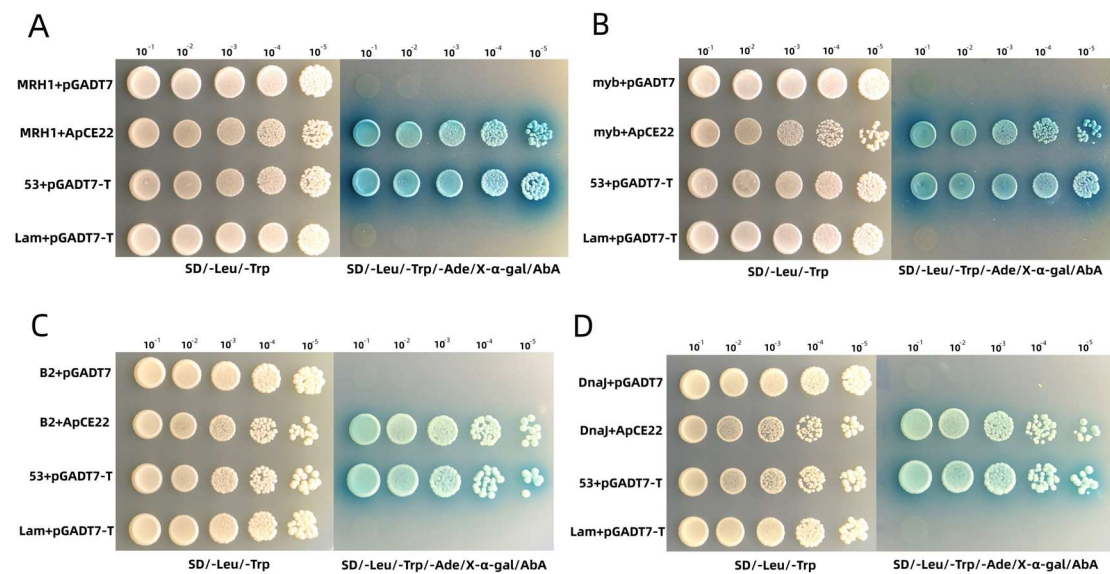**Figure S1.** Self-activation detection of pGBKT7–ApCE22. Note: A: The reaction of the pGBKT7–ApCE22 bait and pGADT7-T was spread on the SD/-Leu/-Trp/X-α-gal medium. B: The reaction of the pGBKT7–ApCE22 bait and pGADT7-T was spread on the SD/-Leu/-Trp/-His/X-α-gal medium. C: The reaction of the pGBKT7–ApCE22 bait and pGADT7-T was spread on the SD/-Leu/-Trp/-His/-Ade/X-α-gal/AbA medium
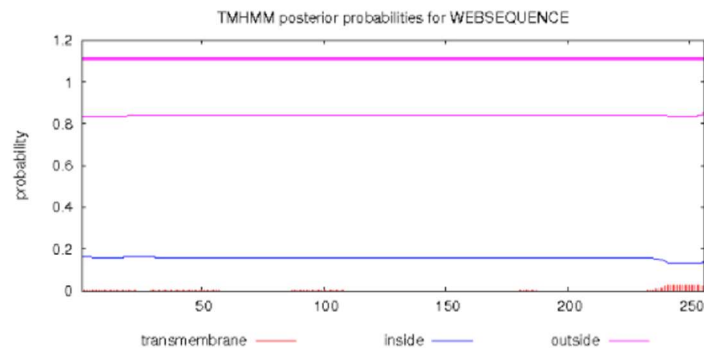

Figure S2. One-to-one yeast two-hybrid results of ApCE22 and the interacting proteins. Note: Interaction proteins were as a bait protein, and ApCE22 protein was as a prey protein.
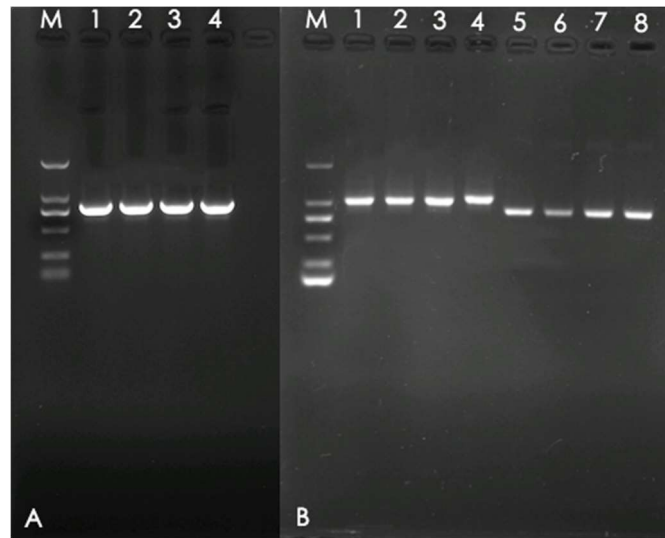
Figure S3. The gene detection results of recombinant plasmid pSPYNE(R) 173-ApCE22, pSPYCE(M)-B2 and pSPYCE(M)-DnaJ. M: DL2000 DNA marker, The labels of the ladder from top to bottom represent 2000, 1000, 750, 500, 250 and 100bp, respectively; 1, 2, 3, 4: ApCE22 gene of pSPYNE(R) 173-ApCE22 was detected by primer ApCE22-F/R; B: pSPYCE(M)-B2. M: DL2000 DNA marker, The labels of the ladder from top to bottom represent 2000, 1000, 750, 500, 250 and 100bp, respectively; 1, 2, 3, 4: B2 gene of pSPYCE(M)-B2 was detected by primer B2-F/R. 5, 6, 7, 8: DnaJ gene of pSPYCE(M)-DnaJ was detected by primer DnaJ-F/R.

