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**Supporting information for article:**

**X-ray crystallographic analysis of the catalytic domain of  
*Paenibacillus glycanilyticus*  $\alpha$ -1,3-glucanase FH1  
overexpressed in *Brevibacillus choshinensis***

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protein are as follows: PgAgl-FH1,  $\alpha$ -1,3-glucanase from *P. glycanilyticus* FH11 (BAP10900): PgAgl-FH2,  $\alpha$ -1,3-glucanase from *P. glycanilyticus* FH11 (BAP10901): BcAgl-KA,  $\alpha$ -1,3-glucanase from *B. circulans* KA-304 (BAE98302): PhMut,  $\alpha$ -1,3-glucanase from *Paenibacillus humicus* (BAI23187): PcMutP,  $\alpha$ -1,3-glucanase from *P. curdlanolyticus* (ADT91063): PkMuA,  $\alpha$ -1,3-glucanase from *Paenibacillus* sp. KSM-35 (BAG15878): PkMuB,  $\alpha$ -1,3-glucanase from *Paenibacillus* sp. KSM-86 (BAF56208): PkMuC1,  $\alpha$ -1,3-glucanase from *Paenibacillus* sp. KSM-126 (BAG15879): PkMuC2,  $\alpha$ -1,3-glucanase from *Paenibacillus* sp. KSM-126 (BAG15880): PkMuE,  $\alpha$ -1,3-glucanase from *Paenibacillus* sp. KSM-138 (BAH10514): PjAPHP0617, APHP domain-containing protein from *Paenibacillus* sp. JDR 2 (WP\_012772618): PjAHPH3616, APHP domain-containing protein from *Paenibacillus* sp. JDR 2 (WP\_015845190): PyAPHP, APHP domain-containing protein from *Paenibacillus* sp. Y412MC10 (WP\_015734695): PpMu22,  $\alpha$ -1,3-glucanase from *Paenibacillus* sp. P22 (CDN41550). Black shading; Threshold 70% for identity. Gray shading; Similarity. Amino acid sequences of catalytic  $\alpha$ -1,3-glucanase domains were aligned by using BioEdit (version 7.0.5; <http://www.mbio.ncsu.edu/BioEdit/bioedit.html>)(Hall, 1999).

**Table S1** Summary of purification of CatAgl-FH1

<b>Purification step</b>	<b>Total activity (U)</b>	<b>Total protein (mg)</b>	<b>Specific activity (U/mg)</b>	<b>Purification (fold)</b>	<b>Yield (%)</b>
Crude extract	49.1	2,459	0.02	1	100
Ammonium sulfate precipitation	30.6	167	0.18	9	62
DEAE-Cellufine	4.90	25	0.20	10	10
Butyl toyopearl	5.00	7	0.71	35	10