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Supporting information for article:

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

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| | | | | |
|------------|-----|---|-----|------------|
| PgAgl-FH1 | 1 | RGAGMPFIVPAGTSNATNG-TLIDPENKPGDNGEASGRSSVYIITIPEWEITISPN--AFVIFNAVAETIC-----TSEAGAVSRSKGFNV | 92 | PgAgl-FH1 |
| PgAgl-FH2 | 1 | RGASMPFPRYITDIDIREGGGLQSAHIDTQDSEASQGYHALPSGSYLONWVTEGEGC-----TMFPTMDPSGCMGILGSLDVYVNNVTKVTL | 100 | PgAgl-FH2 |
| BcAgl-KA | 1 | RGASMPFPRYITDIDIREGGGLQSAHIDTQDSEASQGYHALPSGSYLONWVTEGEGC-----TMFPTMDPSGCMGILGSLDVYVNNVTKVTL | 100 | BcAgl-KA |
| PhMut | 1 | RGASMPFPRYITDIDIREGGGLQSAHIDTQDSEASQGYHALPSGSYLONWVTEGEGC-----TMFPTMDPSGCMGILGSLDVYVNNVTKVTL | 100 | PhMut |
| PcmPtp | 1 | RGASMPFPRYITDIDIREGGGLQSAHIDTQDSEASQGYHALPSGSYLONWVTEGEGC-----TMFPTMDPSGCMGILGSLDVYVNNVTKVTL | 100 | PcmPtp |
| PkmMu | 1 | RGAMPYDNPAEDGVIGGCVVLSNLANTTIGDGEASGRSSVYIITNTGVSWEETITASTN---ITVPEPDPSGCMGILGSLDVYVNNVTKVTL | 97 | PkmMu |
| PkmBu | 1 | RGAMPYDNPAEDGVIGGCVVLSNLANTTIGDGEASGRSSVYIITNTGVSWEETITASTN---ITVPEPDPSGCMGILGSLDVYVNNVTKVTL | 100 | PkmBu |
| PkmMu1 | 1 | RGASMPFPRYITDIDIREGGGLQSAHIDTQDSEASQGYHALPSGSYLONWVTEGEGC-----TMFPTMDPSGCMGILGSLDVYVNNVTKVTL | 100 | PkmMu1 |
| PkmMu2 | 1 | RGASMPFPRYITDIDIREGGGLQSAHIDTQDSEASQGYHALPSGSYLONWVTEGEGC-----TMFPTMDPSGCMGILGSLDVYVNNVTKVTL | 100 | PkmMu2 |
| PkmMu3 | 1 | RGASMPFPRYITDIDIREGGGLQSAHIDTQDSEASQGYHALPSGSYLONWVTEGEGC-----TMFPTMDPSGCMGILGSLDVYVNNVTKVTL | 100 | PkmMu3 |
| PkmMu4 | 1 | RGASMPFPRYITDIDIREGGGLQSAHIDTQDSEASQGYHALPSGSYLONWVTEGEGC-----TMFPTMDPSGCMGILGSLDVYVNNVTKVTL | 100 | PkmMu4 |
| PjAHPH0617 | 1 | RGAMPYDNPAEDGVIGGCVVLSNLANTTIGDGEASGRSSVYIITNTGVSWEETITASTN---ITVPEPDPSGCMGILGSLDVYVNNVTKVTL | 92 | PjAHPH0617 |
| PjAHPH3616 | 1 | RGAMPYDNPAEDGVIGGCVVLSNLANTTIGDGEASGRSSVYIITNTGVSWEETITASTN---ITVPEPDPSGCMGILGSLDVYVNNVTKVTL | 100 | PjAHPH3616 |
| PyAHPH | 1 | RGASMPFPRYITDIDIREGGGLQSAHIDTQDSEASQGYHALPSGSYLONWVTEGEGC-----TMFPTMDPSGCMGILGSLDVYVNNVTKVTL | 100 | PyAHPH |
| PpmMu2 | 1 | RGASMPFPRYITDIDIREGGGLQSAHIDTQDSEASQGYHALPSGSYLONWVTEGEGC-----TMFPTMDPSGCMGILGSLDVYVNNVTKVTL | 100 | PpmMu2 |
