Supplementary Information

Figure S1. Nucleotide and deduced amino acid sequences of ApuASK. Numbers on left side indicate the positions of nucleotide and amino acid, respectively. Residues from −29 to 0 are signal peptide (underlined). Residues A336−T414 constituted CD and pullulan-degrading enzymes N-terminus domain (○). Residues Q452−R912 indicated alpha-amylase catalytic domain (grey highlight). Residues D917−L1001 represented amyC domain (●). Residues T1006−L1092; Q1214−T1302 constituted two fibronectin type III (FnIII) domains (△). Residues T1302−A1399 indicated CBM20 domain (▲). Residues P1531−T1596 represented nine-repeated sequence of PGSGTT with a PGSGTA and PGSGTM (double underlined). Residues E1811−R1874; F1875−A1936; V1944−M2003 indicated three consecutive repeats of S-layer homology (SLH) domain (★). The four conserved regions of the α-amylase family, designated as I, II, III, and IV are shown in rectangular.

```
                                                           GTGGGGAGAAGATGG
                                                            V  G  R  R  W
          AGAAAGCATTTCGCTTATTTCTCAATCTTTTTGCTTTTGGCGCAATTGTTTTCATTTAGTGCAATCGTTCGCGCT
           R  K  H  F  A  Y  F  S  I  F  L  L  L  A  Q  L  F  S  F  S  A  I  V  R  A
     1    AATGAAAACGTGCAAAGCCCTGTCGTAAACGGAAATGAAGTGACGTTCCGTTATGTCGGCACAGGGGAGGAGCAG
     1     N  E  N  V  Q  S  P  V  V  N  G  N  E  V  T  F  R  Y  V  G  T  G  E  E  Q
    76    TCTGTCTTATTAGCCGGATCGTTTAACGGCTGGCAAACAAGTGGAGACAAAAAGATTGAATTGACAAAAGAAAGC
    26     S  V  L  L  A  G  S  F  N  G  W  Q  T  S  G  D  K  K  I  E  L  T  K  E  S
   151    GACCATATTTGGTCAGTCACAAAAACGCTTCCAGACGGAAAGCATATGTACAAGTTTGTTGTGGACGGAAATTGG
    51     D  H  I  W  S  V  T  K  T  L  P  D  G  K  H  M  Y  K  F  V  V  D  G  N  W
   226    AAGCCAGATCCACTAAATAACAATCAAGTAGATGATGGATATGGTGGGAAAAATAGCGTCGTTGTTGTCGGTCAA
    76     K  P  D  P  L  N  N  N  Q  V  D  D  G  Y  G  G  K  N  S  V  V  V  V  G  Q
   301    CCTGTTCAACAACAACGCATCGTCACGCTCGTTGGGAACTTACAAGATGAGTTAGGACATACAGGCGAGTGGGAT
   101     P  V  Q  Q  Q  R  I  V  T  L  V  G  N  L  Q  D  E  L  G  H  T  G  E  W  D
   376    CCAAAAGCGACGGCTACAATTATGAAACATGAAGGCGATGGTTTGTACACGTTTACGGGAACGCTTCCAGCAGGT
   126     P  K  A  T  A  T  I  M  K  H  E  G  D  G  L  Y  T  F  T  G  T  L  P  A  G
   451    ACGTATAAGTACAAATCGCCATTAACGGTAGTTGGGATGAAAATTACGGTGCTGGTGGACGTGATGGTACAGAT
   151     T  Y  K  Y  K  I  A  I  N  G  S  W  D  E  N  Y  G  A  G  G  R  D  G  T  D
   526    ATTCCACTTACGTTAGAAAAAGAAACGAAAGTGACGTTTTACTATCATGACCGCACGCACGCGATTGCGGACTCG
   176     I  P  L  T  L  E  K  E  T  K  V  T  F  Y  Y  H  D  R  T  H  A  I  A  D  S
   601    ACGTGGTATACACCAATTCCAAAGGAGAAGCAACCGCGTTTAGTCGGAACAATTTTGCCAGCGATCGGTTATGAA
   201     T  W  Y  T  P  I  P  K  E  K  Q  P  R  L  V  G  T  I  L  P  A  I  G  Y  E
   676    ACGGAAGTAAACGGATGGACCCCAGAAAAGTCAACAGCATTTCTCATTGATGATAATTTTGACTCCATTTACACG
