

The hemicellulose-degrading enzyme system of the thermophilic bacterium *Clostridium stercorarium* – comparative characterisation and addition of new hemicellulolytic glycoside hydrolases

- Additional file 1 -

Broeker¹, Jannis (jannis.broeker@tum.de), Mechelke¹, Matthias (matthias.mechelke@tum.de), Baudrexl¹, Melanie (melanie.baudrexl@tum.de), Mennerich, Denise (denise.mennerich@tum.de), Hornburg^{2,3}, Daniel (hornburg@stanford.edu), Mann³, Matthias (mmann@biochem.mpg.de), Schwarz¹, Wolfgang H. (wolfgang.schwarz@tum.de), Liebl¹, Wolfgang (wliebl@wzw.tum.de), Zverlov^{1,4*}, Vladimir V. (vladimir.zverlov@tum.de)

¹ Department of Microbiology, TUM School of Life Sciences Weihenstephan, Technical University of Munich, Emil-Ramann-Str. 4, 85354 Freising, Germany

² Present address: School of Medicine, Stanford University, 94305 Stanford, CA, USA

³ Max Planck Institute of Biochemistry, Am Klopferspitz 18, 82152 Martinsried, Germany

⁴ Institute of Molecular Genetics, Russian Academy of Science, Kurchatov Sq. 2, 123182 Moscow, Russia

* Corresponding author: Dr. Vladimir V. Zverlov

email: vladimir.zverlov@tum.de, Tel.: +49-8161-715474

Table S2 Polysaccharide and *p*-nitrophenyl substrates including the final concentration in enzymatic assays.

polysaccharides	final conc.	<i>p</i> NP-glycosides	final conc.
arabinan	0.5% w/v	α -L-arabinofuranoside	4 mM
arabinoxylan (wheat, soluble)	0.5% w/v	α -D-glucopyranoside	4 mM
arabinoxylan (wheat, insoluble)	0.5% w/v	β -D-glucopyranoside	4 mM
4-O-methyl-glucuronoxylan	0.5% w/v	α -D-galactopyranoside	4 mM
xylan (birch)	0.5% w/v	β -D-galactopyranoside	4 mM
xylan (oat spelt)	0.5% w/v	α -D-mannopyranoside	4 mM
xyloglucan	0.5% w/v	β -D-mannopyranoside	4 mM
avicel	0.25% w/v	α -L-rhamnopyranoside	4 mM
β -glucan (barley)	0.5% w/v	α -D-xylopyranoside	4 mM
curdlan	0.5% w/v	β -D-xylopyranoside	4 mM
laminarin	0.5% w/v	β -D-glucuronide	4 mM
lichenin	0.5% w/v	N-acetyl- β -D-glucosaminide	4 mM
pachyman	0.5% w/v		
pullulan	0.5% w/v		
arabinogalactan (larch)	0.5% w/v		
galactan (potato)	0.5% w/v		
galactan (lupin)	0.5% w/v		
pectic galactan (potato)	0.5% w/v		
pectic galactan (lupin)	0.5% w/v		
polygalacturonic acid	0.5% w/v		
mannan	0.5% w/v		
mannan (ivory nut)	0.5% w/v		
galactomannan (guar)	0.5% w/v		
glucomannan (konjac)	0.125% w/v		
gum arabic (acacia)	0.5% w/v		
inulin (dahlia tubers)	0.5% w/v		
sinistrin	0.5% w/v		
rhamnogalacturonan I	0.5% w/v		
chitosan	0.5% w/v		

The polysaccharides used in this study were purchased from: Megazyme (Bray, Ireland): arabinan, wheat arabinoxylan (soluble and insoluble), xyloglucan, barley β -glucan, pachyman, arabinogalactan, potato and lupin galactan and pectic galactan, mannan, ivory nut mannan, galactomannan, glucomannan and rhamnogalacturonan I; Sigma-Aldrich (St. Louis, USA): birch xylan, oat spelt xylan, lichenin, polygalacturonic acid, gum arabic, inulin and chitosan; Serva electrophoresis (Heidelberg, Germany): curdlan and avicel; ICN Biochemical (Irvine, USA): pullulan; Alfa Aesar (Ward Hill, USA): laminarin; and Fresenius Kabi (Graz, Austria): sinistrin. Glucuronoxylan were bought from Sigma-Aldrich and Carbosynth (Compton, GB). The *p*NP-glycosides were purchased from: Carbosynth: α -L-arabinofuranoside, β -D-galactopyranoside, α -D-mannopyranoside, β -D-mannopyranoside and α -D-xylopyranoside; Sigma-Aldrich: α -D-glucopyranoside, α -L-rhamnopyranoside, β -D-xylopyranoside and β -D-glucuronide; Alfa Aesar: β -D-glucopyranoside; Serva electrophoresis: α -D-galactopyranoside; and AppliChem (Darmstadt, Germany): N-acetyl- β -D-glucosaminide.

