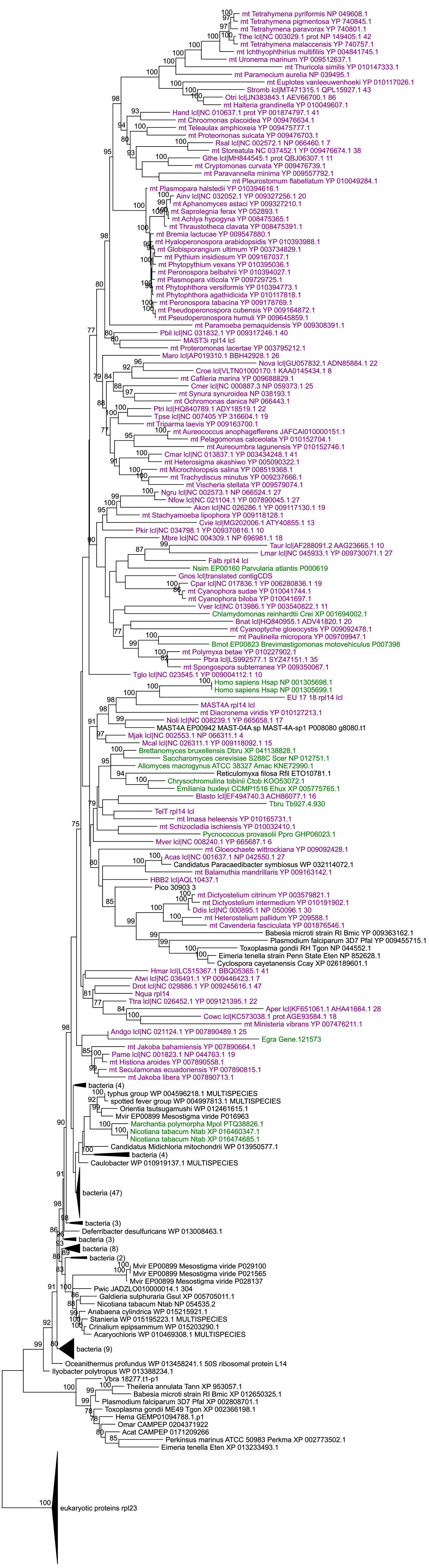
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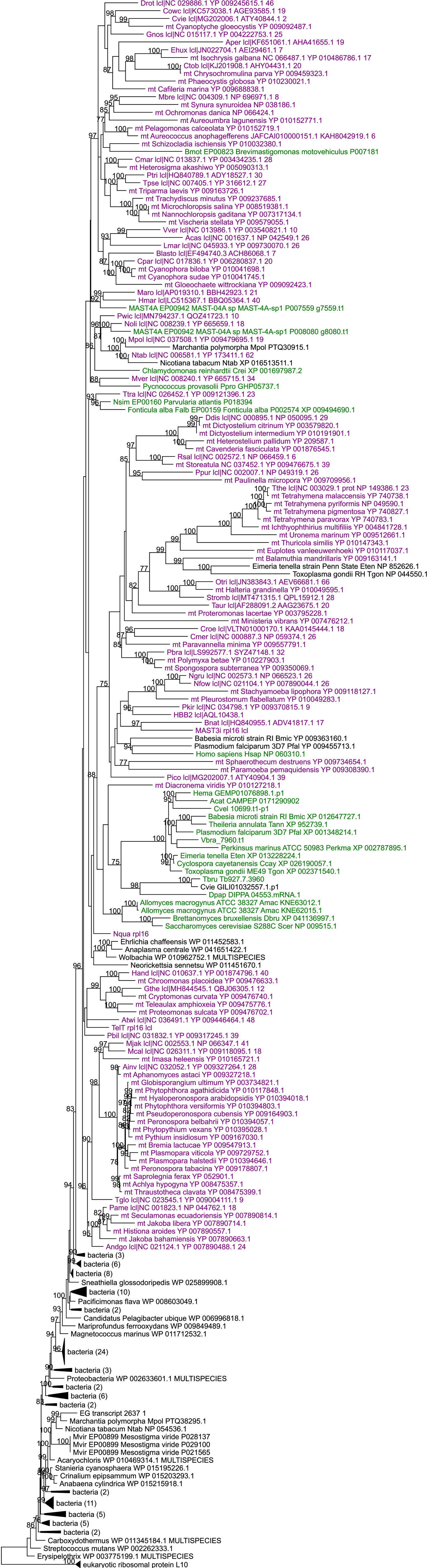


Protein: **rpl11**; alignment timing: trimAl; IQ-TREE2 best-fit model: Q.yeast+R8

0.50

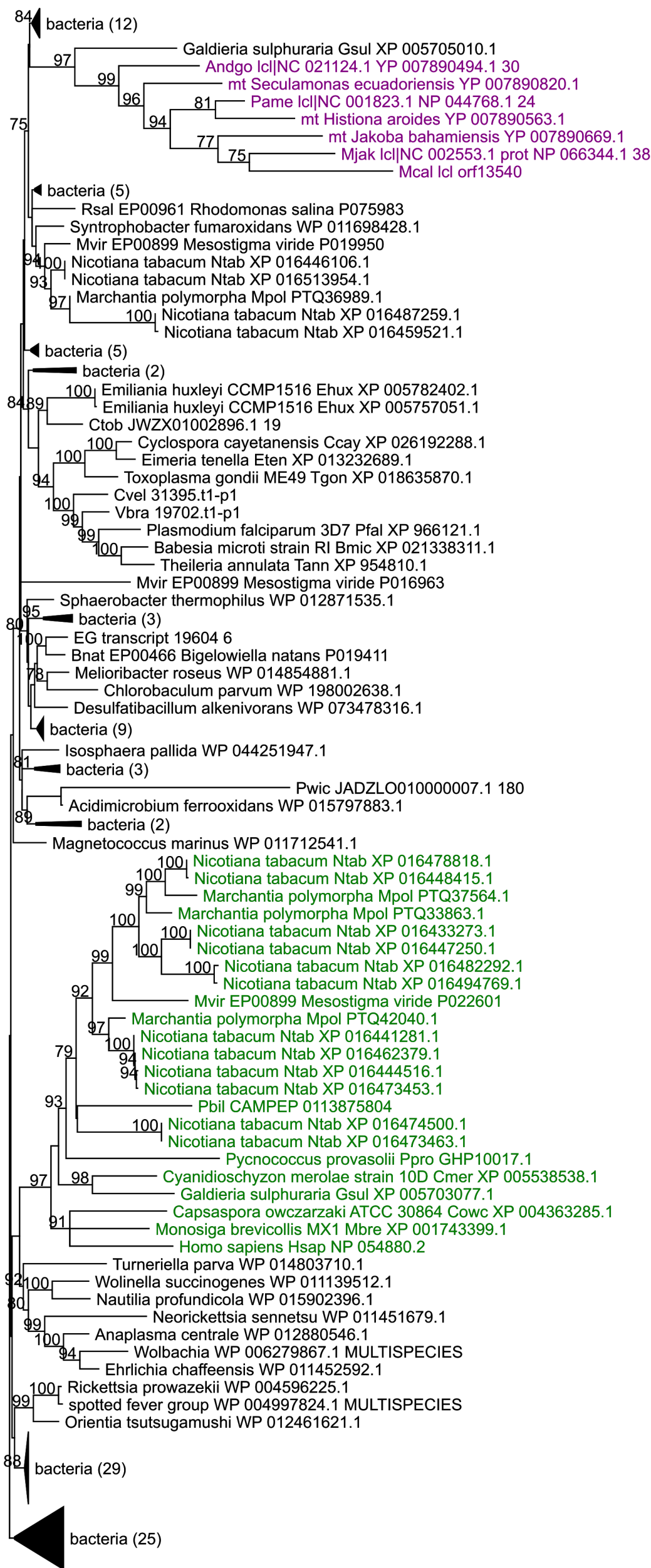


Protein: **rpl14**; alignment timing: trimAl; IQ-TREE2 best-fit model: Q.insect+R7



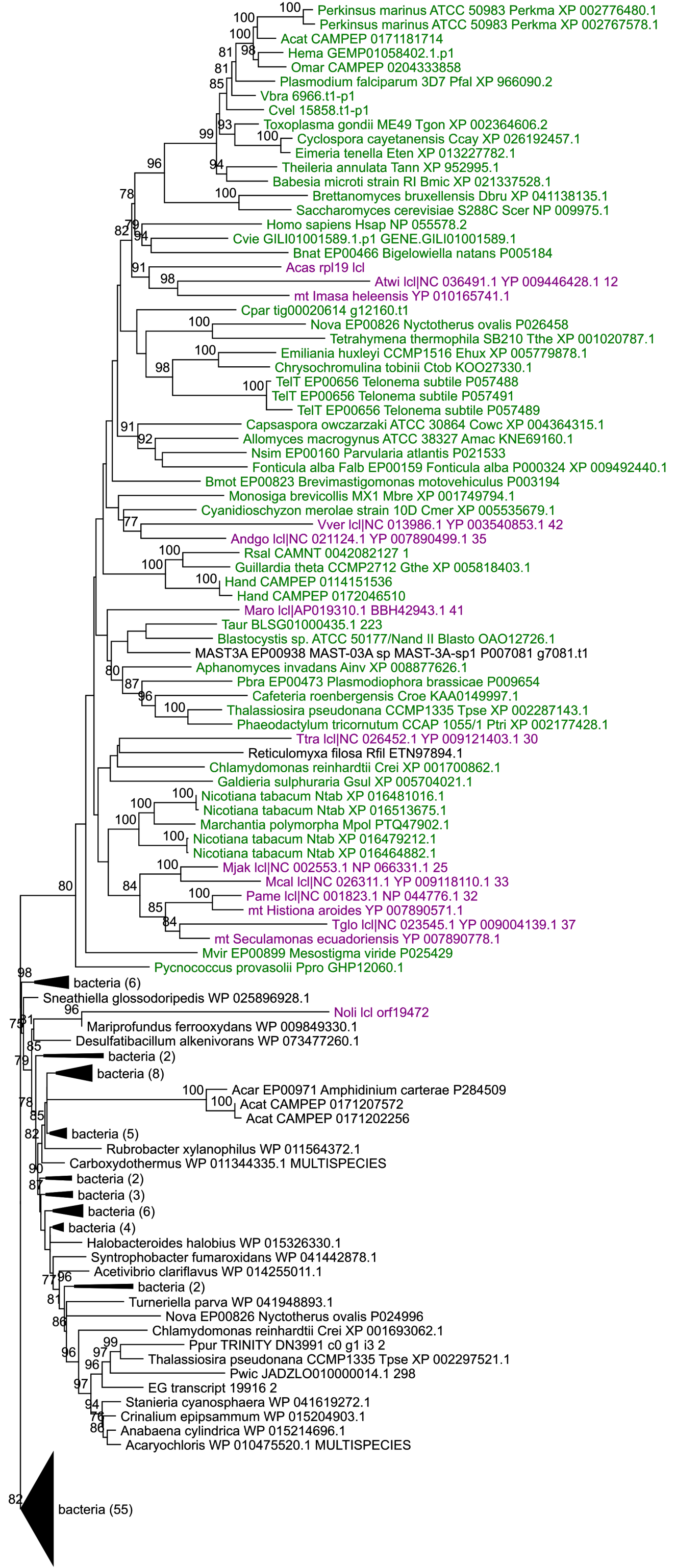
Protein: **rpl16**; alignment timing: trimAl; IQ-TREE2 best-fit model: Q.yeast+R8

