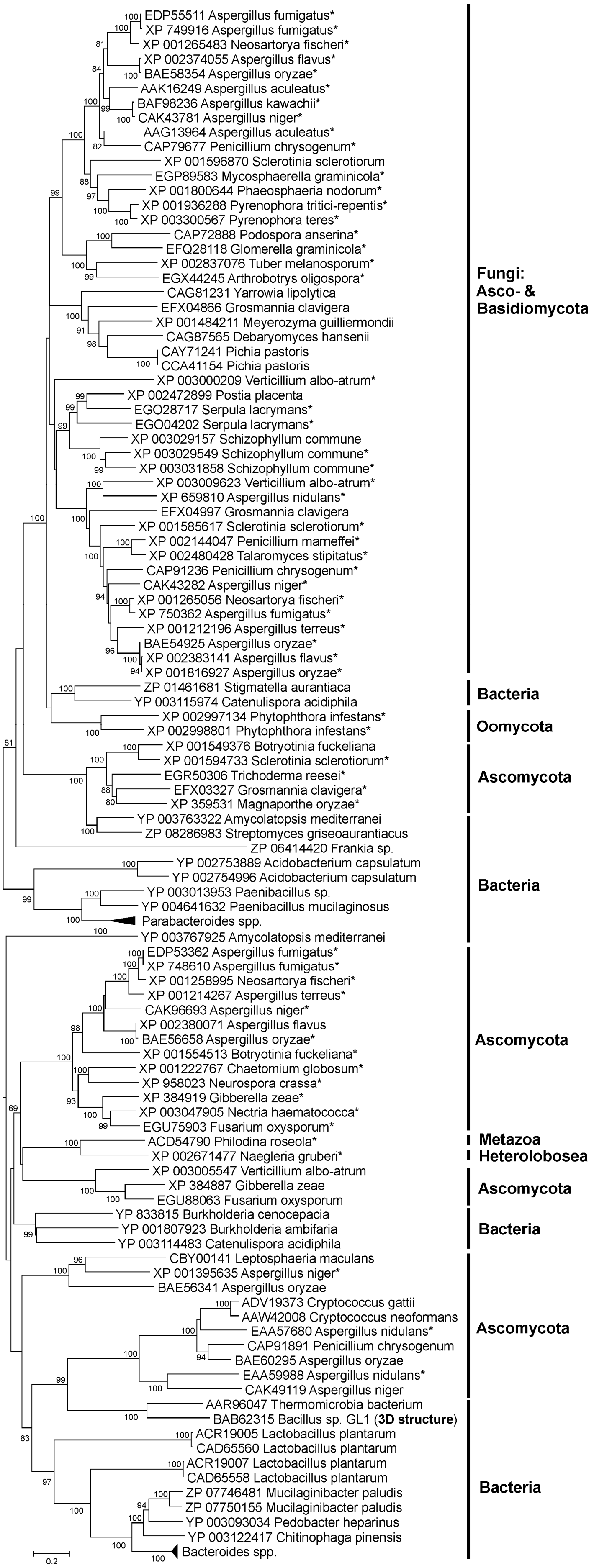

Figure S 4: Evolutionary relationship of eukaryotic and prokaryotic GH78 α-L-rhamnosidases of group II. The evolutionary history was inferred using the Neighbor-Joining method. The optimum tree with the sum of branch length = 35.40476488 is shown. The percentage of replicate trees, in which the associated taxa clustered together in the bootstrap test (1,000 replicates), is shown next to the branches. The evolutionary distances were computed using the Poisson correction method and are given in the units of the number of amino acid substitutions per site. The analysis involved 123 amino acid sequences. All ambiguous positions were removed for each sequence pair. There are a total of 3,634 positions in the final dataset. Appearance of eukaryotic signal peptides were predicted using SignalP 3.0 indicated with (*).