   226     T  E  V  N  G  W  T  P  E  K  S  T  A  F  L  I  D  D  N  F  D  S  I  Y  T
   751    TTCACGGCACGTGTGCCAAAAGGGATGTACGAATTTAAGGTGACATTAGGGAATAGCTGGGCCGAAAATTATCCG
   251     F  T  A  R  V  P  K  G  M  Y  E  F  K  V  T  L  G  N  S  W  A  E  N  Y  P
   826    CAAGATGATGCGAAATTAAACGTATTGGAAGATACGACTATAACGTTTTTCTTTAACGATAAAGAAAAAACGTTA
   276     Q  D  D  A  K  L  N  V  L  E  D  T  T  I  T  F  F  F  N  D  K  E  K  T  L
   901    TACACAGACTATAGCCCAACTGGCTCAGATGGGGCAGTGCAAAAGGATCGTTTAAAACATAACACATGGGATTCG
   301     Y  T  D  Y  S  P  T  G  S  D  G  A  V  Q  K  D  R  L  K  H  N  T  W  D  S
   976    TTATATCGCCAACCGTTCGGTGCAGTAAAAGCAGGAGAAAGCGTGACGCTTCGACTAGCGGCGAAAAAGGGGAT
   326     L  Y  R  Q  P  F  G  A  V  K  A  G  E  S  V  T  L  R  L  A  A  K  K  G  D
                                 ○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○
  1051    TTAACAAAAGCGAACGTATATGTGAAAAATACAACGACAGGAACAGCGAAGTTATATACAATGAACAAAGTTGGA
   351     L  T  K  A  N  V  Y  V  K  N  T  T  T  G  T  A  K  L  Y  T  M  N  K  V  G
          ○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○
  1126    GTCATCGGTGATGATGAATATTGGGAAGCAACGTTTAAGCCTGATGACAAAGGATTGTACGCATATAAGTTCATT
   376     V  I  G  D  D  E  Y  W  E  A  T  F  K  P  D  D  K  G  L  Y  A  Y  K  F  I
          ○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○
  1201    GCGATGGACGGTTCCGCAAAAGCGGAATATGGAGAGGATACACAAGAAGGTCAATGGGGAAGAGCAGTTGATAAA
   401     A  M  D  G  S  A  K  A  E  Y  G  E  D  T  Q  E  G  Q  W  G  R  A  V  D  K
          ○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○○
  1276    AATGCTGAATTGTTCCAGCTAACTGTATACGATCCAAACTATAAAACGCCAGATTGGATGAAGCATGCGGTTGTT
   426     N  A  E  L  F  Q  L  T  V  Y  D  P  N  Y  K  T  P  D  W  M  K  H  A  V  V
  1351    TATCAAATTTTCCCTGATCGTTTCTTTAACGGCAATCCAGACAATGACGATGCTAAATCGAATGCACGAGGAAAT
   451     Y  Q  I  F  P  D  R  F  F  N  G  N  P  D  N  D  D  A  K  S  N  A  R  G  N
```

```
1426  GAACCAATTGAACATCGCGAATGGTCGCAGCTTCCAGACAATCCACGCATGAAAGGGACAGCTGGATATGATGGC
 476   E  P  I  E  H  R  E  W  S  Q  L  P  D  N  P  R  M  K  G  T  A  G  Y  D  G

1501  GATGGCATTTGGTCGAACGACTTTTTCGGTGGAGATATTGCAGGAATTGAACAAAAGCTAGATTATTTACAATCT
 501   D  G  I  W  S  N  D  F  F  G  G  D  I  A  G  I  E  Q  K  L  D  Y  L  Q  S

1576  CTTGGGGTTAATACGTATATATTTAAATCCGATTGCTAAAGCACCATCTAACCATAAATACGATGCGAATGACTAC
 526   L  G  V  N  T  I  Y  L  N  P  I  A  K  A  P  S  N  H  K  Y  D  A  N  D  Y

1651  AAAGAGCTTGATCCAATGTTTGGAACGCCTGAAGAATTTCAATCATTTGTGCAAGCGGTTGCATCTCGTGGTATG
 551   K  E  L  D  P  M  F  G  T  P  E  E  F  Q  S  F  V  Q  A  V  A  S  R  G  M

1726  CACTTAATTTTAGACGGTGTATTTAATCACGTATCAGACGATTCCATTTATTTTGACCGTTATGGAAAATATCCA
 576   H  L  I  L  D  G  V  F  N  H  V  S  D  D  S  I  Y  F  D  R  Y  G  K  Y  P
                      Region I

1801  ACCGTCGGAGCATACGAATATTGGTCGGCTGTGTATGATTTGATGAATGGAAAAGGATTATCAGAAGAACAAGCT