| PgAgl-FH1 | 93 | KESTVIAFPSTLGLRGLYDIAAGAGITATVLYEEACIMLIQVNPAPTRIPIQDAGVYWSWVNLVLTENIAAPFCANDTFTYAVSV--AKRSIDQATE | 190 | PgAgl-FH1 |
| PgAgl-FH2 | 101 | SYNWQYQESGGMGA----DADGEG-----BFLRFPRDEWHRLDITLHGRTIRIQCNG-NDTVEYVHEVEQEYVFAIAEANSVSDIDGADANGDDITI | 193 | PgAgl-FH2 |
| BcAgl-KA | 101 | SYNWQYQESGGMGA----DADGEG-----BFLRFPRDEWHRLDITLHGRTIRIQCNG-NDTVEYVHEVEQEYVFAIAEANSVSDIDGADANGDDITI | 193 | BcAgl-KA |
| PhMut | 101 | SYNWQYQESGGMGA----DADGEG-----BFLRFPRDEWHRLDITLHGRTIRIQCNG-NDTVEYVHEVEQEYVFAIAEANSVSDIDGADANGDDITI | 193 | PhMut |
| PcmPtp | 101 | SYNWQYQESGGMGA----DADGEG-----BFLRFPRDEWHRLDITLHGRTIRIQCNG-NDTVEYVHEVEQEYVFAIAEANSVSDIDGADANGDDITI | 194 | PcmPtp |
| PkmMu | 98 | SESTVIAFPSTLGLRGLYDIAAGAGITATVLYEEACIMLIQVNPAPTRIPIQDAGVYWSWVNLVLTENIAAPFCANDTFTYAVSV--AKRSIDQATE | 190 | PkmMu |
| PkmMu1 | 101 | SYNWQYQESGGMGA----DADGEG-----BFLRFPRDEWHRLDITLHGRTIRIQCNG-NDTVEYVHEVEQEYVFAIAEANSVSDIDGADANGDDITI | 194 | PkmMu1 |
| PkmMu2 | 101 | SYNWQYQESGGMGA----DADGEG-----BFLRFPRDEWHRLDITLHGRTIRIQCNG-NDTVEYVHEVEQEYVFAIAEANSVSDIDGADANGDDITI | 194 | PkmMu2 |
| PkmMu3 | 101 | SYNWQYQESGGMGA----DADGEG-----BFLRFPRDEWHRLDITLHGRTIRIQCNG-NDTVEYVHEVEQEYVFAIAEANSVSDIDGADANGDDITI | 194 | PkmMu3 |
| PkmMu4 | 101 | SYNWQYQESGGMGA----DADGEG-----BFLRFPRDEWHRLDITLHGRTIRIQCNG-NDTVEYVHEVEQEYVFAIAEANSVSDIDGADANGDDITI | 194 | PkmMu4 |
| PjAHPH0617 | 93 | KESTVIAFPSTLGLRGLYDIAAGAGITATVLYEEACIMLIQVNPAPTRIPIQDAGVYWSWVNLVLTENIAAPFCANDTFTYAVSV--AKRSIDQATE | 190 | PjAHPH0617 |
| PjAHPH3616 | 101 | SYNWQYQESGGMGA----DADGEG-----BFLRFPRDEWHRLDITLHGRTIRIQCNG-NDTVEYVHEVEQEYVFAIAEANSVSDIDGADANGDDITI | 193 | PjAHPH3616 |
| PyAHPH | 101 | SYNWQYQESGGMGA----DADGEG-----BFLRFPRDEWHRLDITLHGRTIRIQCNG-NDTVEYVHEVEQEYVFAIAEANSVSDIDGADANGDDITI | 194 | PyAHPH |
| PpmMu2 | 101 | SYNWQYQESGGMGA----DADGEG-----BFLRFPRDEWHRLDITLHGRTIRIQCNG-NDTVEYVHEVEQEYVFAIAEANSVSDIDGADANGDDITI | 193 | PpmMu2 |
| PgAgl-FH1 | 191 | FHQDNIT-----FHGIVVIAPIENTINSKIFIYGR-----ATEVYAGAEWIKVIAVAPC-BOSNTIVGFGNSAIAAAGSHTIDL-----ANGYVYTFDGGKEDID | 277 | PgAgl-FH1 |
| PgAgl-FH2 | 194 | FHQDNIT-----FHGIVVIAPIENTINSKIFIYGR-----ATEVYAGAEWIKVIAVAPC-BOSNTIVGFGNSAIAAAGSHTIDL-----ANGYVYTFDGGKEDID | 278 | PgAgl-FH2 |
