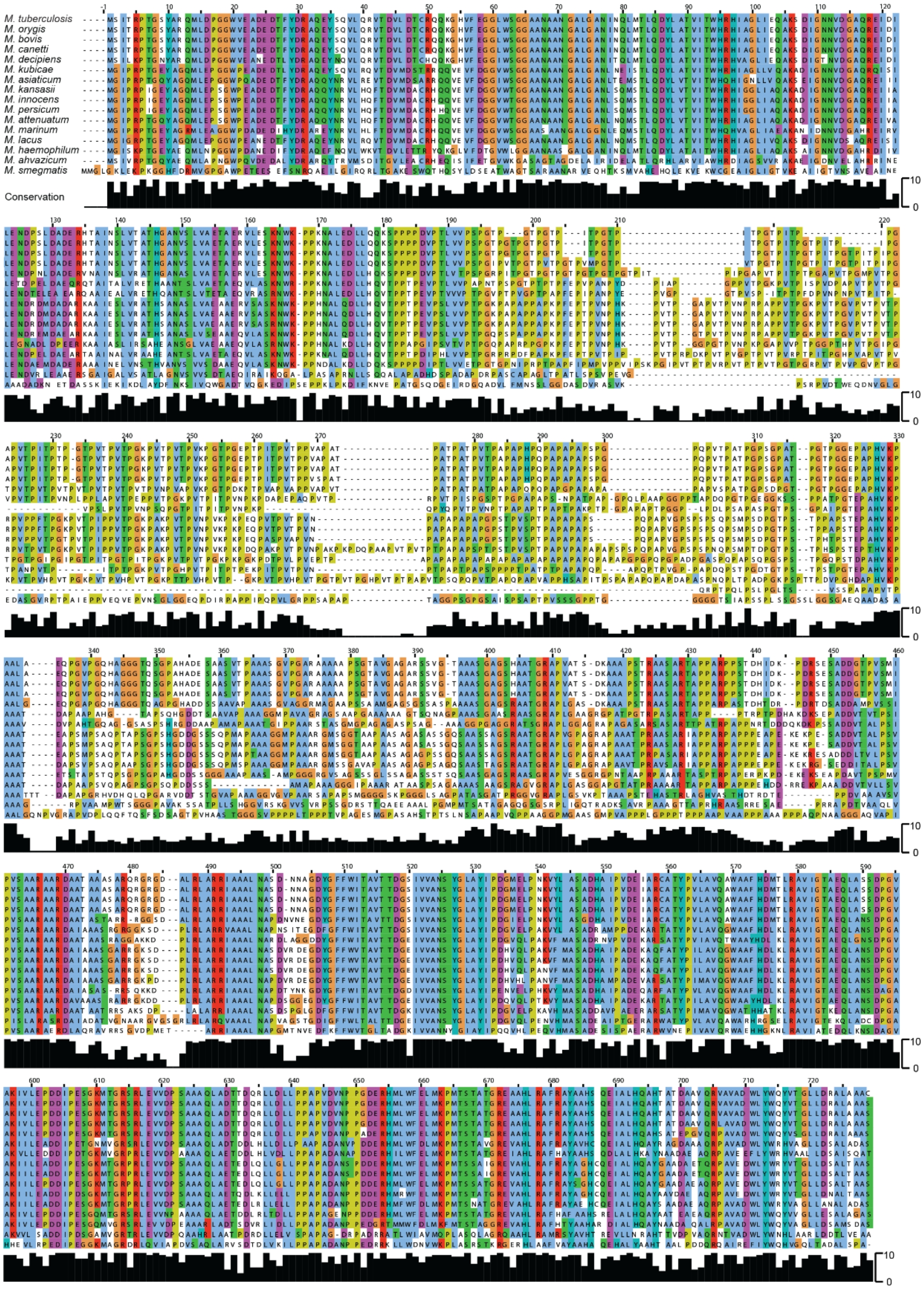
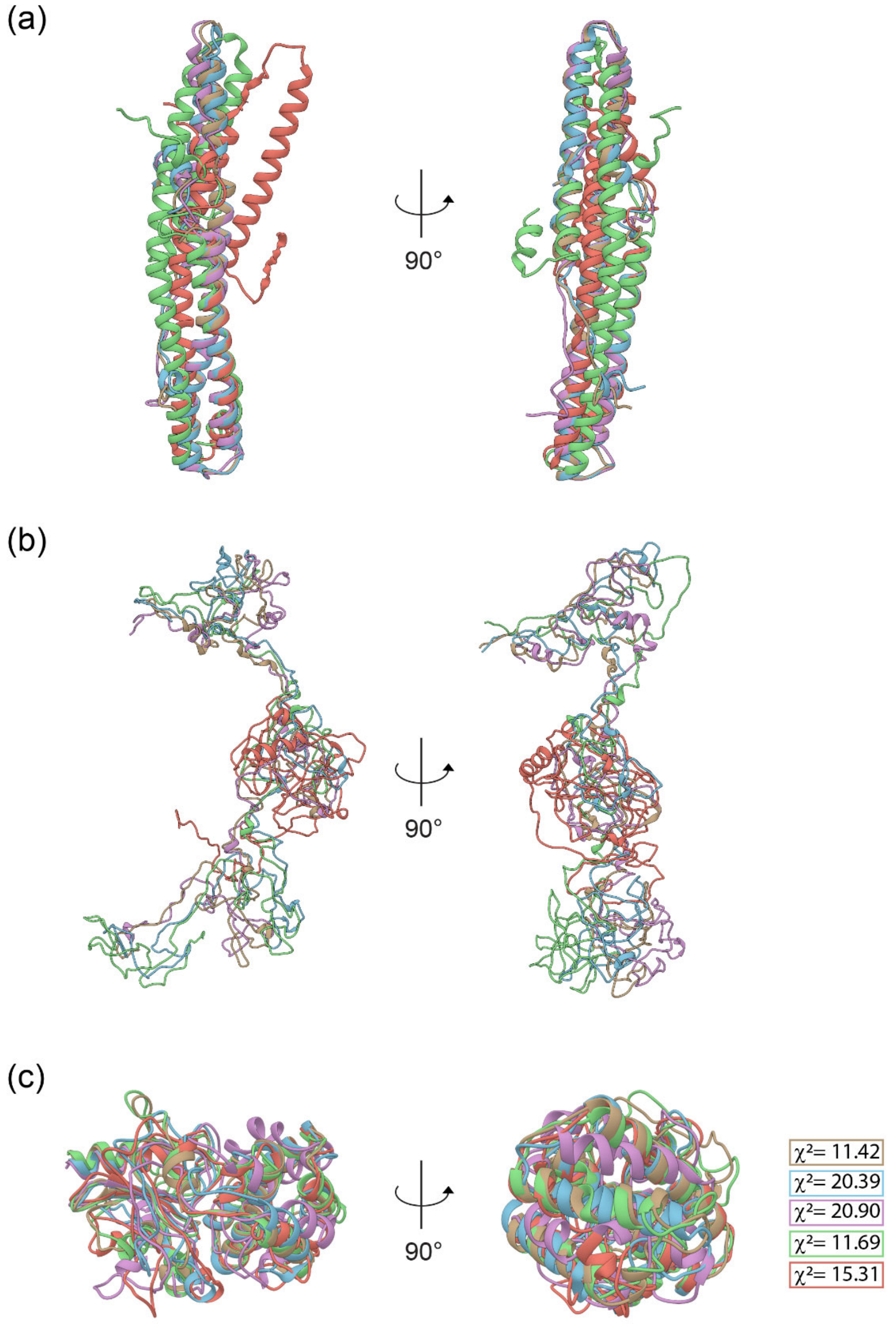
Supplementary material



Supplementary Figure 1. Sequence alignment of EspK from different mycobacterial species. Numbering is based on the sequence of *M. tuberculosis*. Conservation score ranges from 0 (no conservation) to 10 (invariant). Colour scheme of ClustalX is used.



Supplementary Figure 2. Tertiary structure prediction of the different regions of EspK by I-TASSER. Top five models predicted for the N-terminal domain (**a**), the middle region (**b**) and the C-terminal domain (**c**). Each model is represented by different colour. χ^2 represents the correlation between the experimental SAXS data and that calculated for the different I-TASSER models of EspK C-terminal domain.