 601   T  V  G  A  Y  E  Y  W  S  A  V  Y  D  L  M  N  G  K  G  L  S  E  E  Q  A

1876  CGTGCTCAAGTTGAACAAAAGTTTAAAGCTGAGGGACAACAGTTCAGTCCGTACGGATTCCATTTATGGTTTAAT
 626   R  A  Q  V  E  Q  K  F  K  A  E  G  Q  Q  F  S  P  Y  G  F  H  L  W  F  N

1951  ATCGAGAATGAAAAGTAAACGGTGTGTACAAATATCAATCGTGGTGGGATTTGATAGTTTACCAGAATTTAAG
 651   I  E  N  E  K  V  N  G  V  Y  K  Y  Q  S  W  W  G  F  D  S  L  P  E  F  K

2026  TCTGTCACTGGAACGAAAGTAAAGTATGCGAGCGAGTTAAATAACGAACAGCTTGCAAATTACATTTTTTATGAA
 676   S  V  T  G  T  K  V  K  Y  A  S  E  L  N  N  E  Q  L  A  N  Y  I  F  Y  E

2101  GACGATTCTGTCGCCAAAGCTGGATTACGCGCGGAGCTTCAGGTTGGCGCTTAGACGTTGCGAATGAAGTCGAT
 701   D  D  S  V  A  K  S  W  I  T  R  G  A  S  G  W  R  L  D  V  A  N  E  V  D
                                                Region II

2176  ACACAGTTTTGGCGCGAATTTCGTAAAGAGTTGTTGCAAGGTGACTACGACCGTGGCCCAACGTTGAAAAACGGG
 726   T  Q  F  W  R  E  F  R  K  E  L  L  Q  G  D  Y  D  R  G  P  T  L  K  N  G

2251  GAGCAACCGTTAATTCTCGGTGAAATTTGGGATGATGCGTCAAAATACTTCCTAGGCGATCAATACGATTCAGTG
 751   E  Q  P  L  I  L  G  E  I  W  D  D  A  S  K  Y  F  L  G  D  Q  Y  D  S  V
                            Region III

2326  ATGAACTATCGTTTCCGCGGTGCTGTGTTAGACTTTTTACGAAATGGGAAAGCGGAAGATATTGATGCCCGACTA
 776   M  N  Y  R  F  R  G  A  V  L  D  F  L  R  N  G  K  A  E  D  I  D  A  R  L

2401  ACAGCGATTCGTGAAGATTATCCGGAAGAAGCTTTTTATGCGCTAATGAACTTAATTGGTTCACACGATACGGCA
 801   T  A  I  R  E  D  Y  P  E  E  A  F  Y  A  L  M  N  L  I  G  S  H  D  T  A
                                                        Region IV

2476  CGCGCTGTTTTCTTACTTGGAAACGGAACGGATTCATACGAACGTGCTGAACTTGATCCGAATTATAATGAAGAA
 826   R  A  V  F  L  L  G  N  G  T  D  S  Y  E  R  A  E  L  D  P  N  Y  N  E  E

2551  CTCGGTAAAAAGCGATTAAAACTCGCTGCTATTTTACAAATGGGTTATCCAGGTGCGCCGACAATCTACTATGGT
 851   L  G  K  K  R  L  K  L  A  A  I  L  Q  M  G  Y  P  G  A  P  T  I  Y  Y  G

2626  GATGAAGCAGGAGTGACAGGTTCGAAGGATCCGGACGATCGTCGTACGTATCCGTGGGGAAGTGAGGACAAGCAA
 876   D  E  A  G  V  T  G  S  K  D  P  D  D  R  R  T  Y  P  W  G  S  E  D  K  Q

2701  CTCATTGCACATTATCAAAAAGTAGGTGCGATTCGCACGAAGCATCAAGATGTATTAGCGAAAGGAACAATTGAG
 901   L  I  A  H  Y  Q  K  V  G  A  I  R  T  K  H  Q  D  V  L  A  K  G  T  I  E
                                    ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ●

2776  ACAGTATATGCGAAAGGTGATGTATACGTCTTTGCCCGTCAGTACGGAAAAGATGTTGCGCTTATTGCGGTAAAC
 926   T  V  Y  A  K  G  D  V  Y  V  F  A  R  Q  Y  G  K  D  V  A  L  I  A  V  N
       ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ●

2851  CGCGGCAATAGTGAACAAACGGTACAGTTGGATGTCGCTTCACTTATTCCAAATGGCATCAAATTAGTAGATGAA
 951   R  G  N  S  E  Q  T  V  Q  L  D  V  A  S  L  I  P  N  G  I  K  L  V  D  E
       ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ●

2926  CTACATGATTCATATGATGTAACTGTAACAAATGGAAAAGTCACATTACGTGTTCCAGCAATGGACGGTCGAATG
