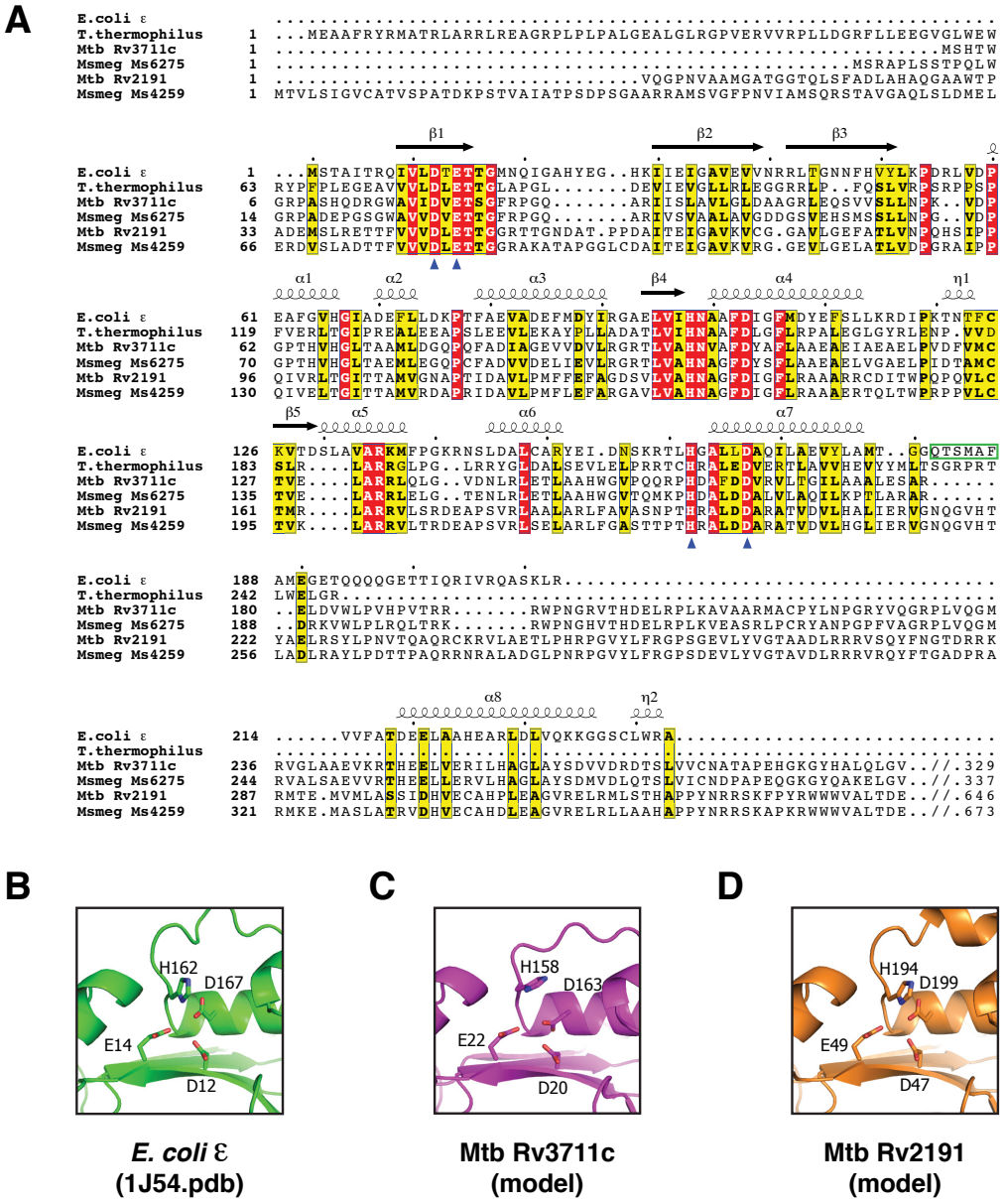

Supplemental Figure 1. *Mycobacterium tuberculosis* (Mtb) and *Mycobacterium smegmatis* contain two ε (*dnaQ*) exonuclease homologues.
(A) Sequence alignment of ε-exonuclease homologues from four different species. Conserved catalytic residues of *E. coli* ε are indicated by blue triangles below the sequences. The clamp binding motif of *E. coli* ε is boxed in green. (B) Active site of the *E. coli* ε-exonuclease. (C) Computational model of the active site of Mtb Rv3711c. (D) Computational model of the active site of Mtb Rv2191.