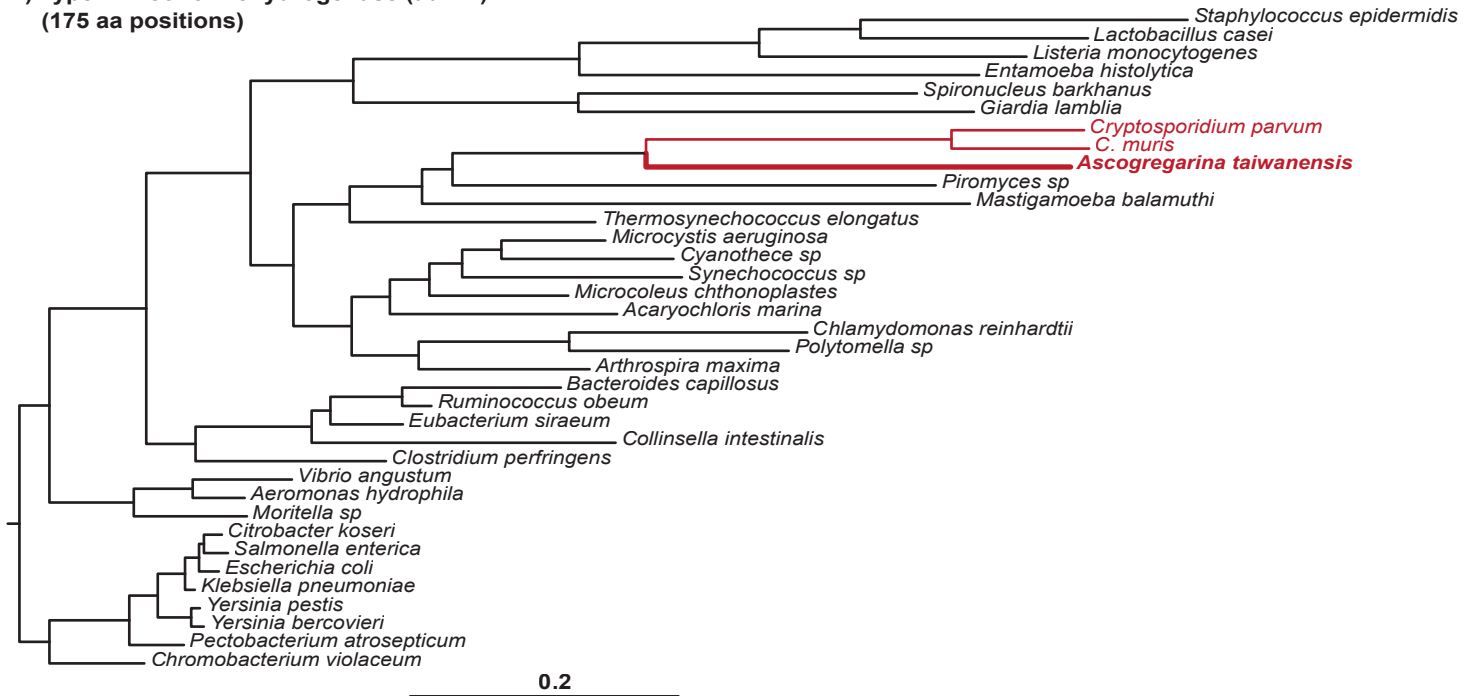


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Figure S1 (A-F). Bacterial-affinity of selected Ascogregarina proteins as inferred by maximum likelihood (ML) analysis (with PROML in the PHYLIP package). Best ML trees are inferred using a JTT amino acid substitution model with the consideration of fraction of invariance (Finv) and 4-rate gamma distribution. Sequences were added randomly with 10 jumps of searches and enabled global rearrangement.