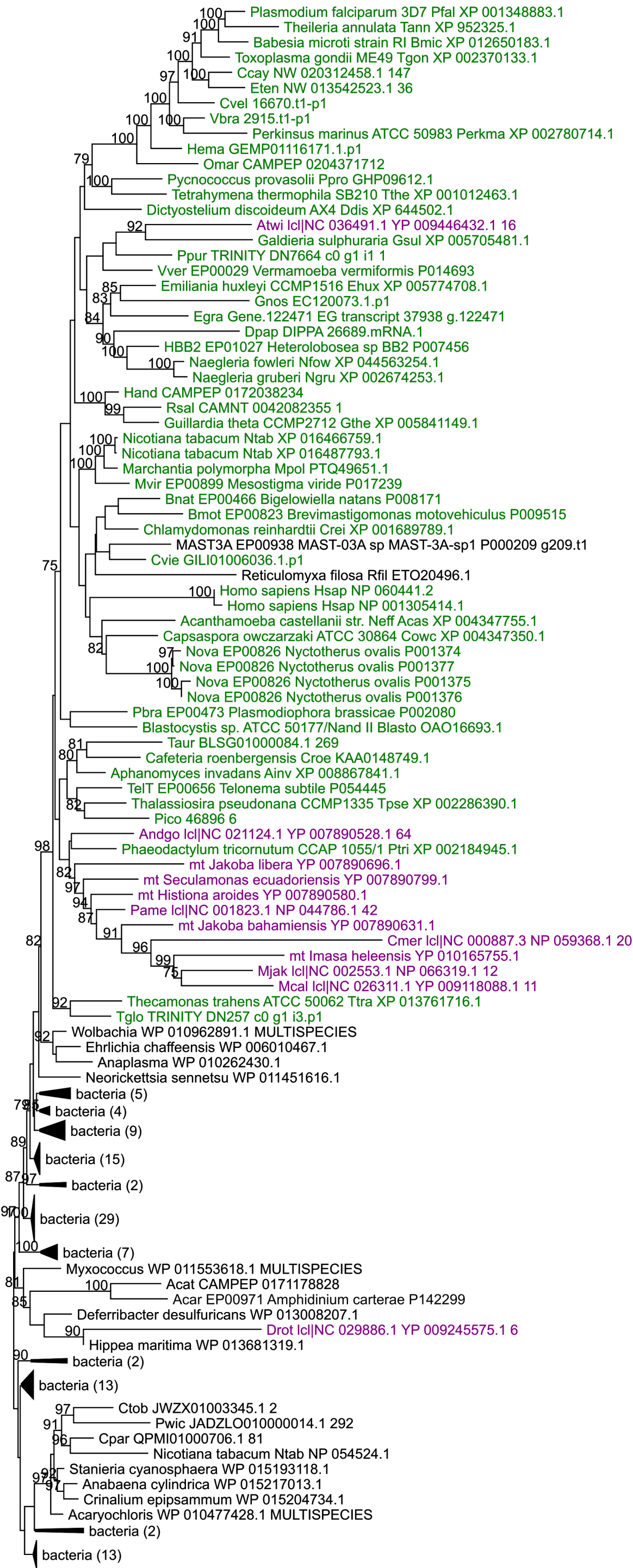
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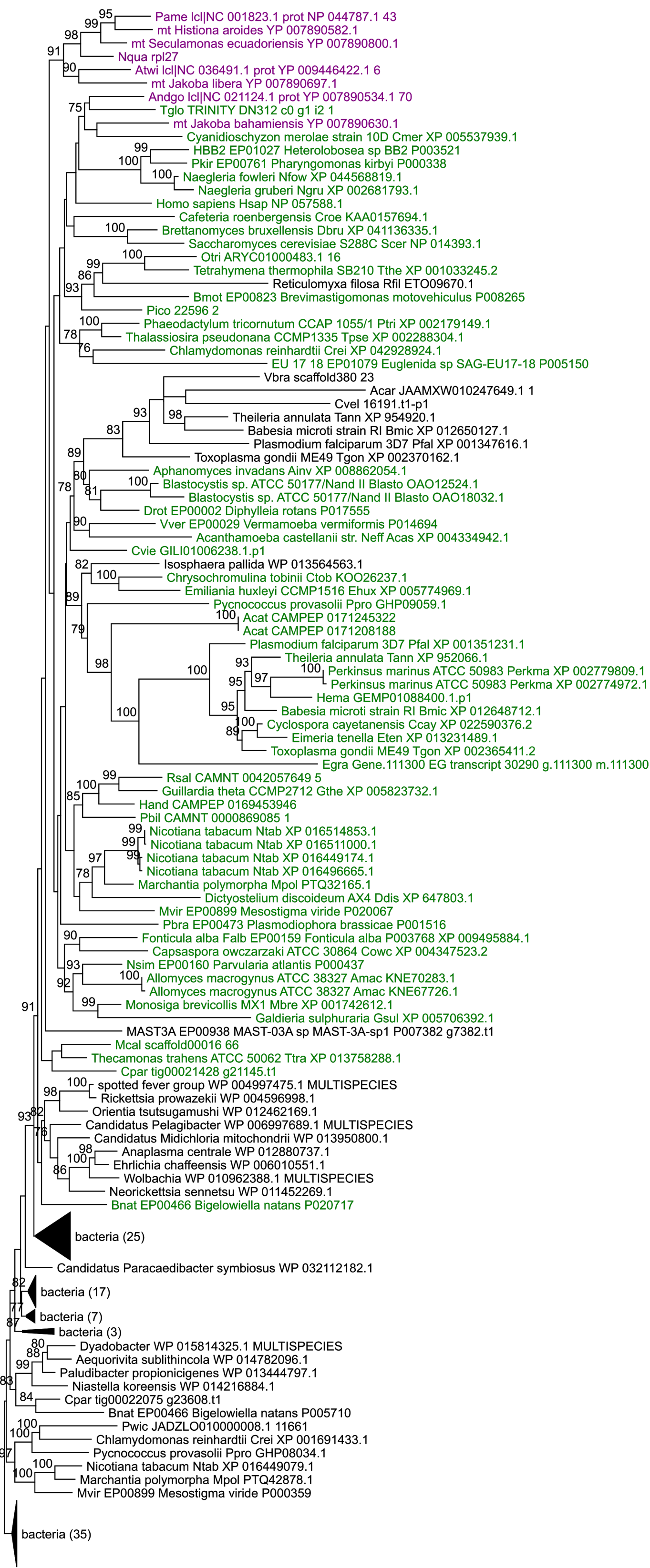
Protein: **rpl18**; alignment timing: trimAl; IQ-TREE2 best-fit model: Q.pfam+G4

