

Letters to the Editor

Backbone assignment of PCF11 CTD binding domain

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The 72 kD Pcf11 protein is a component of cleavage factor I (CF1), which is required for cleavage and polyadenylation of the primary mRNA transcript in *S. cerevisiae*. Its N-terminal CTD-interaction domain (CID) makes a phosphorylation dependent contact with the polymerase II carboxy-terminal domain (CTD) in what is thought to be a crucial step in the recruitment of CF1 to the mRNA processing machinery, (Proudfoot et al., 2002). The flexible polymerase II CTD contains numerous (26 in yeast) repeats of a seven-amino acid-sequence. The crystal structure of the Pcf11 CID in complex with a short CTD-derived peptide revealed that the protein recognizes a phosphorylated serine indirectly (Meinhard and Cramer, 2004).

HNCA and HNCACB – TROSY experiments and a ^{15}N -edited NOESY experiment recorded respectively on ^{15}N ^{13}C ^2H - and ^{15}N -labelled recombinant Pcf11 (residues 1–142) were used to obtain an essentially complete assignment (>95%) of the HN, N, $C\alpha$ and $C\beta$ resonances of Pcf11 CID. Only three NH resonances (D117, S118 and S126) from the flexible loop 7 of the protein could not be assigned. This assignment has allowed the study of the interaction phenomena by crystallography and NMR and we hope that this will pave the way to a deeper understanding of the synergistic regulation of mRNA processing processes. BMRB deposit accession number 6404.

References: Proudfoot, N.J., Furger, A. and Dye, M.J. (2002) *Cell*, **108**, 501–512; Meinhard, A. and Cramer, P. (2004) *Nature*, **430**, 223–226.

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NMR assignments of a low molecular weight protein tyrosine phosphatase (PTPase) from *Bacillus subtilis*

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YwIE (150 amino acids) from *Bacillus subtilis* is identified as a low molecular weight protein tyrosine phosphatase (LMW PTPase) and belongs to protein phosphatase super-family, which is involved in various cellular process and plays important roles, such as signal transduction, proliferation and differentiation (Hunter, 1995; Mijakovic et al., 2003). We here report the nearly complete ^1H , ^{13}C and ^{15}N resonance assignments of YwIE. 2D and 3D heteronuclear NMR experiments were performed with uniformly ^{15}N -, ^{13}C -labeled YwIE. About 96% backbone and 90% side-chain ^1H , ^{13}C and ^{15}N resonance assignments are obtained with the exception of 10 residues, among which, residues T8, G9, T11, C12 and R13 are in the flexible P-loop region, whereas N31, H50, N63, H64 and G121 in other flexible loops. BMRB deposits with accession number 6460.

References: Mijakovic, I. et al. (2003) *EMBO J.*, **22**, 4709–18; Hunter, T. (1995) *Cell*, **80**, 225–236.

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