Structural and functional characterization of a bifunctional GH30-7 xylanase B from the filamentous fungus *Talaromyces cellulolyticus*

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Figure S1. 2D gel electrophoresis analysis (pH4-5) of *T. cellulolyticus* CF-2612 culture grown on birchwood xylan.

CF-2612 was grown on a medium (pH 4.0) containing, per liter: 50 g birchwood xylan, 24 g KH₂PO₄, 1 g Tween 80, 5 g (NH₄)₂SO₄, 1.2 g MgSO₄·7H₂O, 0.01 g ZnSO₄·7H₂O, 0.01 g MnSO₄·6H₂O, 0.01 g CuSO₄·7H₂O, and 4.0 g urea, at 30 °C, 200 rpm, for 72 h in an Erlenmeyer flask. The major protein spots on the gel were treated by endoproteinase Lys-C and analyzed by HPLC peptide mapping. Proteins from the resulting peptide sequences were assigned using a draft genome sequence of *T. cellulolyticus* Y-94. Xyn30B was identified from two peptide sequences (SAEDYLS, FYAESGVPVTHL), and Xyn30A was from two peptide sequences (ATVPPRAVQVF and DFLEIL). Bxy, GH3 β -xylosidase; Cel7A, GH7 cellobiohydrolase I; Xyl10A, GH10 xylanase A; Xyl11A, GH11 xylanase A.



Figure S2. Characterization of purified Xyn30B.

Xylanase activity was measured in a reaction mixture containing purified Xyn30B and 10 mg mL⁻¹ beechwood xylan. (A) Optimal pH. Maximum activity is relatively taken as 100%. The reaction mixture was incubated at 40°C for 15 min in a pH range of 2.0–6.5. (B) Optimal temperature. Maximum activity is relatively taken as 100%. The reaction mixture was incubated at 35–60°C for 15 min in 50 mM sodium acetate (pH 4.0). (C) pH stability. The enzyme was preincubated in a pH range of 2.0–7.0 at 40°C for 30 min, and the residual activity was subsequently measured at 40°C for 15 min in 50 mM sodium acetate (pH 4.0). (D) Thermal stability. The enzyme was preincubated in 50 mM sodium acetate (pH 4.0) at 4–60°C for 30 min (open circle) or 24 hours (filled circle), and residual activity was measured at 40°C for 15 min.

Chain A

Asn60	Man β 1 — 4GlcNAc β 1 — 4GlcNAc β
Asn88	$\begin{array}{c} \text{Man } \alpha 1 < 3\\ \text{Man } \alpha 1 < 6 \end{array} \text{Man } \beta 1 - 4 \text{GlcNAc } \beta 1 - 4 \text{GlcNAc } \beta \\ \text{Man } \alpha 1 < 6 \end{array}$
Asn215	GlcNAc β
Asn334	Man β 1 — 4GlcNAc β 1 — 4GlcNAc β
Asn346	GlcNAc β1
Asn412	GlcNAc β 1 — 4GlcNAc β

Chain B

Asn60	Man $\alpha 1$ — 6Man $\beta 1$ — 4GlcNAc $\beta 1$ — 4GlcNAc β
Asn88	$\begin{array}{c} \text{Man } \alpha 1 < 3 \\ \text{Man } \beta 1 - 4 \text{GlcNAc } \beta 1 - 4 \text{GlcNAc } \beta \\ \text{Man } \alpha 1 - 3 \text{Man } \alpha 1 < 6 \end{array}$
Asn215	GlcNAc β
Asn334	Man β1 — 4GlcNAc β1 — 4GlcNAc β
Asn346	GlcNAc β 1 — 4GlcNAc β
Asn412	GlcNAc β 1 — 4GlcNAc β

Figure S3. *N*-linked carbohydrate moieties and structures in Xyn30B assigned by electron density map shown in Fig. S4.

Two molecules of Xyn30B in an asymmetric unit in the crystal are named as chain A and B.



Figure S4. Fo-Fc omit map (blue) for N-linked carbohydrate moieties, which is calculated without sugar residues, is contoured at 3.0σ .