0.50



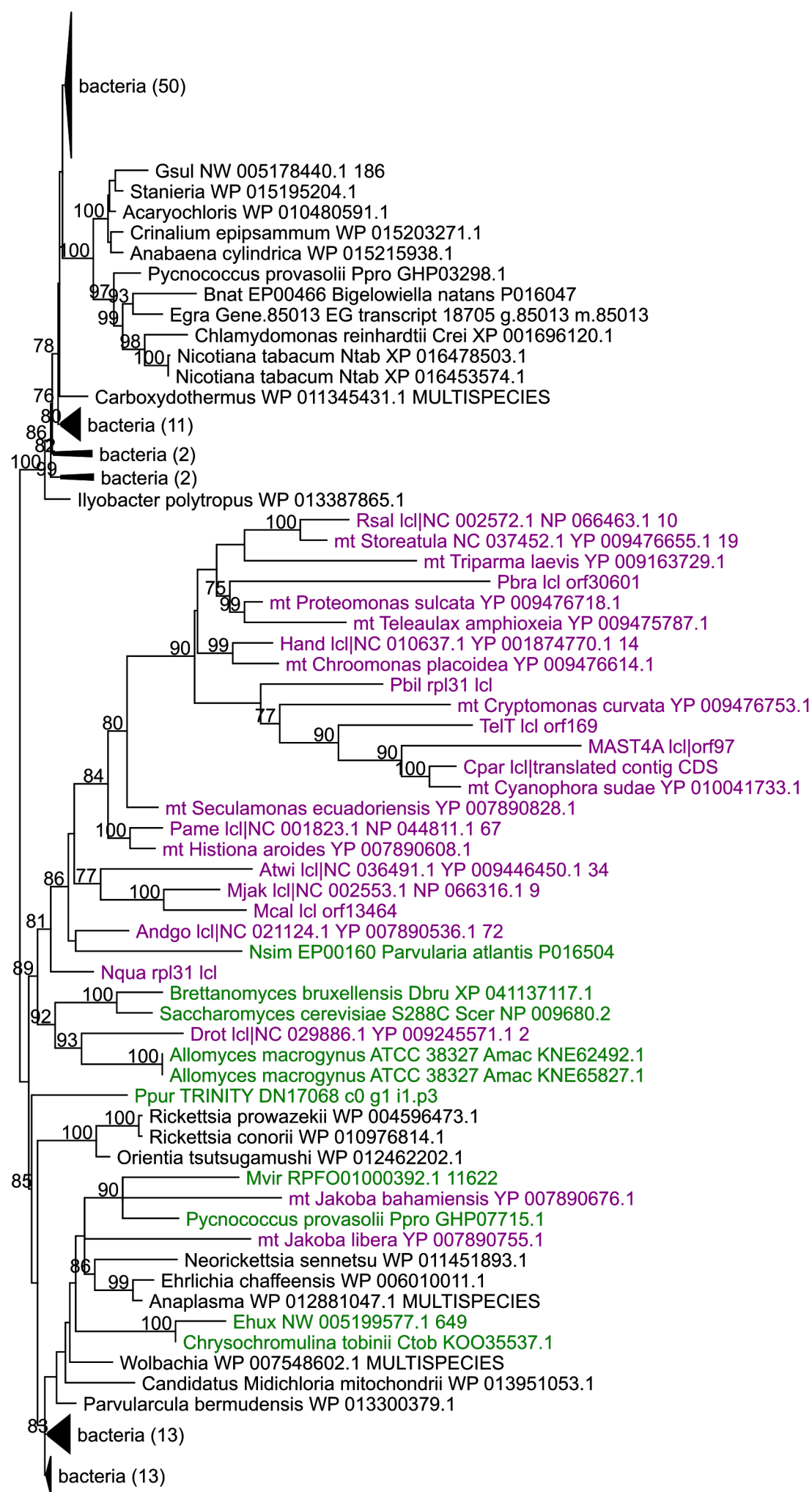


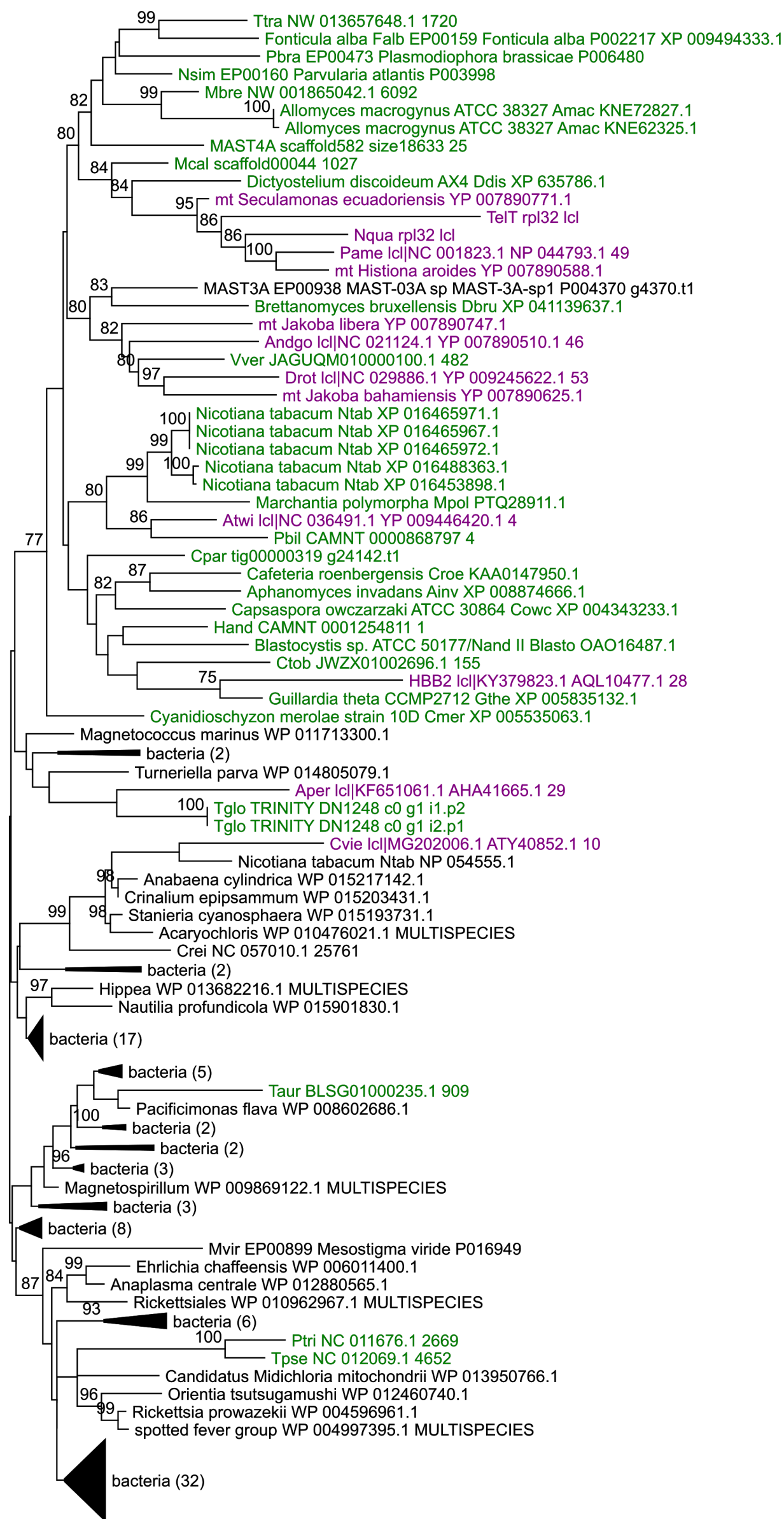




Protein: **rpl27**; alignment timing: ClipKIT; IQ-TREE2 best-fit model: Q.pfam+R6

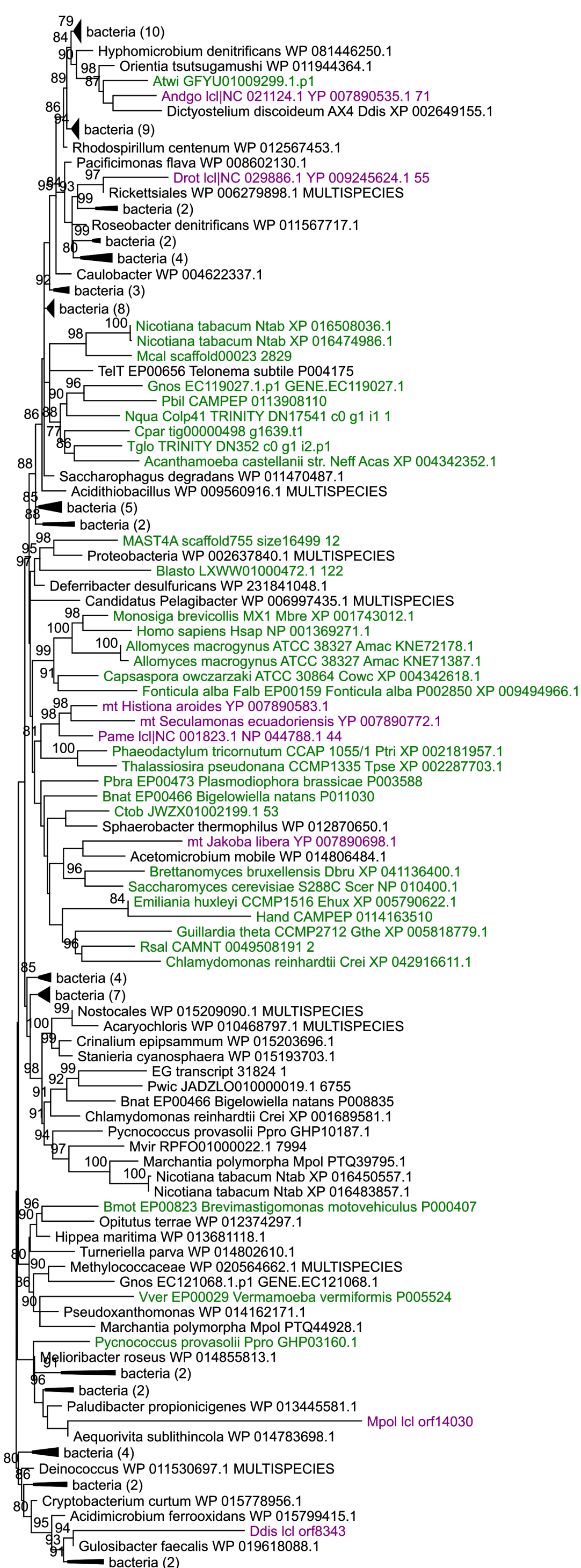
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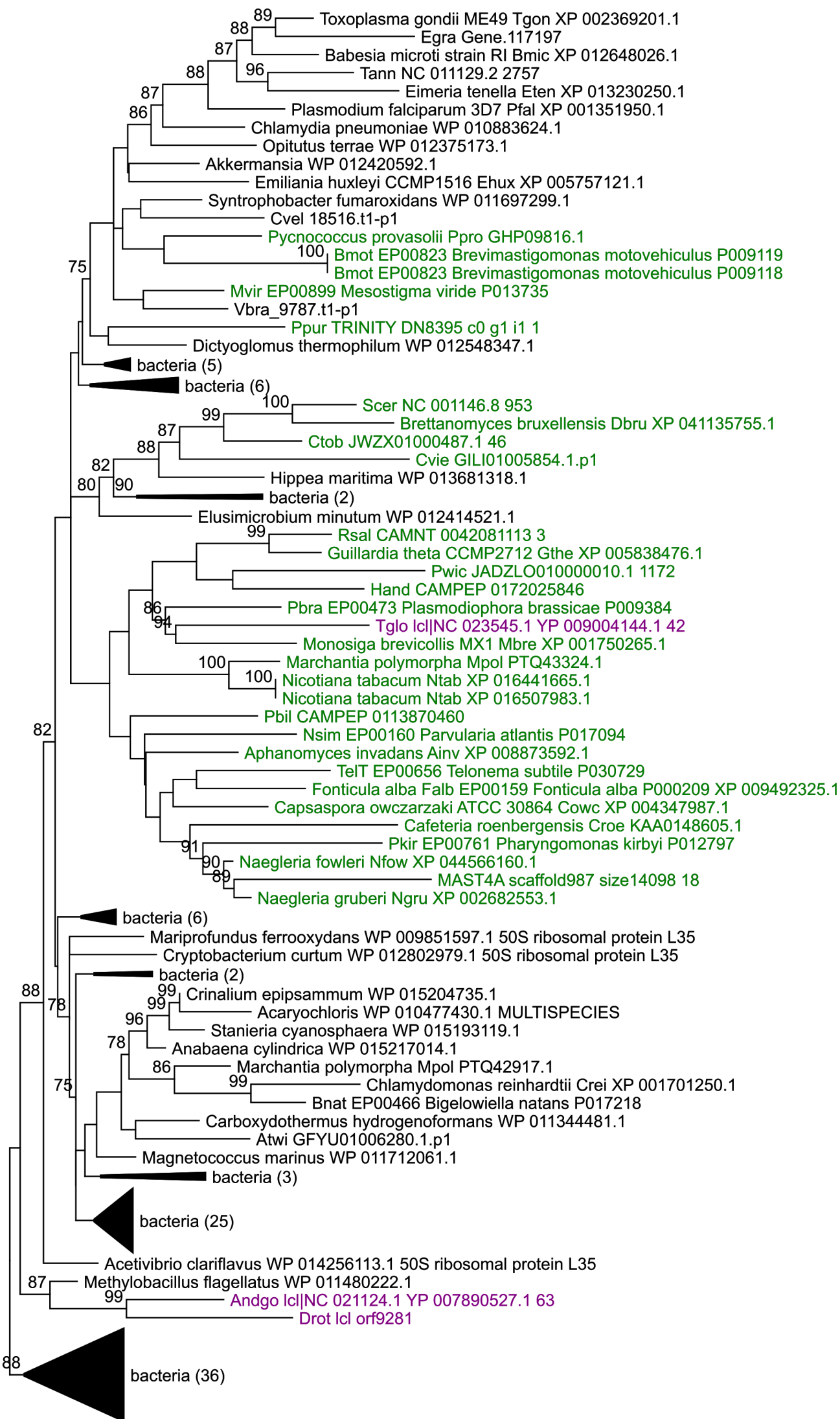


Protein: **rpl32**; alignment timing: ClipKIT; IQ-TREE2 best-fit model: VT+R4

0.50

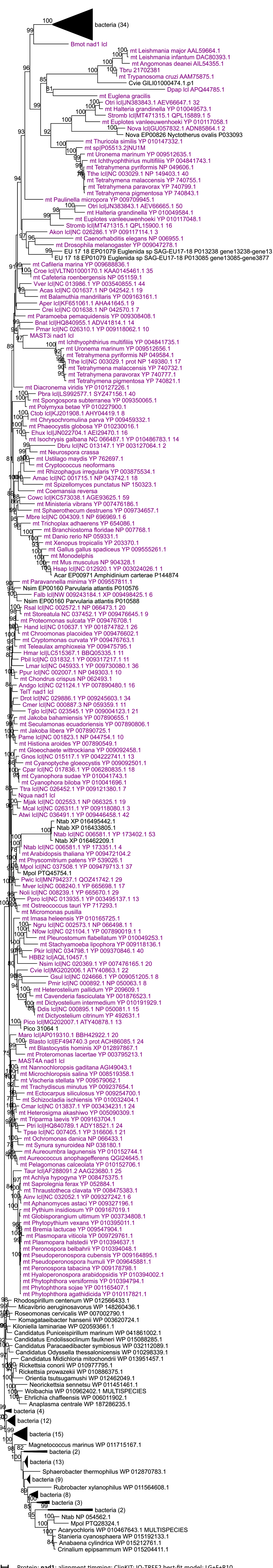


Protein: **rpl34**; alignment timing: ClipKIT; IQ-TREE2 best-fit model: PMB+R4



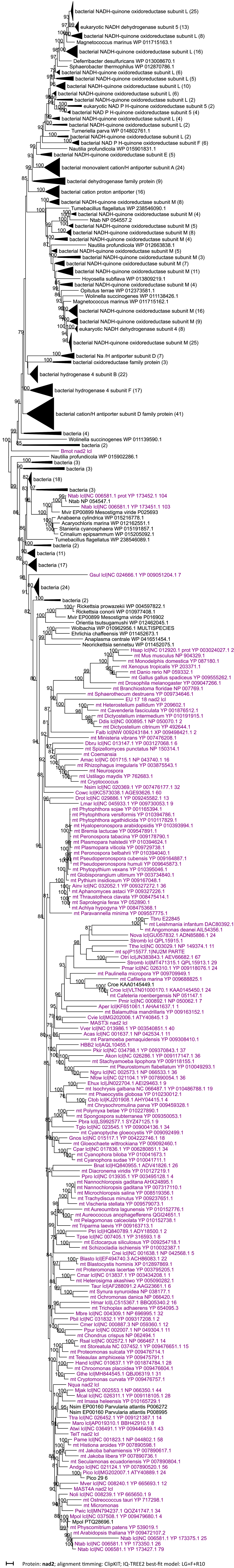
Protein: **rpl35**; alignment timing: trimAl; IQ-TREE2 best-fit model: Q.pfam+R6

