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**Supporting information for article:**

**Expression, purification, crystallization and preliminary X-ray analysis of CttA, a putative cellulose-binding protein from *Ruminococcus flavefaciens***

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**Figure S1** The sequence alignment of the carbohydrate-binding moieties of the *R. flavefaciens* CttA sequences from the six different strains generated by the software packages *mega4* (Tamura *et al.*, 2007) and *BOXSHADE* (Hofmann & Baron, *unpubl.*). CttA5 has an insert of about 100 amino acid residues in the carbohydrate binding moiety between the residues highlighted in yellow.

**Table S1** Pair-wise sequence identities between the carbohydrate binding moieties of the *R. flavefaciens* CttA used in the sequence alignment in Figure S1.

The corresponding GenPept sequence IDs for each CttAs is given in the first column. The residue ranges of the part of the CttAs used in the sequence comparison are given in the third column. CttA1 has an extra long Thr-Ser-rich linker region, whereas CttA5 has an insert of about 100 amino acid residues in the carbohydrate binding moiety (between the residues highlighted in yellow in Figure S1), and CttA6 has a 60 amino acid residues insert at the N-terminus compared to the others. CttA1 is from *R. flavefaciens* strain FD-1, CttA2 from strain 17, CttA3 from strain C94 and CttA6 from strain MC2020. CttA4/5 are as yet unresolved.

	Length	Residue range	CttA1	CttA2	CttA3	CttA4	CttA5	CttA6
CttA1 WP_009986661.1	803	32 to 425	100%	43%	39%	37%	25%	30%
CttA2 WP_019678984.1	738	31 to 409		100%	49%	47%	32%	28%
CttA3 WP_028518574.1	736	30 to 413			100%	45%	30%	29%
CttA4 WP_028521707.1	699	31 to 414				100%	30%	35%
CttA5 WP_028516030.1	838	31 to 540					100%	22%
CttA6 WP_031559918.1	769	98 to 461						100%