 976   L  H  D  S  Y  D  V  T  V  T  N  G  K  V  T  L  R  V  P  A  M  D  G  R  M
       ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ●

3001  TTATTTGGAGAAGCAACTGTTGCTCTTCCGAATAAAGTAACAGATGTTCAAGCGACATCGGGCGTTGGACAAGTG
1001   L  F  G  E  A  T  V  A  L  P  N  K  V  T  D  V  Q  A  T  S  G  V  G  Q  V
       ●             △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △

3076  ACATTAACGTGGGAAGGTGATGCACCAACGTACCGTATTTATCAATCTACATTAAAAGGTGCAGGTTATGAGCTT
1026   T  L  T  W  E  G  D  A  P  T  Y  R  I  Y  Q  S  T  L  K  G  A  G  Y  E  L
       △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △

3151  GTGGAAGAAACGAGTGAAAAGACAGCTGTGATAGACAATTTGAAAAACGGTACCGCATATTACTTTGCGATTACA
1051   V  E  E  T  S  E  K  T  A  V  I  D  N  L  K  N  G  T  A  Y  Y  F  A  I  T
       △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △

3226  GCTGTTGATACAAACGGAAATGAGTCGGCTAAAGTAGAAACAAGCCGCCTTGTCCCACATTATCCATTAGAAGAA
1076   A  V  D  T  N  G  N  E  S  A  K  V  E  T  S  R  L  V  P  H  Y  P  L  E  E
       △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △

3301  GAACACGTTGCTTTACTTTCTGAAGTGAACGGTGGAGTGCTCGATTTAGCTGCTTCAATTACGGTTGAAGCGAAA
1101   E  H  V  A  L  L  S  E  V  N  G  G  V  L  D  L  A  A  S  I  T  V  E  A  K

3376  GTGCAAATCGATAATGTAACGAAACATGGGTTAGCTGACGGTTTACAAGCGGTGTTCCAAGTGAAAAAACCGAAT
1126   V  Q  I  D  N  V  T  K  H  G  L  A  D  G  L  Q  A  V  F  Q  V  K  K  P  N
```

```
3451  AGCGACAAATGGGAAGACATACAAGCAACGTACGACCGACAAGATGGCGATGCGAATGTATTCCGTGCATCGTTC
1151   S  D  K  W  E  D  I  Q  A  T  Y  D  R  Q  D  G  D  A  N  V  F  R  A  S  F

3526  ACTCCGCTACAAGCAGGCACGTACACGTATCGTTATGGCTTTACGACAAATCTCGGTGACAGTTGGGTGCATACA
1176   T  P  L  Q  A  G  T  Y  T  Y  R  Y  G  F  T  T  N  L  G  D  S  W  V  H  T

3601  GAAGAAAAAACGTTTACACTCACTGCAAATGAGGCAGATCAACAAGCACCAGCAAAGGGCATTCAACTTGTTCAA
1201   E  E  K  T  F  T  L  T  A  N  E  A  D  Q  Q  A  P  A  K  G  I  Q  L  V  Q
                                              △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △

3676  CCAGACGTTGAATCCGGTCAAGTGAATTTAACGTGGTCGTTCGTAGATCGAGATGACAATGATGCCTATATGCTT
1226   P  D  V  E  S  G  Q  V  N  L  T  W  S  F  V  D  R  D  D  N  D  A  Y  M  L
       △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △

3751  ATCATTGAGCGTGATGGTCAAATCGTCCATACAACAACGAATATCGGTACATCATTTACTGATTATGATGTTGAA
1251   I  I  E  R  D  G  Q  I  V  H  T  T  T  N  I  G  T  S  F  T  D  Y  D  V  E
       △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △

3826  AACGGAAAAACATATACGTATGTTGTGAAGTTGTATGACCGTGCTGGGAACGTTGTCGCATCAAATGACGTGCAA
1276   N  G  K  T  Y  T  Y  V  V  K  L  Y  D  R  A  G  N  V  V  A  S  N  D  V  Q
       △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △ △

3901  ATTACGCCAGACATCGTGATGGTTCAAGTGACGTTTAAAGTGAAAGCACCAAGCTATACACCGTTAGATACGCGC
1301   I  T  P  D  I  V  M  V  Q  V  T  F  K  V  K  A  P  S  Y  T  P  L  D  T  R
