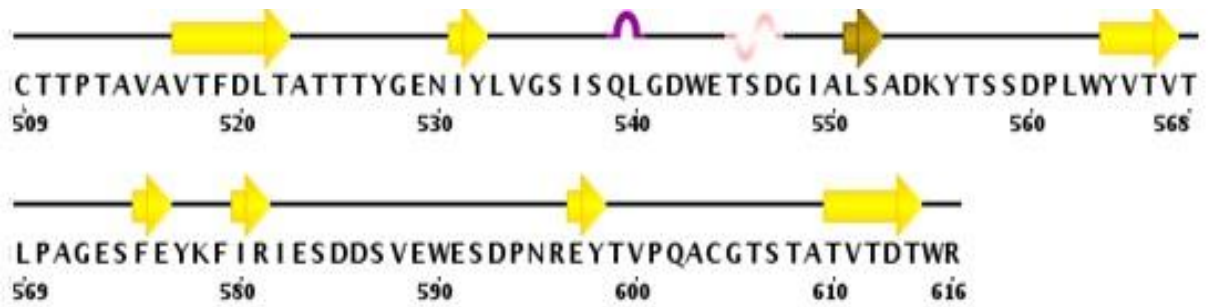
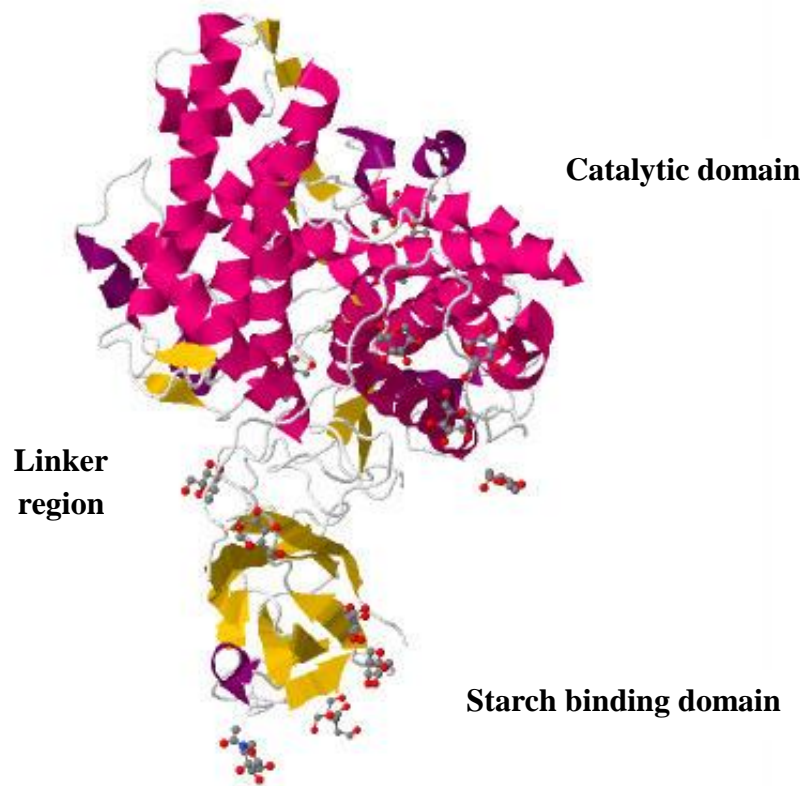