0.50

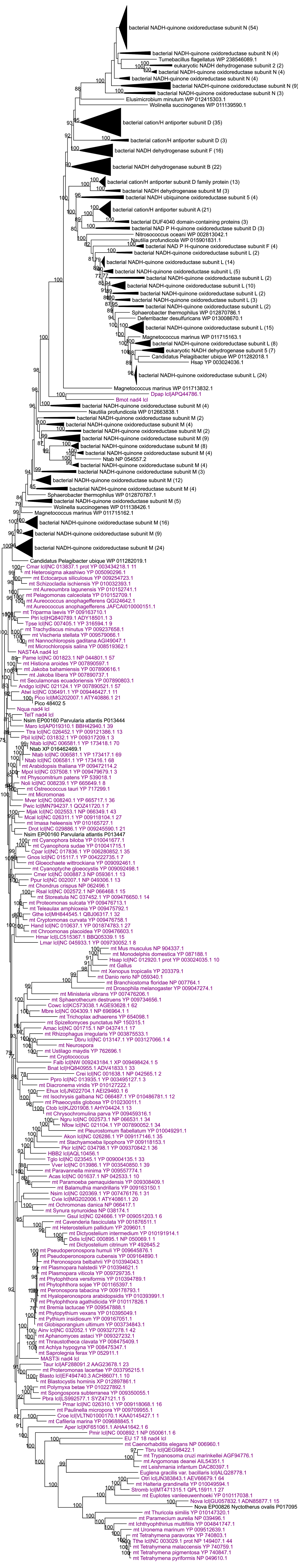


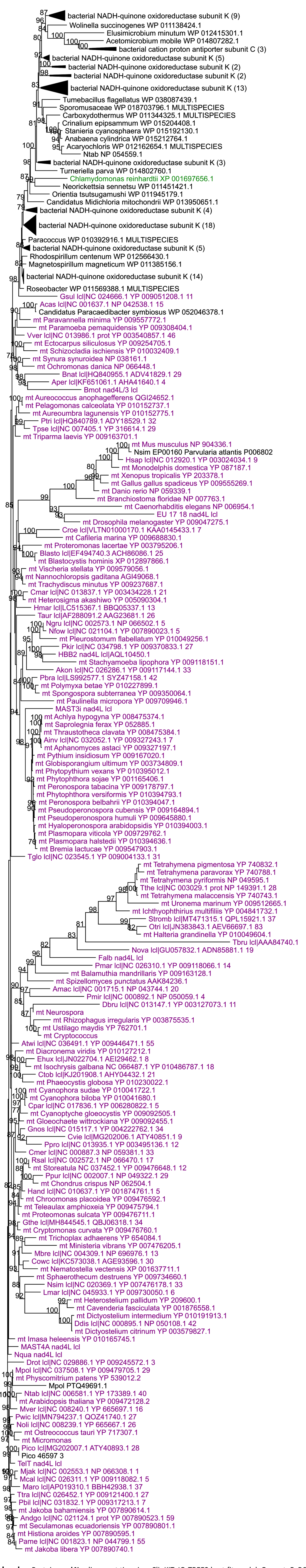
Protein: **nad1**; alignment timming: ClipKIT; IQ-TREE2 best-fit model: LG+F+R10

0.50



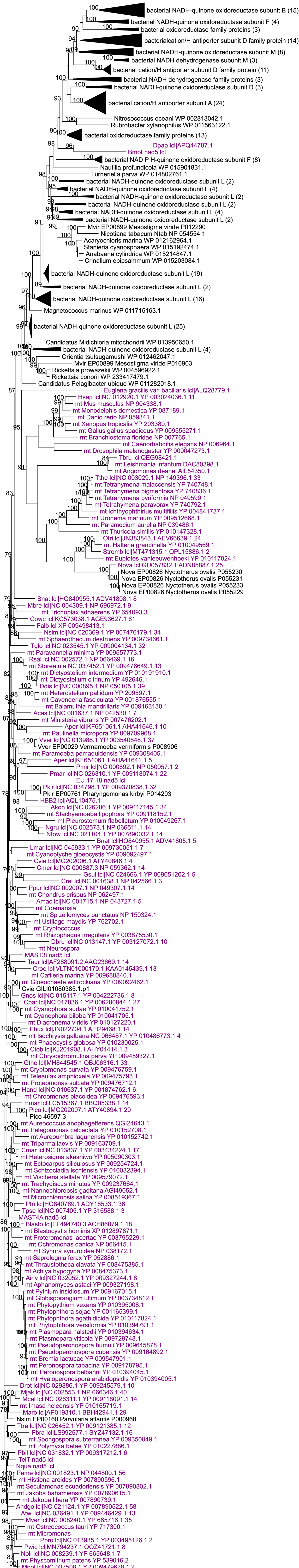




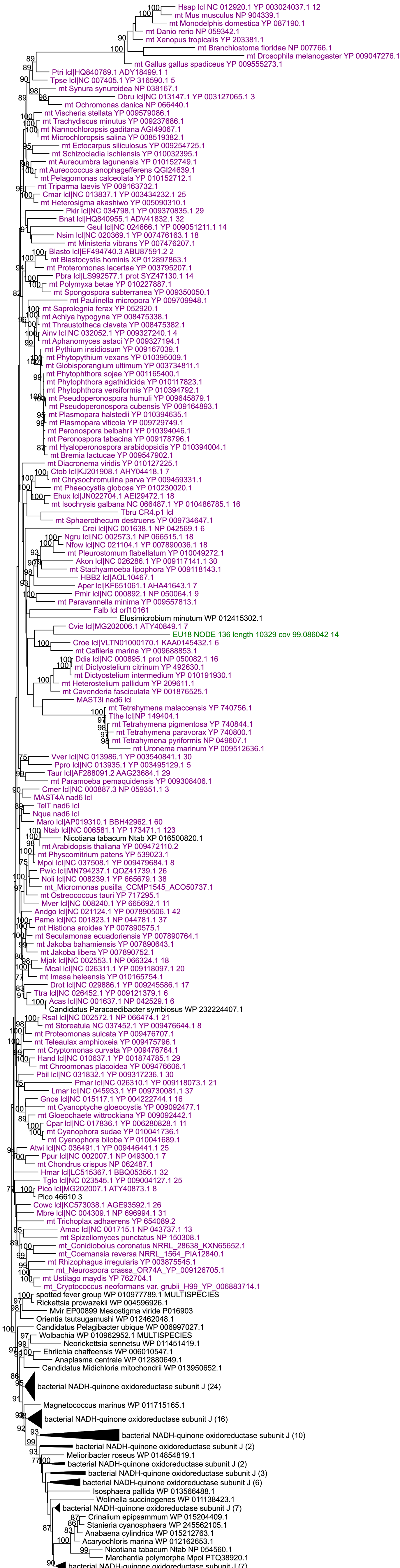


Protein: **nad4L**; alignment timing: ClipKIT; IQ-TREE2 best-fit model: Q.yeast+F+R6

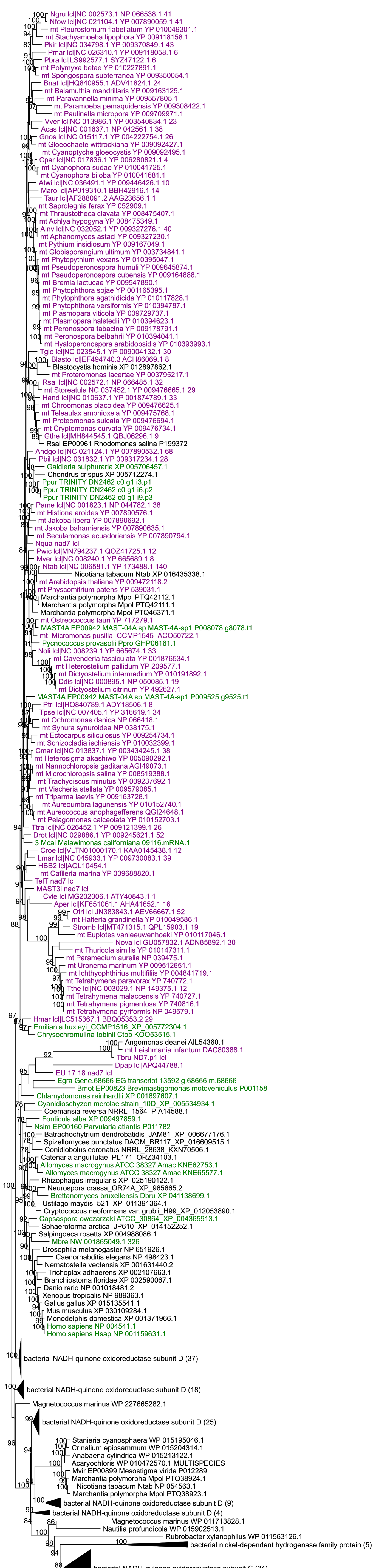
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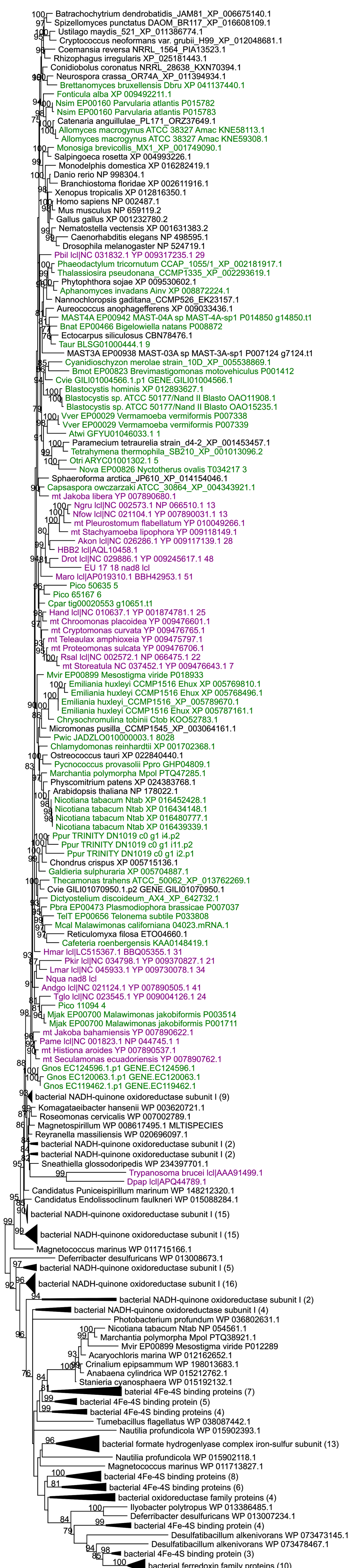
Protein: nad5; alignment timming: ClipKIT; IQ-TREE2 best-fit model: LG+F+R10



H Protein: **nad6**; alignment timming: ClipKIT; IQ-TREE2 best-fit model: Q,yeast+F+R8



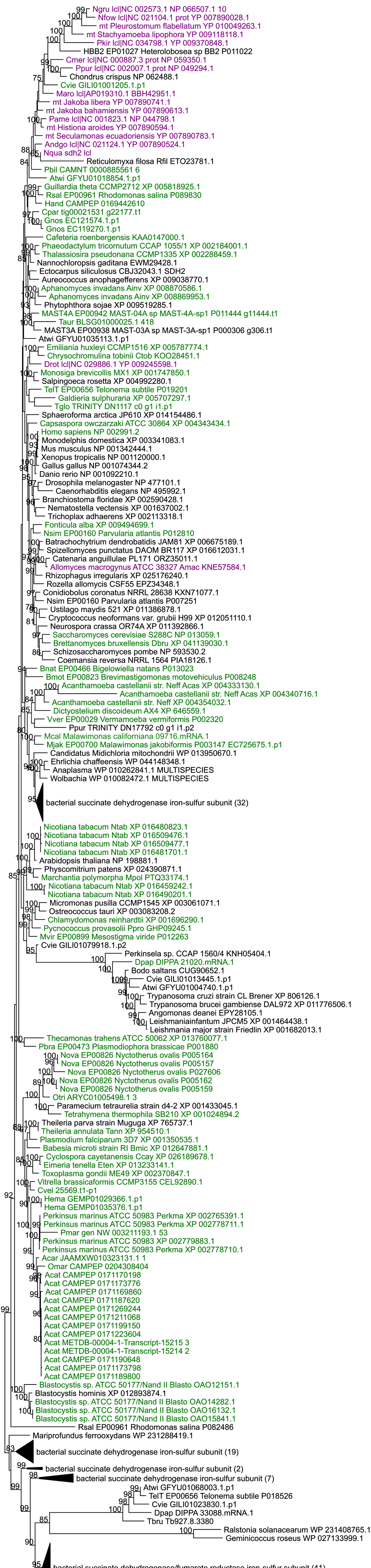
Protein: **nad7**; alignment timing: ClipKIT; IQ-TREE2 best-fit model: LG+R10