A) Type-E Alcohol Dehydrogenase (adh-E)
(175 aa positions)



B) D-Lactate Dehydrogenase (D-LDH)
(76 aa positions)

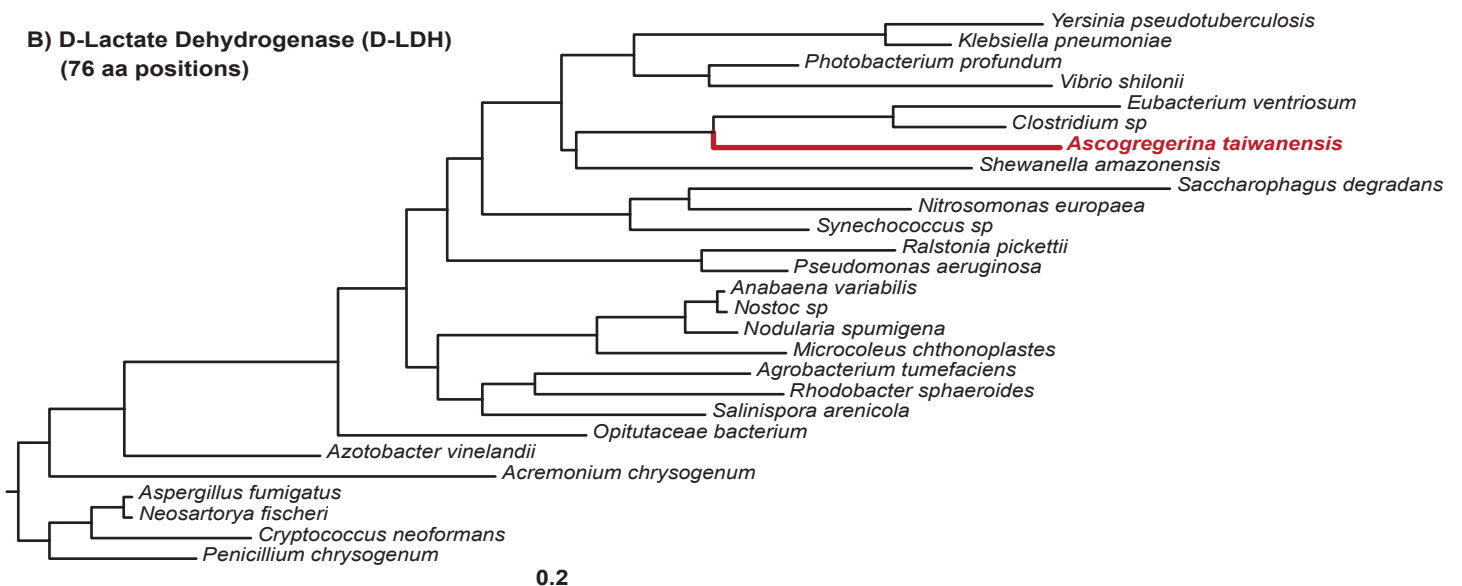
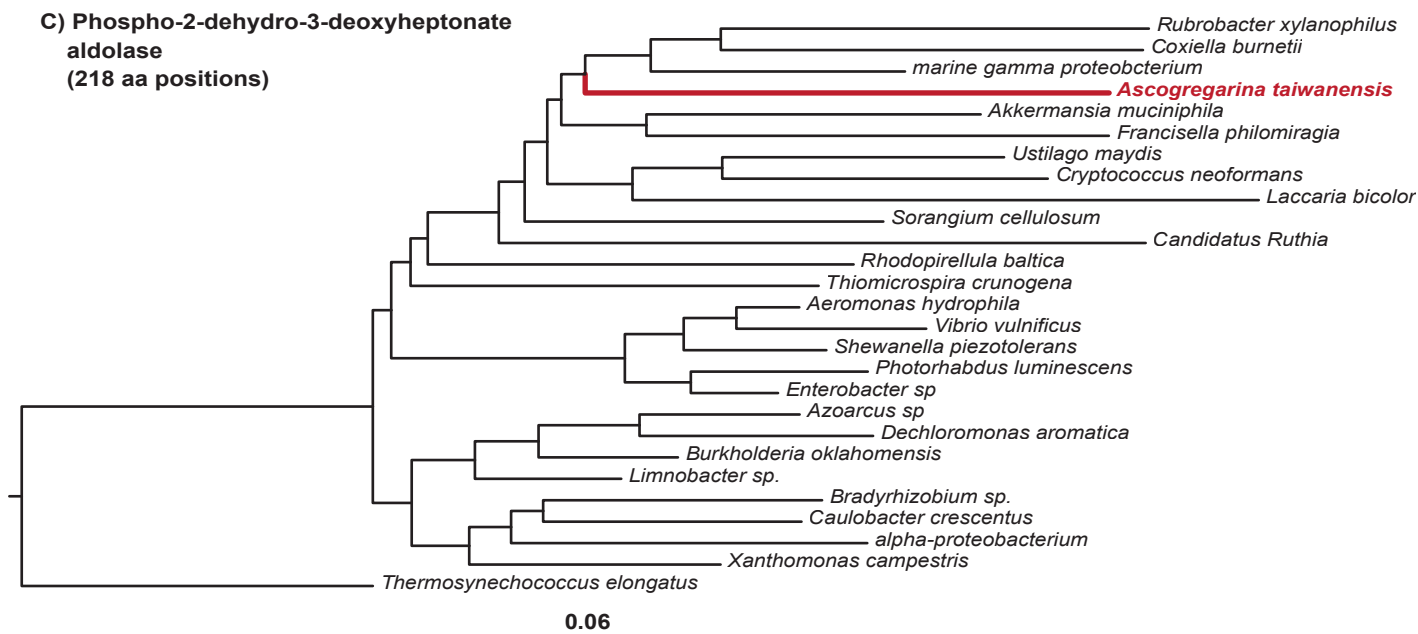


