



**Figure S2. Multispecies alignment of DnaA** Alignment of DnaA protein sequence from Mycobacterium tuberculosis (MTB), Mycolicibacterium smegmatis (MSM), Escherichia coli (Ecoli) and Bacillus subtilis (Bsubt) with clustal omega as implemented on uniprot.org. Visualization was created in boxshade ([https://embnet.vital-it.ch/software/BOX\\_form.html](https://embnet.vital-it.ch/software/BOX_form.html)). Red indicates identity with MTB sequence. Blue indicated similarity with MTB sequence. Sites with similarity in 3 or 4 sequences are annotated in the consensus line with an upper case letter indicating 100% identity across all 4 sequences and lower case letter indicating at least one sequence without amino acid identity.