

Structure of the C-terminal Domain of DipZ from *Mycobacterium tuberculosis*

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DipZ (Rv2874) from *M. tuberculosis* is a member of the CcdA protein family. This family of proteins shares a conserved transmembrane electron transport domain with similarity to CcdA from *Rhodobacter capsulatus* and varies in size from 190 aa to over 750 aa. It has been proposed that the function of the larger proteins has been modified by the acquisition of extra-cytoplasmic protein domains. The transmembrane region functions by passing electrons from the cytoplasm of the cell across the membrane for use by these extra-cytoplasmic domains [1].

The C-terminal soluble domain from DipZ has been crystallised and the structure determined by SAD methods from crystals soaked in K₂PtCl₄. The model reveals a dimeric structure. Each subunit is comprised of two domains, an N-terminal thioredoxin-like fold predicted from earlier sequence alignments, and a C-terminal jelly-roll fold with similarity to the family 6 carbohydrate binding modules. A large cavity is formed at the dimer interface and extends between the two domains of each subunit. Binding studies have demonstrated the ability of this protein construct to bind to cellulose.

These observations suggest a broadening in the functional repertoire of CcdA-like proteins and possible role in carbohydrate processing.

[1] Katzen F., Deshmukh M., Daldal F., Beckwith J., *Embo J.*, 2002, **21**, 3960.

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