Structural Insights into a Glysoside Hydrolase Family 26 lichenase

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Hydrolysis of the glycosidic bond is one of the most critical processes in nature and has considerable technical importance. Glycoside hydrolases have been shown to be extremely proficient at the acceleration of this reaction increasing rates by a factor of 10^{17}, this makes them among the most effective of enzymes. This effectiveness is reflected in the tight binding of the oxocarbenium transition state. Determination of the conformation of the substrate whilst in this transition state is of importance not only for improved understanding of the action of these enzymes but also for the design of specific and powerful enzyme inhibitors. We present here the results of a crystallographic analysis of a member of the glycoside hydrolase family 26. The structure of the native enzyme and the successful structural determination of the enzyme complexed with an inhibitor is described. The enzyme inhibitor interactions revealed as a result of this study are discussed.

Keywords: protein ligand complex, glycoside hydrolase, protein structure