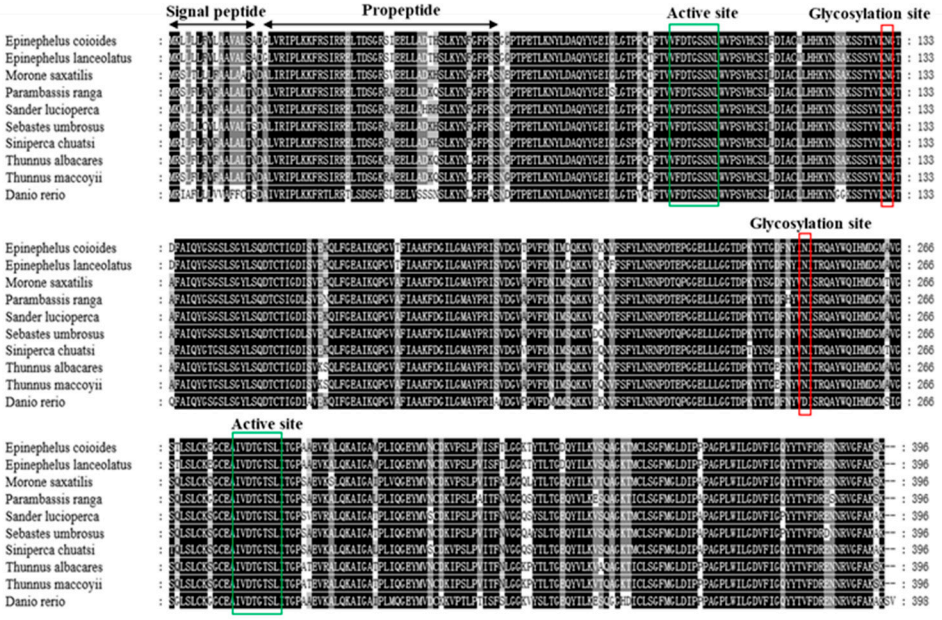
A



B

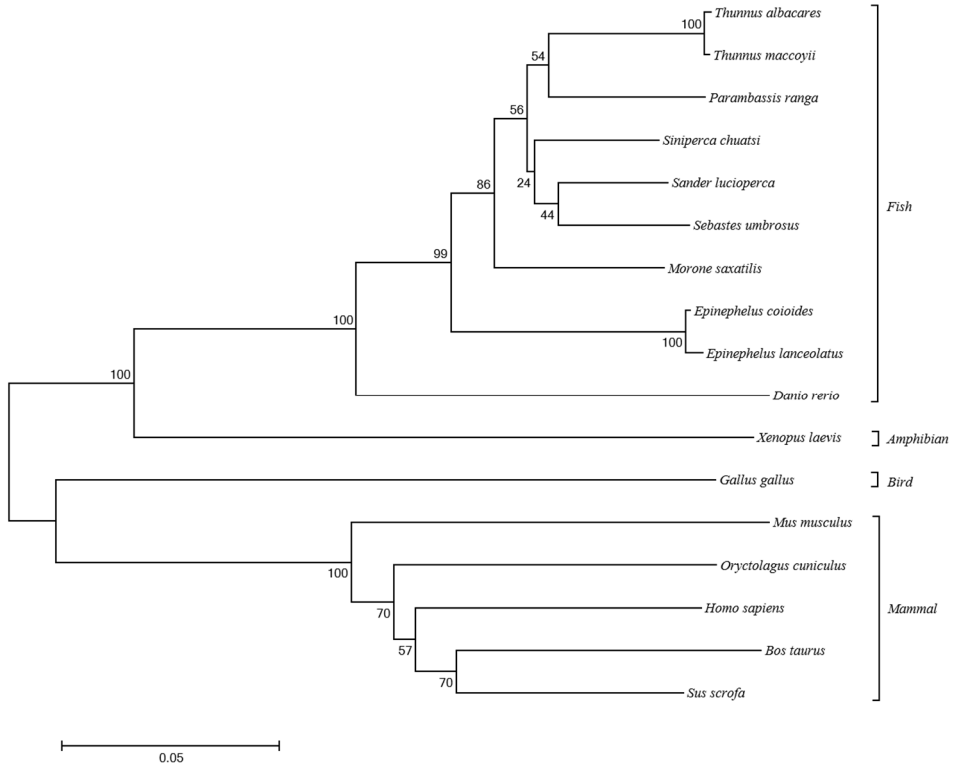


Figure S1. Analysis of Ec-CD proteins. (A) Multiple sequence alignment of Ec-CD and other CD homologs from different species. (B) Phylogenetic analysis of Ec-CD. The phylogenetic tree was constructed according to the sequences of Ec-CD homologs from different species obtained from the NCBI database. Numbers at the nodes denoted the bootstrap values of 1,000 replicates and scale represents the numbers of substitutions per 1,000 bases. GeneDoc program and MEGA5.0 software were used to perform and edit amino acid alignments and the phylogenetic tree.