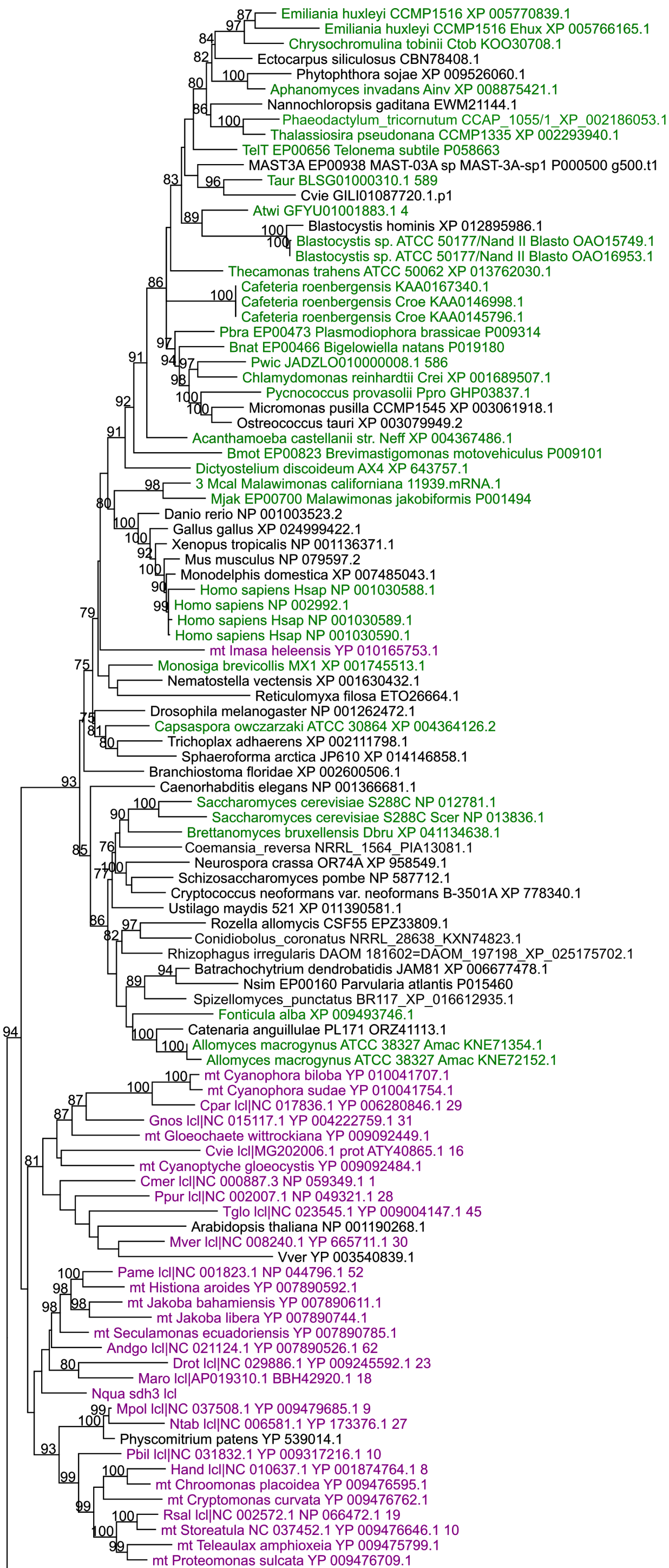
Protein: **nad10**; alignment timing: ClipKIT; IQ-TREE2 best-fit model: Q.pfam+R8





Protein: **sdh2**; alignment timming: trimAl; IQ-TREE2 best-fit model: Q.pfam+R8

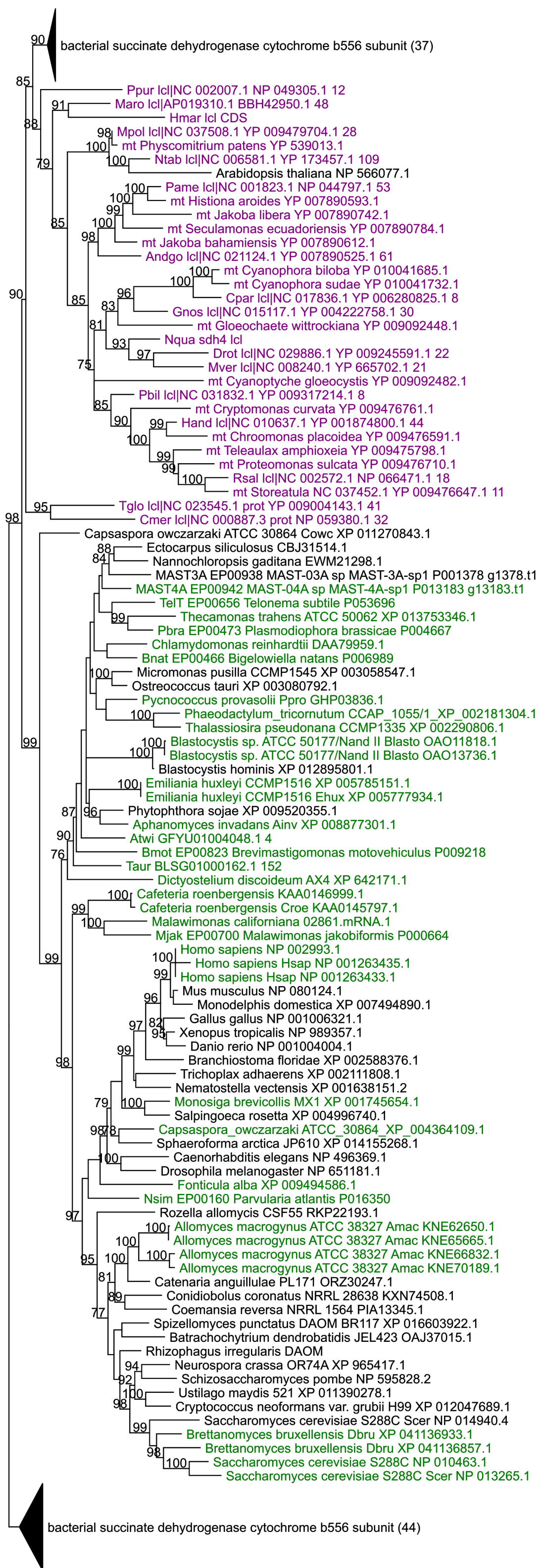
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bacterial succinate dehydrogenase cytochrome b556 subunit (64)

Protein: **sdh3**; alignment timing: ClipKIT; IQ-TREE2 best-fit model: VT+F+R5

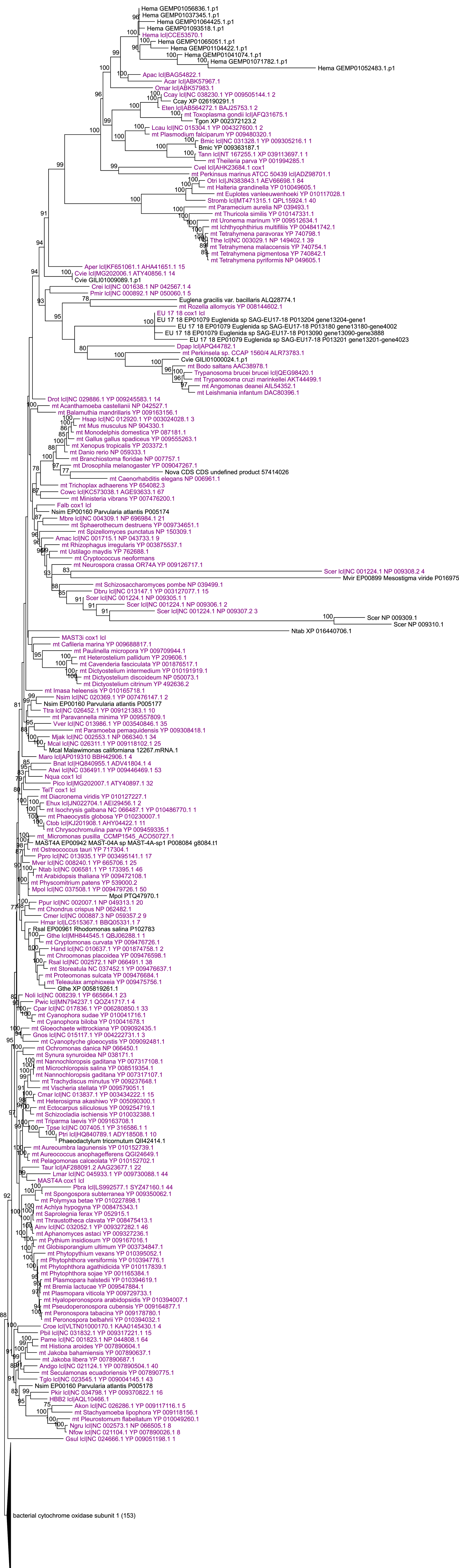
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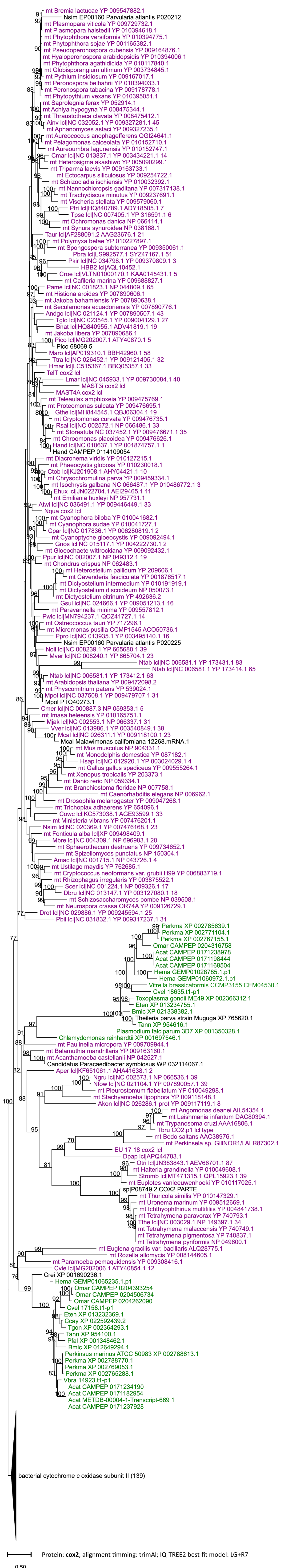


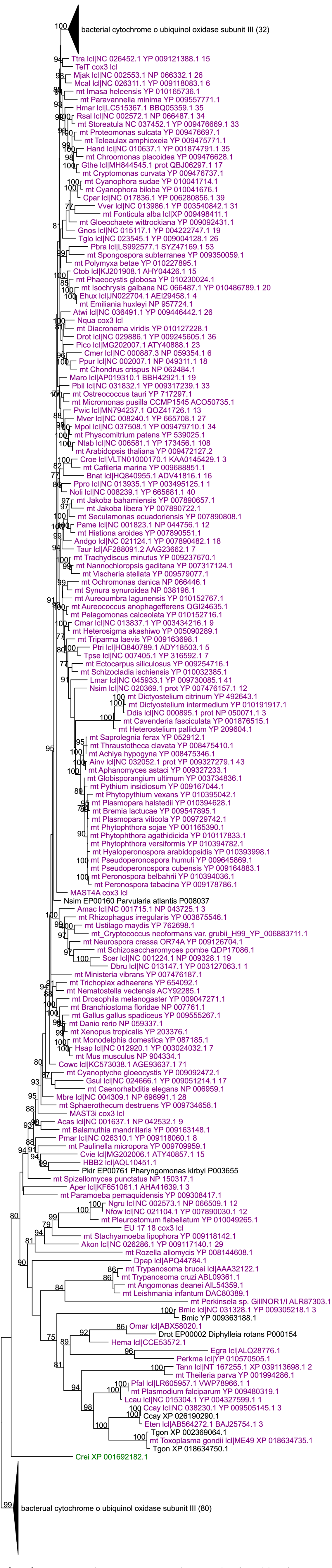
Protein: **sdh4**; alignment timing: ClipKIT; IQ-TREE2 best-fit model: Q.pfam+F+R7