Figure S5. Structural differences in the $\beta 2-\alpha 2$ loops of Xyn30B and *Ec*XynA.

The $\beta 2-\alpha 2$ loops of Xyn30B and *Ec*XynA are shown by red and blue, respectively. Asn-93 of Xyn30B is shown as a stick. Atoms are colored as follows: green, C of Xyn30B; white, C of *Ec*Xyn30A.

	29)																4(6				51
Xyn30B	Q	А	R	Y	Q	S	v	D	G	F	G	с	S	Q	Α	F	Q	R	А	Е	D	Ι	F
T.reesei XYN VI	G	S	К	F	Q	Q	Ι	D	G	F	G	F	S	Q	А	F	G	R	А	R	Е	F	Q
Xyn30A	L	Q	R	Υ	Q	Е	М	Ι	G	G	G	С	S	G	А	F	G	W	А	С	Q	Q	F
F.fujikuroi CCT73001	Ν	К	К	L	Q	v	Ι	D	G	F	G	v	S	Е	А	Y	G	н	А	К	Q	F	Q
T.reesei XYN IV	R	Q	т	Υ	Q	т	М	Ι	G	G	G	С	S	G	А	F	G	Ι	А	С	Q	Q	F
T.terrestris THITE 2123443	G	۷	R	Υ	Q	т	М	М	G	G	G	С	S	G	А	F	G	V	А	С	D	Q	Т
A.oligospora EGX45083	G	т	т	Υ	Q	т	Ι	Е	G	F	G	F	S	Q	А	F	G	R	А	v	Е	F	К
Bispore sp. XYLD	Ν	Е	Е	к	Q	Ι	V	D	G	F	G	F	S	Е	А	F	G	R	А	Е	Ν	V	F
F.fujikuroi CCT73045	Н	٧	R	Υ	Q	Е	L	D	G	F	G	А	S	Q	А	F	Q	R	А	Е	D	Ι	L
L.maculans CBX92400	V	Κ	т	Υ	Q	т	М	D	G	F	G	М	S	Е	т	F	Q	R	А	Ν	Q	М	Κ
L.maculans CBX93583	Т	К	G	Υ	Q	т	Ι	D	G	F	G	v	S	А	А	F	Q	R	А	Ν	L	Ι	V
L.maculans Xy138	V	К	т	Υ	Q	т	М	D	G	F	G	М	S	Е	т	F	Q	R	А	Ν	Q	М	К
P.comata VBB81111	S	R	т	F	Q	т	М	D	G	F	G	А	S	Е	А	F	Q	R	А	٧	т	М	К
P.comata VBB86450	т	R	т	F	Q	К	М	D	G	F	G	F	S	L	А	F	Q	R	А	Ν	L	Ι	т
S.lignohabitans	А	Q	т	Υ	Q	Е	Ι	D	G	F	G	F	S	Е	А	F	Q	R	А	Ν	D	L	Υ
T.purpureogenus AKH40280	К	۷	Q	F	Q	Е	V	D	G	F	G	А	S	Q	А	F	Q	R	А	Е	D	Ι	F
T.terrestris THITE 30409	G	т	Κ	Υ	Q	R	Ι	D	G	F	G	F	S	Q	А	F	G	R	А	А	Е	F	Q
T.thermophila AE055025	S	т	т	Υ	Q	R	Ι	D	G	F	G	т	S	Е	А	F	Q	R	А	v	Q	М	S
T.thermophila AEO57693	S	Q	т	Υ	Q	R	М	D	G	F	G	F	S	L	А	F	Q	R	А	Ν	L	Ι	т
A.albispora AXB42337	А	R	R	Н	Q	Ρ	Ι	D	G	F	G	F	S	Е	А	F	G	R	А	Е	Ι	М	R
