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Identification of new antibacterial targets in RNA polymerase of *Mycobacterium tuberculosis* by detecting positive selection sites.

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Graphical abstract

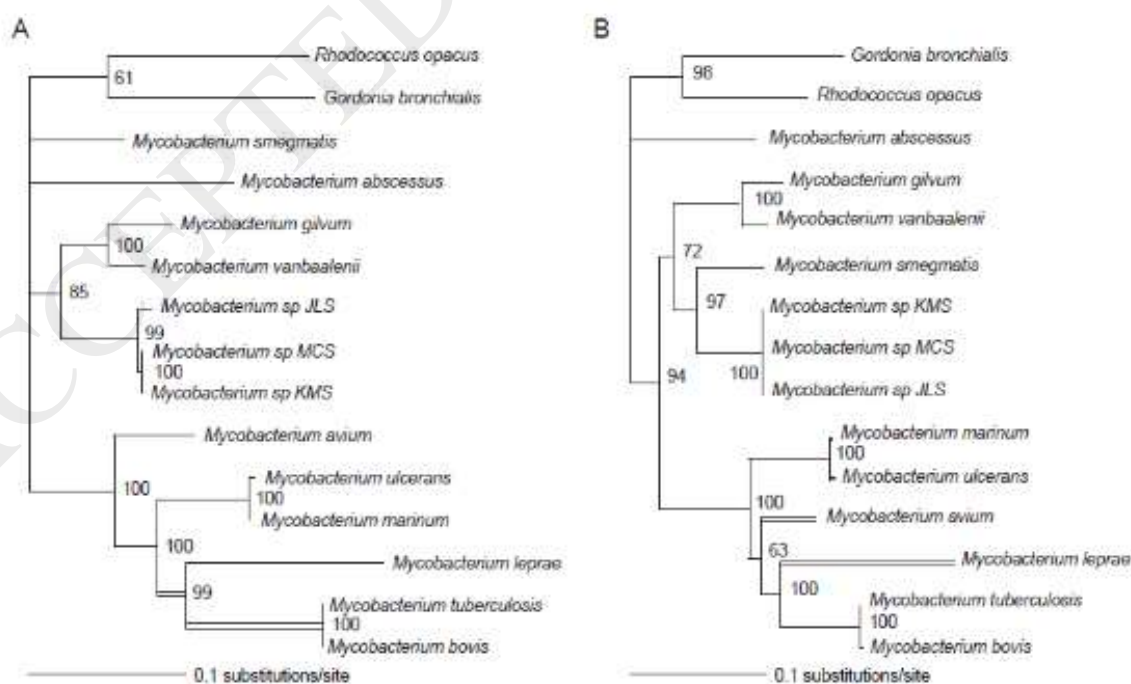


Figure 1. Unrooted phylogenetic trees for rpoB (A) and rpoC (B) constructed by Maximum Likelihood method (— positive selection). Numbers represent boot-strap values for 1000 replicates, unlabeled branches indicate the value less than 500. Bold profile line indicates that this branch is under positive selection.

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