Figure S1 (A-F). Bacterial-affinity of selected Ascogregarina proteins.

C) Phospho-2-dehydro-3-deoxyheptonate aldolase (218 aa positions)



D) Tryptophan synthase (242 aa positions)

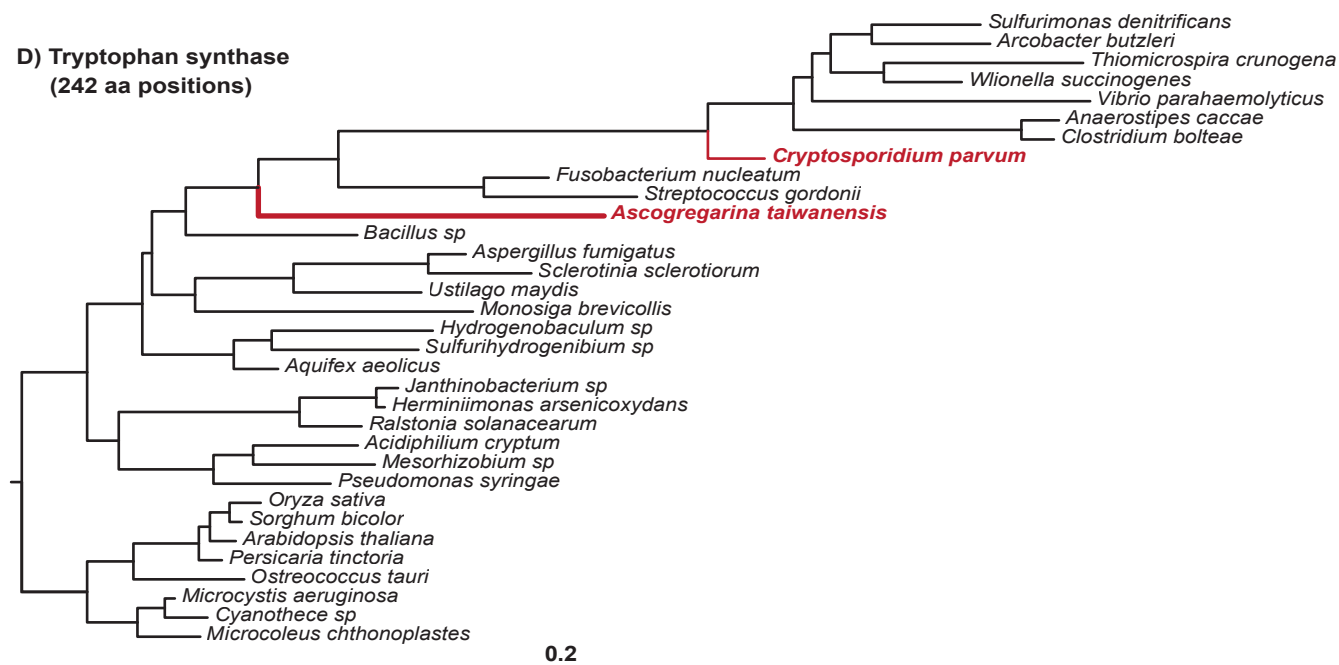


Figure S1 (A-F). Bacterial-affinity of selected Ascogregarina proteins.

