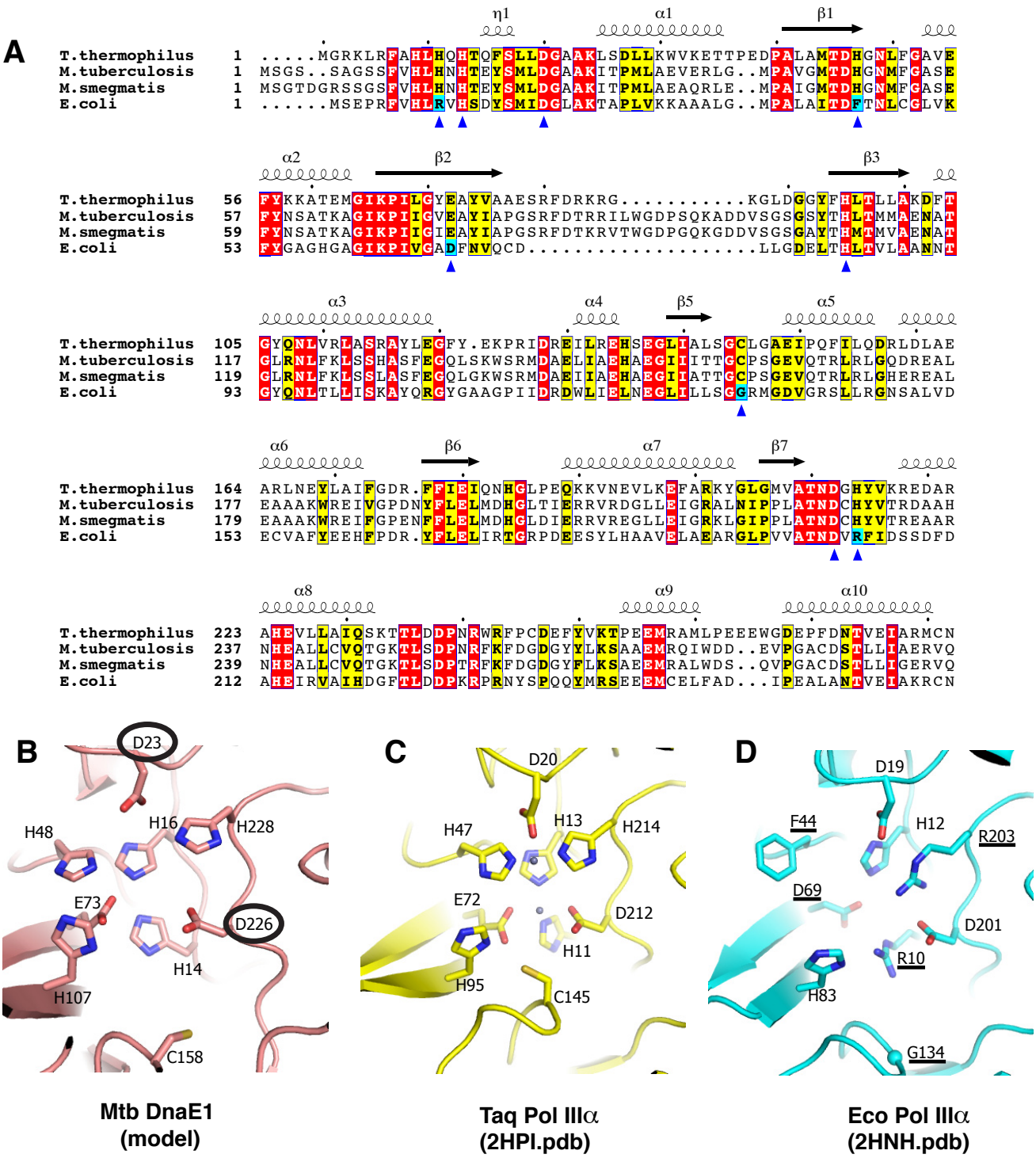

Supplemental Figure 3. PHP domain active sites in bacterial replicative DNA polymerases.

(A) Alignment of PHP domain sequences from replicative DNA polymerases. Conserved metal binding residues of the PHP domain are indicated by blue triangles below the sequences. Cyan squares indicate residues in *E. coli* that deviate from the consensus metal binding motif. **(B)** Computational model of the Mtb DnaE1 PHP domain based on the crystal structure of *T. aquaticus* PolIIIα (shown in panel C). Black circles indicate residues mutated for the experiments performed in this study. **(C)** PHP domain active site of *T. aquaticus* PolIIIα. **(D)** PHP domain active site of *E. coli* PolIIIα. Underlines indicate residues in *E. coli* that deviate from the consensus metal binding motif.