Table S3 Glycoside hydrolase (GH) families present in the *C. stercorarium* genome.

selected	GH2 (5), GH3 (5), GH9, GH10 (4), GH11, GH26, GH27, GH28 (2), GH29, GH31, GH35, GH38, GH39, GH43 (7), GH51, GH53, GH67, GH78, GH88, GH95, GH105 (5), GH115, GH127 (2), GHnc (4)
excluded	GH4, GH13 (5), GH15, GH18 (3), GH23 (2), GH families: GH36 (2), GH48, GH94 (2), GH112, GH130

Enzymes within 24 of 34 GH families were selected and produced in *E. coli*. The number of enzymes is indicated in brackets behind the GH family, if more than one enzyme is present.

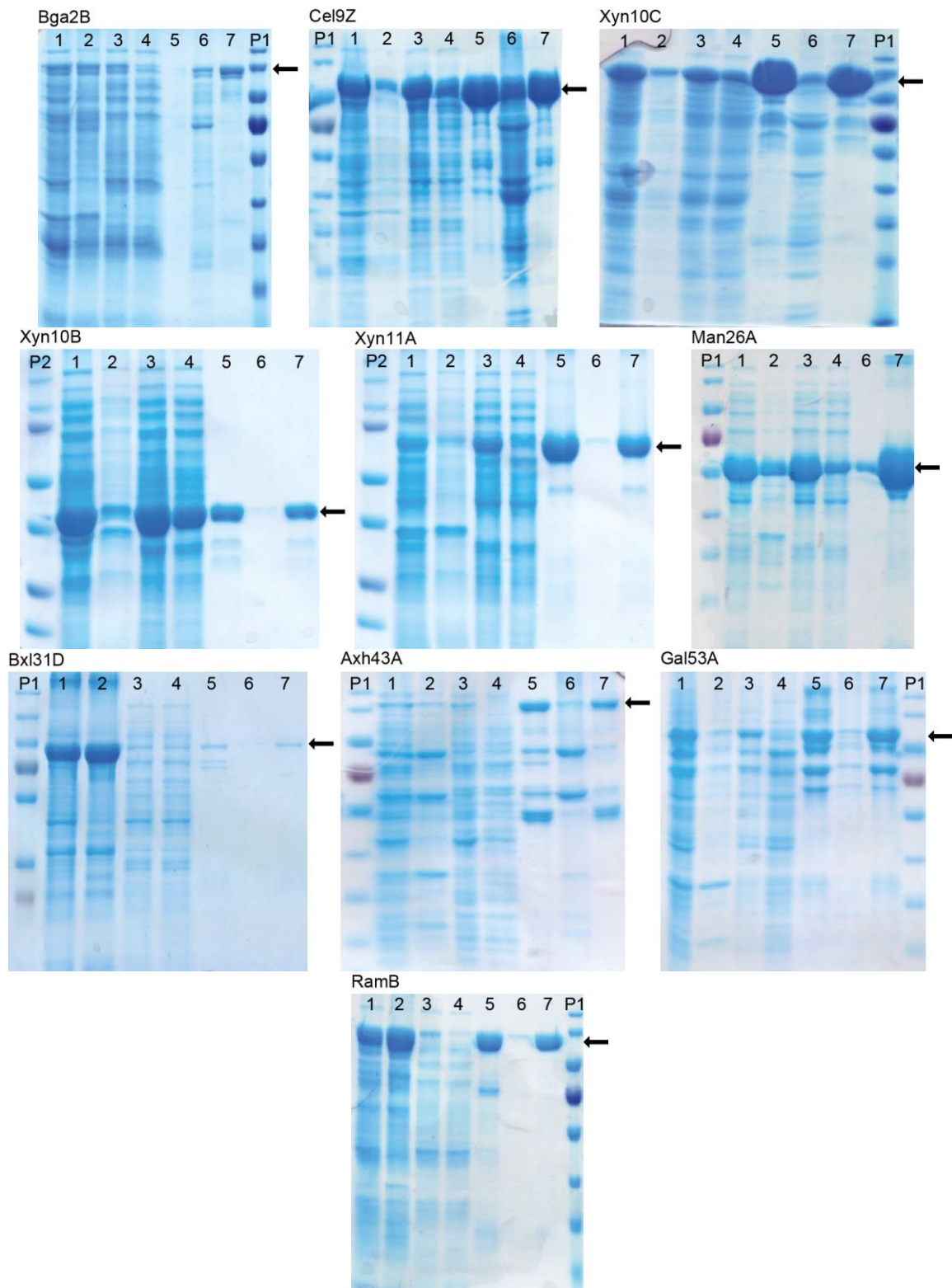


Figure S1 SDS-PAGEs of 10 examples of the 50 *C. stercorarium* proteins recombinantly produced by *E. coli* and purified by IMAC. Purification steps comprises: crude cell extract (1), resuspended cell extract pellet (2), supernatant of the cell extract after centrifugation (3), flow through of IMAC (4) eluate of the IMAC (5), resuspended precipitate of the heat denaturation (6), purified protein solution (7), protein standards with 180, 130, 100, **70**, 55, 40, 35 and 25 kDa (P1) or 250, 150, 100, **75**, 50, 37, **25** and 20 kDa.