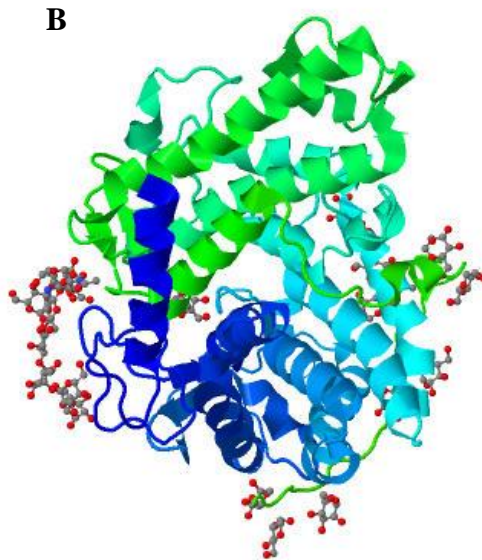
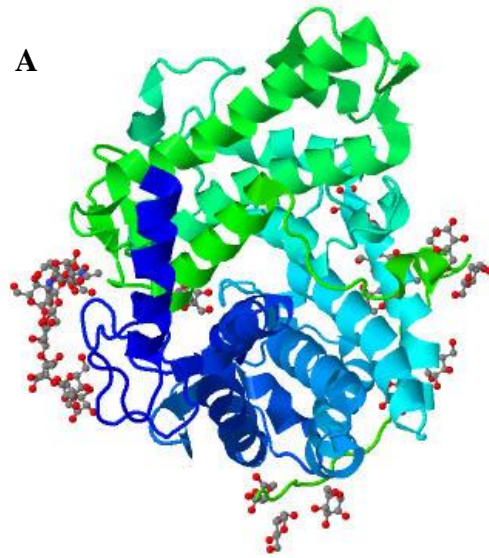
**Figure 2.1.** The amino acid sequence corresponding to mature catalytic domain of *Aspergillus niger* glucoamylase generated by subtilisin cleavage (adapted from Protein Data Bank, entry code: 3EQA). The positions of  $\alpha$ -helices ( ),  $3_{10}$ -helices ( ),  $\beta$ -strands ( ),  $\beta$ -bridges ( ) and turns ( ) are indicated.



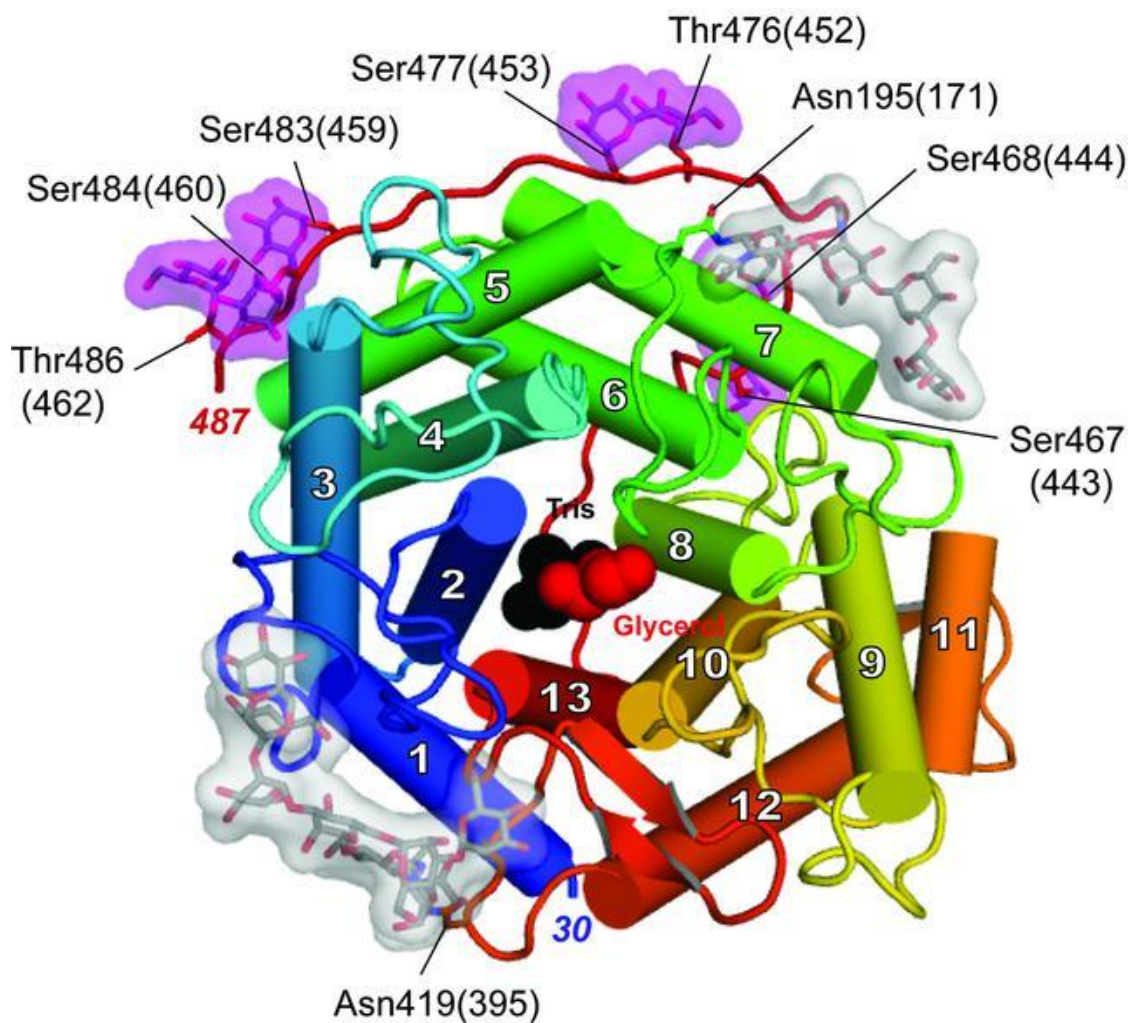
**Figure 2.2.** The amino acid sequence corresponding to mature starch binding domain (SBD) of *Aspergillus niger* glucoamylase (adapted from Protein Data Bank, entry code: 1AC0). The positions of  $3_{10}$ -helices (🌀),  $\beta$ -strands (➡),  $\beta$ -bridges (➡) and turns (↪) are indicated.