| BcAgl-KA | 195 | FHQDNIT-----FHGIVVIAPIENTINSKIFIYGR-----ATEVYAGAEWIKVIAVAPC-BOSNTIVGFGNSAIAAAGSHTIDL-----ANGYVYTFDGGKEDID | 289 | BcAgl-KA |
| PhMut | 194 | FHQDNIT-----FHGIVVIAPIENTINSKIFIYGR-----ATEVYAGAEWIKVIAVAPC-BOSNTIVGFGNSAIAAAGSHTIDL-----ANGYVYTFDGGKEDID | 289 | PhMut |
| PcmPtp | 195 | FHQDNIT-----FHGIVVIAPIENTINSKIFIYGR-----ATEVYAGAEWIKVIAVAPC-BOSNTIVGFGNSAIAAAGSHTIDL-----ANGYVYTFDGGKEDID | 289 | PcmPtp |
| PkmMu | 191 | VEMDTIGG----NLVQYIPLRNQTISKECVYGR-----AKVYAGAEWIKVIAVAPC-BOSNTIVGFGNSAIAAAGSHTIDL-----ANGYVYTFDGGKEDID | 279 | PkmMu |
| PkmMu1 | 195 | FHQDNIT-----FHGIVVIAPIENTINSKIFIYGR-----ATEVYAGAEWIKVIAVAPC-BOSNTIVGFGNSAIAAAGSHTIDL-----ANGYVYTFDGGKEDID | 289 | PkmMu1 |
| PkmMu2 | 195 | FHQDNIT-----FHGIVVIAPIENTINSKIFIYGR-----ATEVYAGAEWIKVIAVAPC-BOSNTIVGFGNSAIAAAGSHTIDL-----ANGYVYTFDGGKEDID | 289 | PkmMu2 |
| PjAHPH0617 | 191 | FHQDNIT-----FHGIVVIAPIENTINSKIFIYGR-----ATEVYAGAEWIKVIAVAPC-BOSNTIVGFGNSAIAAAGSHTIDL-----ANGYVYTFDGGKEDID | 277 | PjAHPH0617 |
| PjAHPH3616 | 194 | FHQDNIT-----FHGIVVIAPIENTINSKIFIYGR-----ATEVYAGAEWIKVIAVAPC-BOSNTIVGFGNSAIAAAGSHTIDL-----ANGYVYTFDGGKEDID | 289 | PjAHPH3616 |
| PyAHPH | 195 | FHQDNIT-----FHGIVVIAPIENTINSKIFIYGR-----ATEVYAGAEWIKVIAVAPC-BOSNTIVGFGNSAIAAAGSHTIDL-----ANGYVYTFDGGKEDID | 289 | PyAHPH |
| PpmMu2 | 194 | FHQDNIT-----FHGIVVIAPIENTINSKIFIYGR-----ATEVYAGAEWIKVIAVAPC-BOSNTIVGFGNSAIAAAGSHTIDL-----ANGYVYTFDGGKEDID | 288 | PpmMu2 |
| PgAgl-FH1 | 278 | GNG-MQVNTQVNLWEEHVLCYNG-----INNSYNTTINRILQVNLWEEHVLCYNG-----INNSYNTTINRILQVNLWEEHVLCYNG-----GSPFLETSIDGSGSYNQGKYNIT | 367 | PgAgl-FH1 |
| PgAgl-FH2 | 289 | FMDMNGCSKINHIIQVNLWEEHFECGFWVGQYAHAT-----GSPFLETSIDGSGSYNQGKYNIT | 388 | PgAgl-FH2 |
| BcAgl-KA | 290 | FMDMNGCSKINHIIQVNLWEEHFECGFWVGQYAHAT-----GSPFLETSIDGSGSYNQGKYNIT | 389 | BcAgl-KA |
| PhMut | 289 | FMDMNGCSKINHIIQVNLWEEHFECGFWVGQYAHAT-----GSPFLETSIDGSGSYNQGKYNIT | 388 | PhMut |
| PcmPtp | 290 | FMDMNGCSKINHIIQVNLWEEHFECGFWVGQYAHAT-----GSPFLETSIDGSGSYNQGKYNIT | 389 | PcmPtp |
| PkmMu | 280 | CN----VLTIDNQVYIPLQVNLWEEHVLCYNG-----INNSYNTTINRILQVNLWEEHVLCYNG-----GSPFLETSIDGSGSYNQGKYNIT | 369 | PkmMu |
| PkmMu1 | 290 | FMDMNGCSKINHIIQVNLWEEHFECGFWVGQYAHAT-----GSPFLETSIDGSGSYNQGKYNIT | 389 | PkmMu1 |
| PkmMu2 | 290 | FMDMNGCSKINHIIQVNLWEEHFECGFWVGQYAHAT-----GSPFLETSIDGSGSYNQGKYNIT | 389 | PkmMu2 |
