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Structures of the surface exposed proteins of Gram positive bacteria

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The Center for Structural Genomics for Infectious Diseases (CSGID) applies structural genomics approaches to biomedically important proteins from human pathogens. It also provides the infectious disease community with a high throughput pipeline for structure determination that carries out all steps of the process, from target selection through structure deposition. Target proteins include drug targets, essential enzymes, virulence factors and vaccine candidates. The CSGID has deposited over 680 structures in the Protein Data Bank. The proteins that are exposed on the surface of Gram positive bacterial pathogens (including Staphylococcus aureus, Bacillus anthracis, Listeria monocytogenes, Streptococcus species and Clostridium species) have been one focus area for the CSGID. So far, the structures of more than 55 of these proteins have been determined. The surface proteins are important in the interactions between the pathogen and its host, but many of them are as yet functionally uncharacterized. Among the examples that will be presented is the Bacillus anthracis SpoIID protein. SpoIID is part of a coordinated cell wall degradation machine that is essential for sporulation and the morphological changes involved. It represents a new family of lytic transglycosylases that degrade the glycan strands of the peptidoglycan cell wall. The two active site clefts in the dimeric enzyme include residues from both subunits, suggesting that the dimer is required for activity. This project has been funded in whole or in part with Federal funds from the National Institute of Allergy and Infectious Diseases, National Institutes of Health, Department of Health and Human Services, under Contracts No. HHSN272200700058C and HHSN272201200026C.

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