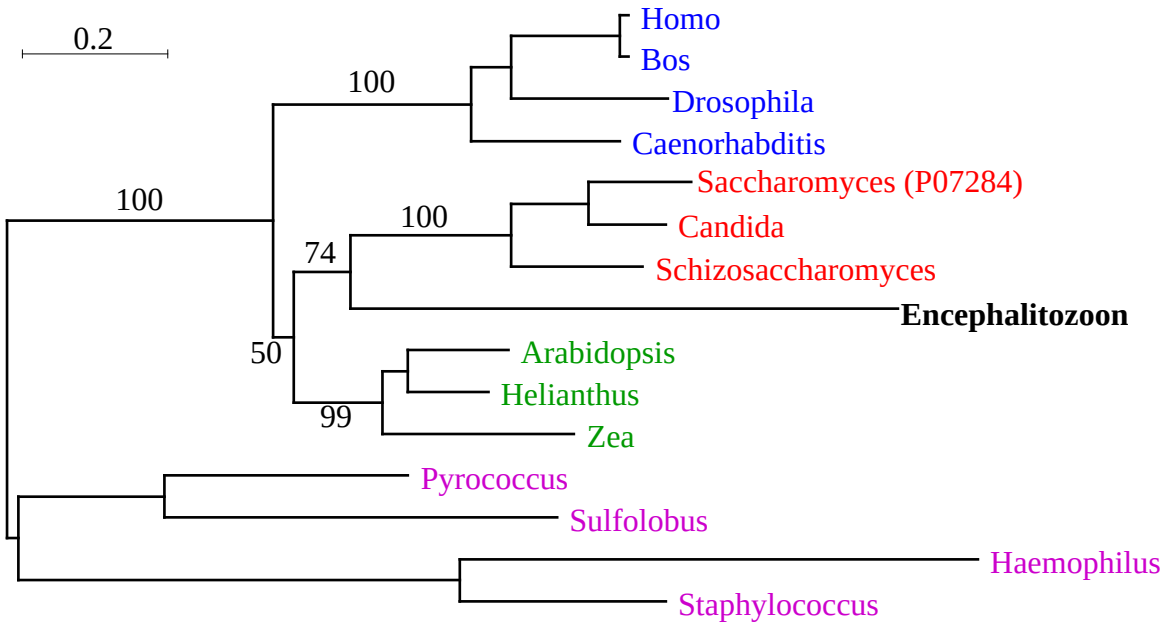
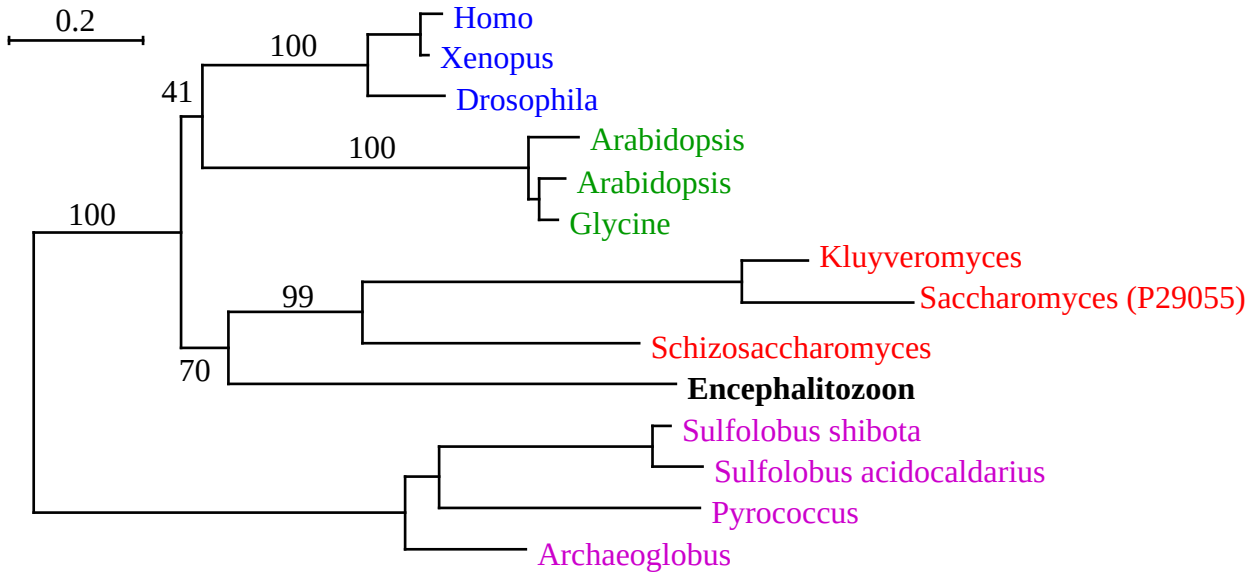
Phylogenetic analyses of 4 putative *Encephalitozoon cuniculi* proteins. Trees were built with BioNJ applied to gamma-corrected ML distances with invariant sites computed with Tree-Puzzle 5.0. Bootstrap scores are in percent of 500 replicates. Color code : animals, fungi, plants, protists, prokaryotes. SWISSPROT accession numbers of *Saccharomyces cerevisiae* orthologs are given. Scale bar : evolutionary distances in replacements per site.

