Appendix C from D. San Mauro et al., “Initial Diversification of Living Amphibians Predated the Breakup of Pangaea”
(Am. Nat., vol. 165, no. 5, p. 590)

Extended Result of the Phylogenetic and Molecular Clock Analyses
Figure C1: Unconstrained (nonultrametric) maximum likelihood phylogram showing the pattern of rate variability.
Figure C2: Topology of maximum likelihood tree with node numbers
Table C1
Statistical support and age estimates for each node

<table>
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<th>BI</th>
<th>ME</th>
<th>MP</th>
<th>Mean</th>
<th>SD</th>
<th>CI</th>
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Note: Statistical support given by bootstrap proportions for maximum likelihood (ML; 100 pseudoreplicates) and minimum evolution and maximum parsimony (ME and MP; 1,000 pseudoreplicates) and by Bayesian posterior probabilities (1,000,000 generations) for Bayesian inference (BI). Age estimates are in millions of years; also included are standard deviations and 95% confidence intervals (CI). Ellipses indicate support values of <50.