0.50





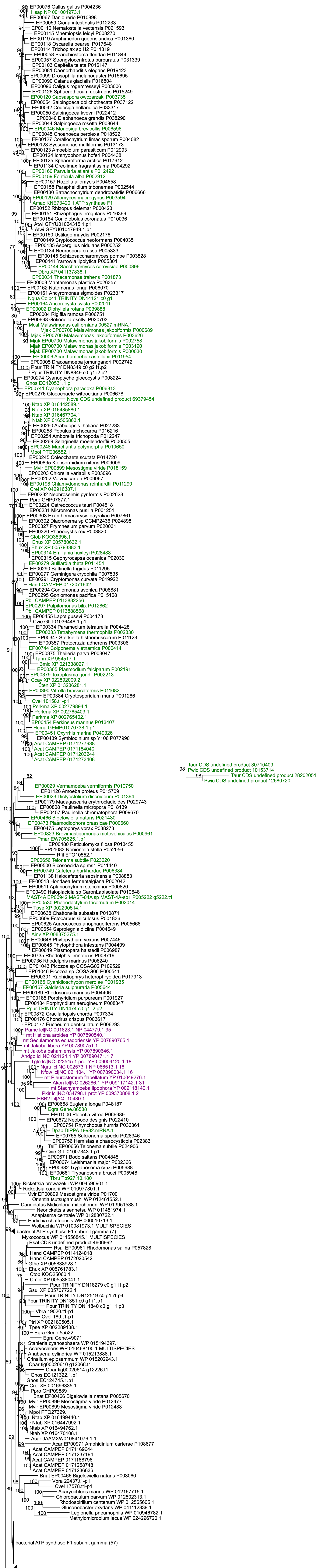


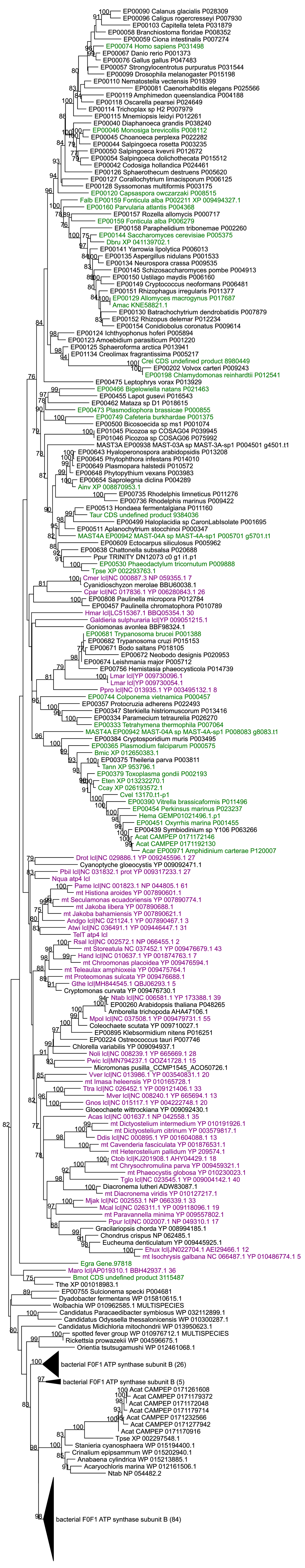


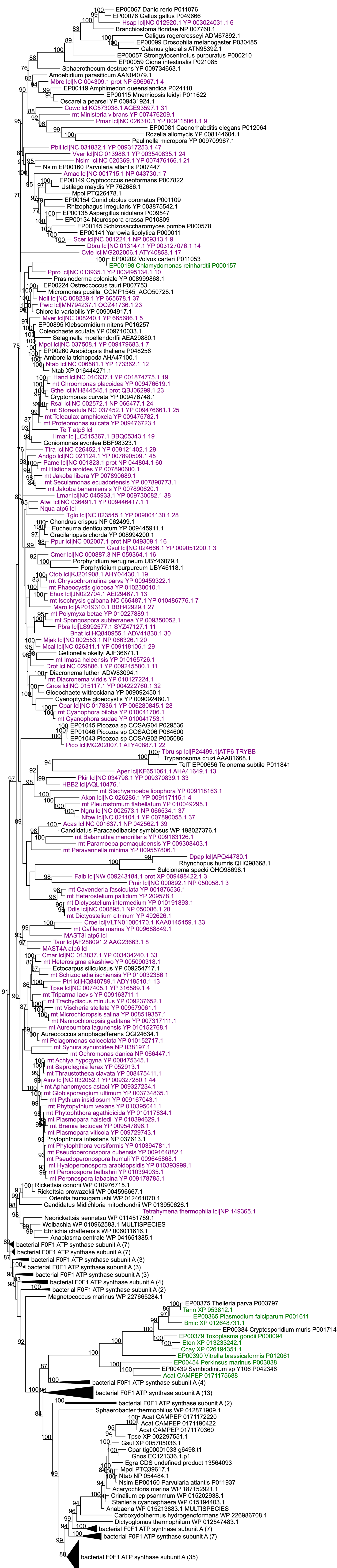


Protein: **atp1**; alignment timming: trimAI; IQ-TREE2 best-fit model: Q.yeast+R10

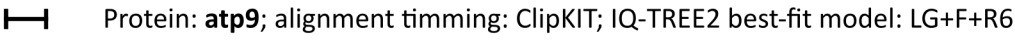
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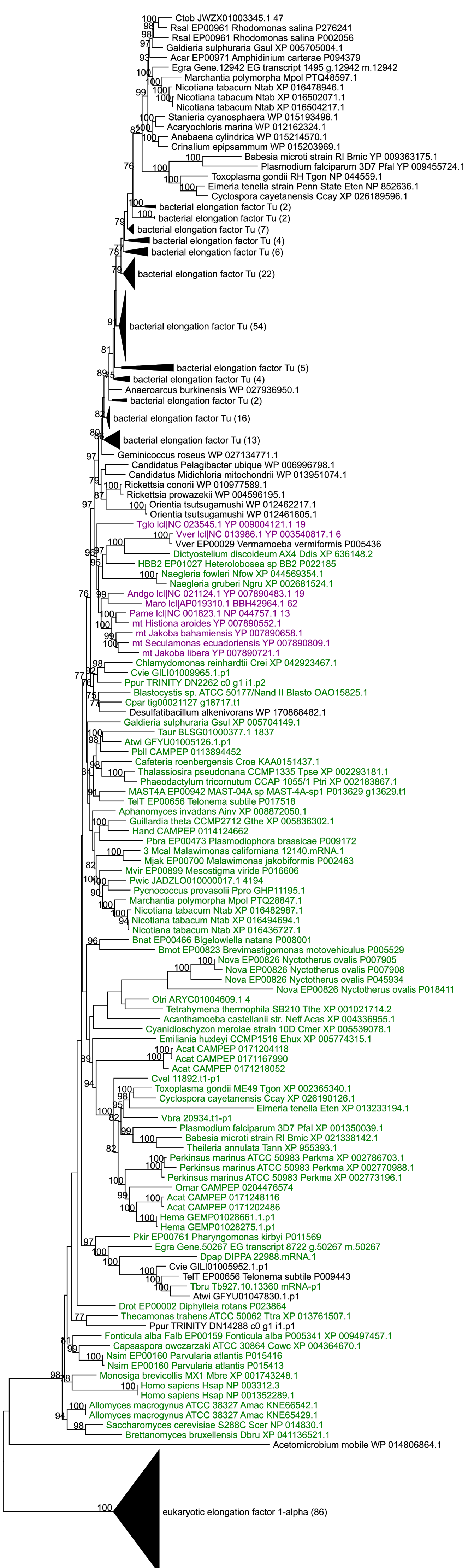






