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Supplementary information

In-Depth Characterization of Debranching Type I Pullulanase from *Priestia koreensis* HL12 as Potential Biocatalyst for Starch Saccharification and Modification

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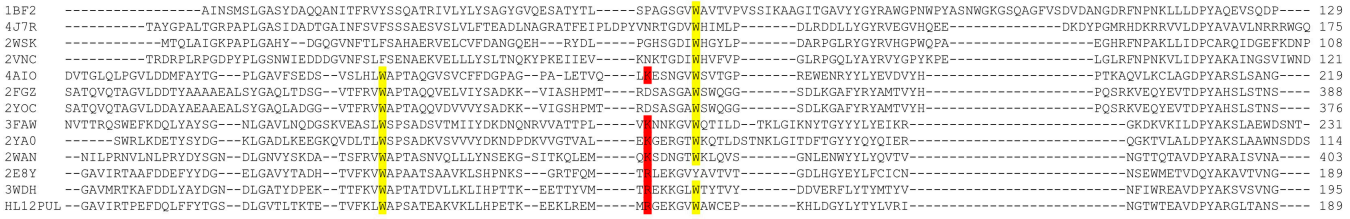

Figure S1. Sequence alignment of CBM48 in HL12Pul and α-glucan debraching enzymes in GH13_11-14 subfamilies [3,9]. Two conserved tryptophans and a functionally important lysine based on [25] are highlighted in yellow and red, respectively. Alpha-glucan debranching sequences in sequence alignment include soamylase from *Chlamydomonas reinhardtii* (4J7R), glycogen debranching enzyme from *Escherichia coli* K-12 (2WSK), isoamylase from *Pseudomonas amyloderamosa* (1BF2), glycogen operon protein GLGX from *Sulfolobus solfataricus* (2VNC), reticulocyte binding protein from *Streptococcus agalactiae* COH1 (3FAW), putative alkaline amylopullulanase from *Streptococcus pneumoniae* (2YA0), limit dextrinase from *Hordeum vulgare* (4AIO), alpha-dextrin endo-1,6-alpha-glucosidase from *Klebsiella pneumoniae* (2FGZ), pullulanase from *Klebsiella oxytoca* (2YOC), type I pullulanase from *Anoxybacillus* sp. LM18-11 (3WDH), pullulanase from *Bacillus acidopullulyticus* (2WAN), and AmyX protein from *Bacillus subtilis* (2E8Y).

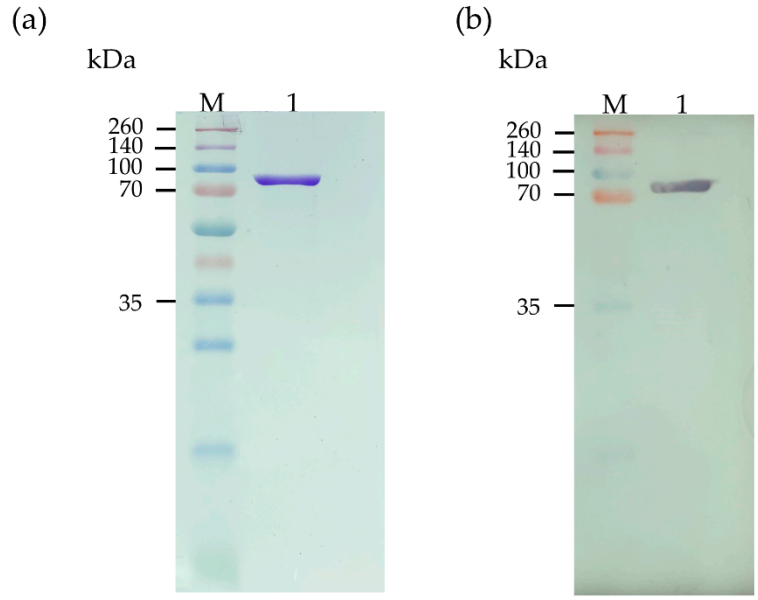

Figure S2. Investigation of recombinant intracellular HL12Pul produced by *E. coli* BL21(DE3). (**a**) Purified HL12Pul on SDS-PAGE analysis (**b**) Purified HL12Pul on Western blot analysis. Lane M: Prestained protein marker (Thermo Scientific). Lane 1: purified HL12Pul fraction.