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**Structures of Sortase B from *Staphylococcus aureus* and *Bacillus anthracis* Reveal Catalytic Amino Acid Triad in the Active Site.** R-g. Zhang<sup>1</sup>, R-y. Wu<sup>1</sup>, G. Joachimiak<sup>1</sup>, S.K. Mazmanian<sup>2,3</sup>, D.M. Missiakas<sup>2,4</sup>, P. Gornicki<sup>3</sup>, O. Schneewind<sup>2,3</sup>, A. Joachimiak<sup>1</sup>. <sup>1</sup>Structural Biology Center, Argonne National Laboratory, 9700 South Cass Ave., Argonne, IL 60439, <sup>2</sup>Committee on Microbiology, Univ. of Chicago, <sup>3</sup>Dept. of Molecular Genetics & Cell Biology, Univ. of Chicago, <sup>4</sup>Dept. of Biochemistry & Molecular Biology, Univ. of Chicago, 920 E. 58<sup>th</sup> St., Chicago, IL 60637, USA.

Surface proteins attached by sortases to the cell wall envelope of bacterial pathogens play important roles during infection. Sorting and attachment of these proteins is directed by C-terminal signals. Sortase B of *S. aureus* recognizes a five-amino acid motif NPQTN, removes the C-terminal sorting signal by cleaving the polypeptide after the T residue and attaches the mature protein to pentaglycine cross-bridges within the cell wall envelope. Sortase B of *B. anthracis* is thought to recognize a similar motif, NPKTG, and presumably attaches surface proteins to m-diaminopimelic acid cross-bridges. We have determined crystal structure of sortase B from *B. anthracis* and *S. aureus* at 1.6 and 2.0 Å resolution, respectively. These structures show a β-barrel fold with α-helical elements on its outside, a structure thus far exclusive to the sortase family. A putative active site located on the edge of the β-barrel is comprised of a Cys-His-Asp catalytic triad and presumably faces the bacterial cell surface. A putative binding site for the sorting signal cleavage motif is located nearby.

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