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Letter to the Editor

NMR assignment of M-crystallin: a Novel Ca^{2+} binding protein of the βγ-crystallin superfamily from *Methanosarcina acetivorans*

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We have cloned and over-expressed the C-terminal βγ-crystallin domain of a protein annotated as a putative βγ-crystallin family protein (accession NP_617429) from the genome of *Methanosarcina acetivorans*, which is the largest of all sequenced archaeal genomes with 5.7 million base pairs (Galagan et al., 2002). We named the protein as M-crystallin. To elucidate the structural and functional properties of this oldest relative of βγ-crystallin, we have initiated to solve the 3D solution structure of this protein. Like some proteins belonging to βγ-crystallin superfamily, M-crystallin also binds Ca^{2+}. 2D and 3D heteronuclear NMR experiments with uniformly ^{15}N-labelled and $^{13}C/^{15}N$ doubly labelled M-crystallin were used for the resonance assignments of almost all ^{1}H, ^{15}N (backbone), $^{13}C^{\alpha}$, $^{13}C^{\beta}$ and $^{13}C'$ spins of M-crystallin in both Ca^{2+} free (apo) and bound (holo) forms (Atreya et al., 2000). It was not possible to assign the resonances for residues M1 and N2 at the N-terminal end of the polypeptide chain, probably because of rapid $^{1}H^{N}$-exchange with solvent. BMRB deposits with accession numbers 6903 (for apo) and 6904 (for holo).

References: Galagan et al. (2002) *Genome Res*., **12**, 532–542; Atreya et al. (2000) *J. Biol. NMR*, **17**, 125–136.

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