Figure S3. Midpoint rooted maximum-likelihood tree based on analysis of Pre-2 predicted amino-acid sequences from members of the Xylariales (red), Sordariomycetes (blue), Pezizomycetes (purple), and Leotiomycetes (brown). Bootstrap values (percent of 1000 replicates) are shown for branches with greater than 65% support. NCBI accession identifiers are present at the end of each branch label. Note that the Xylariales sequences form a single clade among Sordariomycetes sequences, suggesting conservation of this protein among members of the order.