

Backbone and side chain ^1H , ^{13}C , and ^{15}N resonance assignments of AF2241 from *Archaeoglobus fulgidus*

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AF2241 is a 131-residue hypothetical protein from *Archaeoglobus fulgidus*. The protein belongs to a Pfam domain family of unknown function (DUF369), which also includes a number of other hypothetical proteins from archaea and bacteria. Recently, the structure of TM1367 from *Thermotoga maritima*, a member of the DUF369 family, has been determined by X-ray crystallography (Jin et al. 2006). The crystal structure reveals that the protein adopts a similar fold as human cyclophilin A, however, the peptidylprolyl cis-trans isomerases (PPIase) active site is not conserved. We are currently determining the structure of AF2241 using NMR spectroscopy as part of the structural genomics effort to probe the possible function of this family of proteins. 2D and 3D heteronuclear NMR experiments were performed

on a uniformly ^{13}C -, ^{15}N -labeled AF2241 sample. A total of 91.8% of backbone and side chain assignments have been obtained with the exception of residues 1–3 (N-terminal residues), 80–81, 92, 95–96, 107 and 113–116, for which most of them are in the loop regions or turns in the structure that we calculated. BMRB deposit: Accession No. 7271.

References

- Jin KK et al (2006) Crystal structure of TM1367 from *Thermotoga maritima* at 1.90 Å resolution reveals an atypical member of the cyclophilin (peptidylprolyl isomerase) fold. *Proteins* 63:1112–1118

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