E) Indole-3-glycerol-phosphate synthase (I3GPS) (93 aa positions)

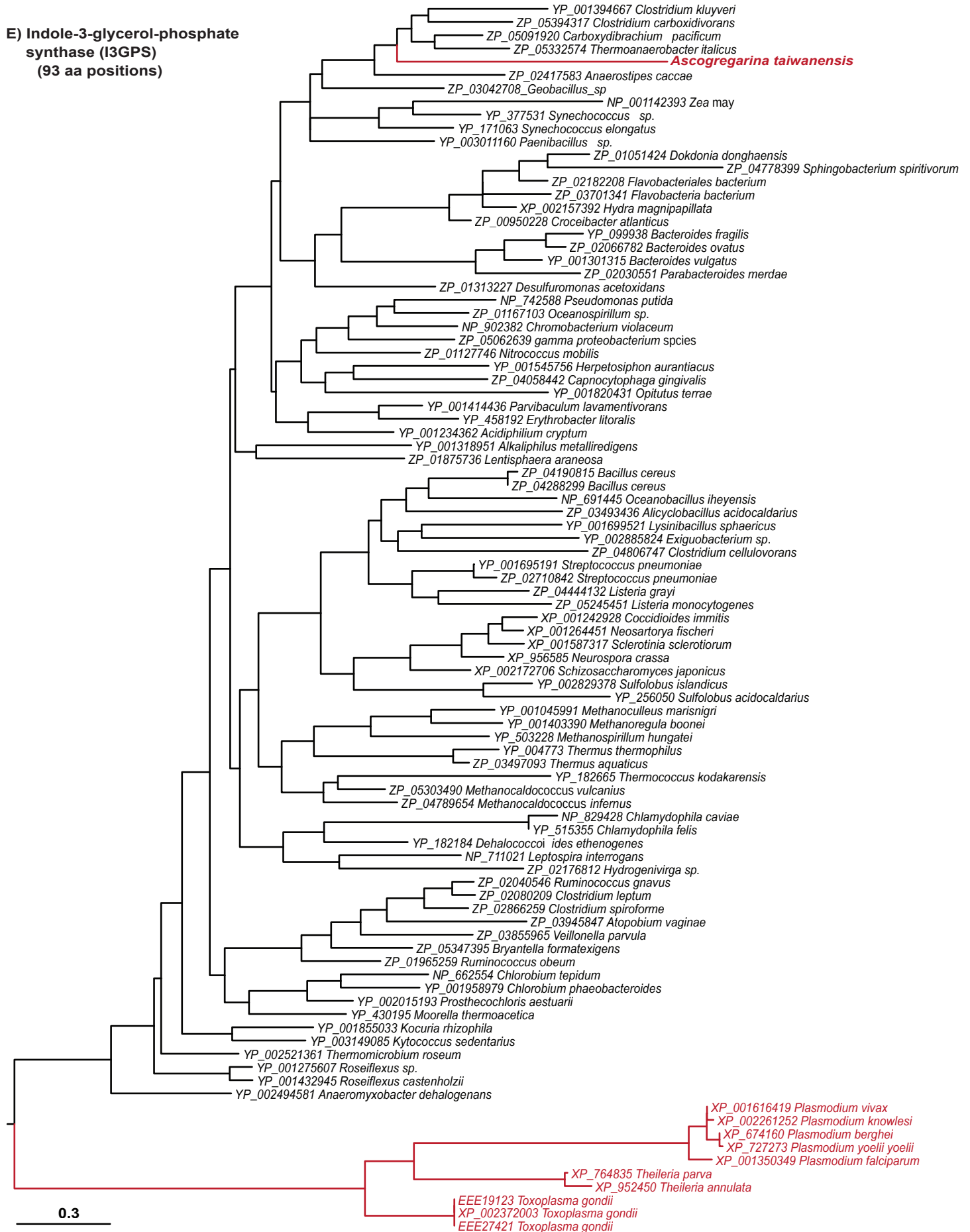


Figure S1 (A-F). Bacterial-affinity of selected Ascogregarina proteins.

