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Letters to the Editor

Sequential backbone assignment of peroxisome proliferator-activated receptor-γ ligand binding domain

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Peroxisome proliferator-activated receptors (PPARs) are transcription factors that belong to the nuclear hormone receptor super family. PPARγ plays an important role in cell cycle regulation, cell differentiation and insulin sensitivity and is a key player in adipogenesis and glucose homeostasis (Cock et al., 2004). The full-length protein can be divided into two distinct structural domains, the DNA binding domain and the ligand binding domain (LBD). PPARγ-LBD (amino acid 207–476) was over expressed and uniformly isotope-enriched in *E. coli*. It shows only approximately half of the expected 266 signals in the ^{1}H, ^{15}N-TROSY-HSQC, upon ligand binding, the quality of spectra is markedly increased and 90% of the expected signals become visible and amenable to sequential assignment (Johnson et al., 2000). Sequential backbone and side chain assignments were accomplished utilising double labelled protein and the spectra HNCO, HCACO and ^{15}N separated NOESY and the triple labelled protein and the TROSY versions of the spectra HNCA, HN(CO)CA, CBCA(CO)NH and by HCCH-TOCSY experiments. Eighty-four percent of the backbone ^{1}Hα, ^{1}HN, ^{15}N and ^{13}CO and ^{13}Cα resonances were assigned. The chemical shifts indicate a well defined globular-fold with an $(\alpha/\beta)_5$ globular structure (Uppenberg et al., 1998). The chemical shifts for PPARγ-LBD have been deposited on the BMRB-Database (http://www.bmrb.wisc.edu) with the Accession Code 6549.

References: Johnson et al. (2000) *J. Mol. Biol.*, **298**; Cock et al. (2004) *EMBO Rep.*, **5**; Uppenberg et al. (1998) *J. Biol. Chem.*, **273**

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^{1}H, ^{13}C and ^{15}N chemical shift assignments of the C-terminal, 133-residue pseudo-receiver domain of circadian input kinase (CikA) in *Synechococcus elongatus*

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CikA is part of the enviromental input pathway that resets the cyanobacterial circadian clock. The sequence of its pseudo-receiver domain (CikAPsR, residues 622–754) shows similarities to the *bona fide* receiver domains of response regulators (RRs) in bacterial two-component systems. The CikAPsR domain has been shown to negatively regulate the autokinase activity of CikA although how this regulation is achieved is presently unknown (Mutsuda et al., 2003). The structure of CikAPsR will provide insight into the regulation of the clock input pathway. Chemical shift assignments were determined from a series of 2D, 3D and 4D NMR expriments with ^{13}C, ^{15}N-labeled CikAPsR. For the entire native sequence, all backbone $^{13}C^{\alpha\beta}$, ^{15}N and ^{1}H resonances were assigned except for residues E635, E636 and D637. All aliphatic ^{1}H and ^{13}C, Gln and Asn amide side chains, and 77% of the aromatic ^{1}H and ^{13}C resonances were also assigned. BMRB deposit 6438.

Reference: Mutsuda et al. (2003) *J. Biol. Chem.*, **278**, 19102–19110.

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