

Phylogenetic Tree View

This tree is based on COBALT multiple alignment [more...](#)

Reset Tree

Cobalt RID 0BNAJYH6212

Number of Seqs 165

Tree method: Fast Minimum Evolution Max Seq Difference: 0.8 Distance: Grishin (protein) Sequence Label: Sequence Title (if a

Mouse over an internal node for a subtree or alignment. Click on tree label to select sequence to download







[Hide legend](#)

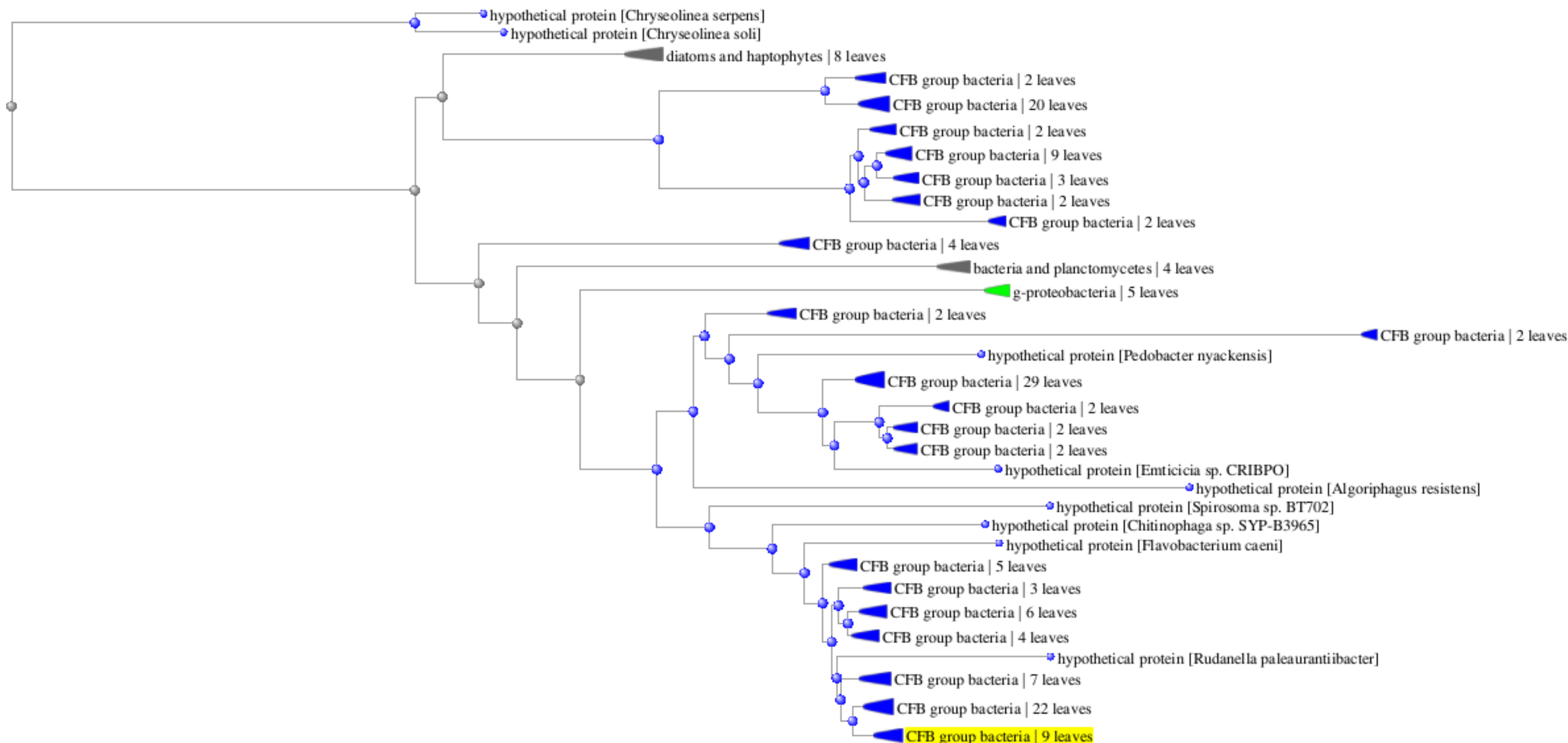
Find: - + TXT

Tools | Upload | ?

Label color map

Blast names color map

	CFB group bacteria
	diatoms
	haptophytes
	planctomycetes
	bacteria
	g-proteobacteria



Success

Nodes 329(0 selected) View port at (0,0) of 1202x576 | 0.1

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National Center for Biotechnology Information, U.S. National Library of Medicine
8600 Rockville Pike, Bethesda MD, 20894 USA

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