

1 ATGAAGGCCATCTATGGACGTAACCTTCAAACCACAAGACTTGAATGCCAAACAGTACACCCACGTCTTGT
1 M K A I Y G R N F K P Q D L N A K Q Y T H V L F
73 GCATTTGCCAAGATCAATGGGCAGACTGGAGAAATCGGTCTTGCTGACCCCTGGGCTGATACAGACATTCAT
25 A F A K I N G Q T G E I G L A D P W A D T D I H
145 TGGGATGAACCCTGGGACCAACCAGGGACCAACCTCTTCGGCATTTCGAGCTTTACAAGCTCAAACGT
49 W D E P W D Q P G T N L F G I F W Q L Y K L K R
217 GCCAACCGAAAGCTCAAGGTGATGTTATCCATAGGTGGATGGACTTACTCCAGGACGGAGACCTCCCTGGC
73 A N R K L K V M L **S I G G W** T Y S Q D G D L P G
Substrate binding site
289 GGTGCGAGTACTCCCGAACGTCGAGATACATTCGCTCGTACAGCCGTCGAAATGGTCAGAAATTTGGCCTC
97 G A S T P E R R D T F A R T A V E M V R N F G L
361 GACGGTGTGACGTCGACTGGGAATACCAAAATGATGCAACTGAAGTCGCCAACTTTGTCGATCTTTAAGA
121 **D G V D V D W E** Y P N D A T E V A N F V D L L R
Active site
433 CGCATCCGCCAGTACCTCGACATACTGAATCCTCGGTTTGAGATCTCAGTTGCTGTACCATGTGGTCTTGAC
145 R I R Q Y L D I L N P R F E I S V A V P C G L D
505 CAGCTCCAAAACCTTGACGCTGCTGGAATGGACAAATATCTCAGCTTCTGGAATTTGATGGCCTACGACTTT
169 Q L Q K L D A A G M D K Y L S F W N L M A Y D F
577 TCAGGTCGTTGGTCTGGTTTCGGGACATGCTTCAAACGTTTATTTCGAAGACGAACCCAGCCTCGACA
193 S G P W S S V S G H A S N V H Y S K T N P A S T
649 GACTATTCATTCGATAAACTCTCGACTTTTTCAAGGGTTCGGTAAAGCCAGAGAACTGGTGATGGGAATG
217 D Y S F D K T L D F F K G S V K P E K L V M G M
721 CCGTTATATGGCCGAGGTTTTGCGGACACAGATGGGCCGGGAAAACCGTACAATGGTGGCGGTGCCGGGCAC
241 P L Y G R G F A D T D G P G K P Y N G G G A G H
793 TGGGAGGCAGGCGTCTGGGATTATAAAGATCTCCCGTTGGCAGGTTGCAAAGTCAATGAGGATCCGTATGCT
265 W E A G V W D Y K D L P L A G S K V N E D P Y A
865 ATCGCCGCTGGAGCTATGATGCCGCTACAAAATAATGGTATCGTTTGACACACCCAACTTGCCAAGTGG
289 I A A W S Y D A A T K L M V S F D T P N V A K W
Chitinase insertion domain
937 AAGGCCAGTATATCAAGGCAAAGGGGCTGGGAGGAGCGATGTGGTGGGAGACTAGTGGGACAAAAGTCGGT
313 K A Q Y I K A K G L G G A M W W E T S G D K V G
1009 TCGGAGTCTCTCGTTCAGACTGTTATAGATGCCCTGGGAGGGACGAAAGCATTGGATACGCACAAGAATACG
337 S E S L V Q T V I D A L G G T K A L D T H K N T
1081 ATTGCATATCCTGGATCTAAATACGACAATGTTTCGACGCTTGGCCTTGA
361 I A Y P G S K Y D N V R S A C A *

Supplementary Fig. S1. Nucleotide sequence and amino acids sequence of chitinase AO-801. Red letters indicated the conserved catalytic domains (SIGGW and LDGVDVDWE) of glycosyl hydrolase family 18; Underlined letters indicated the chitinase insertion domain.