A.derwentensis SDT08346	-	М	S	С	S	Ρ	Ι	D	G	F	G	F	S	Е	Н	F	G	R	А	т	Ι	М	Н
A.orientalis CAA11771	R	Н	S	L	Q	Ρ	Ι	D	G	F	G	F	S	Q	А	F	Q	R	А	А	R	Ι	R
N.gerenzanensis SBO93718	R	۷	R	н	Q	Е	Ι	D	G	F	G	Ι	S	Q	А	F	R	R	Ν	Е	L	L	Е
N.gerenzanensis SBO96059	G	۷	R	н	Q	т	Ι	D	G	F	G	Ι	S	т	А	F	R	R	G	Е	L	L	Κ
Nonomuraea sp. AQZ61832	S	Q	т	Н	Q	т	Ι	D	G	F	G	Υ	S	т	А	F	Q	R	А	т	L	V	Н
Nonomuraea sp. AQZ61834	Q	٧	R	н	Q	Е	Ι	D	G	F	G	Ι	S	т	А	F	R	R	Ν	Е	L	L	К
Nonomuraea sp. AQZ65470	R	۷	R	н	Q	Е	Ι	D	G	F	G	Ι	S	Q	А	F	R	R	Ν	Е	L	L	Κ
Plantactinospora sp. ASW57759	А	Q	т	н	Q	Ρ	Ι	D	G	F	G	Υ	S	Ι	А	F	Q	R	А	S	L	V	Н
S.bingchenggensis ADI10522	G	Q	R	Q	Q	Ρ	Ι	D	G	F	G	F	S	Q	А	F	Q	R	А	D	Ι	М	Н
S.hygroscopicus AQW50539	G	Q	Н	L	Q	Ρ	Ι	D	G	F	G	F	S	Q	А	F	Q	R	А	D	V	М	н
S.iranensis CDR10147	G	R	R	L	Q	Ρ	Ι	D	G	F	G	F	S	Q	А	F	Q	R	А	D	L	Μ	Н
S.lincolnensis ANS64779	S	Т	т	н	Q	Ρ	Ι	D	G	F	G	F	S	Е	н	F	G	R	А	D	Ι	М	R
S.lincolnensis AXG57013	S	Т	т	н	Q	Ρ	Ι	D	G	F	G	F	S	Е	Н	F	G	R	А	D	Ι	Μ	R
S.rapamycinicus AGP58059	G	R	Н	L	Q	Ρ	Ι	D	G	F	G	F	S	Q	А	F	Q	R	А	D	L	М	Н
S.venezuelae ALO06247	R	А	А	L	Q	Ρ	Ι	D	G	F	G	F	S	М	А	F	Q	R	А	D	L	L	н
S.venezuelae CCA60025	R	А	Е	L	Q	Ρ	Ι	D	G	F	G	F	S	М	А	F	Q	R	А	D	L	L	н
S.venezuelae CUM43504	R	А	А	L	Q	Ρ	Ι	D	G	F	G	F	S	М	А	F	Q	R	А	D	L	L	н
S.vietnamensis AJF69043	R	А	D	L	Q	Ρ	Ι	D	G	F	G	F	S	М	А	F	Q	R	А	D	L	L	н
Streptomyces sp. ASQ94399	G	Q	Н	L	Q	Ρ	Ι	D	G	F	G	F	S	Q	А	F	Q	R	А	D	V	М	Н
Streptomyces sp. AXE85427	S	т	R	н	Q	Ρ	Ι	D	G	F	G	Ι	S	Е	Н	F	G	R	А	Е	Ι	М	R
A.derwentensis SDT07978	Т	т	R	Υ	Q	R	Ι	D	G	F	G	Ι	S	Е	А	F	G	т	А	Ν	Q	L	R
BsXynC	S	А	Е	к	Q	v	Ι	R	G	F	G	G	Μ	Ν	Н	Ρ	А	W	А	G	D	L	т
EcXynA	Ν	V	Ν	Υ	Q	Ι	Ι	Q	G	F	G	G	Μ	S	G	V	G	W	Ι	Ν	D	L	т

