REFINED STRUCTURE FOR THE COMPLEX OF ACARBOSE WITH GLUCOAMYLASE FROM ASPERGILLUS AWAMORI VAR.X100 TO 2.4-A RESOLUTION

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The three-dimensional structure of the complex of pseudotetrasaccharide acarbose with glucoamylase II–(471) from *Aspergillus awamori* var.X100 has been determined to 2.4-A resolution. The model includes residues corresponding to residues 1–471 of glucoamylase I from *Aspergillus niger*, the molecule of bound acarbose and 535 sites for water molecules. The crystallographic R factor from refinement is 0.124, and the root-mean-squared deviation in bond distances is 0.012 A. The inhibitor complex confirms the location of the active site in the packing void of the α/α-barrel as proposed by Aleshin et al. [1]

Interactions of acarbose with the enzyme at its the first site involve Arg 54, Asp 55, Arg 305, Trp 52 and carbonyl 177, at the second site Glu 180, Arg 305, Tyr 48, Tyr 50, Trp 120. The third unit of acarbose has besides stacking interaction with Trp 120 also two hydrogen bonds with the enzyme. The position of the fourth residue of acarbose is not firmly determined because of interaction with the neighboring molecule of the protein. The structural arrangement of functional groups near the inhibitor molecule suggests that Glu 179 is a catalytic acid, Glu 400 a catalytic base, and water 500 the attacking nucleophile in the hydrolysis of maltooligosaccharides.

REFERENCES

1. *Aleshin A., Golubev A., Firsov L.M., Honzatko R.B.* J.Biol.Chem., 1992. V.267. P.19291–19298.