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Protein structure of a glycoside hydrolase family 30, subfamily 12 endo-1,4- β -xylanase. Corrigendum

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Two corrections are made to the article by St John *et al.* (2026).

The following corrections are made to the article by St John *et al.* (2026). The last sentence of the caption to Fig. 1 is corrected. The corrected sentence should read ‘The two red dots represent the locations of the two catalytic glutamate residues, Glu143, the acid/base catalyst after the β 4 strand, and Glu256, the catalytic nucleophile at the end of the β 7 strand’.

A correction is also made to an amino-acid label in Fig. 5. The corrected figure is shown below.

References

St John, F. J., Crooks, C., Endres, M., Pakdaman, L., Koch, L., Bynum, L., Kuch, N., Joachimiak, A. & Tan, K. (2026). *Acta Cryst. D* **82**, 370–382.

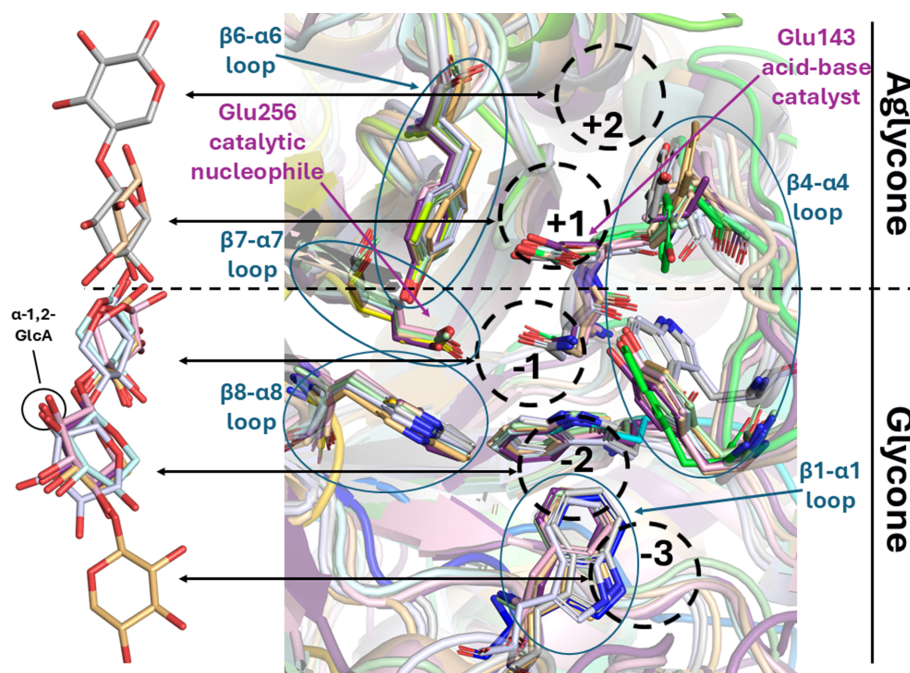


Figure 5

Amino-acid conservation in the XBC. Pair fitting alignment reveals the closeness between related GH30 subfamilies. The overlaid sugar ligands resulting from the alignment are shifted to the left side for clarity and subsites are indicated as well as the catalytic center and five loop regions. Pair fitting of *AchXyn30A* (in rainbow) with two GH30_7 dual-function GX/XBH enzymes [*TcXyn30B* (PDB entry 6krm) in pale cyan and *TtXyn30A* (PDB entry 7o0e) in light pink], a GH30_7 enzyme with REX activity and a GH30_7 EX with −2 subsite affinity [*TcXyn30A* (PDB entry 8idq) in wheat and *TcXyn30C* (PDB entry 6m5z) in pale green], three GH30_8 bacterial GXs [*EcXyn30A* (PDB entry 2y24) in light orange, *BsXyn30C* (PDB entry 3k15) in blue white and *CtXyn30A* (PDB entry 5a6m) in gray] and lastly a GH30_10 XBH [*AcXbh30A* (PDB entry 7n6o) in light blue]. The glycone region ligands obtained from the listed GX GH30_8 enzymes each contained a GlcA substituted α -1,2 on the −2 subsite xylose. This appendage has been removed for clarity and its location is noted in the figure.