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## Review Article

# The Importance of Surface-Binding Site towards Starch-Adsorptivity Level in $\alpha$ -Amylase: A Review on Structural Point of View

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Starch is a polymeric carbohydrate composed of glucose. As a source of energy, starch can be degraded by various amylolytic enzymes, including  $\alpha$ -amylase. In a large-scale industry, starch processing cost is still expensive due to the requirement of high temperature during the gelatinization step. Therefore,  $\alpha$ -amylase with raw starch digesting ability could decrease the energy cost by avoiding the high gelatinization temperature. It is known that the carbohydrate-binding module (CBM) and the surface-binding site (SBS) of  $\alpha$ -amylase could facilitate the substrate binding to the enzyme's active site to enhance the starch digestion. These sites are a noncatalytic module, which could interact with a lengthy substrate such as insoluble starch. The major interaction between these sites and the substrate is the CH/ $\pi$ -stacking interaction with the glucose ring. Several mutation studies on the *Halothermothrix orenii*, *SusG Bacteroides thetaiotamicron*, *Barley*, *Aspergillus niger*, and *Saccharomycopsis fibuligera*  $\alpha$ -amylases have revealed that the stacking interaction through the aromatic residues at the SBS is essential to the starch adsorption. In this review, the structural appearance of SBS in various  $\alpha$ -amylases is also presented. Therefore, based on the structural point of view, SBS is suggested as an essential site in  $\alpha$ -amylase to increase its catalytic activity, especially towards the insoluble starch.

## 1. Introduction

Starch is the most abundant form of storage of many economically important crops such as wheat, rice, maize, tapioca, and potato [1, 2]. Starch-containing crop is an essential constituent of the human diet, and a large proportion of the food consumed by the world's population originates from them. Starch is harvested and used as its original form or chemically or enzymatically processed into a variety of different products, for example, starch hydrolysates, glucose syrups, fructose, starch or maltodextrin derivatives, or cyclodextrins [1].

Degradation of starch into a variety of different products is performed by amylolytic enzymes, such as  $\alpha$ -amylase, glucoamylase,  $\beta$ -amylase, isoamylase, pullulanase, exo-1,4- $\alpha$ -D-glucanase,  $\alpha$ -D-glycosidase, and cyclomaltodextrin-D-glucotransferase [3].

The amylases are multidomain proteins. Interestingly, about 10% of them contain a distinct noncatalytic module that is known to facilitate binding and degradation of raw starch [4]. Initially, only two types of starch-binding domains (SBDs) were recognized: either very frequent C-terminal SBD or very scarcely occurring N-terminal SBD [5] and sometimes substrate bind in the one or more surface region