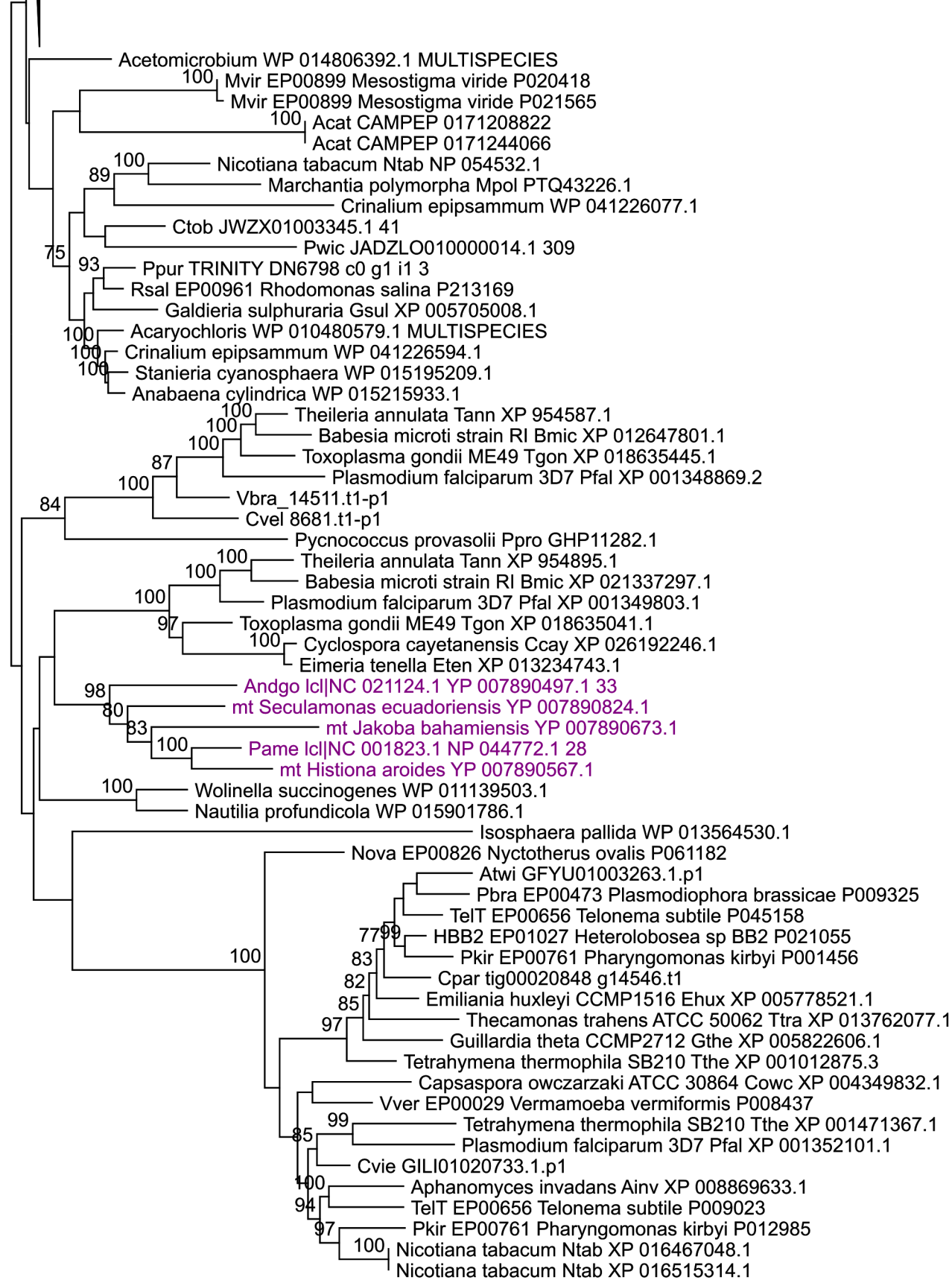




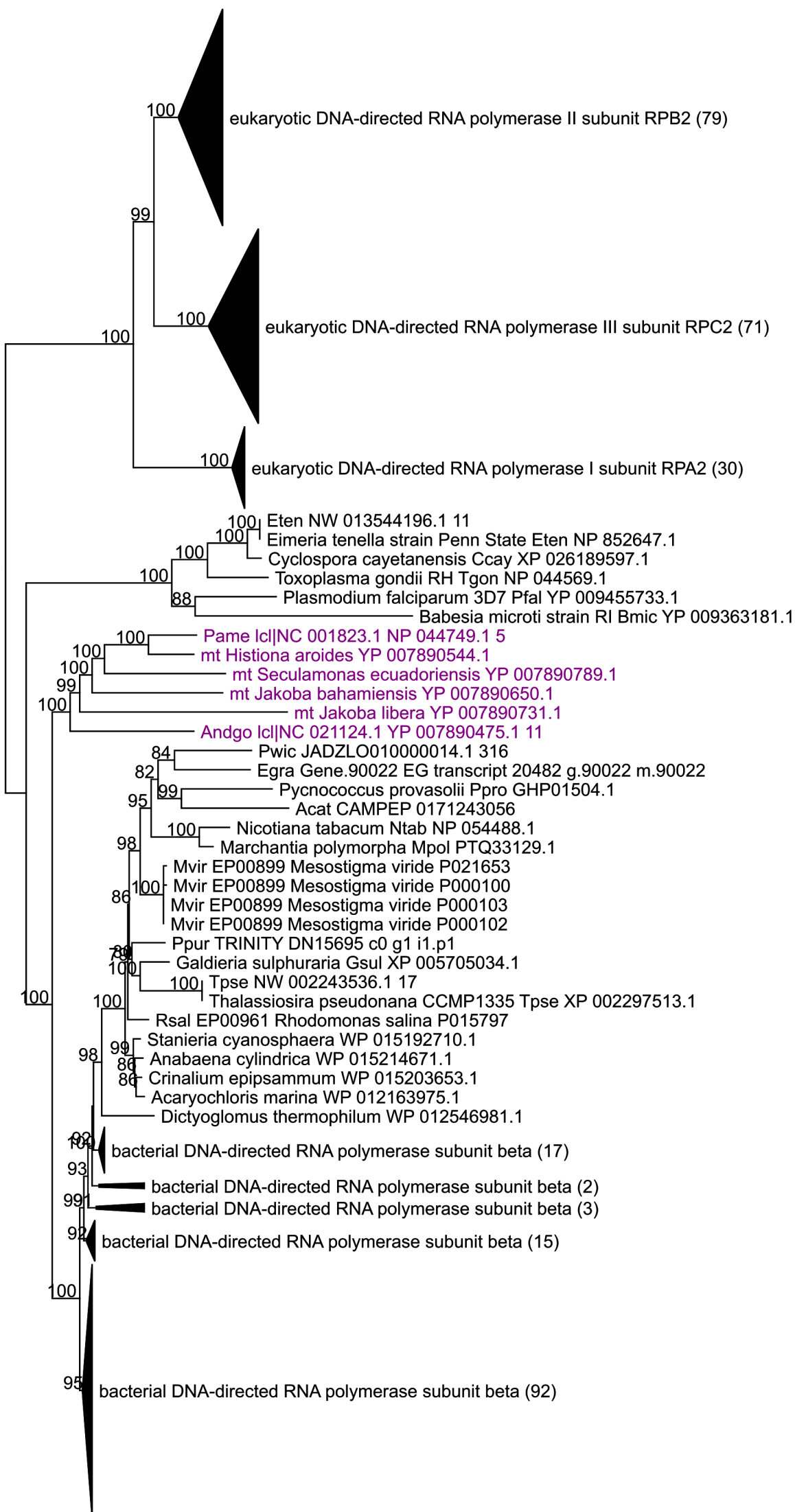


bacterial DNA-directed RNA polymerase subunit alpha (110)

78



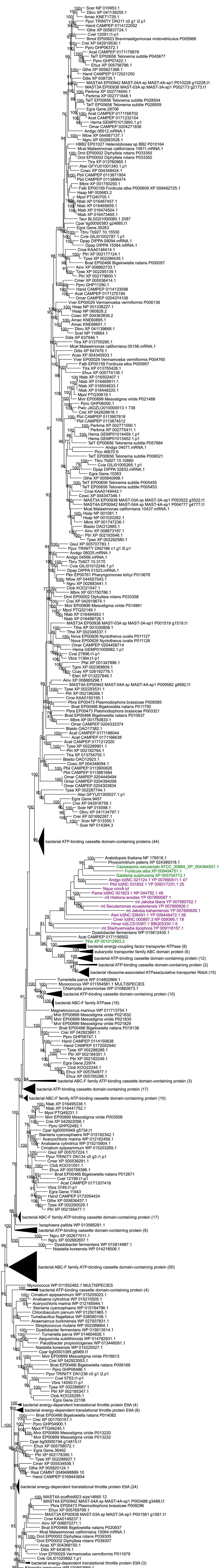
Protein: **rpoA**; alignment timing: trimAl; IQ-TREE2 best-fit model: LG+R6

