Crystal structure of amylomaltase from Corynebacterium glutamicum in complex with maltopentaose

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Amylomaltase (AM; EC 2.4.1.25) belongs to the 4-α-glucanotransferase group of the α-amylase family. The enzyme catalyzes the transfer of an α-1,4-D-glucan unit, producing linear and cyclic oligosaccharides. Here, we report the crystal structure of amylomaltase from a mesophilic bacteria, Corynebacterium glutamicum (CgAM), in complex with maltopentaose. CgAM contains three main domains, namely domain A, B and N (Fig. 1a). Domain A consists of a typical TIM barrel, while Domain B locates on the top of the TIM barrel of domain A. The domain N, consisting of four α-helices and eleven β-strands, presents in CgAM and amylomaltase from Escherichia coli [1], but not in thermophilic amylomaltases [2,3]. The catalytic Asp460 was mutated to Asn460 to produce an inactive CgAM (D460N). Fig. 2b shows clear visible electron density map that fits five glucose units within the active site of D460N mutant. The residue Asn460 is oriented in an unfavourable position for catalysis. The glucose at subsite -1 shows hydrogen bondings with His560 and the catalytic residue Asp561, while the glucose at subsite -2 interacts with Asn661 and Gly664.

Figure 1. (a) Overall structure of D460N CgAM-Maltopentaose. Maltopentaose (yellow sticks) bound to D460N CgAM (green). The omit electron density map (Fo-Fc) was displayed at a contour level of 3s.


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