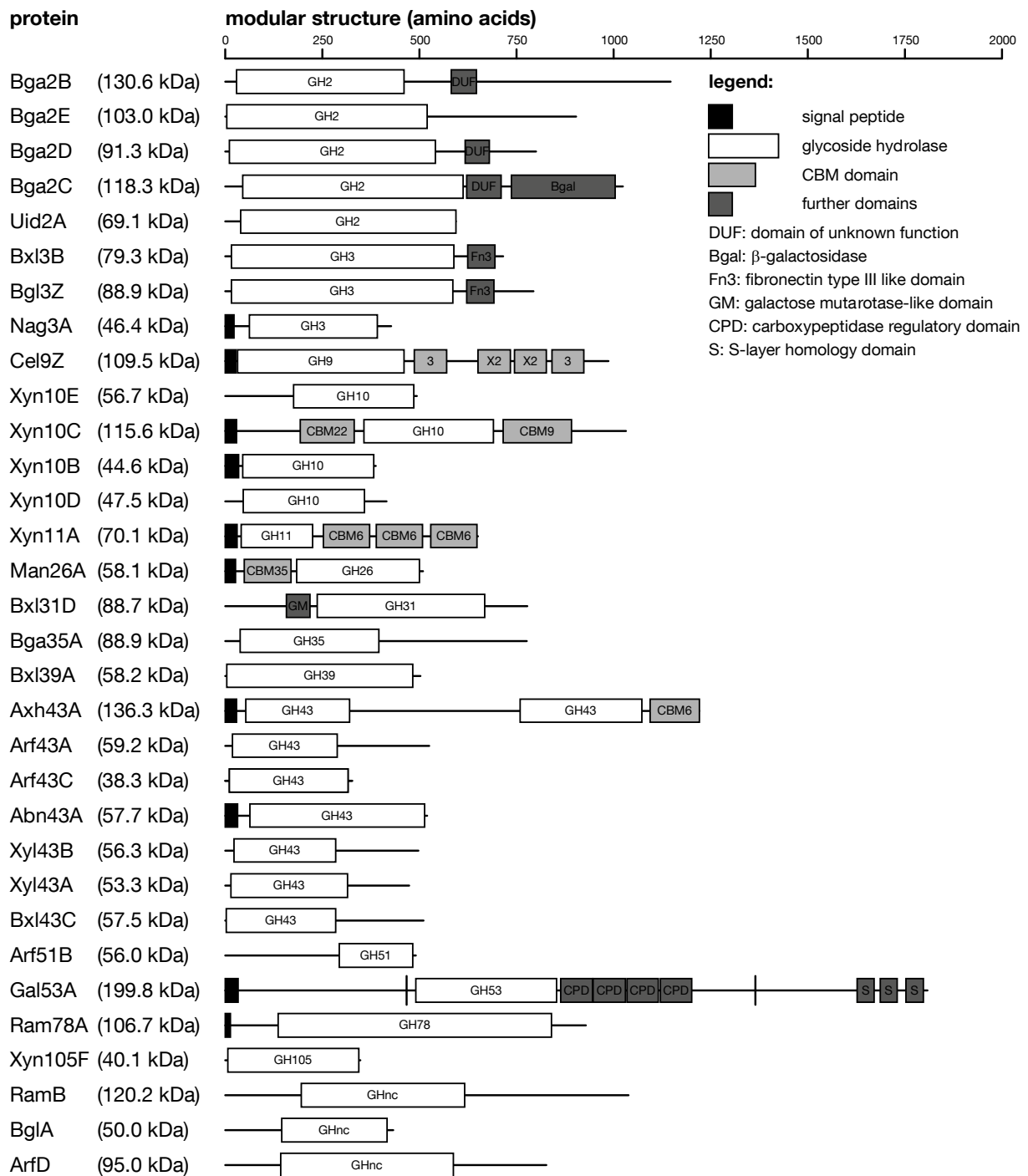
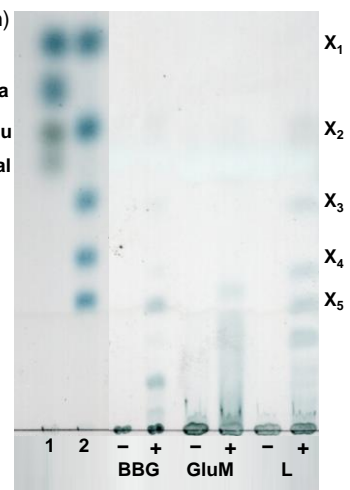
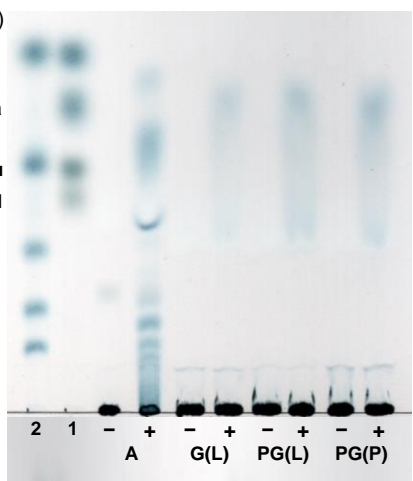
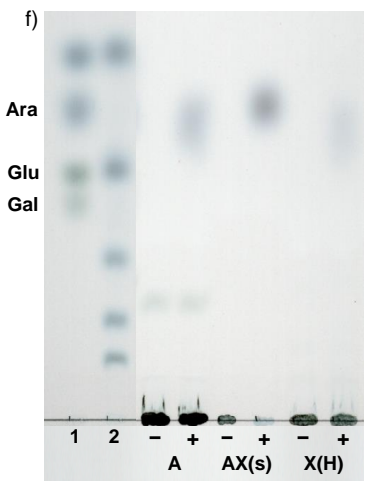
