

The use of Carbohydrate Binding Modules (CBMs) to elucidate the relationship between fibrillation, hydrolyzability, and accessibility of cellulosic substrates

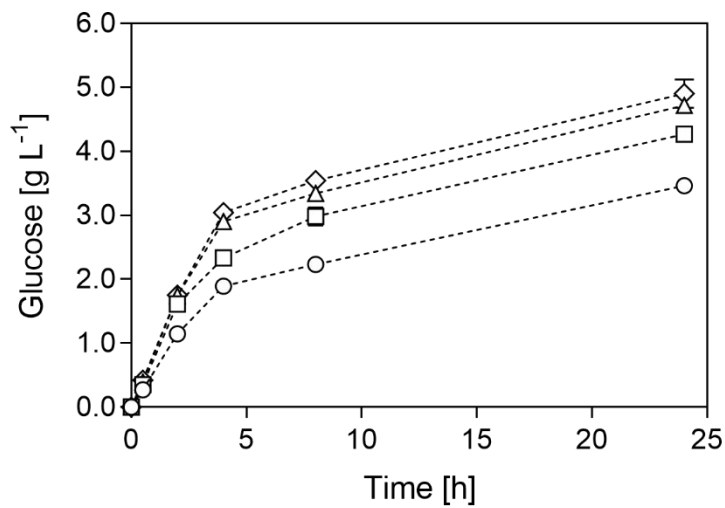
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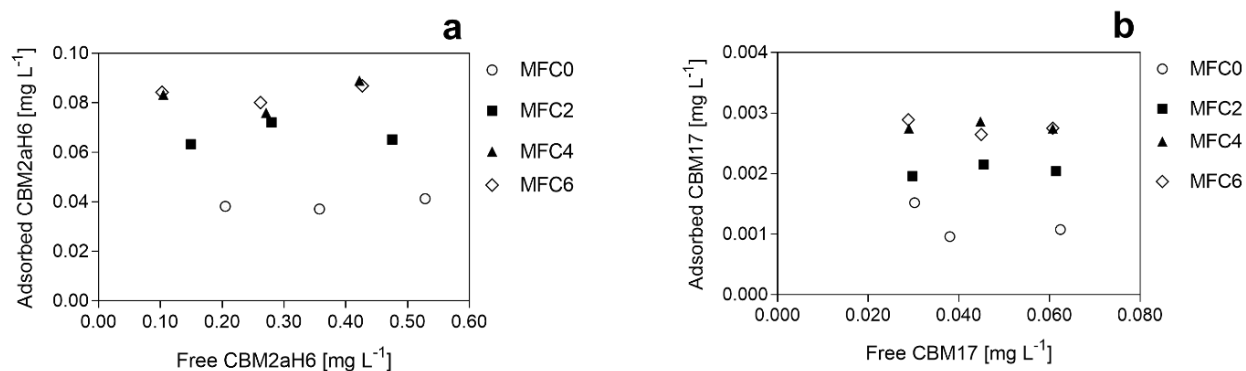
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S1: Time course of enzymatic hydrolysis reactions of MFC0 (0 kWh ton⁻¹, circles), MFC2 (500 kWh ton⁻¹, squares), MFC4 (1000 kWh ton⁻¹, triangles), and MFC6 (1500 kWh ton⁻¹, diamonds).

S2: Adsorption of CBM2a on increasingly refined substrates **b)** Adsorption of CBM17 on increasingly refined substrates



Supplementary Figure S1: Time course of enzymatic hydrolysis reactions of MFC0 (0 kWh ton⁻¹, circles), MFC2 (500 kWh ton⁻¹, squares), MFC4 (1000 kWh ton⁻¹, triangles), and MFC6 (1500 kWh ton⁻¹, diamonds). All hydrolysis reactions were performed with a substrate and enzyme loading of 10 g dry mass substrate per L and 5 FPU per g dry mass substrate, respectively. Data represent mean values of 2 independent experiments. Error bars show the spread.



Supplementary Figure S2: a) Adsorption of CBM2a on increasingly refined substrates b)

Adsorption of CBM17 on increasingly refined substrates: MFC0 (0 kWh ton⁻¹, circles), MFC2 (500 kWh ton⁻¹, squares, MFC4 (1000 kWh ton⁻¹, triangles), and MFC6 (1500 kWh ton⁻¹, diamonds). CBM2a binding indicates accessible crystalline cellulose. CBM17 binding indicates accessible paracrystalline cellulose.