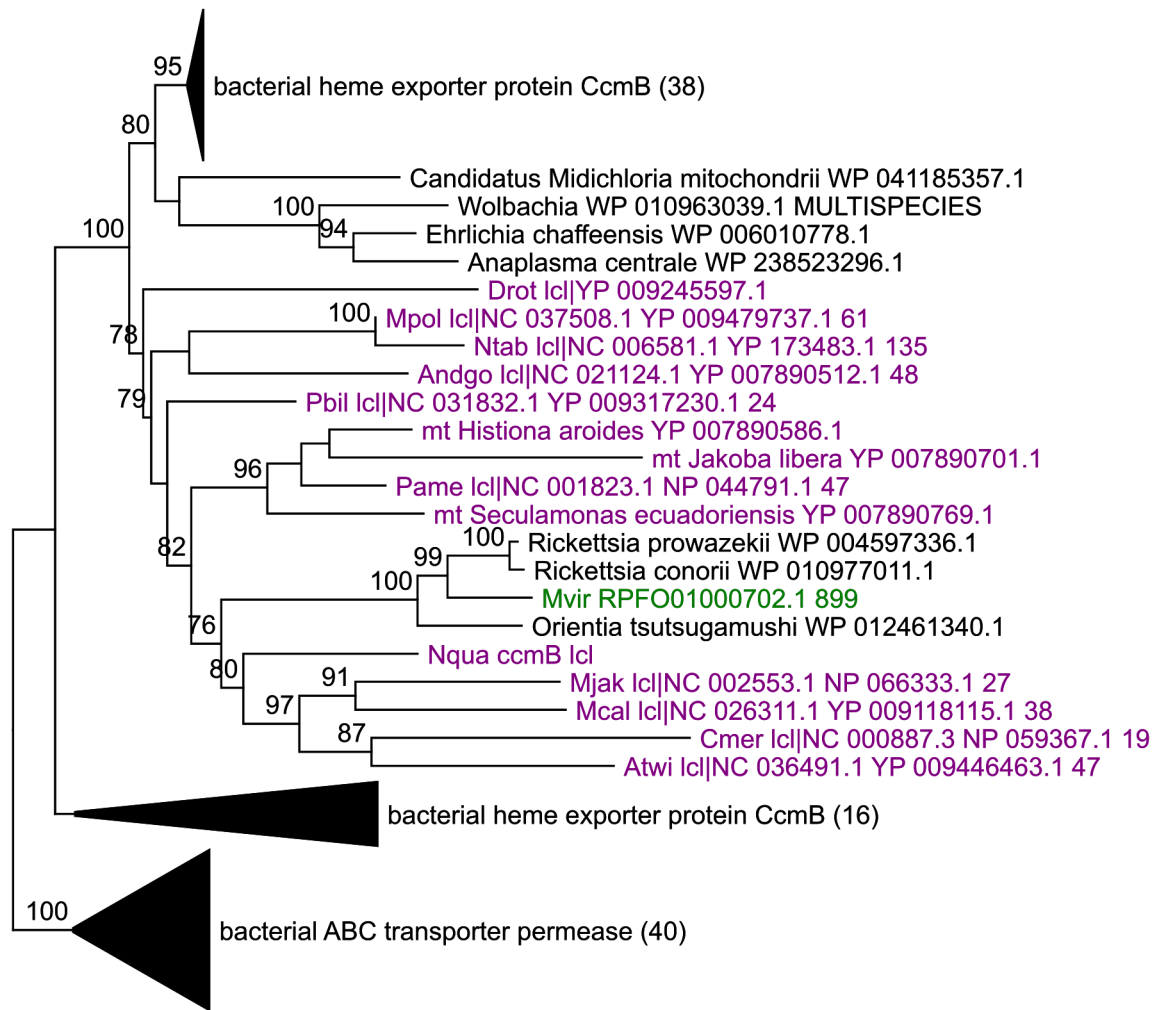


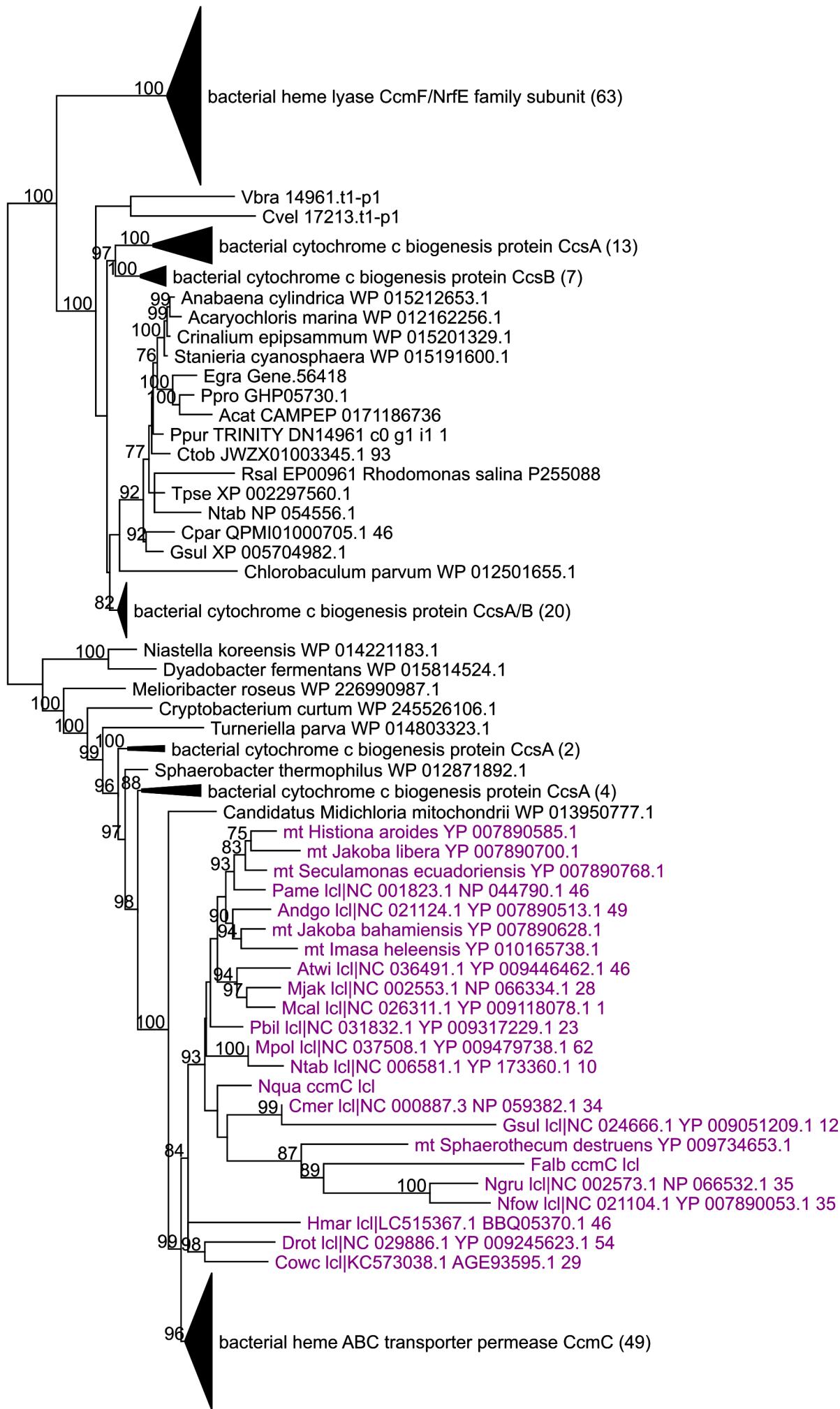


Protein: **rpoD**; alignment timing: trimAl; IQ-TREE2 best-fit model: LG+R9

0.50

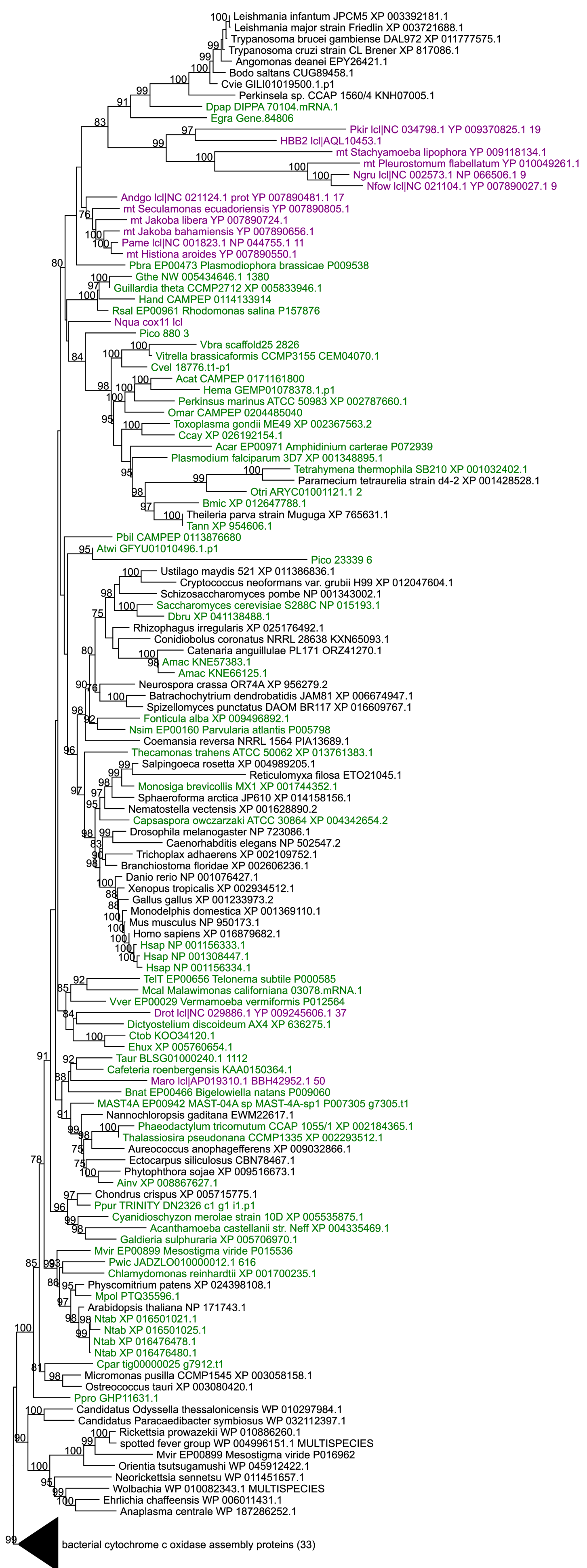


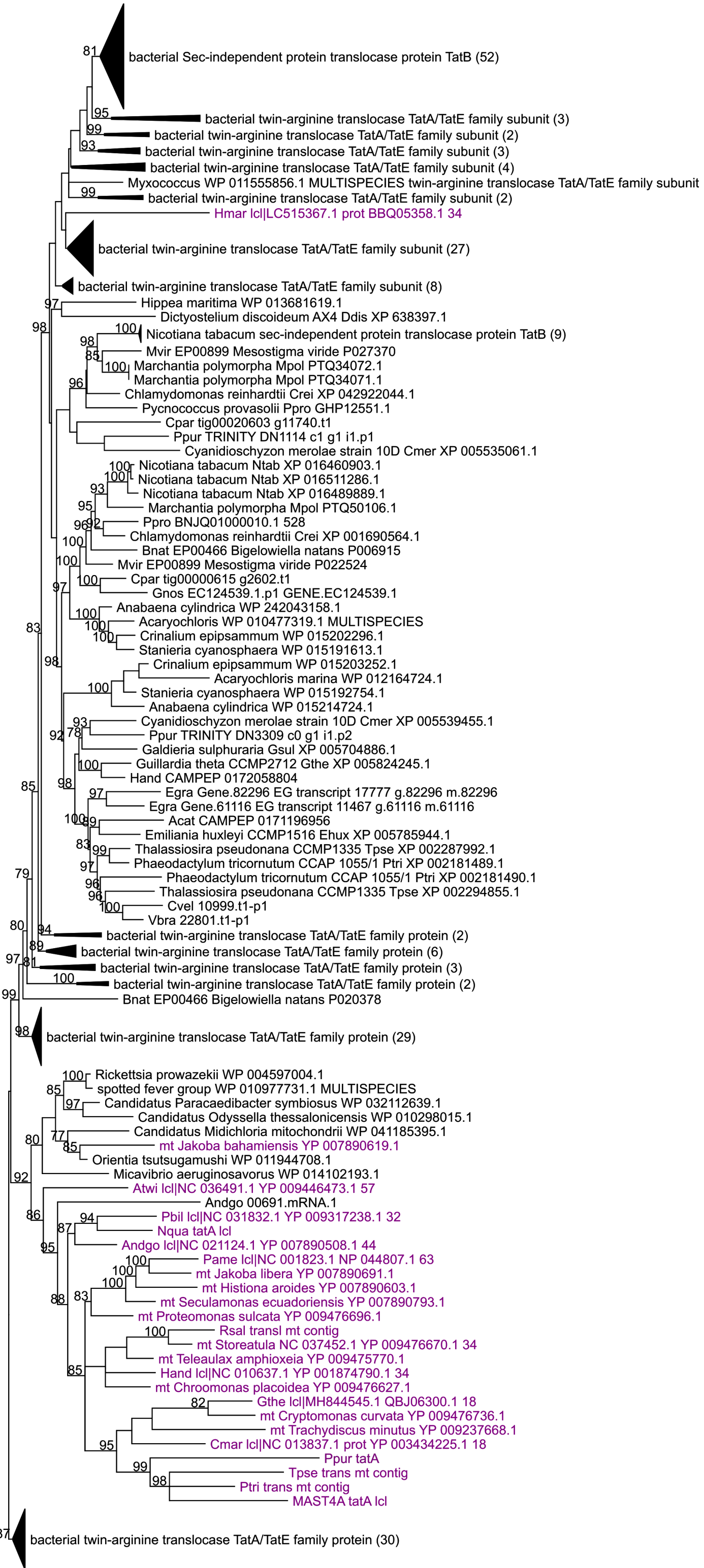




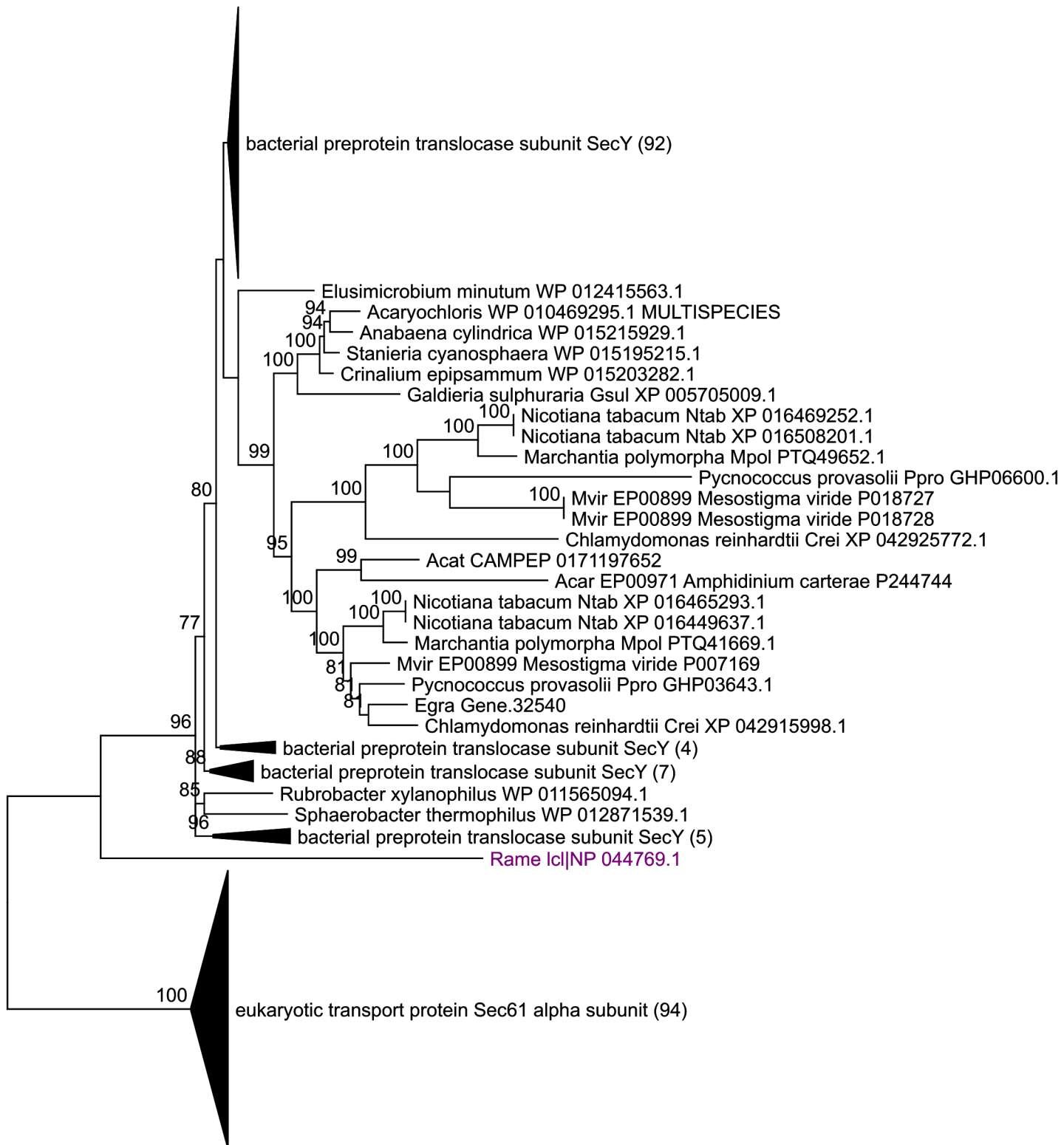
Protein: **ccmC**; alignment timing: trimAl; IQ-TREE2 best-fit model: LG+F+R8







Protein: **tatA**; alignment timing: ClipKIT; IQ-TREE2 best-fit model: Q.pfam+R5



Protein: **secY**; alignment timming: trimAl; IQ-TREE2 best-fit model: LG+F+R7

0.50