Figure S6. Amino acid sequence alignment of GH30-7 enzymes.

Amino acid sequence alignment of the region around Arg46 of Xyn30B was conducted using program MEGA7 (1). Amino acid sequences used for the alignment were from the following fungal GH30-7 enzymes: *T. cellulolyticus* Xyn30B (NCBI protein ID: GAM36763), *T. reesei* XYN VI (EGR45006), *T. cellulolyticus* Xyn30A (GAM43270), *T. reesei* XYN IV (AAP64786), *Arthrobotrys oligospora* ATCC24927 AOL_s00173g184

(EGX45083), Bispora sp. MEY-1 XylD (ADG62369), Fusarium fujikuroi IMI58289 FFUJ 12899 (CCT73001), F. fujikuroi IMI58289 FFUJ 12945 (CCT73045), Leptosphaeria maculans Xyl38 (AAO49459), L. maculans JN3 LEMA P044840.1 (CBX93583), L. maculans JN3 LEMA P051060.1 (CBX92400), Podospora comate PODCO 503770 (VBB81111), P. comate PODCO 702000 (VBB86450), Sugiyamaella lignohabitans AWJ20 568 (ANB12318), Talaromyces purpureogenus XynC (AKH40280), Thermothelomyces thermophila ATCC42464 Gxhl (AEO55025), T. thermophila ATCC42464 THITE 30409 (AEO57693) and bacterial GH30-7 enzymes: Actinoplanes derwentensis DSM43941 SAMN04489716_2447 (SDT07978), A. derwentensis DSM43941 SAMN04489716 2458 (SDT08346), Amycolatopsis albispora WP1 A4R43 07175 (AXB42337), Amycolatopsis orientalis PCZA361.14 (CAA11771), Nonomuraea gerenzanensis ATCC39727 BN4615 P5575 (SBO96059), N. gerenzanensis ATCC39727 BN4615_P3232 (SBO93718), Nonomuraea sp. ATCC55076 BKM31 32010 (AQZ65470), Nonomuraea sp. ATCC55076 BKM31 10440 (AQZ61834), Nonomuraea sp. ATCC55076 BKM31 10430 (AQZ61832), Plantactinospora sp. KBS50 CIK06 16110 (ASW57759), Streptomyces bingchenggensis BCW-1 SBI_07402 (ADI10522), Streptomyces hygroscopicus XM201 SHXM 04002 (AQW50539), Streptomyces iranensis SIRAN6727 (CDR10147), Streptomyces lincolnensis LC-G SLCG 5858 (AXG57013), S. lincolnensis NRRL2936 SLINC 2555 (ANS64779), Streptomyces rapamycinicus NRRL5491 M271 33220 (AGP58059), Streptomyces sp. 11-1-2 CGL27 16155 (ASQ94399), Streptomyces sp. Go-475 XynC (AXE85427), Streptomyces venezuelae ATCC10712 SVEN 6739 (CCA60025), S. venezuelae ATCC15439 BN2537 15973 (CUM43504), S. venezuelae ATCC15439 AQF52 0650 (ALO06247), Streptomyces vietnamensis GIM4.0001 SVTN 36865 (AJF69043) and bacterial GH30-8 enzymes: Bacillus subtilis subsp. subtilis str. 168 BsXynC (CAA97612) and Dickeya chrysanthemi D1 EcXynA (AAB53151). The amino acid numbering is according to the Xyn30B sequence. The Arg residues and the other residues corresponding to Arg-46 of Xyn30B are highlighted by green and blue, respectively. Highly conserved residues are highlighted by yellow.

References

1. Kumar, S., Stecher, G., and Tamura, K. (2016) MEGA7: molecular evolutionary genetics analysis version 7.0. molecular biology and evolution. *Mol. Biol. Evol.* **33**, 1870–1874

	Products (mM)												
Reaction time (h)	Xyl	Xyl ₂	Xyl ₃	Xyl ₄	Xyl ₅	Xyl ₆							
1	ND	0.35	0.013	0.031	ND	0.025							
6	0.0079	1.1	0.033	0.22	0.018	0.075							
12	0.02	1.6	0.061	0.37	0.034	0.13							

Table S1. Xylooligosaccharides generated by Xyn30B reaction

ND, not detected

Table S1. The release of linear xylooligosaccharides from 10 mg mL⁻¹ beechwood xylan was performed using 100 μ g mL⁻¹ Xyn30B in 50 mM sodium acetate pH 4.0 at 40°C for 1, 6, or 12 hours. The reactions were stopped by incubation at 99°C for 5 min. Each resultant sample was analyzed by a HPAEC-PAD method.