

The X-Ray Diffraction Structure of a Glycosyl Hydrolase Family 32 protein: 1-Fructan Exohydrolase IIa of *Cichorium Intybus*, Maureen Verhaest,^a Wim Van den Ende,^b Camiel De Ranter,^a André Van Laere^b and Anja Rabijns^{a*}, ^a*Laboratorium voor Analytische Chemie en Medicinale Fysicochemie, K.U. Leuven, E. Van Evenstraat 4, 3000 Leuven, Belgium, and* ^b*Laboratorium voor Moleculaire Plantenfysiologie, K.U.Leuven, Kasteelpark Arenberg 31, 3001 Heverlee, Belgium.* E-mail: Anja.Rabijns@pharm.kuleuven.ac.be

Keywords:protein crystallization; 1-fructan exohydrolase IIa; glycosyl hydrolase

About 15% of flowering plants use fructans, fructose based oligo- or polysaccharides, as a storage carbohydrate instead of starch or sucrose [1]. In addition, fructans are recognized to enhance cold and drought tolerance of plants. Food industries are interested in fructans for their different health-promoting effects. However, fructan degradation causes an important drawback for industrial harvesting. Fructan exohydrolase (FEH), a glycosyl hydrolase, catalyzes this breakdown. FEH belongs to family 32 of the glycosyl hydrolases, a classification based on general amino acid sequence similarities [2]. At present, no structural information is available for any member of this family. Therefore, elucidating the structure of FEH can not only contribute to a better understanding of its catalytic mechanism, but can also provide a model for the other enzymes of family 32. Consequently, 1-FEHIIa from Chicory (*Cichorium intybus*) [3] has been crystallized using the hanging drop vapor diffusion method [4]. The structure was determined by the Single Anomalous Dispersion method to a resolution of 2.35 Å. The crystals are tetragonal, belonging to space group P4₁2₁2. The structure comprises an N-terminal five fold β-propeller domain followed by a second domain existing of 2 β-sheets. The active site is located completely in the β-propeller structure and is formed by highly conserved amino acids within the glycosyl hydrolase family 32. The 2 β-sheets domain is thought to be important for fructan binding.

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