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Letters to the Editor

NMR assignment of the six zinc fingers of MTF-1 in the free and DNA-bound states

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Metal-response element-binding transcription factor-1 (MTF-1) coordinates the expression of genes involved in eukaryotic zinc homeostasis. MTF-1 has a 6 Cys_2His_2 zinc finger DNA-binding domain (F1–6) that responds to zinc through metal coordination (Lichtlen and Schaffner, 2001). To gain insight into MTF-1 function, NMR structural, dynamics and metal binding studies of murine F1–6 (residues 138–312) in DNA-free and DNA-bound forms (17 bp and 22 bp complexes) are ongoing. 2D and 3D heteronuclear NMR experiments were recorded using uniformly ^{15}N-, ^{13}C-labelled F1–6 proteins. F1–6 complexes with DNA were also 80% ^{2}H-labeled. Nearly complete backbone ^{1}H, ^{13}C, ^{15}N, and $^{13}C\beta$ resonances (all >92%) were assigned for all F1–6 constructs. Approximately 90% of the side chain ^{1}H and ^{13}C resonance assignments for DNA-free F1–6 are also reported. BMRB accession numbers are 6275 (DNA-free), 6276 (17 bp DNA complex), and 6445 (22 bp DNA complex).

References: Lichtlen, P. and Schaffner, W. (2001) *Swiss Medical Weekly*, **131**, 647–652.

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NMR assignment of the reduced and oxidized forms of the human ADAP hSH3-1 domain

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The protein ADAP is a hematopoeitic adapter protein that regulates T cell receptor mediated integrin activity and cytokine production. ADAP contains several protein interaction sites that include a SH2 docking sequence for the Fyn tyrosine kinase SH2 domain, an EVH1 binding site, proline-rich motifs and two SH3-like domains (Heuer et al., 2004). We found that the N-terminal hSH3 domain exists in two forms, an oxidized and a reduced form that are reversibly interchanged by the addition of H_2O_2 and DTT, respectively. 2D and 3D heteronuclear NMR experiments with $^{15}N/^{13}C$-labeled ADAP hSH3-1 were used for spectral assignments.

The backbone assignment of the reduced form is complete for residues 497–579, with residues 509 and 546 being proline. The backbone assignment for the oxidized form is complete for residues 497–576, except for V512, P509 and P546. The sidechain assignment is ~95% complete for both forms. The chemical shift assignments have been deposited at the BMRB (http://www.bmrb.wisc.edu) under accession number 6536 for the reduced form and accession number 6539 for the oxidized form of the human ADAP hSH3-1 domain.

References: Heuer, K. et al. (2004) *Structure (Camb.)*, **12,** 603–610.

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