F) glutamine amidotransferase class-I
anthranilate synthase (GAT1-AS)
(91 aa positions)

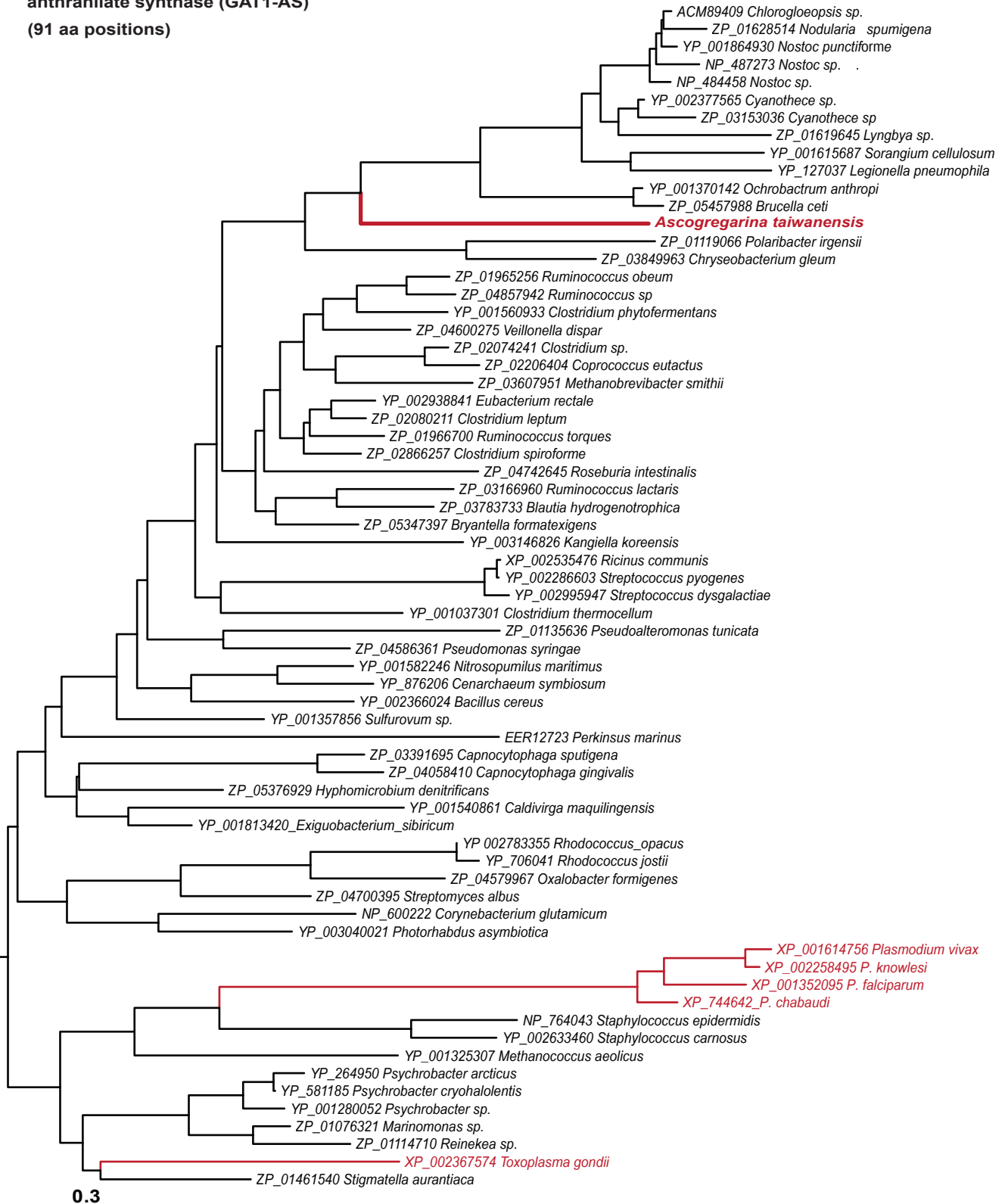


Figure S1 (G-J). Plant-affinity of selected Ascogregarina proteins as inferred by maximum likelihood (ML) analysis (with PROML in the PHYLIP package). Best ML trees are inferred using a JTT amino acid substitution model with the consideration of fraction of invariance (Finv) and 4-rate gamma distribution. Sequences were added randomly with 10 jumps of searches and enabled global rearrangement.

