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 α-helices ( ), 3₁₀-helices ( ), β-strands ( ), β-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 ( ), β-strands ( ), β-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. XI00 (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) α-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 β-cyclodextrin (B) (PDB entry code: 1AC0).
Figure 2.7. Representation of the direction and alignment of the β-strands (numbered 1 to 8) in the starch binding domain of *Aspergillus niger* glucoamylase. The first and the last residues in each strand are marked at the ends of the arrows. [Reprinted from Sorimachi et al. (1996)].