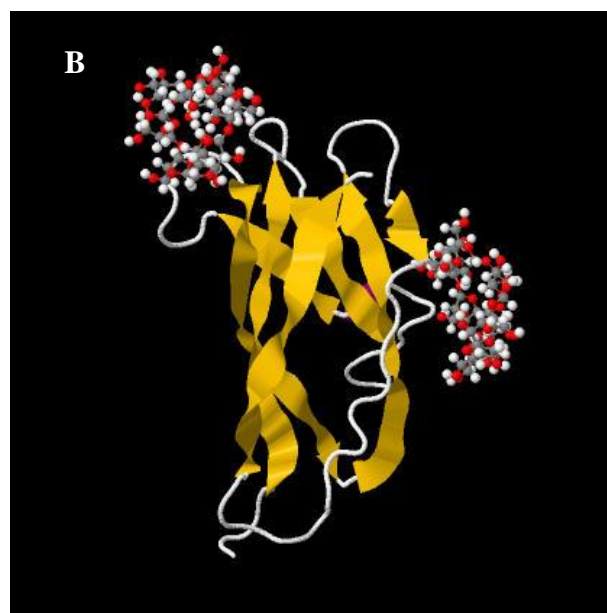
**Figure 2.3.** Three-dimensional structure of *Hypocrea jecorina* glucoamylase (PDB entry code: 2VN4), showing the location of different domains.