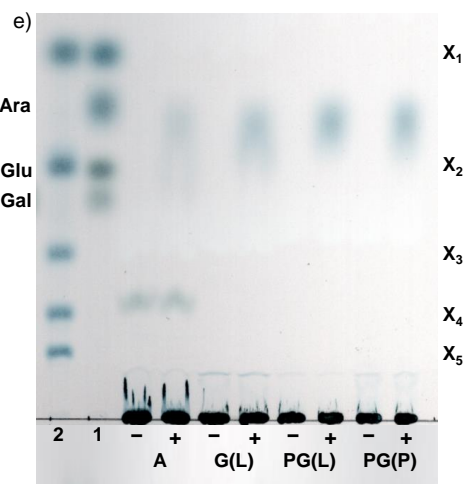
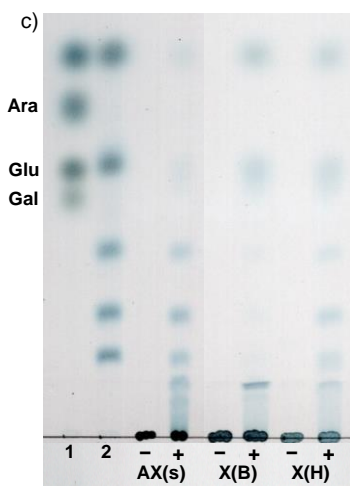
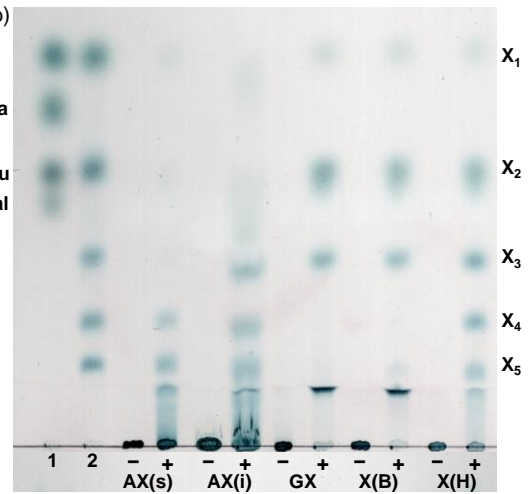
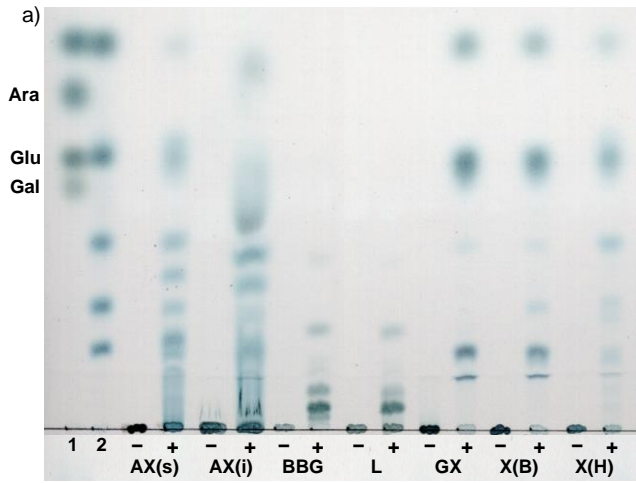