       △ △ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲

3976  ATTACGATTCCAAATAGTATTAACGGTTGGAATACAGGTGCATGGGAAATGACGCGTGGTGGAGCGGTCACACCT
1326   I  T  I  P  N  S  I  N  G  W  N  T  G  A  W  E  M  T  R  G  G  A  V  T  P
       ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲

4051  GATTGGGAATTTACAACGGAGCTTCAAGAAGGCGAAACAATTACTTATAAGTATGTAAAGGGTAGCTCATGGGAT
1351   D  W  E  F  T  T  E  L  Q  E  G  E  T  I  T  Y  K  Y  V  K  G  S  S  W  D
       ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲

4126  CAAGAAGGGCTAGCTGATCATACACGTGATGATCAAACAGATGATGATGTTAGCTATTATGGCTATGGTGCGATC
1376   Q  E  G  L  A  D  H  T  R  D  D  Q  T  D  D  D  V  S  Y  Y  G  Y  G  A  I
       ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲ ▲

4201  GGAACGGATTTAAAAGTTACGGTACAAAATCAAGGCAATAACAAAATGATCATTCAAGATTACATTTTACGTTGG
1401   G  T  D  L  K  V  T  V  Q  N  Q  G  N  N  K  M  I  I  Q  D  Y  I  L  R  W

4276  ATCGATATGCCTGTCGTTGTTGAAGAAGTGAAAAAAGATGGCGATCGCGTCACGATAAAAGGAAACGCGATTAAA
1426   I  D  M  P  V  V  V  E  E  V  K  K  D  G  D  R  V  T  I  K  G  N  A  I  K

4351  GATGGCGTGTTAACGATCAATAAAGAACGTGTCACGATTCAAGACGACATGTCATTTACGTACACGTTCACACCA
1451   D  G  V  L  T  I  N  K  E  R  V  T  I  Q  D  D  M  S  F  T  Y  T  F  T  P

4426  GCAGCCAATCAAAAAGAAGTGGCCATCCACATCGAACCGTCTGAACGAAGTAAGTCAGACATCTTTAAAAATGAT
1476   A  A  N  Q  K  E  V  A  I  H  I  E  P  S  E  R  S  K  S  D  I  F  K  N  D

4501  GGCGGTGCCATTGCGAAAAATACGAAAAACTACGTACTAAATATCGAAACAAAACAATTGCGCGAAGGTGTGTTG
1501   G  G  A  I  A  K  N  T  K  N  Y  V  L  N  I  E  T  K  Q  L  R  E  G  V  L

4576  CAAGAGGATACAACACCGGGCAGTGGCACAACACCAGGCAGCGGTACAACACCAGGCAGTGGCACAGCACCAGGT
1526   Q  E  D  T  T  P  G  S  G  T  T  P  G  S  G  T  T  P  G  S  G  T  A  P  G
                    ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾

4651  AGCGGCACAACACCAGGTAGCGGCACAATGCCGGGCAGCGGCACAACACCGGGCAGTGGCACAACACCGGGCAGT
1551   S  G  T  T  P  G  S  G  T  M  P  G  S  G  T  T  P  G  S  G  T  T  P  G  S
       ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾

4726  GGCACAACACCGGGCAGCGGCACAACACCAGGAAGTGGCACAACACCAGGAAGTGGCACAACACCAGTGAAGGGT
1576   G  T  T  P  G  S  G  T  T  P  G  S  G  T  T  P  G  S  G  T  T  P  V  K  G
       ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾

4801  GAAAATGGTACGGTTGTTTTACAGCCGAAAGTAGAGACGAAAGAAAAAGACGGCAAAGTAGTAGAAAAAGTGGCA
1601   E  N  G  T  V  V  L  Q  P  K  V  E  T  K  E  K  D  G  K  V  V  E  K  V  A

4876  ACTATTTCAACAAATGAAGTTGAAGCGATTGTCAAGGAGCTGTCGAATGAAAATAAACAAGTCGTCGTCTCCCTC
1626   T  I  S  T  N  E  V  E  A  I  V  K  E  L  S  N  E  N  K  Q  V  V  V  S  L

4951  GGCTCGCTTCCAAAAGGTGTAGCCACAAAAGTAGATGTGCCAGCTACATTATTTACAAAAGCGGCAAATAAGCAA
1651   G  S  L  P  K  G  V  A  T  K  V  D  V  P  A  T  L  F  T  K  A  A  N  K  Q

5026  GGAGAAGCAACGATTGTGAGTGCAACTGAGCAGGCGACATACAAATTGCCAGCAAAGAAGTACAAGCGTCTCTG
