

Poster Presentation

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Crystal structure of amyloamylase from Corynebacterium glutamicum

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Amyloamylase (AM; EC 2.4.1.25) belongs to the 4- α -glucanotransferase (4 α GTase) 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. Amyloamylase 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* amyloamylase (CgAM) was overexpressed, purified and crystallized [3]. X-ray crystal structure of CgAM differs from *Th. aquaticus* amyloamylase in the presence of an additional N-terminus domain. The acarbose- and maltotriose- bound structures revealed the residues involved in substrate binding.

[1] Y. Terada, K. Fujii, T. Takaha et al. *Appl Environ Microbiol*, 1999, 65, 910-915., [2] W. Srisimarat, A. Powviriyakul, J. Kaulpiboon et al. *J Incl Phenom Macrocycl Chem*, 2011, 70, 369-375., [3] W. Srisimarat, S. Murakami, P. Pongsawasdi et al. *Acta Crystallogr Sect F Struct Biol Cryst Commun*, 2013, 69, 1004-1006.

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