

## Letters to the Editor

### <sup>1</sup>H, <sup>13</sup>C and <sup>15</sup>N NMR assignments for AlgH, a putative transcriptional regulator from *Pseudomonas aeruginosa*

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AlgH (20.2 kDa, 189 residues) from *Pseudomonas aeruginosa* is known to regulate the biosynthesis of the exopolysaccharide alginate, as well as siderophore, protease, rhamnolipid and nucleoside diphosphate kinase, putatively at the transcriptional level, and has been suggested to be a 'global regulator of several functions' (Schlichtman et al., 1995). The mechanism by which AlgH acts has not been defined, and no functional or structural information is currently available for any members of the AlgH family (Pfam PF02622). We have demonstrated previously the production, labeling and purification of this stable, folded, globular protein (Bieber Urbauer et al., 2005). Heteronuclear 2D and 3D methods were used to obtain nearly complete main chain <sup>1</sup>H, <sup>13</sup>C, and <sup>15</sup>N (>95%) and aliphatic side chain <sup>1</sup>H, and <sup>13</sup>C assignments (>93%). Unassigned resonances include the 14 Pro <sup>15</sup>N resonances and many <sup>13</sup>C and <sup>1</sup>H resonances of aromatic groups. The BMRB deposit has Accession No. 6644.

References: Schlichtman et al. (1995) *J. Bacteriol.*, **177**, 2469–2474; Bieber Urbauer et al. (2005) *Prot. Expr. Purif.* **43**, 57–64.

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### <sup>1</sup>H, <sup>13</sup>C and <sup>15</sup>N resonance assignments of the AT-Rich Interaction Domain (ARID) of Jumonji

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Jumonji (Jmj) is a ubiquitous, transcriptional repressor protein which plays important roles in development, cell growth and gene expression (Takeuchi et al., 1995). Jmj is a member of Jmj transcription factor family, which contains an AT-rich interaction domain (ARID) (Wilsker et al., 2002) and Jumonji-like domains (JmjN/JmjC). Jmj ARID is a putative DNA-binding domain, which shares about 30% sequence identity to the ARID family members. In this study, we prepared non-labeled, uniformly <sup>15</sup>N-labeled and <sup>13</sup>C/<sup>15</sup>N-labeled Jmj ARID (116 residues, L615 to K730) to determine the solution structure of the protein and to examine the structure–function relationships of the protein by NMR experiments. NMR spectra were acquired on a Bruker AVANCE 500 spectrometer equipped with <sup>1</sup>H/<sup>13</sup>C/<sup>15</sup>N cryogenic probe at 15 and 25°C. Most of backbone (99% of <sup>15</sup>N and HN, 98% of <sup>13</sup>CO, 98% of <sup>13</sup>C $\alpha$ , 99% of H $\alpha$ , 96% of <sup>13</sup>C $\beta$ , 95% of H $\beta$ ) and side-chain resonances (approximately 86% of <sup>1</sup>H and <sup>13</sup>C resonances) were assigned. BMRB deposit with accession number 6607.

References: Takeuchi et al. (1995) *Genes Dev.*, **9**, 1211–1222; Wilsker et al. (2002) *Cell Growth Differ.*, **13**, 95–106.

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