**Supplemental Information**

# Characterization of guided entry of tail-anchored proteins 3 homologues in *Mycobacterium tuberculosis*

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This supplementary document contains three figures.

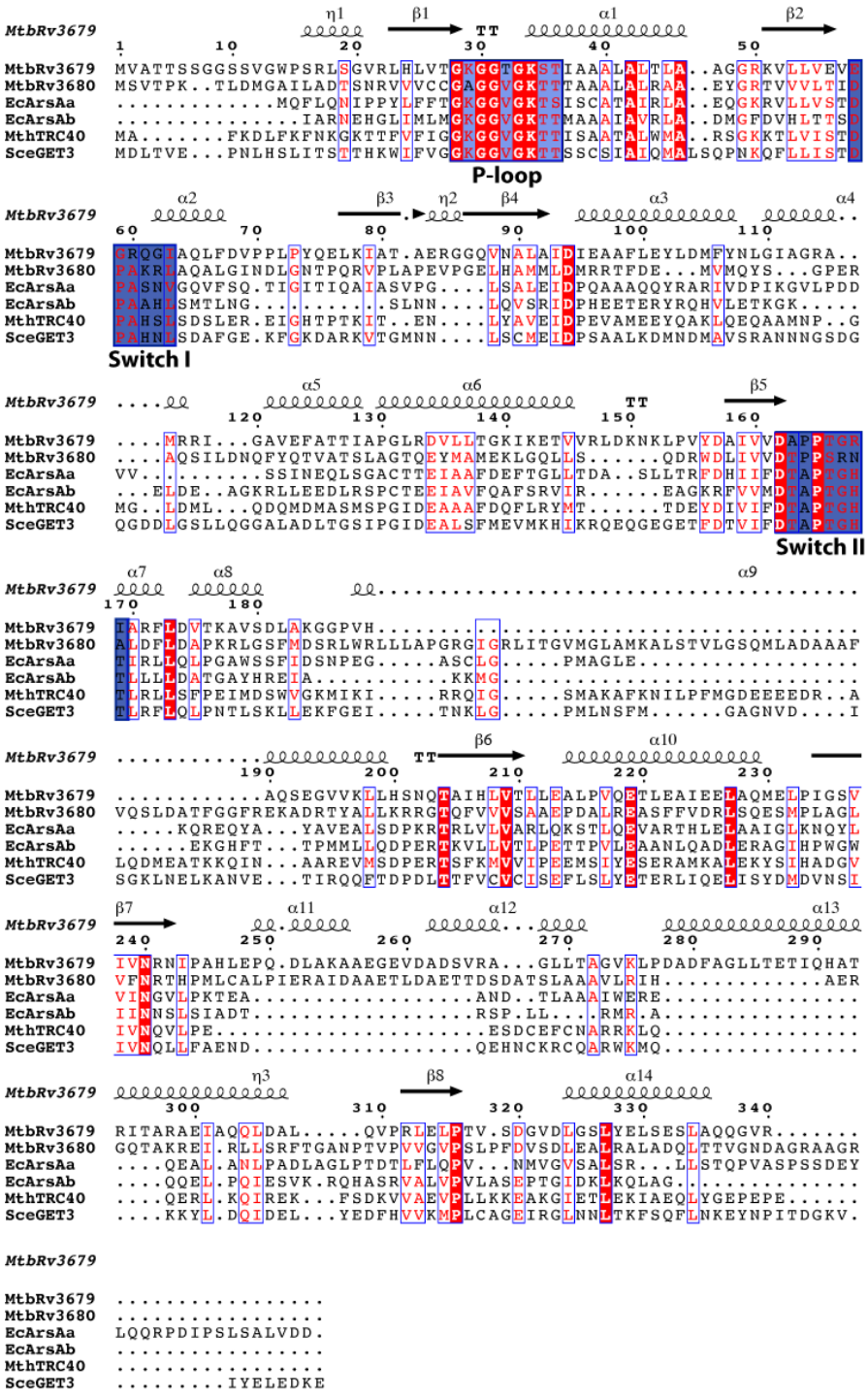


**Figure S1.** Sequence alignment of Rv3679 (BagA) and Rv3680 (BagB) from *Mycobacterium tuberculosis*, Get3 from *Saccharomyces cerevisiae*, ArsA from *Escherichia coli* (ArsAa and ArsAb represent the N- and C-terminal ATPase domain), and TRC40 from *Methanothermobacter thermautotrophicus*. Three conserved ATPase motifs (P-loop, switch I, and switch II) are shown in blue.

