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Letters to the Editor

NMR backbone assignment of the mitogen-activated protein (MAP) kinase p38

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MAP kinase p38 is an important anti-inflammatory drug target (Lee et al., 1994). The construct p38(−2-349) of mouse p38 is very stable and suitable for applications in drug discovery. We have partially assigned p38 using principles developed for the catalytic domain of protein kinase A (Langer et al., 2004). 3D heteronuclear NMR experiments with ^{2}H, ^{13}C, ^{15}N p38, 2D NMR experiments with selectively ^{15}N-Tyr, Phe, Met, Ile, Val, Leu labeled p38 and distance information from a paramagnetic adenosine derivate were used. 254 (75.4%) of the expected 337 amide signals were found. Backbone and C_{β} shifts for 216 of these (85.0, 64.0% based on the sequence) were assigned and are mapped onto the sequence in Figure 1 (supplementary material), BMRB deposit with Accession number 6468.

References: Langer, et al. (2004) *Chembiochem.*, **5**, 1508–1516; Lee, et al. (1994) *Nature.*, **372**, 739–746.

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Resonance assignments for the DNA binding domain of ERCC-1/XPF heterodimer

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Nucleotide excision repair (NER) is a sophisticated DNA repair mechanism that eliminates a wide variety of DNA lesions. The endonuclease ERCC-1/XPF (Excision Repair Cross Complementation group 1/ Xeroderma Pigmentosum group F) complex is the structure-specific endonuclease that participates in the repair of DNA damage by making the 5′ incision. In the ERCC-1/XPF heterodimer, C-terminal domains of both subunits contain two tandemly repeated helix–hairpin–helix DNA binding motifs. The heterodimeric DNA binding domain in the ERCC-1/XPF complex plays a crucial role in positioning it at the appropriate location containing irregular DNA structures. We initiated a NMR structure determination of the heterodimeric DNA binding domain of the ERCC-1/XPF to explore its binding mode to unusual DNA structures. Here, we report nearly complete ^{1}H, ^{13}C and ^{15}N resonance assignment of the DNA binding domain in human ERCC-1/XPF heterodimer; ERCC-1 and XPF subunits consist of 79 residues (residues 219–297) and 96 residues (residues 810–905), respectively. BMRB deposit with accession number 6502.

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