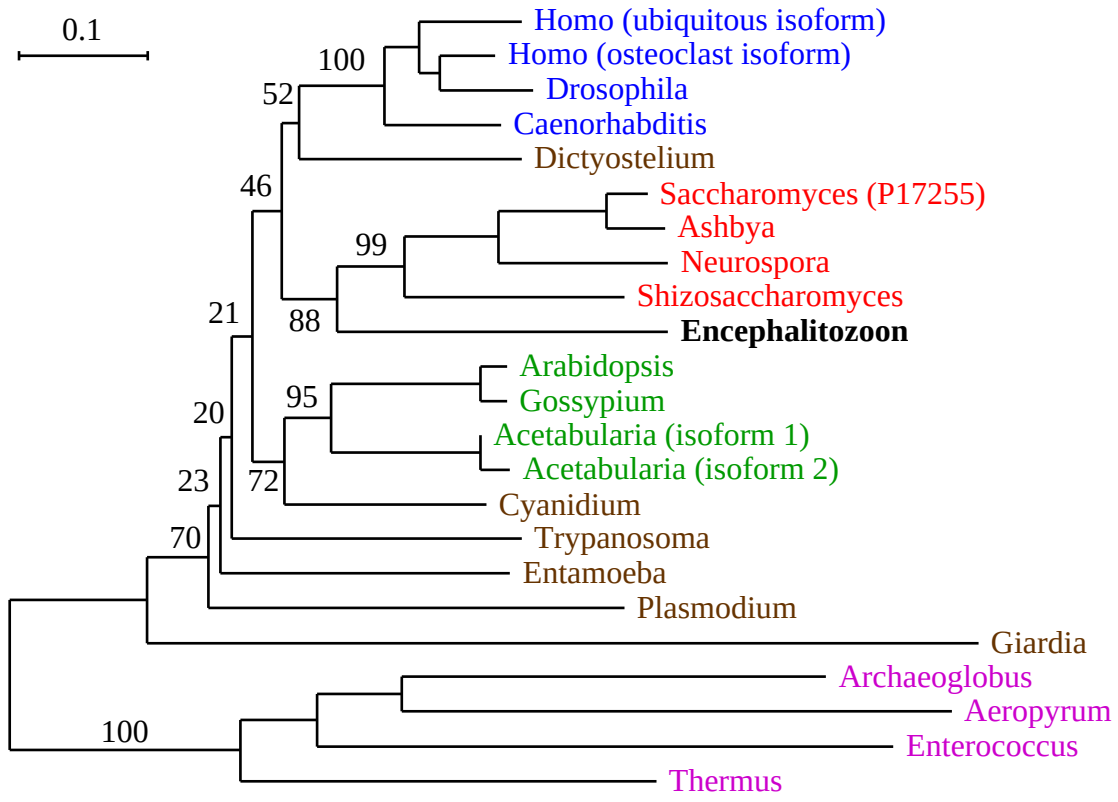
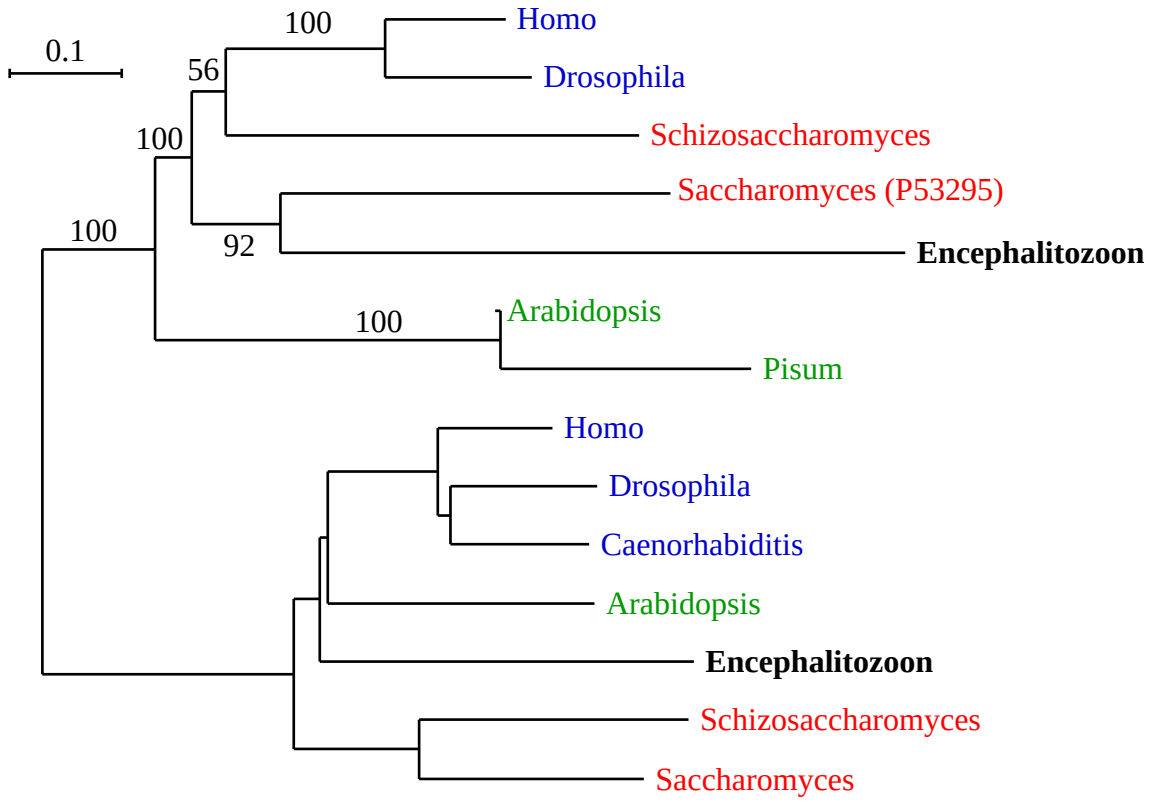
Seryl-tRNA synthetase



Transcription initiation factor II B



vacuolar ATPase subunit A



GTP-binding protein