

Supplementary materials

Secretory expression fine-tuning and directed evolution of diacetylchitobiose deacetylase by *Bacillus subtilis*

Running title: diacetylchitobiose deacetylase

Zhu Jiang^a, Tengfei Niu^a, Xueqin Lv^{a, b}, Yanfeng Liu^{a, b}, Jianghua Li^b, Wei Lu^c, Guocheng Du^{a, b}, Jian Chen^b,
Long Liu^{a, b†}

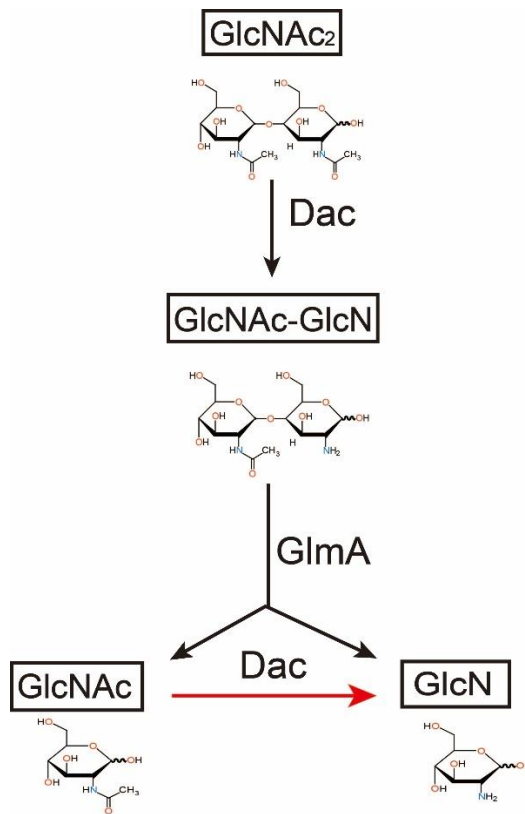
^a Key Laboratory of Carbohydrate Chemistry and Biotechnology, Ministry of Education, Jiangnan University, Wuxi 214122, China

^b Key Laboratory of Industrial Biotechnology, Ministry of Education, Jiangnan University, Wuxi 214122, China

^c Shandong Runde Biotechnology CO., LTD, Taian 271200, China

†Corresponding author: Long Liu, Tel.: +86-510-85918312, Fax: +86-510-85918309, E-mail:

