

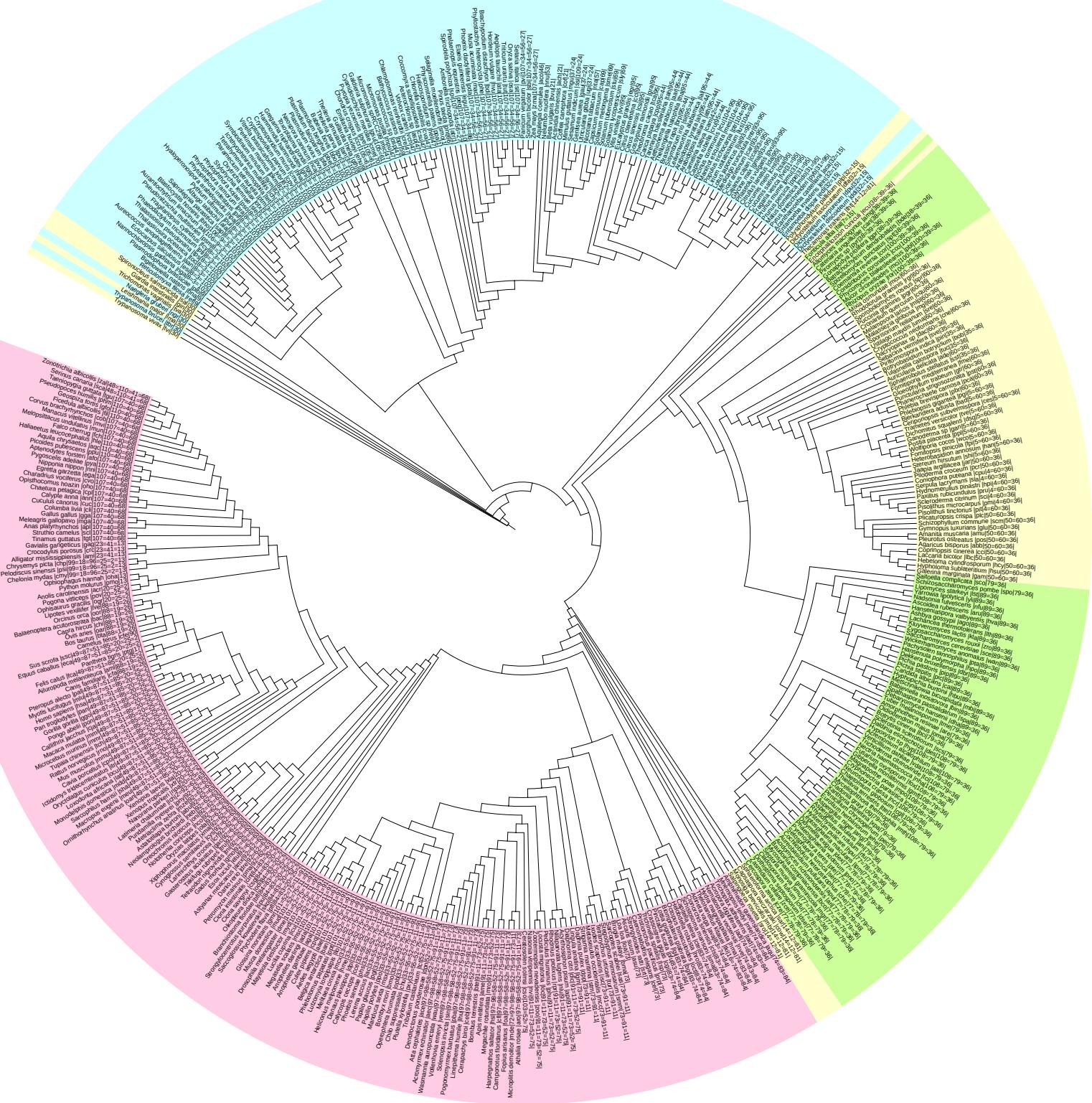
Groups

Protist

Metazoa

Viridiplantae

Fungi



SMO. Bibliography for the molecular phylogenies used to manually curate the “reference supertree of eukaryotes”.

Lozada-Chávez I., Stadler,P.F., and Prohaska, S.J. (2018). bioRxiv,doi.org/10.1101/283549. Re-submitted (2022)

Genome-wide features of introns are evolutionary decoupled among themselves and from genome size throughout Eukarya.

<https://www.biorxiv.org/content/early/2018/03/18/283549>

Example taken from the Reference supertree topology for 461 species that is depicted above:

The phylogenetic relationships of the below three species are supported by the molecular phylogenies reported by both the genome project (denoted with the species abbreviated name) and specific lineages (denoted with numbers) reconstructed with different phylogenetic methods and/or genetic markers/orthologs.



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