The Crystal Structure of Mannosylglycerate Synthase from *Rhodothermus marinus* at 2.5 Å Resolution

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Mannosylglycerate (MG) is a compatible solute widely distributed among thermophilic and hyperthermophilic organisms. It accumulates in response to salt and heat stress in *R. marinus* and was found to protect several enzymes against heat inactivation [1,2]. The pathways for the synthesis of MG in *R. marinus* have been characterized in detail [1]. Mannosylglycerate synthase (MGS) is involved in the single-step pathway converting GDP-mannose and D-glycerate to MG, similarly to the GDP-mannose:α-mannosyltransferase GT55 family of Glycosyltransferases (EC 2.4.1.-), which retain the anomeric configuration of the substrate [1,3]. To date no 3D structure is known for any enzyme belonging to this family.

A Se-Met derivative of MGS has been recently crystallized and a Se K-edge MAD experiment was carried out on ESRF beamline ID29. The crystals belong to trigonal space group $P3_221$, with unit cell parameters $a = b = 148$, $c = 155$ Å. Preliminary structural analysis suggests that MGS may function as a dimer and that each monomer has two distinct domains: one mainly α-helical and the other predominantly β-sheet.

[1] Martins et al., *J. Biol. Chem.*, 1999, **274**, 35407-35414. [2] Ramos et al., *Appl. Environ. Microbiol.*, 1997, **63**, 4020-4025. [3] Borges et al., *J. Biol. Chem.*, 2004, **279**, 9892-9898.

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