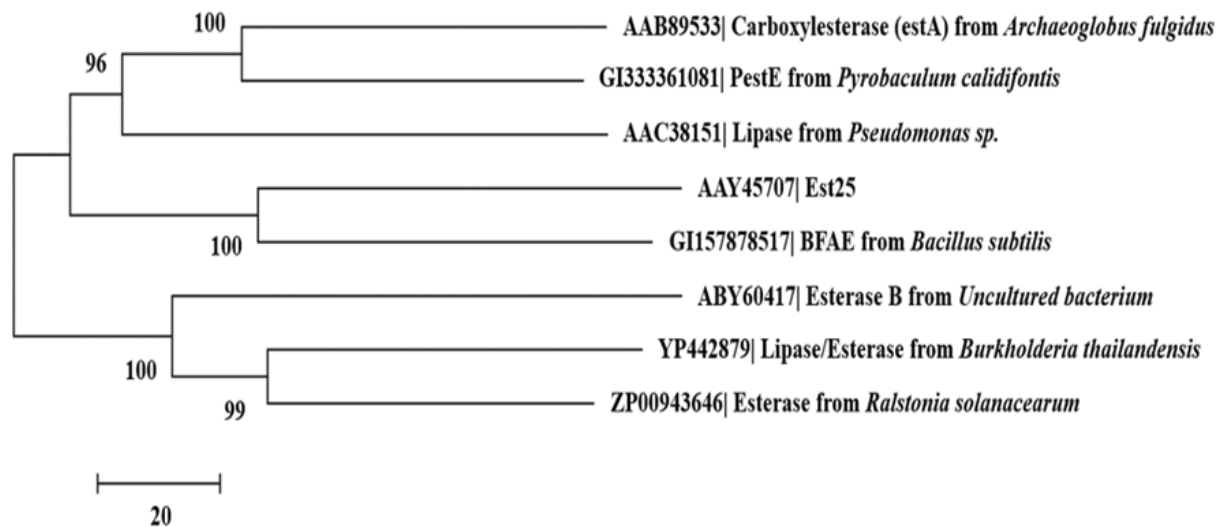
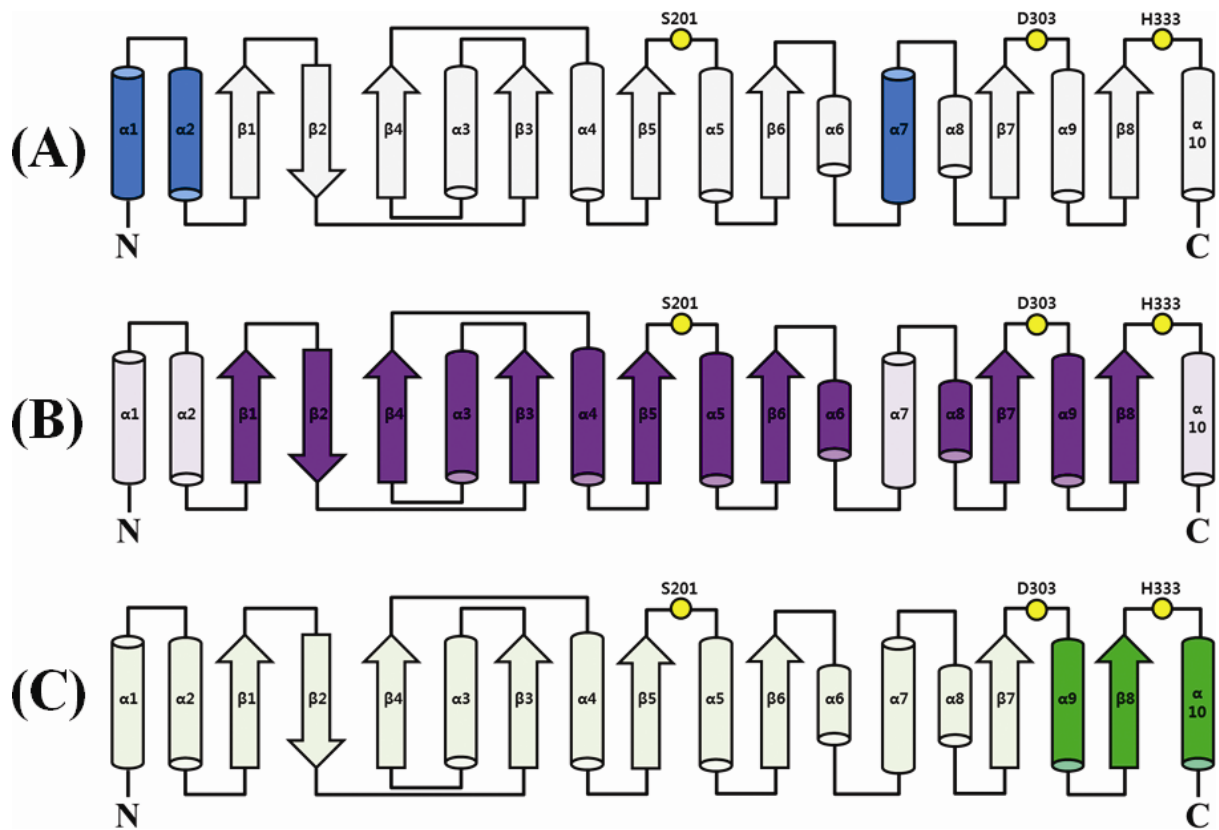


Supplementary Material



Supplementary Figure S1. Phylogenetic analysis of Est25. Unrooted neighbor-joining phylogenetic analysis of Est25 and representative members of bacterial family IV lipolytic enzyme families. Amino acid sequences of esterases and lipases were retrieved from GenBank. Please note the very close distances among Est25(AAY45707), BFAE(GI157878517), PestE(GI3333610810), and AFEST(AAB89533). The scale bar represents the number of changes per amino acid position, and the length of the branches indicates the differences in the protein sequences.



Supplementary Figure S2. Classification of secondary structures of Est25 based on their structural roles. (A) Three helices in the cap domain are shown in blue. (B) The α/β -hydrolase fold is shown in deep purple. (C) Dimerization interface helices and strand are shown in green. Three residues in the catalytic triad are shown in yellow circle.