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Supporting information for article:

Expression, purification and crystallization of a novel carbohydrate-binding module from *Ruminococcus flavefaciens* cellulosome

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(a)

CBM-Rf1	APLADGEKLYGKKSEGTVTFET-KAIGDNAFVEIKTGADTGF<small>MNGCLGFS</small>--ESIDGKNY	57
WP_022411635	-TTEGIHAKITEDSGYNISFAPKSMGKTVYLVEANSNVAFANGCLGV--ATVDGTDY	57
WP_021680671	-EGKGEAAKIVADSGYNISFK-QSIGNSVDLTFLSDDVS KANGCIGIS --ANVDGVDY	56
WP_009986452	ADPNKSFAKLSNAEGNVNIFP--EASQTVYLRIDLPDDCTYANGGLGV--IPVDGKY	56
WP_022050916	-IENAIMGDIKKDGSTVKVIFD-RSMGKEVHLIVLDLDDSLGYANGCVGVS--VKVDGVDY	56
WP_022428282	QPENGTAGQIKKSTNGYTITFD-RAMEDEVLVLDAKSPVNANGCGLGV--VTVDGTDY	57
EWM52390	SNVSESDKIYGDNGSGTVNFG-TSIGETA <small>F</small> VDFQFAGNTNF <small>MNGCLGFS</small> --PQLNGKSY	57
WP_019680477	SNVSESDKIYGDNGSGTVNFG-TSIGETA <small>F</small> VDFQFAGNTNF <small>MNGCLGFS</small> --PQLNGKSY	57
WP_024860388	ANVSESDKIYGDNGNGTVNFG-TSIGETA <small>F</small> VDFQFAGNTNF <small>MNGCLGFS</small> --PQLNGKSY	57
WP_022495183	VILKKSDWVKGDVLPTGTISFD-QAIGDKLKLEVEVDEKAGYVNGCIGFSVTDTSTGKY	59
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CBM-Rf1	WVAYVWQTKKSDTISIDMSSPVQIAEIIGTE-TQEVTDA <small>D</small> TICKLTDKIKTEKSALLQW	116
WP_022411635	WVSYKWEISKSGTISVLDKDVS--YNIITYNNGKDTVTDEDLIAKIVEVVKKQTDMVQIW	115
WP_021680671	WLNYKWLDSTDEVTAKLDKP---YNIITYNNGKDEVTDADMIIKISDEAIKQKNAQVQIW	113
WP_009986452	WANVKWEATASGDKVVDLIDNL--LNVTL--GTD A VEDEDIAAVKEALVKQTD F QGQVW	112
WP_022050916	WVSYKWEASKSDDVTVSLDADN-VYNVTFNNGSGTVKADQIAKIAEEAAQKEKEAQFQVW	115
WP_022428282	WVSYKWEIASGNGQDVAVDLNT-PTEASTNNNGKDKVTD P DLAKIAEEAAKAQKTAEVQIW	116
EWM52390	WVSYVWEAKKSGTITLDMMNPQVMDVSNEP-AEAVTDSNVKKQLIEMIKKEKSALLQAW	116
WP_019680477	WVSYVWEAKKSGTITLDMMNPQVMDVSNEP-AEAVTDSNVKKQLIEMIKKEKSALLQAW	116
WP_024860388	WVSYVWEAKKSGIITLDMMNPQVMDVSTEP-SEA V TADVKKQLIDMIKNEKSALLQAW	116
WP_022495183	WISYKWEASASDTITINMNSPFQIVDVTDSENTIDVEDEELREKLIGIVKSSKSASI QFW	119
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CBM-Rf1	YASDKTGKQIDPADSASESIEVYIPSA	143
WP_022411635	WANDGPESIATSN--VVLTDAYLPES	140
WP_021680671	WVANGAGDTLESSN--VKLTGAYLPKS	138
WP_009986452	YAANG-ADALDSTDG-VYISAAYIKKG	137
WP_022050916	WANDKEGEKD TT K--ATLVAAYLPDE	140
WP_022428282	WANDAGGKETATSN--VTLVGAYLPNK	141
EWM52390	YASDKSGKEITPPASGAESIKAFI SS	143
WP_019680477	YASDKSGKEITPPASGAESIKAFI SS	143
WP_024860388	YASDKSGKEITPPASGAESIKAFIVAS	143
WP_022495183	WASDASGEELSPASDYATLVSASVCAA	146
.. : :	

(b)

Figure S1 (a) Schematic showing the modular architecture of the full-length *Ruminococcus flavefaciens* glycoside hydrolase family 5 containing protein. SP is the N-terminal signal peptide, GH5_4 the catalytic module belonging to glycoside hydrolase family 5 and CBM-Rf1 is the putative carbohydrate binding module with the dockerin module (DOC) at the C-terminal. The CBM-Rf1 construct used in this study covers the range 438 to 586. The linker regions between the defined modules are expected to be flexible. (b) Sequence comparison of CBM-Rf1 family members. The aromatic amino acids conserved between all CBMs are shaded in yellow. The alignment was made using ClustalW2 (Thompson *et al.*, 1994).

Reference

Thompson, J. D., Higgins, D. G. & Gibson, T. J. (1994). *Nucleic Acids Res* **22**, 4673-4680.