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Letters to the Editor

NMR assignment of the periplasmic domain of peptidoglycan-associated lipoprotein (Pal) from *Haemophilus influenzae*

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Pal is part of the Pal-Tol network of proteins that is responsible for protein import and translocation of group A colicins through the cell envelope (Lazzaroni et al., 2002). Pal is anchored to the outer membrane of Gram-negative bacteria through an N-terminal myristoyl attachment and contains a signature sequence that confers peptidoglycan recognition (Koebnik, 1995). One of the roles of Pal is to stabilize the outer membrane by providing a structural link to the peptidoglycan layer. We obtained ^{1}H, ^{13}C, and ^{15}N resonance assignments for the 134-residue periplasmic domain of *H. influenzae* Pal in the presence of a biosynthetic precursor of the peptidoglycan layer, UDP-*N*-acetylmuramyl-L-Ala-D-Glu-*m*-Dap-D-Ala-D-Ala. This work provides the foundation for understanding the molecular basis for peptidoglycan recognition. Sequence-specific assignments were completed for residues 3-134 for more than 90% of the H_{α} and side chain protons as well as many of the ^{13}C and ^{15}N resonances. The chemical shifts have been deposited in the BMRB (accession number BMRB-6465). Supporting information is available.

References: Lazzaroni et al. (2002) *Biochimie*., **84**, 391–397; Koebnik (1995) *Mol. Microbiol.*, **16**, 1269–1270.

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NMR assignment of the R2 domain of pneumococcal choline binding protein A (CbpA)

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Choline binding protein A (CbpA) binds on the surface of the human pathogen, *Streptococcus pneumoniae*, and functions biologically as a specific adhesin for polymeric immunoglobulin receptor (pIgR) found in the membrane of human nasopharyngeal epithelial cells. CbpA first causes pneumococci to bind to pIgR-expressing cells, followed by invasion of these cells and entry into the bloodstream. The R2 domain of CbpA (CbpA-R2; residues 327–442) binds specifically and with high affinity to pIgR and the sequence of this domain is highly conserved in more than 40 pneumococcal strains. We have undertaken solution NMR studies of CbpA-R2 to advance our understanding of (i) the structure of this disease-associated protein and (ii) the relationship between structure and its role in pneumococcal pathogenesis. 2D, 3D, and 4D NMR experiments were performed with ^{15}N, $^{13}C/^{15}N$- and $^{2}H/^{13}C/^{15}N$-labeled CbpA-R2. Based on these data, complete backbone and near complete side chain ^{1}H, ^{13}C, and ^{15}N resonances assignments were made (BMRB accession number 6528). Analysis of chemical shifts reveals three α-helices between residues 330–357, 366–390, and 396–425.

References: Zhang, et al. (2000) *Cell*., **102**, 827–837.

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