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Letters to the Editor

^{1}H, ^{13}C and ^{15}N backbone and side chain resonance assignments of *Haloferax volcanii* DHFR1

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Haloferax volcanii is an archael species which exploits the niche of hyper-saline environments. To understand how enzymes can adapt to function in very different salt concentrations, the salt-dependence of the properties of dihydrofolate reductases (DHFRs) from *H. volcanii* (*hv*DHFR1) and *E. coli* (*ec*DHFR) are being studied (Wright et al., 2002). To test the relationship between stability, activity and flexibility, we propose to investigate the flexibility of *ec*DHFR and *hv*DHFR1 through NMR relaxation studies at varying salt concentrations. Nearly complete chemical shift assignments of 50% ^{2}H and uniformly ^{15}N and ^{13}C labeled *hv*DHFR1 in 3.5 M NaCl have been accomplished through 2D and 3D heteronuclear NMR experiments. The high viscosity of the solvent makes the protein's correlation time more like a 25 kDa protein. Therefore we used ~50% ^{2}H labeling, which resulted in interpretable data. Chemical shift assignments were accomplished for 97% of the backbone amides, the residues A10, E11, R13, D18, and R69 were unassigned. In total, 98% of $^{13}C^{\alpha}$, 96% of $^{13}C^{\beta}$, 92% of ^{13}CO, 97% of $^{1}H^{\alpha}$ and 97% of $^{1}H^{\beta}$ were assigned. BMRB accession Nr. 6645.

Reference: Wright et al. (2002) *J. Mol. Biol.*, **323**, 327–344.

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NMR Assignment of HI1506, a novel two-domain protein from *Haemophilus influenzae*

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HI1506 is a 128-residue hypothetical protein of unknown function from *H. influenzae*. It was originally annotated as a shorter 85-residue protein but a sequence correction conducted in our laboratory revealed that the full-length protein has an additional 43 residues on the C-terminus, corresponding with a region initially ascribed to HI1507. As part of a larger effort to understand the functions of hypothetical proteins from Gram-negative bacteria, and *H. influenzae* in particular, we report here the NMR assignments for the corrected full-length HI1506 protein. Sequence-specific ^{1}H, ^{13}C, and ^{15}N assignments were completed for more than 95% of the backbone atoms. Most side chain atoms have also been assigned. Our results indicate that HI1506 has two domains connected by a short linker. The assignments provide the basis for structure determination and, potentially, further insight into function. The chemical shifts have been deposited in the BMRB (accession number BMRB-6780).

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