Figure S2 Schematic structure of the glycoside hydrolases with proven activity from *C. stercorarium*. Molecular masses are given in brackets. The size of each enzyme and domain is scaled according to the corresponding amino acid chain length. Classification of GH and CBM modules were obtained from the CAZy database [40]. Domain structure was obtained from the Pfam database [58]. The CAZy database lists only the two CBM3 modules for Cel9Z whereas the four listed CBM61 modules of Gal53A and the second CBM22 module of Xyn10C could not be identified using the Pfam database. Protein Gal53A was shortened in PCR at indicated (I) sites.

Table S4 Studied enzymes in the secretome or intracellular proteome of *C. stercorarium* analysed by LC-MS/MS.

protein name	iBAQ SU	rank SU	iBAQ PE	rank PE
Bga2B	9,47	32 %	12,32	21 %
Bga2E	6,35	67 %	7,47	80 %
Bga2D	3,22	93 %	6,37	88 %
Bag2C	6,66	63 %	11,37	30 %
Uid2A	8,26	44 %	11,85	26 %
Bxl3B	7,12	57 %	8,48	69 %
Bgl3Z	11,16	16 %	12,67	18 %
AGC67350.1	3,44	92 %	8,97	63 %
AGC68204.1	6,40	66 %	9,54	56 %
Nag3A	4,80	81 %	7,88	75 %
Cel9Z	16,11	1 %	4,95	96 %
Xyn10E	5,48	75 %	8,98	63 %
Xyn10C	11,38	14 %	9,20	60 %
Xyn10B	9,07	35 %	-	-
Xyn10D	10,63	19 %	13,26	13 %
Xyn11A	14,27	3 %	-	-
Man26A	6,51	65 %	5,31	95 %
AGC68671.1	8,18	45 %	10,19	46 %
AGC67830.1	9,88	28 %	11,90	25 %
AGC67947.1	11,05	17 %	12,61	18 %
AGC67128.1	6,57	64 %	8,43	70 %
Bxl31D	-	-	5,92	91 %
Bga35A	6,28	68 %	8,86	64 %
AGC68033.1	6,11	69 %	7,66	78 %
Bxl39A	8,77	38 %	12,14	23 %
Axh43A	-	-	-	-
Arf43A	10,04	26 %	11,40	30 %
Arf43C	-	-	4,39	97 %
Abn43A	5,17	77 %	6,98	84 %
Xyl43B	6,57	64 %	10,25	46 %
Xyl43A	9,34	32 %	11,84	26 %
Bxl43C	5,71	73 %	9,49	57 %
Arf51B	10,46	21 %	12,99	15 %
Gal53A	7,64	52 %	5,46	93 %
AGC69355.1	6,63	63 %	10,79	38 %
Ram78A	2,46	96 %	7,70	77 %
AGC69452.1	8,94	36 %	11,15	33 %
AGC67127.1	-	-	3,42	99 %
Xyn105F	-	-	-	-
AGC67892.1	-	-	-	-
AGC67946.1	9,49	31 %	12,18	22 %
AGC68044.1	5,05	78 %	9,52	56 %
AGC68046.1	-	-	9,49	57 %
AGC67967.1	7,90	50 %	10,48	42 %
AGC67053.1	7,63	52 %	10,54	41 %
AGC67292.1	0,86	100 %	3,55	99 %
RamB	1,80	98 %	6,09	90 %
BglA	-	-	-	-
AGC69032.1	4,62	83 %	8,64	67 %
ArfD	4,30	86 %	7,95	74 %

C. stercorarium was grown in GS2 medium with 0.5% w/v cellobiose for 24 h. The protein length normalised log₂ protein intensities (iBAQ) and the percentage rank of the protein in the secretome (SU) and intracellular proteome (PE) are given. Some proteins weren't detected (-).



