



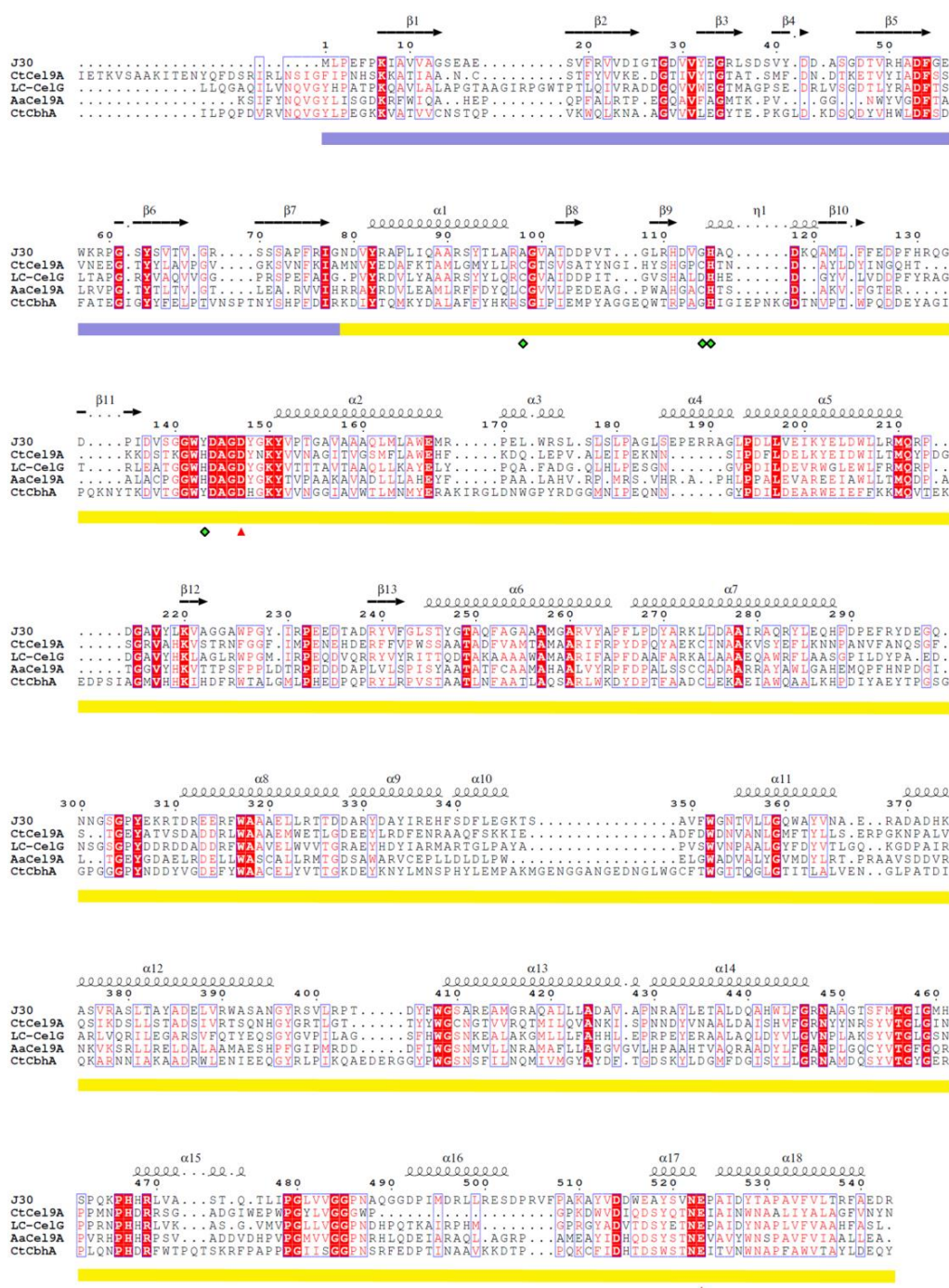
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**Supporting information for article:**

**Engineering glycoside hydrolase stability by the introduction of zinc binding**

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**Figure S1** Sequence alignment based on the crystal structures of J30 and its closest homologs. The amino-acid numbering, domain color coding (same as in Figure 1) and secondary-structure elements refer to J30 wt ( $\alpha$ :  $\alpha$ -helices;  $\beta$ :  $\beta$ -strands;  $\eta$ :  $3_{10}$ -helix). The covered residues comprise those present in the crystal structures of CtCel9A (amino acids 35-575), LC-CelG (30-577), AaCel9A (7-534) and CtCbha (208-815). Green and black diamonds denote the locations of the Zn<sup>2+</sup>-coordinating residues in the triple mutant J30 CCH, and red triangles point towards the catalytic residues. The bipartite  $\beta$ -strand 7 (residues 70-72 and 75-77) is depicted as a continuous strand for the sake of simplicity.