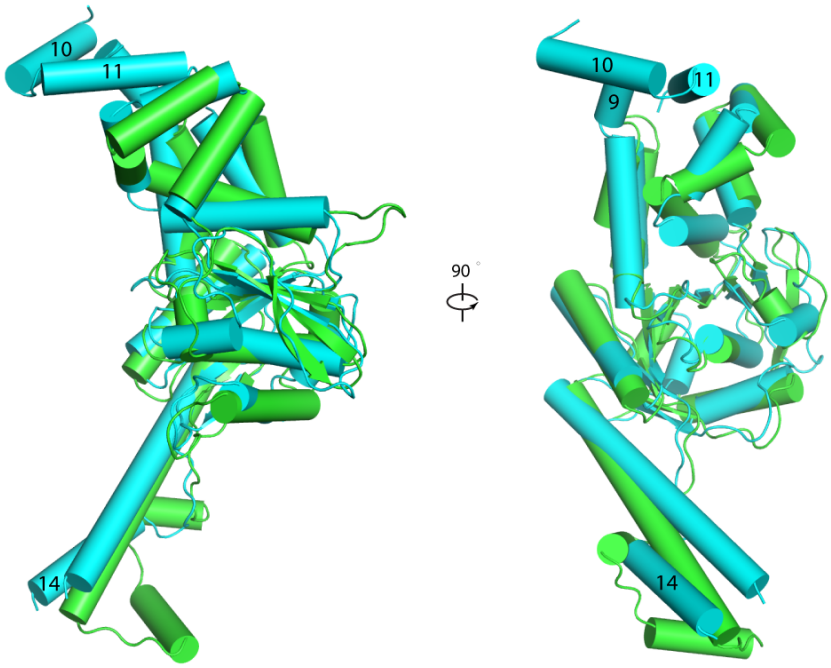


**Fig. S2.** Structural alignment of BagA (green) and BagB (cyan). Each helix of BagB has its correspondent one in BagA except for α9-11 and 14, which are localized in helical domains flanking the nucleotide-binding domain.

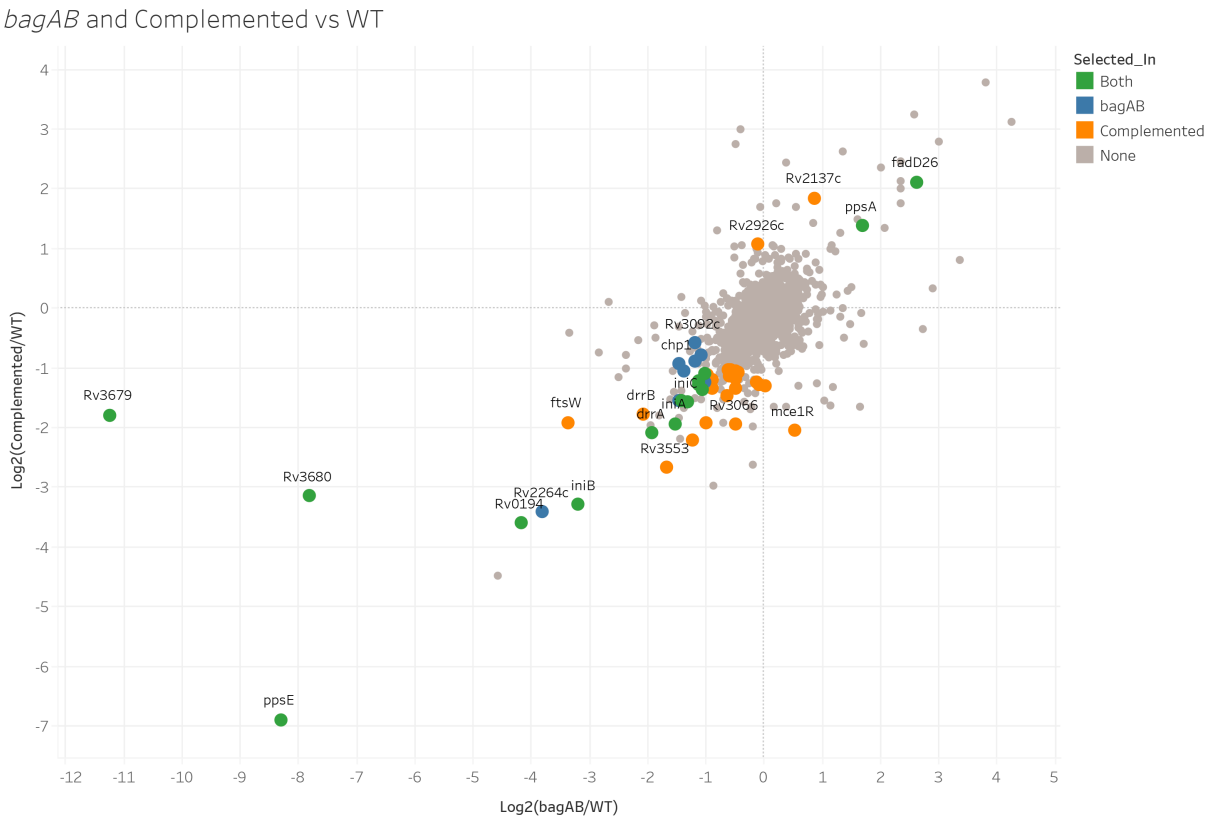


**Fig. S3.** Scatterplot of the fold changes of proteins in the WT/*bagAB* and WT/complemented strains. For each detected protein the log2 fold change for both *bagAB*/WT and complemented/WT data sets are shown. Based on based on the quantitative results, green dots indicate proteins that were altered in both the mutant and complemented strains relative to the WT strain, the orange dots represent proteins that were different between the complemented and WT strains, and the blue dots represent proteins that were different only in the *bagAB* strain compared to the WT strain.