J Biomol NMR (2007) 38:185
DOI 10.1007/s10858-006-9116-8

LETTER TO THE EDITOR

NMR resonance assignments of the human high mobility group protein HMGA1

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Received: 6 October 2006 / Accepted: 27 October 2006 / Published online: 6 January 2007

Human high mobility group protein HMGA1 is a 107-residue, non-histone chromatin protein with a wide sphere of influence including embryogenesis, apoptosis, differentiation, cell proliferation, and cancer development (Reeves 2001). Due to the repetitive nature of the three DNA-binding domains, C-terminal strings of glutamic acid residues, and unstructured nature in the absence of A-T rich regions of DNA and/or other proteins, resonance assignments were challenging. Especially useful was the HNN experiment (Panchal et al. 2001), a set of truncated HMGA1 constructs, and some high resolution NMR data (^{1}H 900 MHz). Except for absolute assignment of R60 and R86, all 82 amides were assigned to cross peaks in the ^{1}H-^{15}N HSQC spectrum and many of the side chain ^{13}C and ^{1}H resonances were assigned (BMRB—7279). The intensity of the amide cross peaks for residues E3–S9 and S64–K67 were much weaker than the other amide cross peaks in the ^{1}H-^{15}N HSQC spectrum suggesting that even in this unstructured protein there are regions experiencing motion different from the molecule as a whole.

Acknowledgements This work was supported by an LDRD project at EMSL, a national scientific user facility sponsored by a US. DOE BER program located at PNNL.

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Electronic supplementary material The online version of this article (doi: 10.1007/s10858-006-9116-8) contains supplementary material, which is available to authorized users.

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