1676   G  E  A  T  I  V  S  A  T  E  Q  A  T  Y  K  L  P  A  K  E  V  Q  A  S  L

5101  GCAGCGATTGCAAAAACACTCGGTGCAACAGTCGAACAAGTAAACATCTCGATCGAAATGAAAGTAAAAGATGCT
1701   A  A  I  A  K  T  L  G  A  T  V  E  Q  V  N  I  S  I  E  M  K  V  K  D  A

5176  CCACAACTACGTGCGAAAGCATTATCTGATGCAGTAGAGTTTCATGTTGTGGCGAAGGCAAACGGAAAAGAACAA
1726   P  Q  L  R  A  K  A  L  S  D  A  V  E  F  H  V  V  A  K  A  N  G  K  E  Q

5251  GTGATTGATCGTTTTACTCAATATGTTGAACGTGAAATCGTATTGAAGCAGGCGGTGAATGCAAGTCGTTCTATT
1751   V  I  D  R  F  T  Q  Y  V  E  R  E  I  V  L  K  Q  A  V  N  A  S  R  S  I

5326  GTGGTGCGTGTAAACGATGACGGTTCCATTACACCTGTACCGACCACATTTGTTGGCAACAAAGCGGTCATCAAG
1776   V  V  R  V  N  D  D  G  S  I  T  P  V  P  T  T  F  V  G  N  K  A  V  I  K

5401  TCATTGACGAACTCGACATACGTCGTCGTTGAAGGAACACATACATTTGGCGACATCGAGCAACATTGGGCGAAA
1801   S  L  T  N  S  T  Y  V  V  V  E  G  T  H  T  F  G  D  I  E  Q  H  W  A  K
                                  ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★

5476  GGATATATCGAAACATTGGCAGCTAAACGCTTGTGAAAGGTATGACAGAAACAGCATACCGACCAAATGAGCAG
1826   G  Y  I  E  T  L  A  A  K  Q  L  V  K  G  M  T  E  T  A  Y  R  P  N  E  Q
       ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★ ★
```

```
5551   ATGACACGTGCCCAGTTTGCTGTGTTGCTTGTACGCGCATTAGCATTGCCACATGAAACATATGACGGTCGATTT
1851    M  T  R  A  Q  F  A  V  L  L  V  R  A  L  A  L  P  H  E  T  Y  D  G  R  F
       ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★

5626   GCTGATGTAAAAGGCACAGAATGGTTTAACAAAAACGGTGAATTAGCGGCTGCAGTCAAACTAGGTATCATTCAA
1876    A  D  V  K  G  T  E  W  F  N  K  N  G  E  L  A  A  A  V  K  L  G  I  I  Q
       ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★

5701   GGAAAAACAGCCAATACGTTTGCGCCGAATGAGCCAATCACTCGCGCCGAAGCAGCTGTTATGATCGAGCGAGCA
1901    G  K  T  A  N  T  F  A  P  N  E  P  I  T  R  A  E  A  A  V  M  I  E  R  A
       ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★

5776   TTGAAGCTTTCGTTTGTTGGCTATAATGAAGCAACAAACGACAAAACGAAAAAGGTAACAGATTTCCGCGATGCA
1926    L  K  L  S  F  V  G  Y  N  E  A  T  N  D  K  T  K  K  V  T  D  F  R  D  A
       ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★              ★  ★  ★  ★  ★  ★  ★  ★  ★

5851   AAACAATTGCCAACATGGGCAAAACAGGCGATTGAAGCAGTATACCAAGCAGGAGTCATGCAAGGACGAGATAAT
1951    K  Q  L  P  T  W  A  K  Q  A  I  E  A  V  Y  Q  A  G  V  M  Q  G  R  D  N
       ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★

5926   GGAAGCTTTGATCCTACGAGCCATATGACGCGTGCCGAAATGGCGAAAGTATTGGTGGAGTTTTTAGGAAAAGTA
1976    G  S  F  D  P  T  S  H  M  T  R  A  E  M  A  K  V  L  V  E  F  L  G  K  V
       ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★  ★

6001   AAATTGATGTAA
2001    K  L  M
       ★  ★  ★
```

Figure S2. The comparison of conserved regions of various α-amylase (Amy), cyclodextrin glucanotransferase (CGTase), type I pullulanase (Pul), and amylopullulanase (Apu) using WebLogo 3.3.
