

Poster Presentation

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Helicobacter pylori Csd4 is a peptidoglycan metallo-carboxypeptidase

A. Chan¹, Y. Liu², K. Blair³, E. Firdich¹, E. Gaynor¹, N. Salama³, M. Tanner², M. Murphy¹

¹University of British Columbia, Department of Microbiology and Immunology, Vancouver, Canada, ²University of British Columbia, Department of Chemistry, Vancouver, Canada, ³Fred Hutchinson Cancer Research Center, Division of Human Biology, Seattle, USA

The bacterial cell wall is a polymeric structure that determines the overall shape of the cell and undergoes constant remodelling during cell growth, requiring enzymes that cleave the existing peptidoglycan structure. Csd4 is an enzyme important for cell shape as deleting it in *Helicobacter pylori* causes the helical-shaped cells to become rod-like. Csd4 is a zinc carboxypeptidase that can cleave the tripeptide moiety found in peptidoglycan (i.e. L-Ala- γ -D-Glu-m-DAP) to release meso-diaminopimelic acid (mDAP). Structures of Csd4 were solved by X-ray crystallography up to 1.75 Å resolution in space group P212121 with zinc and substrate/product bound and contain the same unit cell dimensions. Csd4 is a monomeric enzyme with three domains: an N-terminal M14-family carboxypeptidase domain followed by two smaller domains likely important in protein-protein or protein-peptidoglycan interactions. Key interactions are observed between the protein and substrate in the active site, supporting specific substrate recognition by Csd4. A water or hydroxide molecule, which is required for catalytic activity, is also observed bound to the zinc and is poised to interact with the substrate molecule upon activation.

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