| PjAHPH0617 | 295 | FMDMNGCSKINHIIQVNLWEEHFECGFWVGQYAHAT-----GSPFLETSIDGSGSYNQGKYNIT | 394 | PjAHPH0617 |
| PjAHPH3616 | 278 | GNG-MQVNTQVNLWEEHVLCYNG-----INNSYNTTINRILQVNLWEEHVLCYNG-----GSPFLETSIDGSGSYNQGKYNIT | 367 | PjAHPH3616 |
| PyAHPH | 289 | FMDMNGCSKINHIIQVNLWEEHFECGFWVGQYAHAT-----GSPFLETSIDGSGSYNQGKYNIT | 388 | PyAHPH |
| PpmMu2 | 289 | FMDMNGCSKINHIIQVNLWEEHFECGFWVGQYAHAT-----GSPFLETSIDGSGSYNQGKYNIT | 388 | PpmMu2 |
| PgAgl-FH1 | 368 | AATVVERAFLPVGCGSDLQLYGAATYGTISYSSGNTLQGQ-DTVIGA-----GDFWTSGVADKINEQYNG-----YTGSRKFLN | 466 | PgAgl-FH1 |
| PgAgl-FH2 | 389 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 476 | PgAgl-FH2 |
| BcAgl-KA | 390 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 477 | BcAgl-KA |
| PhMut | 389 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 476 | PhMut |
| PcmPtp | 390 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 477 | PcmPtp |
| PkmMu | 370 | SILAAVQYVAGAEYATRINLQVNLWEEHVLCYNG-----GASPINNEI-----TJFAGHWG-----ACIFQAWFNSAVKFGV | 459 | PkmMu |
| PkmMu1 | 390 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 477 | PkmMu1 |
| PkmMu2 | 390 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 477 | PkmMu2 |
| PjAHPH0617 | 395 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 482 | PjAHPH0617 |
| PjAHPH3616 | 368 | AATVVERAFLPVGCGSDLQLYGAATYGTISYSSGNTLQGQ-DTVIGA-----GDFWTSGVADKINEQYNG-----YTGSRKFLN | 466 | PjAHPH3616 |
| PyAHPH | 389 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 476 | PyAHPH |
| PpmMu2 | 389 | FMDMNGCSKINHIIQVNLWEEHFECGFWVGQYAHAT-----GSPFLETSIDGSGSYNQGKYNIT | 388 | PpmMu2 |
| PgAgl-FH1 | 368 | AATVVERAFLPVGCGSDLQLYGAATYGTISYSSGNTLQGQ-DTVIGA-----GDFWTSGVADKINEQYNG-----YTGSRKFLN | 466 | PgAgl-FH1 |
| PgAgl-FH2 | 389 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 476 | PgAgl-FH2 |
| BcAgl-KA | 390 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 477 | BcAgl-KA |
| PhMut | 389 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 476 | PhMut |
| PcmPtp | 390 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 477 | PcmPtp |
| PkmMu | 370 | SILAAVQYVAGAEYATRINLQVNLWEEHVLCYNG-----GASPINNEI-----TJFAGHWG-----ACIFQAWFNSAVKFGV | 459 | PkmMu |