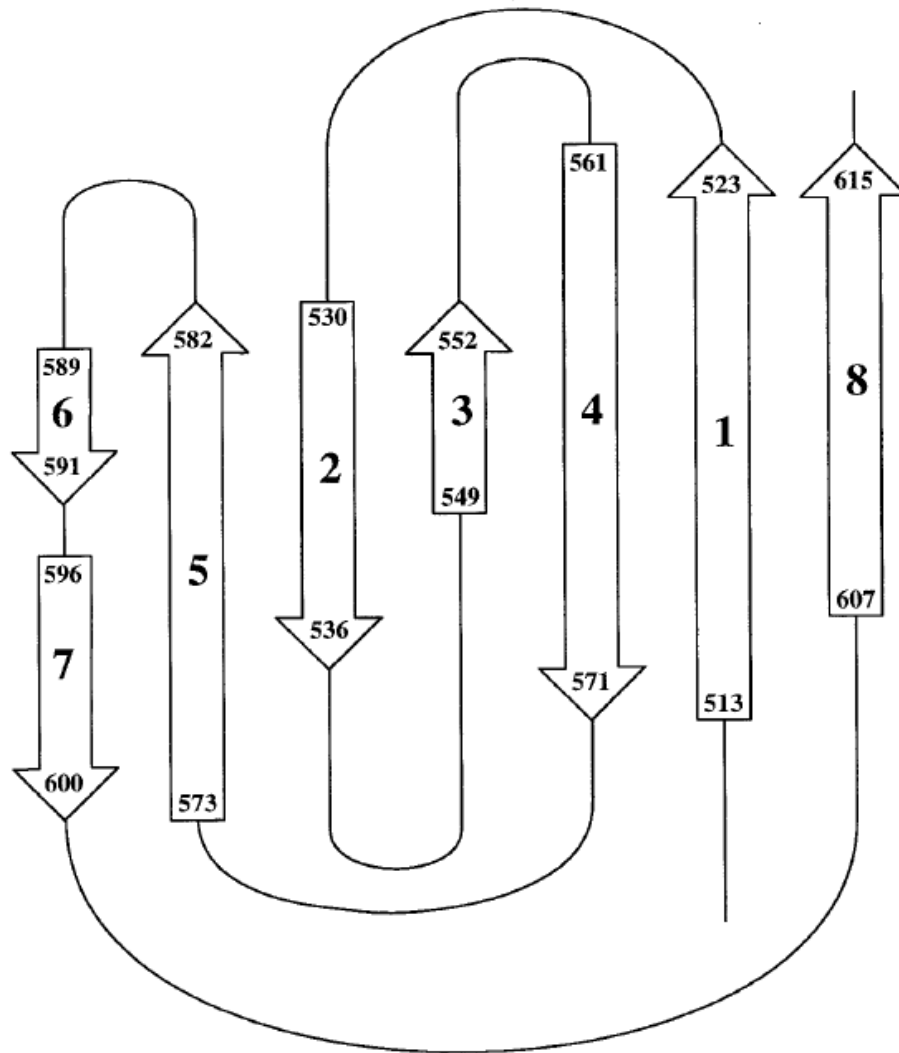
**Figure 2.4.** Three-dimensional structures of the catalytic domain of glucoamylase from (A) *Aspergillus niger* complexed with tris and glycerol (PDB entry code: 3EQA) and (B) *Aspergillus awamori* var. X100 (PDB entry code: 1GLM).



**Figure 2.5.** Three-dimensional structure of the catalytic domain [residue 30 (blue) to 487 (red)] of *Aspergillus niger* glucoamylase. Thirteen (13)  $\alpha$ -helices, shown as cylinders, are numbered from the N-terminus. The glycosylation sites of the mannose (magenta) and NAG oligosaccharides (grey) as well as the active-site-bound Tris (black) and glycerol (red) are highlighted. [Reprinted from Lee and Paetzel (2011)].



**Figure 2.6.** Three-dimensional structures of the starch binding domain of *Aspergillus niger* glucoamylase both in the free form (A), (PDB entry code: 1KUL) and in complex with  $\beta$ -cyclodextrin (B) (PDB entry code: 1AC0).



**Figure 2.7.** Representation of the direction and alignment of the  $\beta$ -strands (numbered 1 to 8) in the starch binding domain of *Aspergillus niger* glucoamylase. The first and the last residues in the each strand are marked at the ends of the arrows. [Reprinted from Sorimachi *et al.* (1996)].