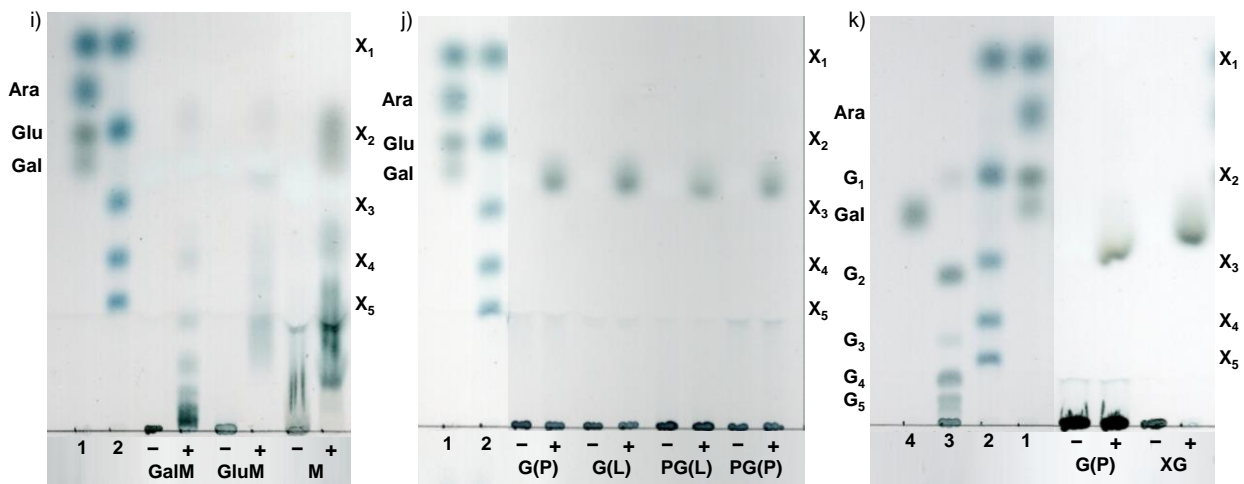


Figure S3 Hydrolytic products of different polysaccharides analysed by Thin-layer chromatography (TLC). Polysaccharides were hydrolysed by a) Xyn10C, b) Xyn11A, c) Xyn10D, d) Arf51B, e) Arf43C, f) Axb43A, g) Abn43A, h) Cel9Z, i) Man26A, j) Bga35A, k) Bga2B. The experiments were performed overnight (16 h) at pH 6.5 and 60 °C with 5.0 mg/L enzyme and 0.5% substrate in 0.1 M MOPS reaction buffer. Arabinan (A), soluble wheat arabinoxylan (AX(s)), insoluble wheat arabinoxylan (AX(i)), barley β -glucan (BBG), galactan lupin (G(L)), galactan potato (G(P)), galactomannan (GalM), glucomannan (GluM), glucuronoxylan (GX), lichenin (L), mannan (M), pectic galactan lupin (PG(L)), pectic galactan potato (PG(P)) xylan (birch) (X(B)), xylan (oat spelt) (X(H)), xyloglucan (XG) negative control (-), hydrolysate (+), standards: xylose, arabinose, glucose, galactose (1), xylose, xylobiose, xylotriose, xylotetraose, xylopentatose (2), glucose, cellobiose, cellotriose, cellotetraose, cellopentaose (3), galactose (4).

