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Letters to the Editor

NMR assignment of the novel *Helicobacter pylori* protein JHP1348

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Helicobacter pylori is a pathogenic bacterium that infects a large proportion of the population worldwide. It is the causative agent for most cases of gastritis, gastric ulcer, and can lead to gastric cancer. Although the genomes of two strains of *H. pylori* have been sequenced, approximately one third of the open reading frames have no known homologs and no assigned functions (Tomb et al., 1997). Using a structural genomics paradigm, we searched the genome of *H. pylori* strain J99 for open reading frames encoding for functionally uncharacterized proteins with properties that would make their structural determination feasible by solution NMR techniques. JHP1348 is a putative periplasmic protein of 113 amino acids. Nearly all backbone and sidechain ^{1}H, ^{13}C, and ^{15}N resonances have been assigned using 2D and 3D heteronuclear NMR experiments (Sattler et al., 1999). Only C' resonance assignments for L18, which precedes a proline, and E111, which is the C-terminal residue, are missing. Over 87% of sidechain ^{1}H, ^{13}C, and ^{15}N resonances have been assigned. The chemical shifts have been deposited in the BioMagResBank under accession number 6640.

References: Tomb et al. (1997) *Nature*, **388**, 539–547; Sattler et al. (1999) *Prog. NMR Spectrosc.*, **34**, 93–158.

Brendan N. Borin[a], Andrei Popescu[a], Andrzej M. Krezel[a,*]

[a]*Department of Biological Sciences and Center for Structural Biology, Vanderbilt University, Nashville, TN, 37232, U.S.A*

*To whom correspondence should be addressed. E-mail: Andrzej.M.Krezel@Vanderbilt.edu

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^{1}H, ^{13}C and ^{15}N backbone resonance assignment of the Hsp90 binding domain of human Cdc37

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Cdc37 belongs to the cohort of cochaperones that assist Hsp90 to function correctly and is mainly associated with Hsp90. Most of the client proteins interacting with Hsp90/Cdc37 are crucial elements of signaling pathways inside the cell. A predominant group herein are protein kinases. Hence, Cdc37 was assigned as a kinase targeting subunit of Hsp90 (MacLean and Picard, 2003). Cdc37 can be dissected into three different domains. An N-terminal client binding domain, a middle domain binding Hsp90 and a C terminal domain without yet known function. Recently, a crystal structure of the middle domain bound to the N-terminal ATP-binding domain of Hsp90 became available (Roe et al. 2004). The Hsp90 binding domain of human Cdc37 comprising amino acids 147–276 were overexpressed in *E. coli* and 3D heteronuclear NMR experiments with ^{2}H, ^{13}C, ^{15}N and 2D NMR experiments with uniformly ^{15}N labelled protein were used for assignment. For the 130 residue fragment of Cdc37 the backbone assignments are essentially complete with exception of Pro 230. From the triple resonance experiments, further backbone and non-aromatic side chain assignments were made to the following extents: 98% of C_{α}; 86% of H_{α}; 97% of C_{β}, 73% of H_{β}; and 96% of CO. BMRB deposit with accession number BMRB-6586.

References: MacLean and Picard (2003) *Cell Stress Chaperones*, **8**, 114–119; Roe et al. (2004) *Cell*, **116**, 87–96.

Sridhar Sreeramulu[a], Jitendra Kumar[a], Christian Richter[a], Martin Vogtherr[a], Krishna Saxena[a], Thomas Langer[a], Harald Schwalbe[a,*]

[a]*Institut für Organische Chemie und Chemische Biologie, Zentrum für Biologische Magnetische Resonanz, Johann Wolfgang Goethe-Universität Frankfurt, Marie Curie Straße 11, D-60439, Frankfurt*

*To whom correspondence should be addressed. E-mail: schwalbe@nmr.uni-frankfurt.de

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