Table S1. The pH and temperature optima for the β-glycoside hydrolases.

Enzyme	Optimal pH	Optimal temperature
CfXyl3A	7.0	50°C
CfBgl3A	7.5	55°C
CfBlg3B	6.5	30°C
CfBgl3C	7.0	30°C
CfBgl1	7.5	40°C

These activities were measured using *p*NP-glycoside substrates.

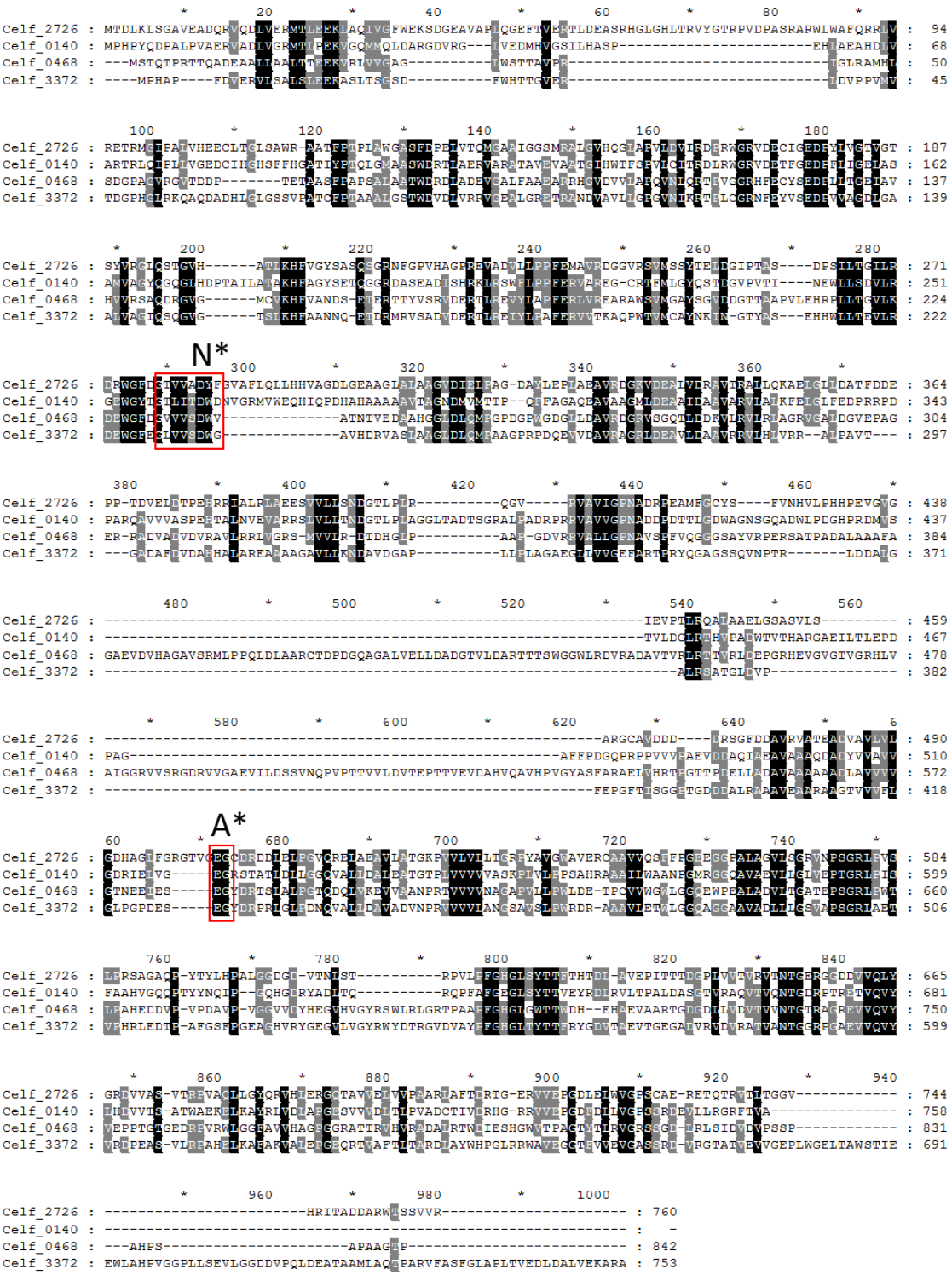

Fig. S1 Multiple amino acid sequence alignment of four GH3 family enzymes from *C. fimi* ATCC484. Dark shading indicates highly conserved residues in all sequences, lighter shading indicated conserved residues in 3 of the 4 sequences. Alignment was generated using ClustalX2.1 and formatted with Genedoc. Putative catalytic residues are labelled as N* for nucleophile and A* as acid/base catalyst.

