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# Structure of the diaminopimelate epimerase DapF from *Mycobacterium tuberculosis*

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# Crystal structure of diaminopimelate epimerase

## *Mycobacterium tuberculosis* DapF

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### Captions for Supplementary Figures

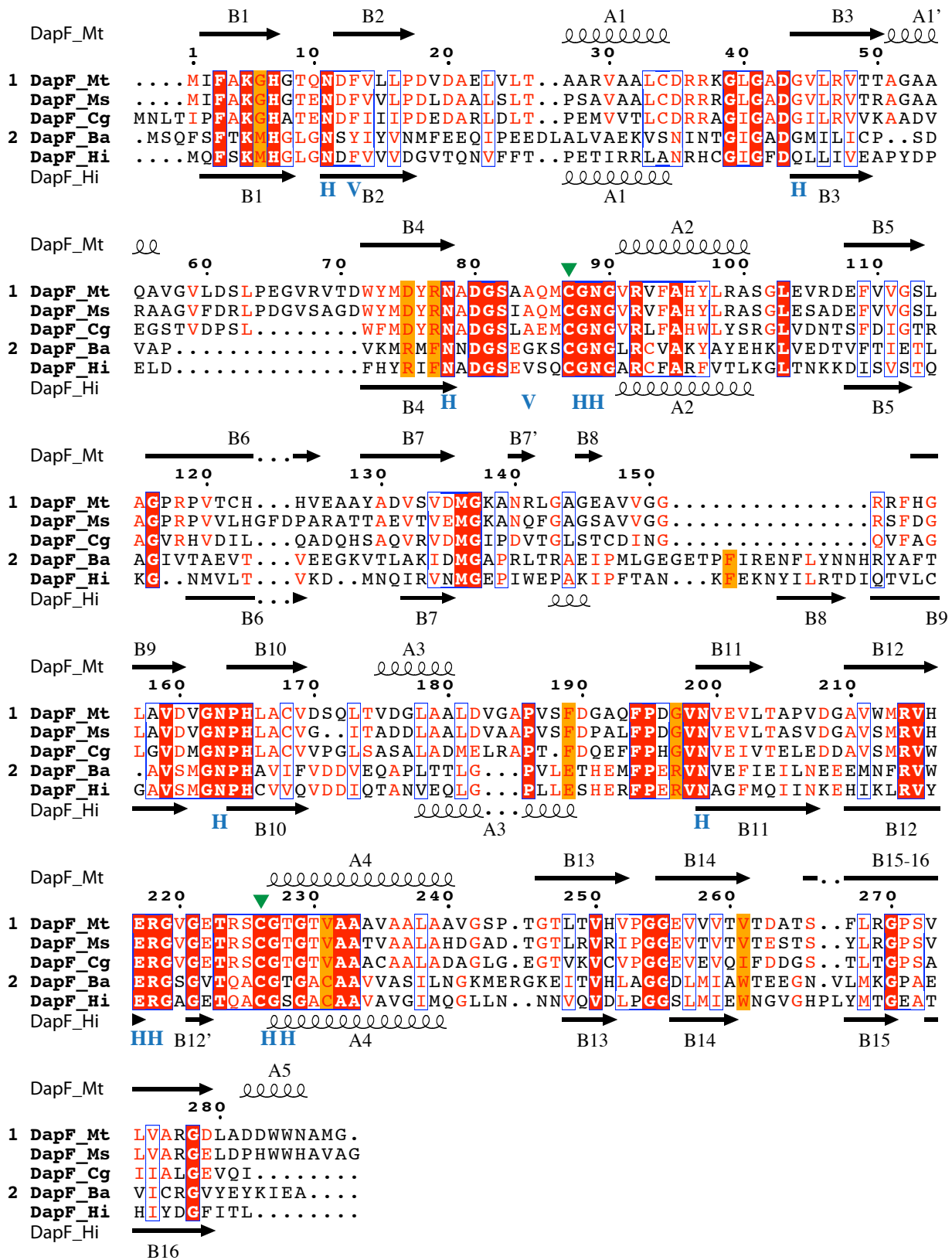
#### **Supplementary Figure S1. Sequence alignment and secondary structure assignment of DapF.**

Amino acid sequences of DapF orthologues aligned using ClustalW. Species abbreviations: Mt = *M. tuberculosis*, Ms = *Mycobacterium smegmatis*, Cg = *Corynebacterium glutamicum*, Ba = *Bacillus anthracis*, Hi = *Haemophilus influenzae*. Secondary structure assignments of the bottom sequence reflects that of PDB entry 1bwz. Green triangles mark the catalytic Cys residues. Blue letters H, V denote residues in H-bond or van der Waals contact, respectively, with L,L-AziDAP in PDB entry [2gke](#) (Pillai et al., 2006). Alignment formatted using ESPript (<http://esprict.ibcp.fr/>).

#### **Supplementary Figure S2. Distribution of atomic displacement factors**

Ribbon diagram of *Mt*DapF coloured according to atomic displacement factors. Colour ramp is from dark blue (min. B = 31 Å<sup>2</sup>) to dark red (max. B = 110 Å<sup>2</sup>).

# Supplementary Figure S1



# Supplementary Figure S2

