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Supporting information for article:

Structural insight into industrially-relevant glucoamylases: flexible positions of starch-binding domains

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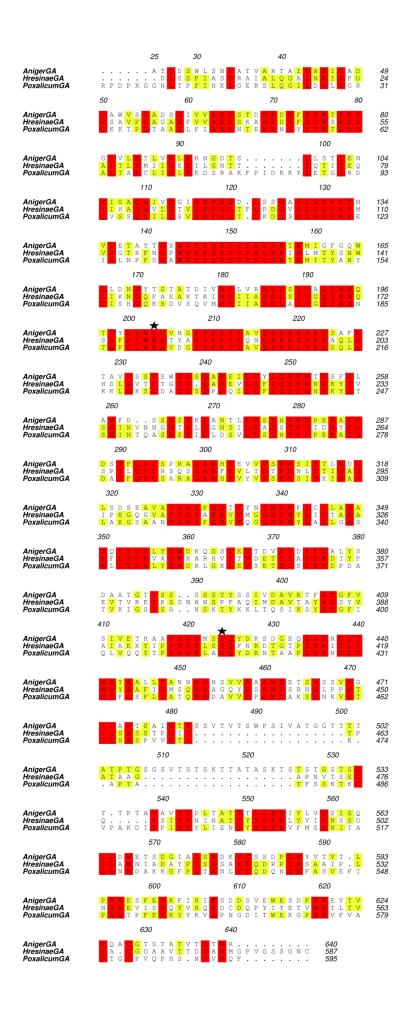


Figure S1 Sequence alignment of AnGA, HrGA and PoGA obtained using MUSCLE (Edgar, 2004) and visualized using ALINE (Bond & Schuttelkopf, 2009). Amino acids identical for all three proteins are outlined in red, for two – in yellow. The catalytic acid and base are marked with a star.

Figure S2 Schematic representation of the interaction of acarbose in the active site of HrGA. Hydrogen bonds are shown as dotted lines and the monomers of acarbose are numbered according their position in the subsites of the GA binding site Figure was prepared using ChemDraw (Perkin Elmer Informatics Inc.).