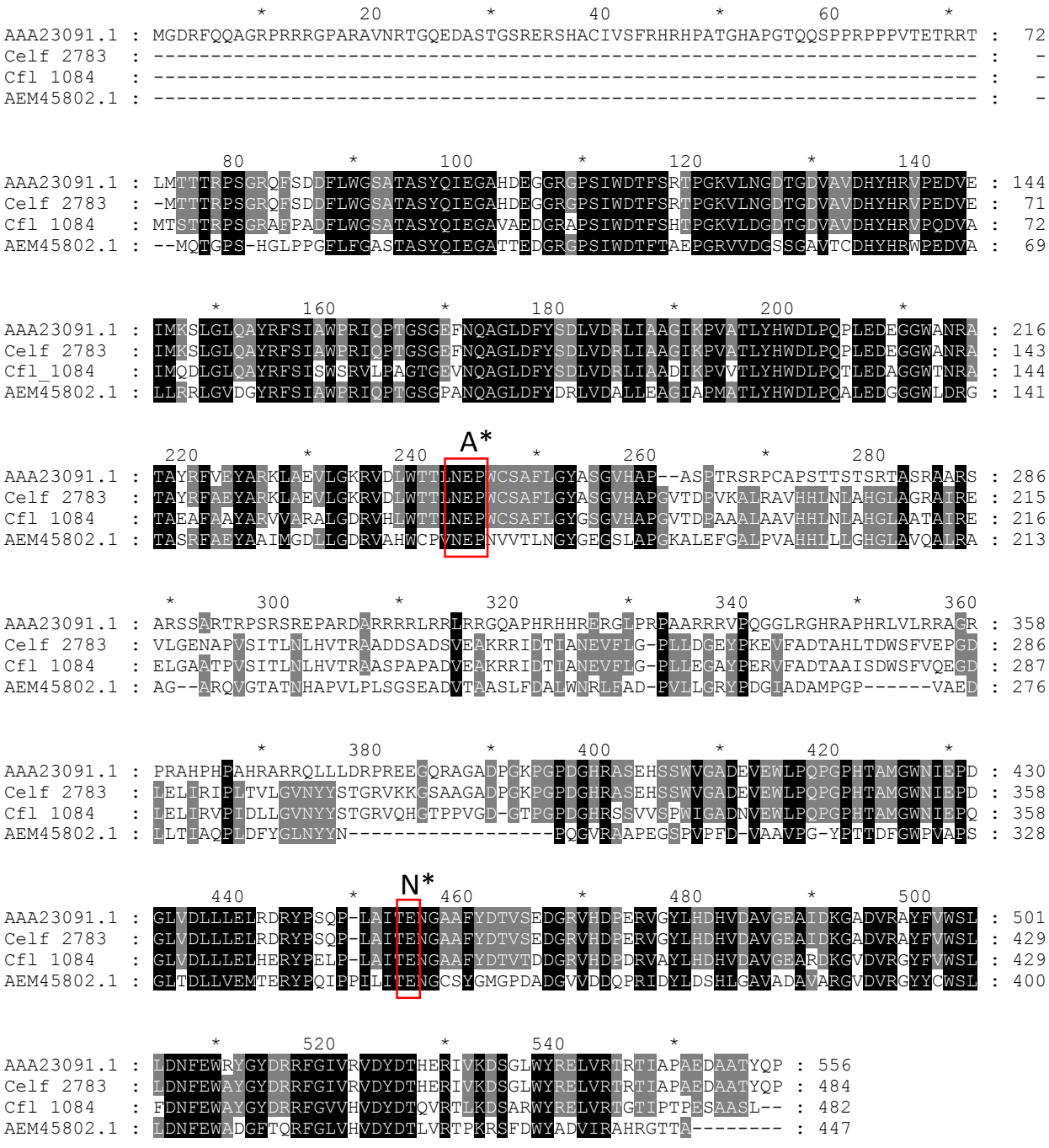

Fig. S2. Multiple amino acid sequence alignment of GH1 family enzymes. The GH1 protein sequences rom *C. fimi* ATCC484, *C. flavigena* ATCC482, and Genebank enteries AAA23091.1, putative C. fimi GH1, and AEM45802.1, GH1 from *Cellulomonas biazotea*. Dark shading indicates highly conserved residues in all sequences, lighter shading indicated conserved residues in 3 of the 4 sequences. Putative catalytic residues are labelled as N* for nucleophile and A* as acid/base catalyst. The alignment was generated using ClustalX2.1 and Genedoc.

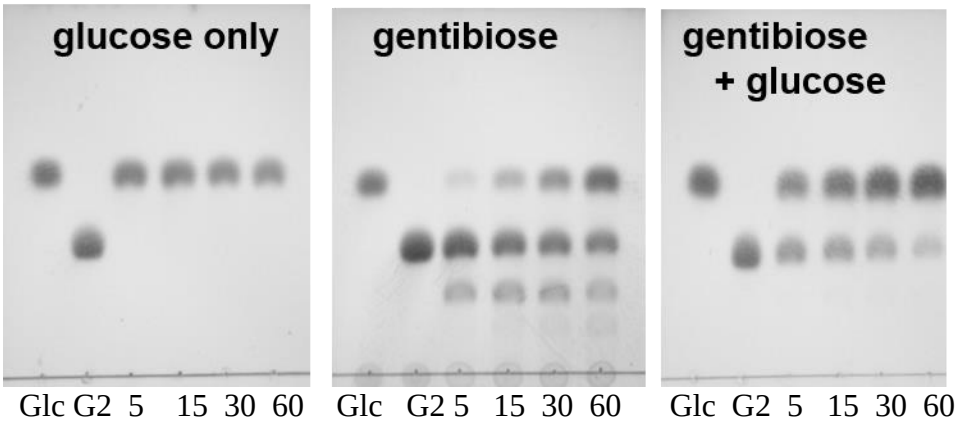

Figure S3. Inhibition of transglycosylation of CfBgl3B gentibiose by glucose.
CfBgl3B was incubated with 25 mg/ml glucose, 5 mg/ml gentibiose, or a mixture of the two sugars. The reaction progress was followed by TLC.