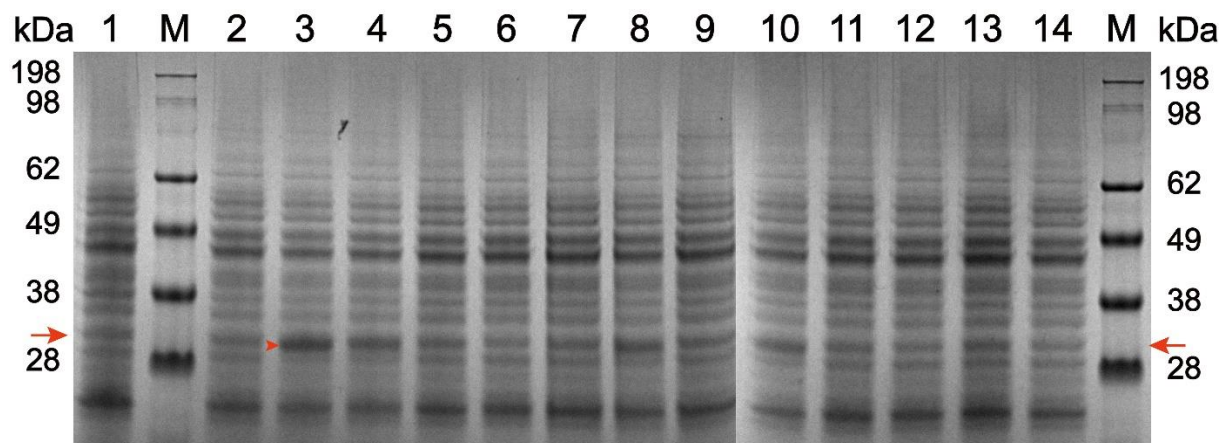
longliu@jiangnan.edu.cn



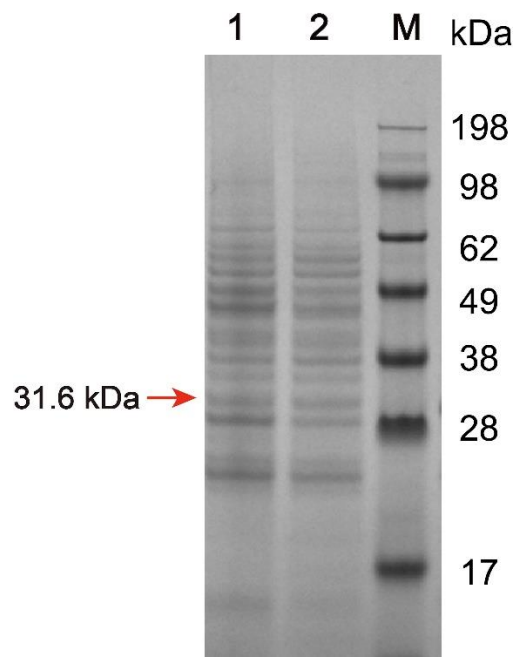
(Figure. S1)

1 ATGGTCGTCA ACATGTTCGA GGACATCGAC ACGTTCGAGG AAGCGTTTAA CAAGCTGCTG CGCGAAGTCC TGGAAATTTGA TCTGCAAAAT CCGTTCAAAG
101 ACGCGAAGAA AGTCCTTTGC ATCGAACCGC ATCCGGACGA TTGCGTTATT GGAATGGGCG GCACAATCAA AAAACTGAGC GATATGGGCG TCGAAGTCAT
201 CTACGTTTGC ATGACAGACG GCTATATGGG CACAACAGAC GAAAGCCTGT CAGGACACGA ATTAGCAGCA ATCCGCCGCA AAGAAGAAGA AGAAAGCGCA
301 CGCCTGCTGG GCGTAAAAA GATCTATTGG CTGAACTACC GCGATACAGA ACTGCCGTAT TCACGCGAAG TCCGCAAAGA TCTGACGAAA ATTCTGCGCA
401 AAGAACAACC GGACGGAGTT TTTGCACCAG ATCCTTGGCT TCGTACGAA TCACATCCGG ATCATAGACG CACAGGCTTT CTGGCGATTG AATCAGTTGC
501 GTTAGCCAG CTGCCGAATT TTAGCAACAC GGATCTGGAC ATTGGCCTGA ATCCGTATAA CAGCGGAAGC TTTATCGCGC TGTACTACAC GCACAAACCG
601 AACTACATCG TCGACATCAC GGACCTGATG GAACTGAAAC TGAAGCCGAT TCGCGTCCAT AGAAGCCAGT TTCCGGACGA TATTTGGGAG AAATGGGAAC
701 CGTTCCTGAG AACAAATCGG ATGTTCTACG GCGAAAAAAT CGGCGTTCGC TACGGAGAAG GCTTTAGAAT TATGCCGGGC CTGTTCTACC ACATCACACC
801 GTTTACGGAC CTGATCTGA

(Figure. S2)



(Figure. S3)

