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Letters to the Editor

Backbone NMR assignment of the low-molecular-weight protein tyrosine phosphatase (MPtpA) from *Mycobacterium tuberculosis*

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The majority of cellular functions depend on protein phosphorylation by kinases and dephosphorylation by phosphatases. Malfunction of protein phosphorylation contributes to the development of many human diseases, ranging from cancer to neurological disorders and diabetis.
Moreover several bacterial pathogens produce eukaryotic-like protein phosphatases that are involved in virulence. One particularly important example is *Mycobacterium tuberculosis*, the main causative agent of tuberculosis (TB). Genome analysis of *M. tuberculosis* revealed the presence of two functional phosphatases (MPtpA (17.5 Da) and MPtpB (30 kDa)) which are secreted by mycobacterial cells (Koul et al., 2000). These phosphatases are believed to mediate mycobacterial survival in hosts and are therefore new potential anti-TB drug targets. Recently, the crystal structure of MPtpA (Madhurantakam et al., 2005) was solved, providing the basic for structure based drug design. To gain further insight into possible protein ligand interaction, 3D heteronuclear NMR experiments with ^{13}C, ^{15}N-labelled MPtpA were recorded to assign the backbone and Cβ atoms. For 10 residues out of 157 observable residues (6.4 %) a signal in the HSQC spectra is missing (H-1, T12, H31, W48, D90, L97, R98, H132, V138, F139). All observed residues were complete assigned. BMRB deposit with accession number 6722.

References: Koul et al. (2000) *J. Bacteriol.*, **182**, 5425–5432; Madhurantakam et al. (2005) *J. Bacteriol.*, **187**, 2175–2181.

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NMR assignment of the N-terminal domain *a* of the glycoprotein chaperone ERp57

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ERp57 is a glycoprotein chaperone, structurally the closest homologue of protein disulfide isomerase, PDI (Ellgaard and Ruddock, 2005). One function of PDI is to act as the β subunit of collagen prolyl 4-hydroxylase (C-P4H), an $\alpha_2\beta_2$ tetramer. Although ERp57 and PDI are 56% similar in primary structure, ERp57 cannot substitute for PDI in C-P4H assembly (Koivunen et al., 1996). To understand the differences between these two enzymes we initiated NMR structural studies of the individual domains of ERp57. For the N-terminal domain we used a set of 2D and 3D NMR spectra recorded on ^{15}N and $^{15}N/^{13}C$ labeled samples. Ninety-eight percent of backbone and side chain ^{1}H, ^{13}C and ^{15}N nuclei have been assigned. Missing backbone amides include residues participating in the catalytic activity, namely W32, C33, H35 and G93. BMRB deposition with Accession No. 6308.

References: Ellgaard and Ruddock (2005) *EMBO Rep.*, **6**, 28–32; Koivunen et al. (1996) *Biochem. J.*, **316**, 599–605.

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