

Thiomidoyl glycosides hydrolysis by glycoside hydrolase require remote activation for efficient activity

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Supplemental figure

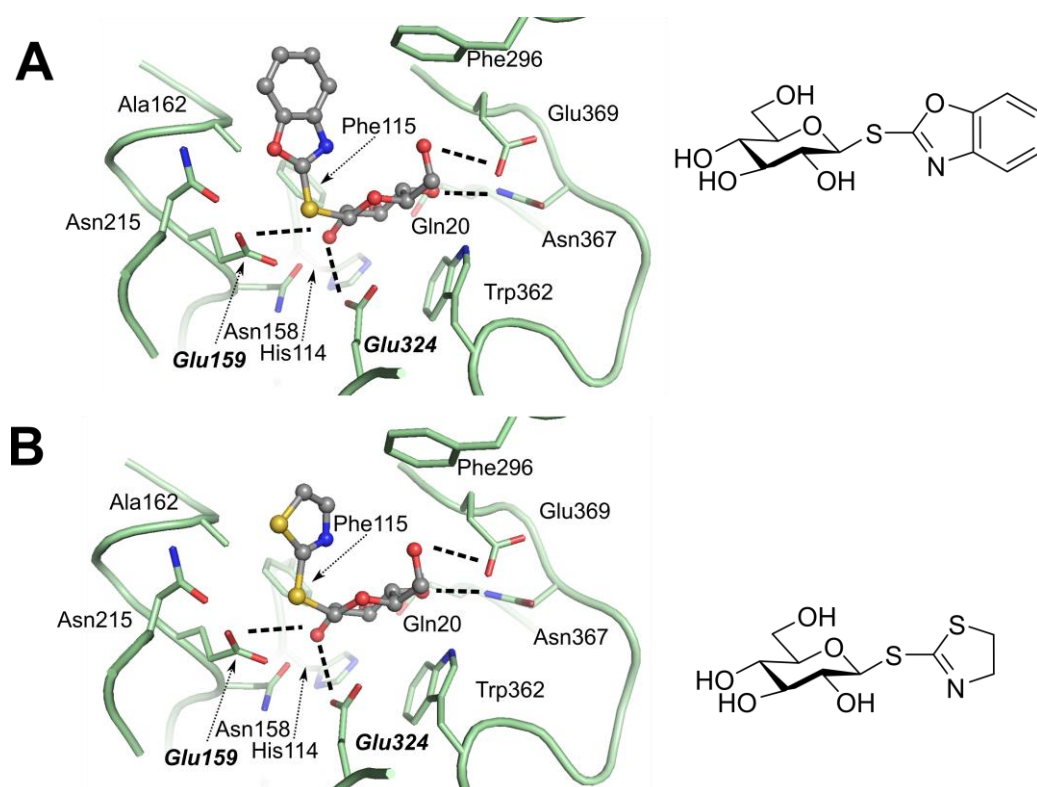


Figure S1. Model of docked GlcSBox (A) and GlcSTaz(B) in *DfGly* active site. Residues surrounding the ligand binding pocket are depicted as sticks. For clarity purposes, hydrogens are not represented. Catalytic residues Glu159 (acid/base) and Glu324 (nucleophile) are highlighted in bold. H-bonds are indicated as dashed lines.