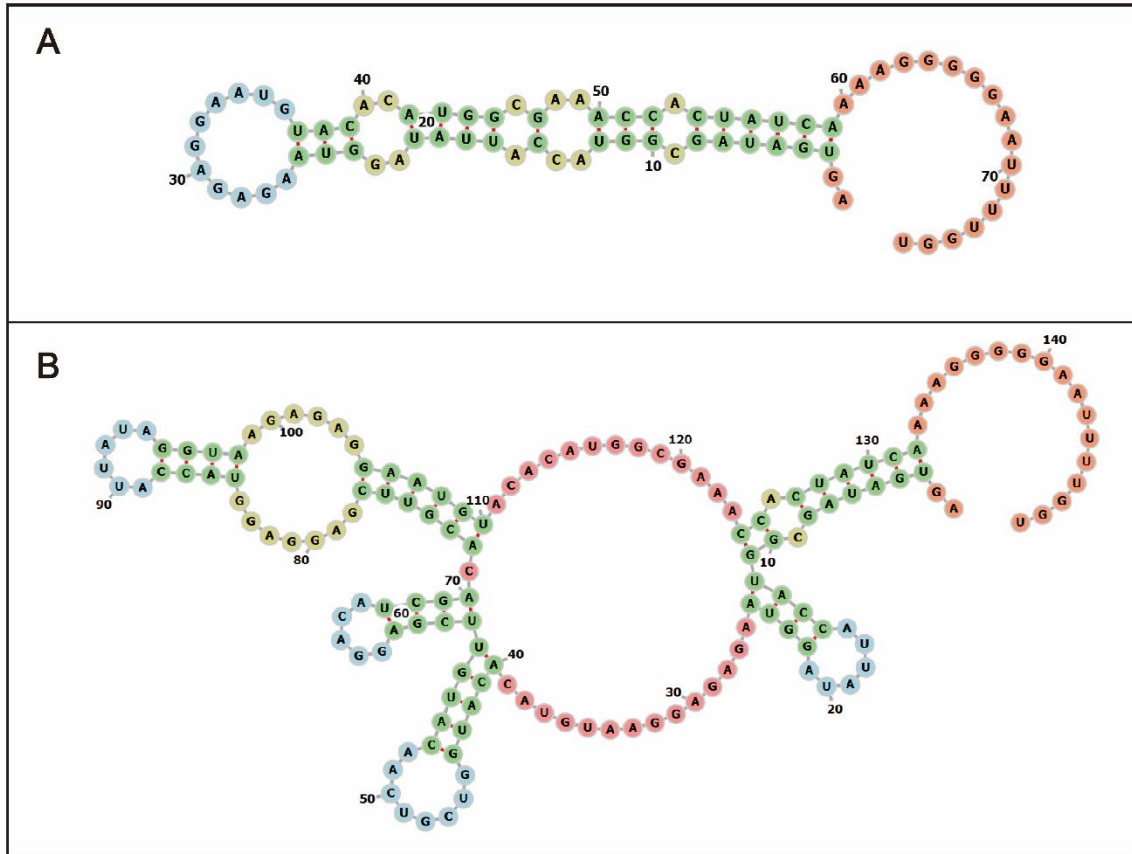


(Figure. S4)

transcription start region



(Figure. S5)



(Figure. S6)

1 **Figure legends**

2 **Fig. S1** The catalysis process of GlcNAc₂ by Dac.

3 **Fig. S2** Nucleotide sequences of Dac after codon optimization.

4 **Fig. S3** SDS-PAGE analysis of extracellular Dac of the recombinant strains. M: protein marker; 1–
5 14 represent *B. subtilis* WB600 expressing different plasmid respectively. 1: pMA0911 (without Dac
6 gene); 2: pMA0911NS (expression Dac without signal peptide); 3: pMA0911J (Dac with YncM), 4:
7 pMA0911C (Dac with Bpr); 5: pMA0911M (Dac with YwbN); 6: pMA0911Z (Dac with AnsZ); 7:
8 pMA0911O (Dac with YvgO); 8: pMA0911A (Dac with AmyE); 9: pMA0911F (Dac with OppA); 10:
9 pMA0911G (Dac with Vpr); 11: pMA0911L (Dac with LipA); 12: pMA0911H (Dac with WapA); 13:
10 pMA0911E (Dac with Epr); 14: pMA0911I (Dac with YclQ).

11 The Dac bands are indicated by arrows. The recombinant strains were grown in fermentation
12 medium (see the “Materials and methods” section) containing 10 mg/L of kanamycin in 250-mL
13 flask and incubated at 37°C and 220 rpm for 60 h.

14 **Fig. S4** SDS-PAGE analysis of the recombinant Dac in the pellet of cell lysate. M: protein marker;
15 1: Control group, *B. subtilis* WB600 harboring pMA0911 plasmid (without Dac); 2: *B. subtilis* WB600
16 harboring pMA0911-YncM-Dac plasmid. The recombinant strains in this work were collected and
17 broken by ultrasonic cell disruption system.

18 **Fig. S5** The 5'-terminal sequencing map after RACE experiments in different strains. A: The 5'-
19 terminal sequencing map in recombinant strain WB-NMK/Dac. B: The 5'-terminal sequencing map
20 in recombinant strain WB-NMKmut/Dac.

21 **Fig. S6** The secondary structure formed by mRNA of 5'-UTR in different strains. A: The secondary
22 structure of 5'-UTR in recombinant strain WB-NMK/Dac. B: The secondary structure of 5'-UTR in
23 recombinant strain WB-NMKmut/Dac.