Crystal structure of amylomaltase from Corynebacterium glutamicum

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Amylomaltase (AM; EC 2.4.1.25) belongs to the 4-α-glucanotransferase (4αGTase) group of the α-amylase family. The enzyme can produce cycloamylose (CA) or large-ring cyclodextrin (LR-CD) through intramolecular transglycosylation or cyclization reactions of α-1,4 glucan. Amylomaltase from the mesophilic bacterium Corynebacterium glutamicum yielded different LR-CD production profile from that of the well-characterized Thermus aquaticus enzyme [1,2]. C. glutamicum amylomaltase (CgAM) was overexpressed, purified and crystallized [3]. X-ray crystal structure of CgAM differs from Th. aquaticus amylomaltase in the presence of an additional N-terminus domain. The acarbose- and maltotriose- bound structures revealed the residues involved in substrate binding.


Keywords: Amylomaltase, Corynebacterium glutamicum, large-ring cyclodextrin