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Letter to the Editor

NMR assignment of peptidyl-tRNA hydrolase from *Mycobacterium tuberculosis* H37Rv

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Peptidyl-tRNA hydrolase (PTH, EC 3.1.1.29) is an enzyme essential for the viability of bacteria and is responsible for alleviating the toxic effects of accumulation of prematurely dissociated peptidyl-tRNA in the cytosol. We have cloned and over-expressed the protein annotated as a putative PTH (ORF Rv1014c) from the genome of *Mycobacterium tuberculosis* H37Rv. In order to understand the dynamic structure of this protein and the protein and peptidyl-tRNA interactions in solution, we have initiated determination of its 3D solution structure. *M. tuberculosis* PTH (mtPTH) consists of 191 residues and has a molecular weight of 20,550.3 Da. Using 2D and 3D heteronuclear NMR experiments on uniformly ^{13}C,^{15}N-labeled mtPTH, we have assigned 171 out of a total of 179 non-proline amide residues. The amide residues that could not be assigned are Met1, Ala2, Glu3, Ala15, Asn16, Lys44, Gly111, Asn116, and Arg143. In addition, assignment of 97% of C^{α}, C^{β}, and CO, 95% of non-aromatic and non-carbonyl side-chain carbons, 89% of H^{α}, and 86% of H^{β} is complete. Based on the chemical shifts obtained, 7 β-strands and 10 α-helices were identified. The overall fold of mtPTH is similar to that of *E. coli* PTH, with which it has 52% sequence homology (Schmitt et al., 1997). BMRB deposits with accession number 7055.

Reference: Schmitt et al. (1997) *EMBO J.*, **16**, 4760–4769.

Naresh C. Bal[a], Himanshu Agrawal[a], Akshaya K. Meher[a], S. V. S. R. Krishna Pulavarti[a], Anupam Jain[a], Geoff Kelly[b], Thomas A. Frenkiel[b], Annalisa Pastore[b] & Ashish Arora[a,*]

[a]*Molecular and Structural Biology, Central Drug Research Institute, Chattar Manzil Palace, Lucknow, 226 001, India;*[b]*Molecular Structure Division, National Institute for Medical Research, London, NW7 1AA, UK*

*To whom correspondence should be addressed. E-mail: ashishcdri@yahoo.com
Naresh C. Bal and Himanshu Agrawal have contributed equally to this work.

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