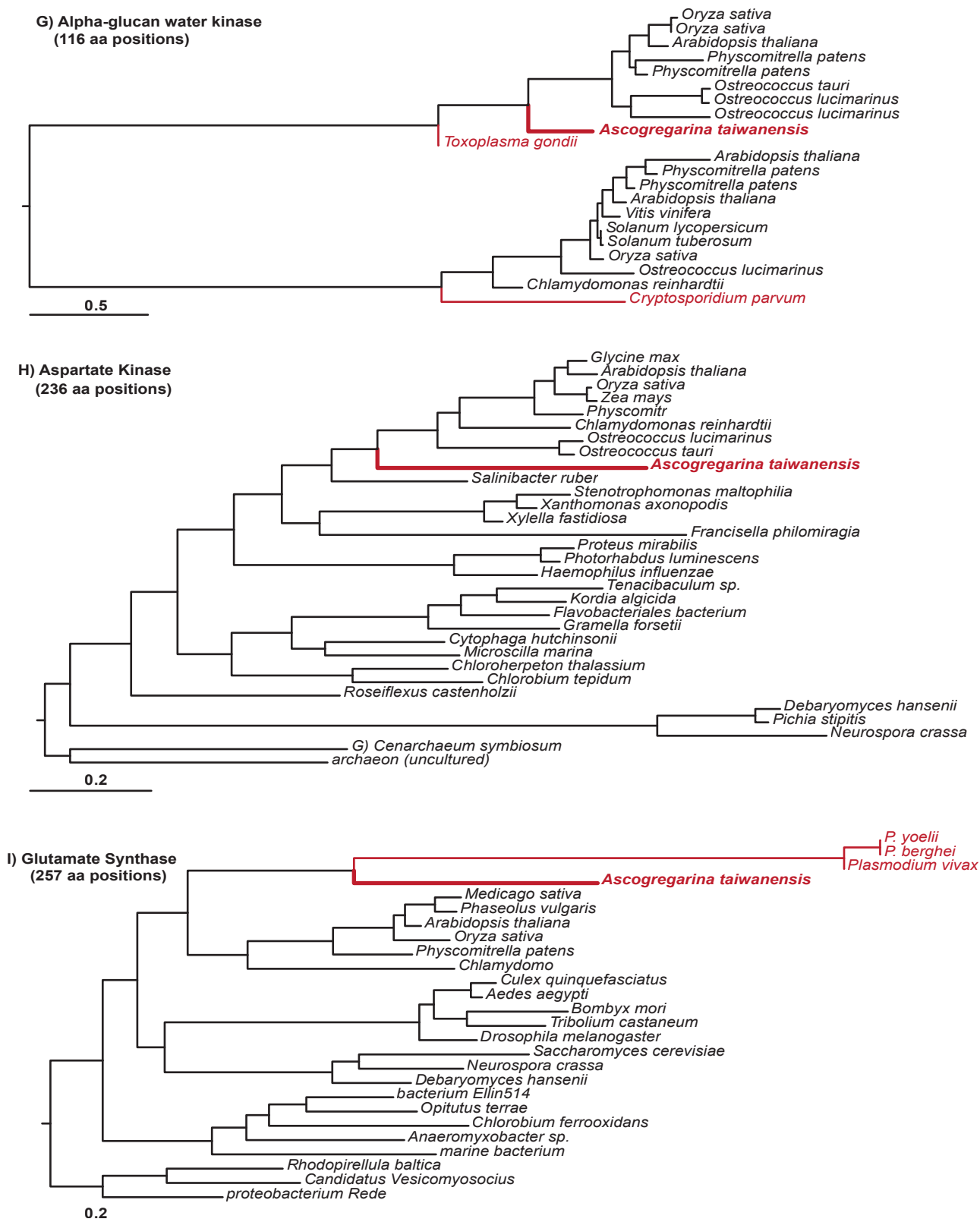


Figure S1 (G-J). Plant-affinity of selected Ascogregarina proteins

**J) Trehalose-6-P synthase
(218 aa positions)**