| PkmMu1 | 390 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 477 | PkmMu1 |
| PkmMu2 | 390 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 477 | PkmMu2 |
| PjAHPH0617 | 395 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 482 | PjAHPH0617 |
| PjAHPH3616 | 368 | AATVVERAFLPVGCGSDLQLYGAATYGTISYSSGNTLQGQ-DTVIGA-----GDFWTSGVADKINEQYNG-----YTGSRKFLN | 466 | PjAHPH3616 |
| PyAHPH | 389 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 476 | PyAHPH |
| PpmMu2 | 389 | IENNWRAPIAAFFFGGSKHDKHNIVDTVGGSQ-----RNTVFFG-----TSDIDNGERGAIDLEASIDIKNTV | 476 | PpmMu2 |
| PgAgl-FH1 | 467 | IPNDIDINPVYFCQVNLQFQS-----MSPN-----MCN-----ENVNV-----TINH-----RYGIMLVRAECC-----GSPFLETSIDGSGSYNQGKYNIT | 553 | PgAgl-FH1 |
| PgAgl-FH2 | 477 | IPNDIDINPVYFCQVNLQFQS-----MSPN-----MCN-----ENVNV-----TINH-----RYGIMLVRAECC-----GSPFLETSIDGSGSYNQGKYNIT | 565 | PgAgl-FH2 |
| BcAgl-KA | 478 | IPNDIDINPVYFCQVNLQFQS-----MSPN-----MCN-----ENVNV-----TINH-----RYGIMLVRAECC-----GSPFLETSIDGSGSYNQGKYNIT | 566 | BcAgl-KA |
| PhMut | 477 | IPNDIDINPVYFCQVNLQFQS-----MSPN-----MCN-----ENVNV-----TINH-----RYGIMLVRAECC-----GSPFLETSIDGSGSYNQGKYNIT | 565 | PhMut |
| PcmPtp | 478 | IPNDIDINPVYFCQVNLQFQS-----MSPN-----MCN-----ENVNV-----TINH-----RYGIMLVRAECC-----GSPFLETSIDGSGSYNQGKYNIT | 566 | PcmPtp |
| PkmMu | 460 | VNDIDIDIPYXHMEQINQVNLWEEHVLCYNG-----GSPFLETSIDGSGSYNQGKYNIT | 556 | PkmMu |
| PkmMu1 | 478 | IPNDIDINPVYFCQVNLQFQS-----MSPN-----MCN-----ENVNV-----TINH-----RYGIMLVRAECC-----GSPFLETSIDGSGSYNQGKYNIT | 566 | PkmMu1 |
| PkmMu2 | 478 | IPNDIDINPVYFCQVNLQFQS-----MSPN-----MCN-----ENVNV-----TINH-----RYGIMLVRAECC-----GSPFLETSIDGSGSYNQGKYNIT | 566 | PkmMu2 |
| PjAHPH0617 | 478 | IPNDIDINPVYFCQVNLQFQS-----MSPN-----MCN-----ENVNV-----TINH-----RYGIMLVRAECC-----GSPFLETSIDGSGSYNQGKYNIT | 571 | PjAHPH0617 |
| PjAHPH3616 | 477 | IPNDIDINPVYFCQVNLQFQS-----MSPN-----MCN-----ENVNV-----TINH-----RYGIMLVRAECC-----GSPFLETSIDGSGSYNQGKYNIT | 566 | PjAHPH3616 |
| PyAHPH | 478 | IPNDIDINPVYFCQVNLQFQS-----MSPN-----MCN-----ENVNV-----TINH-----RYGIMLVRAECC-----GSPFLETSIDGSGSYNQGKYNIT | 566 | PyAHPH |
| PpmMu2 | 477 | IPNDIDINPVYFCQVNLQFQS-----MSPN-----MCN-----ENVNV-----TINH-----RYGIMLVRAECC-----GSPFLETSIDGSGSYNQGKYNIT | 565 | PpmMu2 |
