



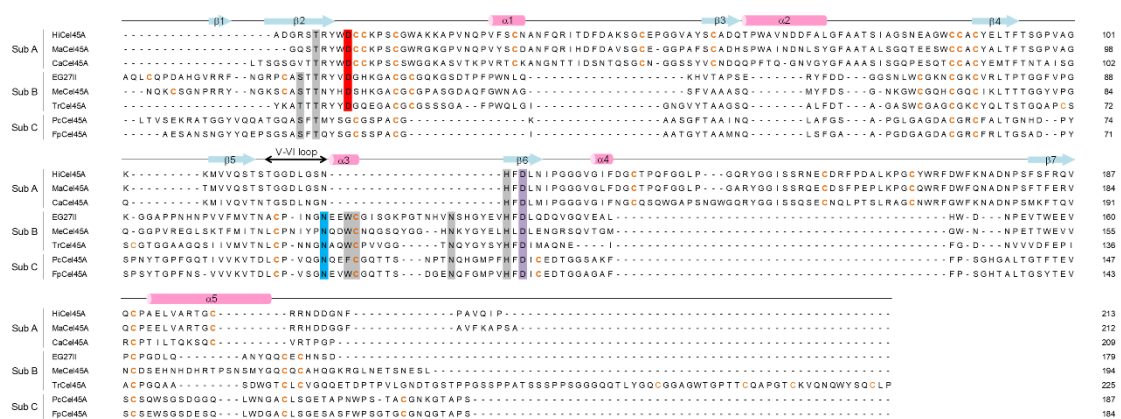
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**Supporting information for article:**

**High-resolution crystal structures of the glycoside hydrolase family 45 endoglucanase EG27II from the snail *Ampullaria crossean***

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**Figure S1** Multiple alignment of the amino acid sequences of GH45 endoglucanases. The amino acid sequence of EG27II (GenBank accession number: ABR92638) was aligned with *HiCel45A* (CAB42307), *MaCel45A* (CAD56665), *CaCel45A* (ACV50414), *MeCel45A* (CAC59695), *TrCel45A* (CAA83846), *PcCel45A* (BAG68300), and *FpCel45A* (BAI58030) using Clustal OMEGA (Sievers F, *et al.*, 2011). The signal peptides in these sequences were predicted by SignalP 4.1 Server (Nielsen, 2017) and removed from the sequences before using the multiple alignment. The catalytic acid residues are shown in a purple box, and the catalytic base residues of subfamily A and C are shown in a red and blue box, respectively. The proton relay residues in subfamily C and the corresponding homologous residues in subfamily A and B are shown in grey boxes. Cysteine residues are shown in orange letters. The secondary structure of EG27II was shown above the alignment.