



Figure S3. Molecular phylogenetic analysis of *SmMCO2* and related genes based on deduced amino acid sequences. The tree was inferred from 225 aligned amino acid sites using the maximum likelihood method. Bootstrap values based on 1,000 replications are shown as percentages on the nodes (only values $\geq 50\%$ are shown). Sequences obtained in this study are underlined and in bold type. Sequence accession numbers are shown in brackets.