

## Letter to the Editor

### NMR assignment of $^2\text{H}$ , $^{13}\text{C}$ and $^{15}\text{N}$ labeled amino-terminal domain of apo-pantothenate synthetase from *E. coli*

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Pantothenate (vitamin  $\text{b}_5$ ) is an essential precursor for the biosynthesis of coenzyme A (CoA), an essential metabolite for many important cellular processes (Brown et al., 1987). Pantothenate Synthetase (PS) catalyzes the ATP dependent condensation of D-pantoate with  $\beta$ -alanine to give rise to pantothenate. Our interest lies in studying the solution-state inter-domain interactions in *E. coli* PS that results in formation of the catalytic site. As a first step we have cloned and over-expressed an isotopically enriched sample of the dimeric amino-terminal domain (residues 1–176) of *E. coli* PS. Here we report the backbone and side-chain assignments for HN,  $^{13}\text{C}$  ( $\text{C}^\alpha$ ,  $\text{C}^\beta$  & CO) and  $^{15}\text{N}$  nuclei of the protein, obtained using triple resonance NMR experiments (Yamazaki et al., 1994). CSI and NOE data indicates that the protein is well folded containing both  $\alpha$ -helices and  $\beta$ -sheet. Assignment for  $\sim 95\%$  of backbone and side-chain resonances for the catalytic domain has been obtained and deposited in BMRB (accession # 6940).

References: Brown et al. (1987) *Escherichia coli* and *Salmonella typhimurium: Cellular and Molecular Biology*, Neidhart, F. C. (Ed.), A.S.M., Washington (D.C), pp. 521–538; Yamazaki et al. (1994) *JACS*, **116**, 11656–11666.

Kalyan Sundar Chakrabarti & Siddhartha P. Sarma\*

*Molecular Biophysics Unit, Indian Institute of Science, Bangalore 560012, India*

\*To whom correspondence should be addressed. E-mail: sidd@mbu.iisc.ernet.in

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