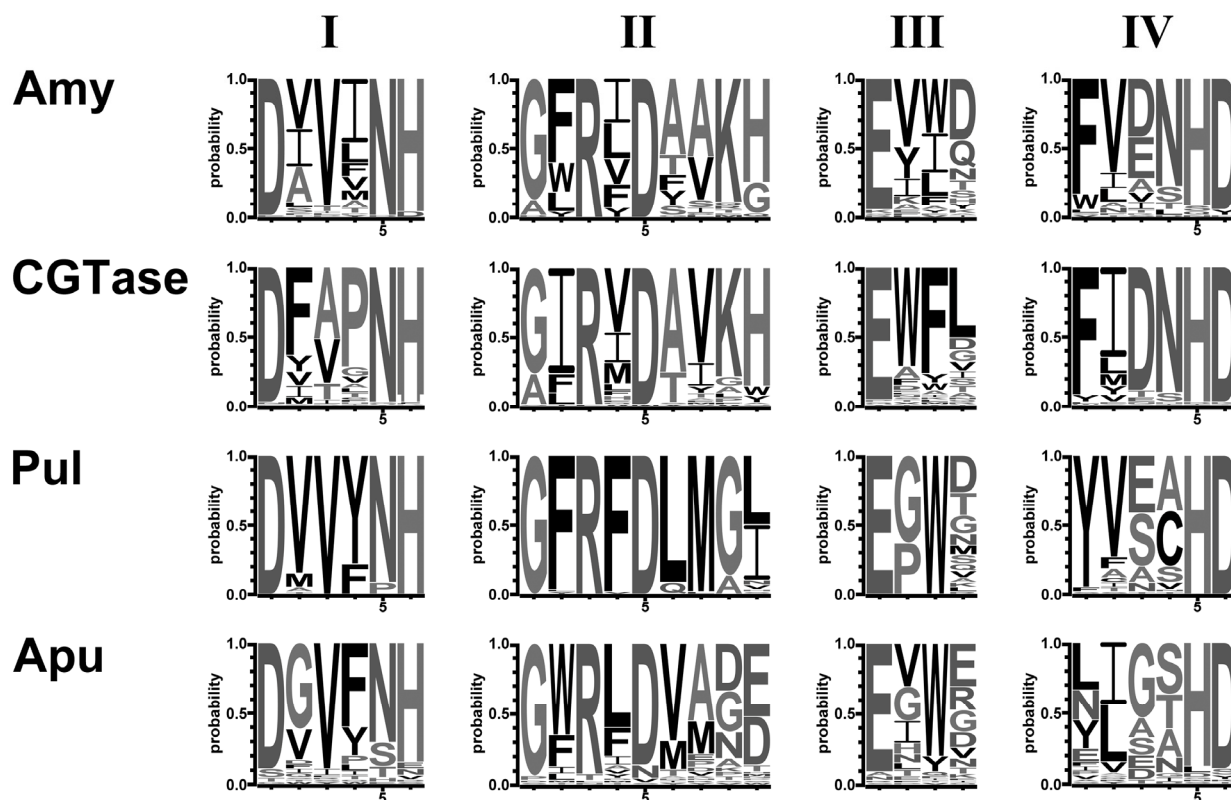
Figure S3. (**a**) SDS-PAGE (12%) and (**b**) Native-PAGE (12%) of the purified ApuASK. Zymogram for (**c**) pullulytic activity and (**d**) amylolytic activity of the purified ApuASK. Lane 1, standard molecular weight marker; Lane 2, purified ApuASK. Arrows pointing the band correspond to the purified ApuASK.