Supplementary Online Material

Table S1. Thermodynamic parameters of CBM monomer-polysaccharide interactions as determined by ITC.

CBMs	Ligand	K_a (M^{-1})	ΔH (kcal/mol)	TΔS (kcal/mol)	Number of binding sites
CBM4-2	FAX	$4.6 \pm 0.2 \times 10^4$	-5.5 ± 0.1	0.9	1.0
CBM X-2	FAX	Too low to determine			
CBM G-4	FAX	No binding			

Table S2. Comparison of CBM diffusion in buffer obtained by two experimental techniques. D_{ref} is derived from FRAP experiments (mean values and standard deviations from at least 5 measurements, for each probe) and D_{th} is derived from R_H calculated from light scattering experiments (see Table 1), both for monomeric and dimeric CBMs.

	D_{ref} ($\mu m^2 \times s^{-1}$)	D_{th} ($\mu m^2 \times s^{-1}$)	Variation between D_{ref} and D_{th}
Monomeric CBMs	96.2 ± 7.9	97.3	+1.1%
Dimeric CBMs	65.1 ± 3.2	63.0	-3.2%

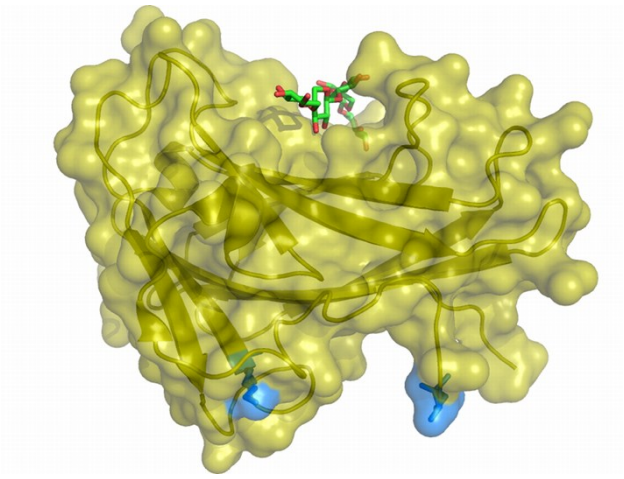

Figure S1. 3D structure of the monomeric CBM X-2. CBM (yellow) is complexed with a xylopentaose (green; PDB ID: 2Y6L), the location of the amino groups (N-terminal residue and Lys55) that can be labelled by fluorescent dyes is indicated (blue). These functions are located on the side opposite to the carbohydrate binding site (situated on top of the molecules in this projection), as indicated by the presence of the xylopentaose ligand.

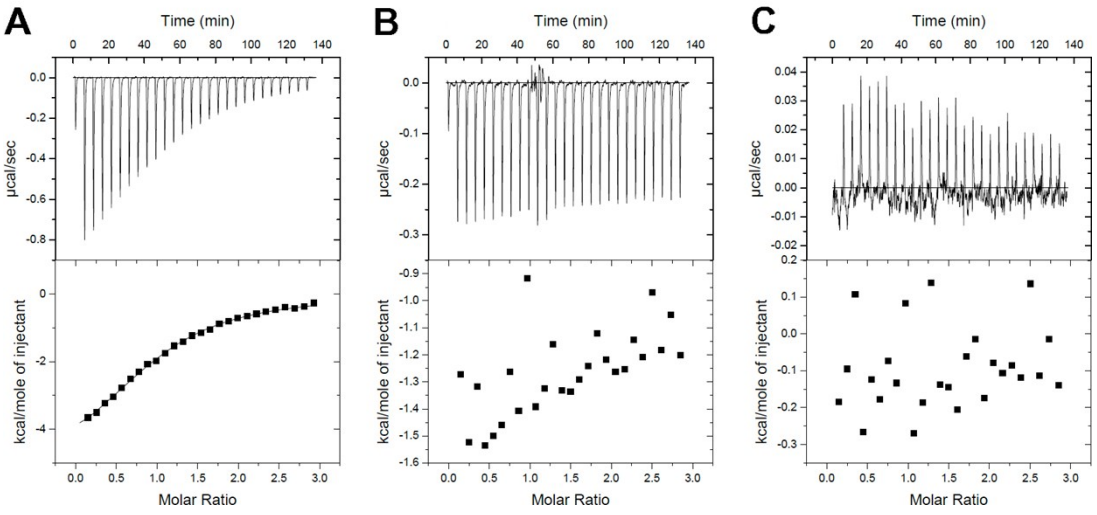

Figure S2. Binding of CBMs to FAX measured by ITC. (A) CBM4-2, (B) CBM X-2 and (C) CBM G-4. Only CBM4-2 interacts substantially to FAX.

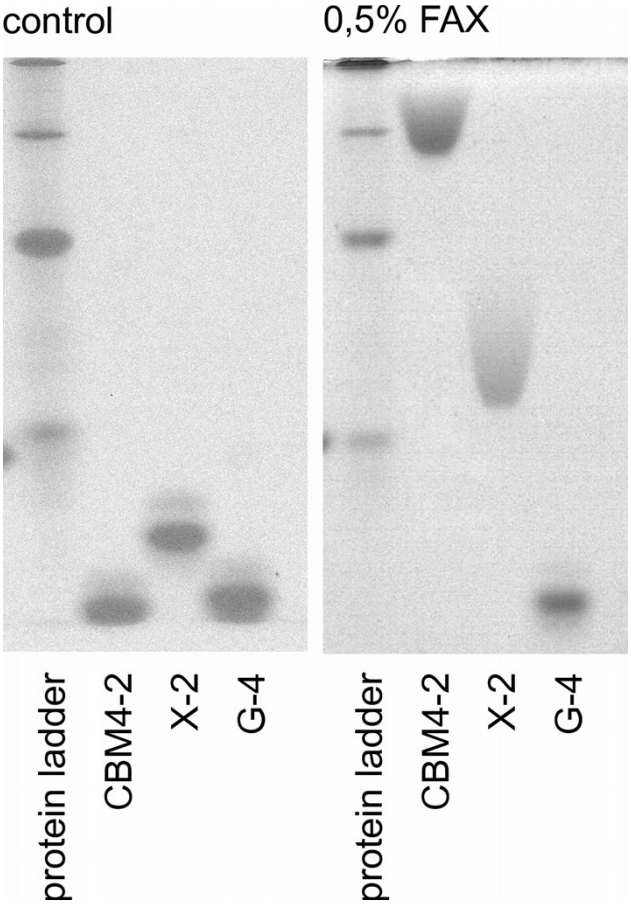

Figure S3. Binding of CBMs to FAX measured by AE. Migration in gels containing 0.5% FAX is compared to migration in a control gel with no polysaccharide present. Monomeric CBM4-2 and CBM X-2 are retained in the gel containing FAX. Monomeric CBM G-4, a CBM with no affinity for carbohydrates, is not retained at all in the polysaccharide gel.