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Letters to the Editor

Assignments for the *Bombyx mori* pheromone-binding protein fragment BmPBP(1–128) at pH 6.5

The 142-residue silkworm moth pheromone-binding protein transports pheromones across the sensillar lymph to the membrane-standing receptor. It undergoes a pH-dependent conformational transition from a form at pH 6.5 containing a large preformed pheromone-binding cavity (Lee et al., 2002) to a form at pH 4.5 where this cavity is occupied by a helix of the C-terminal dodecapeptide (Horst et al., 2001). To investigate the role played by this C-terminal helix in ligand binding and ejection, we initiated an NMR structure determination of the recombinant protein BmPBP (1–128), which is devoid of the C-terminal helix. 3D heteronuclear NMR experiments with ^{13}C, ^{15}N-labeled BmPBP (1–128) were analyzed with CARA (www.nmr.ch) to obtain ^{1}H, ^{13}C and ^{15}N assignments, which are complete except for H^N and N of S1 and Q2, C′ of S1, γCH_2, δCH_2 and εCH_2 of K6, Hδ1 of H69, εCH_3 of M86, and δ1 ^{15}N—H of H80, H95, and H123, BMRB deposit 6313.

References: Horst, R. et al. (2001) *Proc. Natl. Acad. Sci., USA*, **98**, 14374–14379; Lee, D. et al. (2002) *FEBS Lett*., **531**, 314–318.

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NMR resonance assignments for the DNA-supercoiling domain of the human protein DEK

The highly abundant nuclear protein DEK, first discovered in the context of a fusion product of an in-frame chromosomal translocation in acute myeloid leukemia, has since been implicated in disease and biological processes as diverse as cancer, lupus, viral transcription. We previously determined the NMR structure of the C-terminal domain (Devany et al., 2004). Here we report the resonance assignments for the N-terminal domain of DEK (DEK78–208), which contains a structured region reported to induce DNA supercoiling (Waldmann et al., 2002). The on-going structure determination will provide further insight into the biological function of DEK and the DNA binding mechanism of this novel DNA-binding sequence. Sequential assignment of the DNA supercoiling domain of DEK was achieved using a ^{13}C and ^{15}N labeled DEK78–208 recombinant construct and standard 2D and 3D NMR experiments. Nearly complete backbone assignments were obtained, 95% of the HN, N, HA, CA, C′ shifts for the structured residues (78–187), and 88% assignment for the entire native sequence. The majority (85%) of side chain assignments for the structured region were also completed. Chemical shift index values and NOE patterns indicate DEK78–208 consists of five α-helices: residues 92–99, 103–113, 120–129, 140–163, and 172–183. BMRB accession number 6361.

References: Devany et al. (2004) *Protein Sci*., **13**, 2252–2259; Waldmann et al. (2002) *J. Biol. Chem.,* **28**, 24988–24994.

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