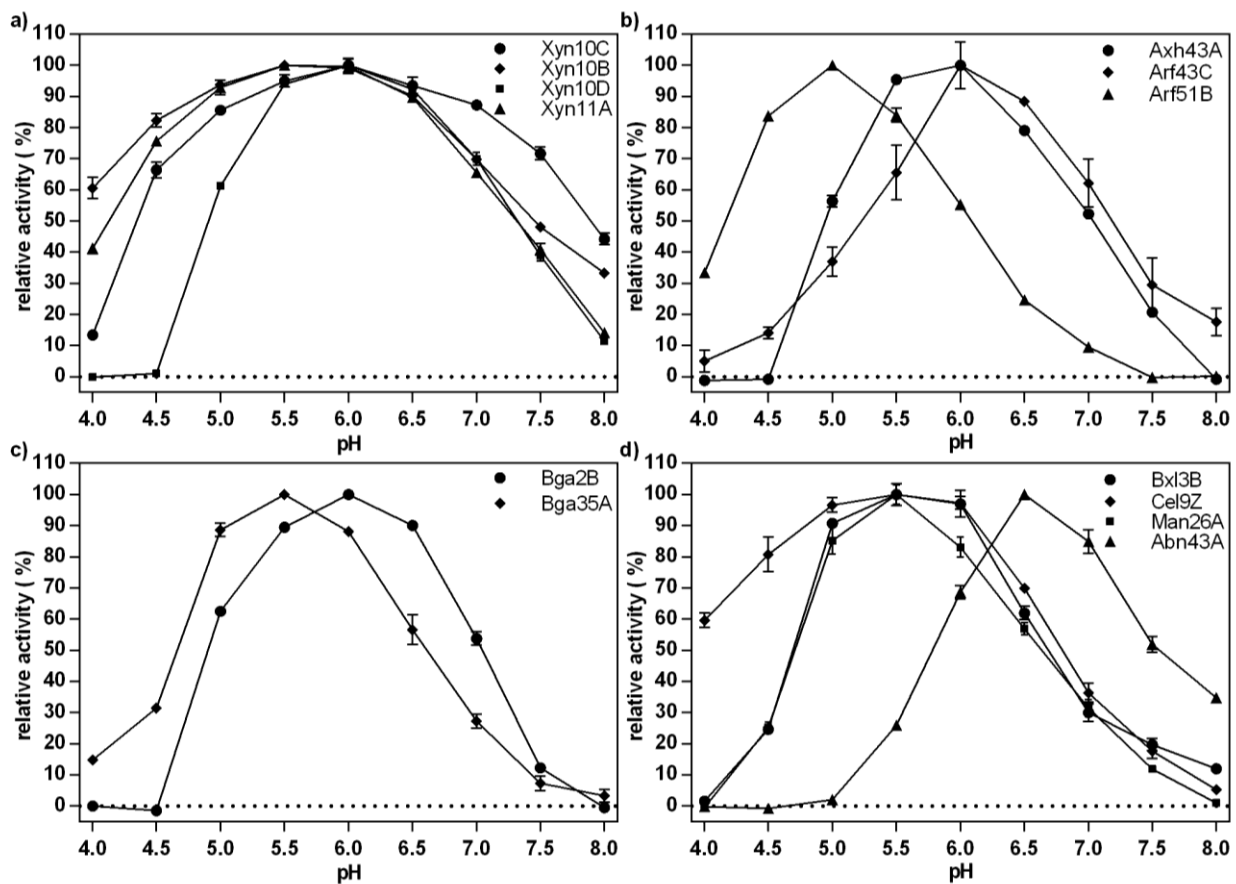


Figure S4 Relative activity of characterised enzymes at different pH. pH profiles of a) xylanases Xyn11A & Xyn10B-D, b) Axb43A and α -arabinofuranosidases Arf51B & Arf43C, c) β -galactosidases Bga3B & Bga35A, d) Bxl3B, Cel9Z, Man26A, and Abn43A. Experiments were performed for 30 min, 60 min (Bga2B, Bga35A and Arf51B) or 120 min (Bxl3B) at 60 °C in 0.1 M citrate-phosphate reaction buffer with 0.05 mg/L Xyn11A, 0.1 mg/L Xyn10B, 0.5 mg/L Xyn10C & Cel9Z, 0.6 mg/L Man26A, 1.0 mg/L Abn43A, 1.5 mg/L Axb43A, 5.0 mg/L Xyn10D & Arf43C, 8.0 mg/L Bga2B, 10.0 mg/L Arf51B & Bga35A and 24.0 mg/L Bxl3B.