| PgAgl-FH1 | 554 | TRVSGNNW 561 | | PgAgl-FH1 |
| PgAgl-FH2 | 566 | N----- 566 | | PgAgl-FH2 |
| BcAgl-KA | 567 | Q----- 567 | | BcAgl-KA |
| PhMut | 566 | K----- 566 | | PhMut |
| PcmPtp | 567 | Q----- 567 | | PcmPtp |
| PkmMu | 557 | N-VNF----- 560 | | PkmMu |
| PkmMu1 | 567 | Q----- 567 | | PkmMu1 |
| PkmMu2 | 567 | H----- 567 | | PkmMu2 |
| PkmMu3 | 567 | H----- 567 | | PkmMu3 |
| PkmMu4 | 567 | N----- 567 | | PkmMu4 |
| PkmMu5 | 572 | Q----- 572 | | PkmMu5 |
| PjAHPH0617 | 554 | TRVSGNNW 561 | | PjAHPH0617 |
| PjAHPH3616 | 566 | N----- 566 | | PjAHPH3616 |
| PyAHPH | 567 | E----- 567 | | PyAHPH |
| PpmMu2 | 566 | K----- 566 | | PpmMu2 |

Figure S1 Multiple alignments of amino acid sequence of catalytic α -1,3-glucanase domains.

Abbreviations and accession number of the α -1,3-glucanases and APHP domain-containing

protein are as follows: PgAgl-FH1, α -1,3-glucanase from *P. glycanilyticus* FH11 (BAP10900): PgAgl-FH2, α -1,3-glucanase from *P. glycanilyticus* FH11 (BAP10901): BcAgl-KA, α -1,3-glucanase from *B. circulans* KA-304 (BAE98302): PhMut, α -1,3-glucanase from *Paenibacillus humicus* (BAI23187): PcMutP, α -1,3-glucanase from *P. curdlanolyticus* (ADT91063): PkMuA, α -1,3-glucanase from *Paenibacillus* sp. KSM-35 (BAG15878): PkMuB, α -1,3-glucanase from *Paenibacillus* sp. KSM-86 (BAF56208): PkMuC1, α -1,3-glucanase from *Paenibacillus* sp. KSM-126 (BAG15879): PkMuC2, α -1,3-glucanase from *Paenibacillus* sp. KSM-126 (BAG15880): PkMuE, α -1,3-glucanase from *Paenibacillus* sp. KSM-138 (BAH10514): PjAPH0617, 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, α -1,3-glucanase from *Paenibacillus* sp. P22 (CDN41550). Black shading; Threshold 70% for identity. Gray shading; Similarity. Amino acid sequences of catalytic α -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

| Purification step | Total activity (U) | Total protein (mg) | Specific activity (U/mg) | Purification (fold) | Yield (%) |
|--------------------------------|-----------------------|-----------------------|-----------------------------|---------------------|-----------|
| 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 |