

Supplementary data

Rational re-design of *Lactobacillus reuteri* 121 inulosucrase for product chain length control

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Table S1. Oligonucleotide primers for site-directed mutagenesis

Primer name	Sequence (5' - 3')
F_NdeI	GGTACATATGCTAGAACGCAAGGAACATAAAAAAAT
R_699HIS	GGTGCTCGAGTTTTAATCCATAACCAATTAAG
F_R483A	CCAATGATGATATTAAGAGTGCGCAACTTGGG
R_R483A	CCCAAGTTGCCGCACTCTTAATATCATCATTGG
F_R483F	CCAATGATGATATTAAGAGTTTCGCAACTTGGG
R_R483F	CCCAAGTTGCGAACTCTTAATATCATCATTGG
F_R483Y	CCAATGATGATATTAAGAGTTACGCAACTTGGG
R_R483Y	CCCAAGTTGCGTAACTCTTAATATCATCATTGG
F_R483W	CCAATGATGATATTAAGAGTTCCGCAACTTGGG
R_R483W	CCCAAGTTGCGGAACTCTTAATATCATCATTGG

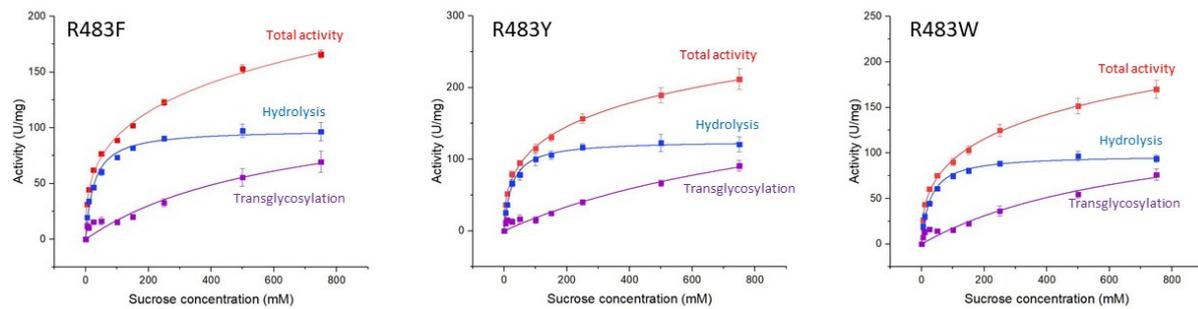


Fig. S1 Graphs of relationship between initial velocity (V) and sucrose concentration for wild-type and mutant inulosucrase. The kinetic parameters were determined based on activity versus sucrose concentration curve, using 'OriginPro' as curve fitting software.