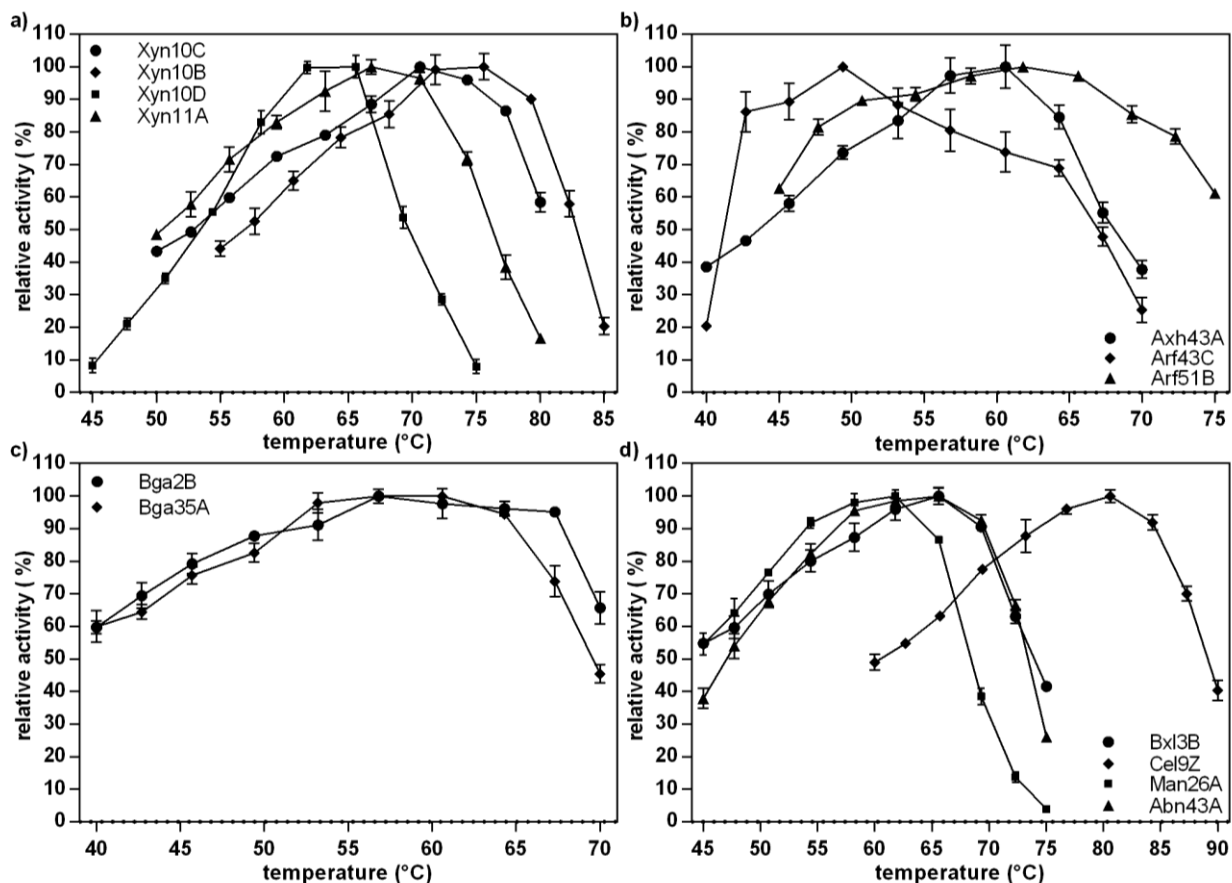


Figure S5 Relative activity of characterised enzymes at different temperatures. Temperature profiles of a) xylanases Xyn11A & Xyn10B-D, b) Axh43A and α -arabinofuranosidases Arf51B & Arf43C, c) β -galactosidases Bga2B & Bga35A, d) Bxl3B, Cel9Z, Man26A, and Abn43A. Experiments were performed for 30 min, 60 min (Bga2B, Bga35A and Arf51B) or 120 min (Bxl3B) at the optimal pH of each enzyme in in 0.1 M citrate-phosphate reaction buffer with 0.05 mg/L Xyn11A, 0.1 mg/L Xyn10B, 0.5 mg/L Xyn10C & Cel9Z, 0.6 mg/L Man26A, 1.0 mg/L Abn43A, 1.5 mg/L Axh43A, 5.0 mg/L Xyn10D & Arf43C, 8.0 mg/L Bga2B, 10.0 mg/L Arf51B & Bga35A and 24.0 mg/L Bxl3B.

References:

38. Architecture et Fonction des Macromolécules Biologiques: Carbohydrate-Active Enzymes database. <http://www.cazy.org/> (2014). Accessed 24 Jul 2014.
58. European Bioinformatics Institute: Pfam database. <https://pfam.xfam.org/> (2017). Accessed 24 Jul 2017.