# Modular Assembly of the Cellulosome Revealed by X-Ray Crystallography

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*Clostridium thermocellum* is an anaerobic bacterium isolated from hot springs which converts hemicellulose into ethanol. These microorganisms express multienzyme complexes dedicated to the degradation of the plant cell wall. These complexes (cellulosomes) are composed of modules assembled by an integrating protein (scaffoldin), composed of several type I cohesins, which bind type I dockerins. A type II dockerin of the scaffoldin binds to a type II cohesin and anchors the whole complex to the cell. Other modules named Carbohydrate Binding Modules (CBM), are responsible for adherence to the substrate.

The crystal structure of type I cohesin-dockerin complex was solved to 2.2 Å and revealed for the first time how protein-protein recognition is achieved in the complex [1]. The 2.5 Å crystal structure of the type II cohesion, solved by MIR/MAD will be described. Subtle differences between type I and type II cohesins give insight into the structural determinants of cohesin-dockerin specificity. We will also report the 1.98 Å structure (MAD-SeMet) of the family 11 CBM belonging to a cellulosomal enzyme. The structure of the CBM11 reveals a concave side that forms a potential carbohydrate binding cleft [2].

[1] Carvalho A.L., et al., *Proc. Natl. Acad. Sci. USA*, 2003, **100**, 13809-14. [2] Carvalho A.L., et al., *J. Biol: Chem.*, 2004, **279**, 34785-93.

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