

### **Results of Branch-Site, Site Specific Selection Analyses**

For analyses of the branch leading to all snakes, the ln likelihood value of M2a(null) was -433795.05 versus that for M2a(alt.) at -433376.37. The likelihood ratio test favors the alternative model with positive selection allowed on the branch leading to all snakes at  $P \ll 0.001$ . The same test for positive selection at sites along the branch leading to the Alethinophidia yielded ln likelihood values of M2a(null) = -433795.05 and M2a(alt) = -433465.10. The likelihood ratio test also strongly supported the alternative model allowing some sites to be under positive selection along the Alethinophidian branch at  $P \ll 0.001$ . Based on these two analyses, the estimates of sites that are under positive selection along these two branches are provided in Table 1 (all proteins) and Table S3 for COI, based on Bayes empirical Bayes posterior probability support for each site.