Crystal Structures of pmbA and CsrA: Both Reveal New Folds

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The crystal structure of pmbA reveals a new fold. PmbA, which is encoded by the TM0727 gene of *Thermatoga maritima*, functions in the production of the antibiotic peptide microcin B17[1]. Additionally, pmbA is a putative modulator of DNA gyrase that may function with carbon storage regulator A (CsrA)[2]. The structure was determined using MAD phasing, and two monomers were refined to 1.95Å. The pmbA monomer is composed of two domains, with the N-terminal domain forming a long anti-parallel six-stranded β-sheet, and the C-terminal domain containing three anti-parallel β-sheets, five α-helices and regions of extended coil.

The crystal structure of the carbon storage regulator A (CsrA) gene of *Pseudomonas putida* also reveals a new fold. The structure of dimeric CsrA was determined with MAD phasing and refined to 2.05Å. Each monomer is composed of five consecutive anti-parallel β-strands and one α-helix, with the dimer formed by the intertwining of a pair of β-strands. *E. coli* CsrA is an RNA binding protein which, in conjunction with CsrB-RNA, negatively regulates glycogen biosynthesis, glyconeogenisis and glycogen metabolism, while having a positive regulatory effect on glycolysis[3].

[1] Rodriguez-Sainz M.C., Hermandez-Chico C., Moreno F., *Mol. Microbiol.*, 1990, **4**, 1921. [2] Murayama N., Shimizu H., Takiguchi S., Baba Y., Amino H., Horiuchi T., Sekimizu K., Miki T., *J. Mol. Biol.*, 1996, **256**, 483. [3] Romeo T., *Mol. Microbiol.*, 1998, **29**, 1321.

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