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--- PhyML v3.0 (179M) +M3L ---

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PhyML is a simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood

Stephane Guindon & Olivier Gascuel
<http://www.atgc-montpellier.fr/phyml>

+M3L is a modification of the PhyML source code to accommodate multiple branch-length ratios, and to estimate statistical support for clades as posterior probability values using an empirical Bayesian MCMC strategy to sample phylo-parameter space.

Victor Hanson-Smith, Bryan Kolaczkowski, John St. John, and Joe Thornton
<http://phylo.uoregon.edu/software/phyml-m3l>

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. Enter the sequence file name > examples/cox2cds.phy
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