WEBSEQUENCE Length: 256
WEBSEQUENCE Number of predicted TMHs: 0
WEBSEQUENCE Exp number of AAs in TMHs: 0.62391
WEBSEQUENCE Exp number, first 60 AAs: 0.11594
WEBSEQUENCE Total prob of N-in: 0.16261
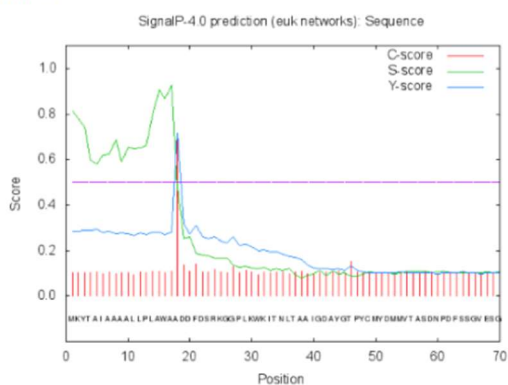WEBSEQUENCE   TMHMM2.0   outside   1   256

A

TMHMM posterior probabilities for WEBSEQUENCE

transmembrane ——   inside ——   outside ——

plot in postscript, script for making the plot in gnuplot, data for plot

SignalP-4.0 euk predictions
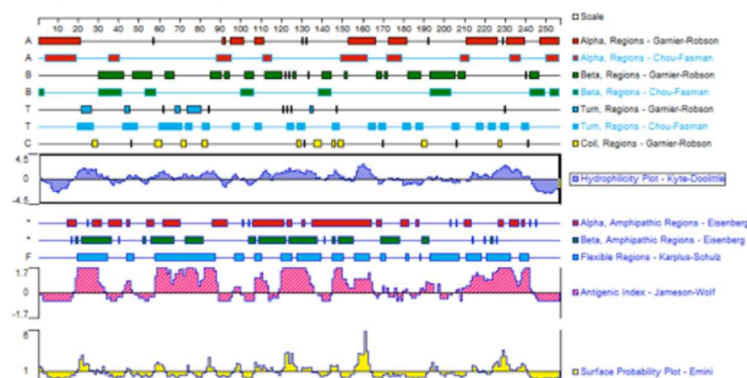>Sequence

B

SignalP-4.0 prediction (euk networks): Sequence

Measure Position Value   Cutoff   signal peptide?
  max. C   18   0.694
  max. Y   18   0.715
  max. S   17   0.927
  mean S   1-17   0.714
      D   1-17   0.715   0.450   YES
Name=Sequence   SP='YES' Cleavage site between pos. 17 and 18: AWA-AD D=0.715 D-cutoff=0.450 Networks=SignalP-noTM

C

Figure S4. Analysis of transmembrane region, signal peptide and hydrophilicity of effector ApCE22 sequence

TMHMM result

Figure part A — TMHMM result:

```
# WEBSEQUENCE Length:  346
# WEBSEQUENCE Number of predicted TMHs:  0
# WEBSEQUENCE Exp number of AAs in TMHs:  0.00439000000000001
# WEBSEQUENCE Exp number, first 60 AAs:  0.00097
# WEBSEQUENCE Total prob of N-in:  0.01697
WEBSEQUENCE   TMHMM2.0   outside   1   346
```

TMHMM posterior probabilities for WEBSEQUENCE

transmembrane ——   inside ——   outside ——

SignalP-4.1 prediction (euk networks): Sequence

```
# Measure  Position  Value   Cutoff   signal peptide?
  max. C      39      0.146
  max. Y      39      0.139
  max. S       7      0.187
  mean S     1-38     0.133
  D          1-38     0.136   0.450    NO
Name=Sequence   SP='NO' D=0.136 D-cutoff=0.450 Networks=SignalP-noTM
```
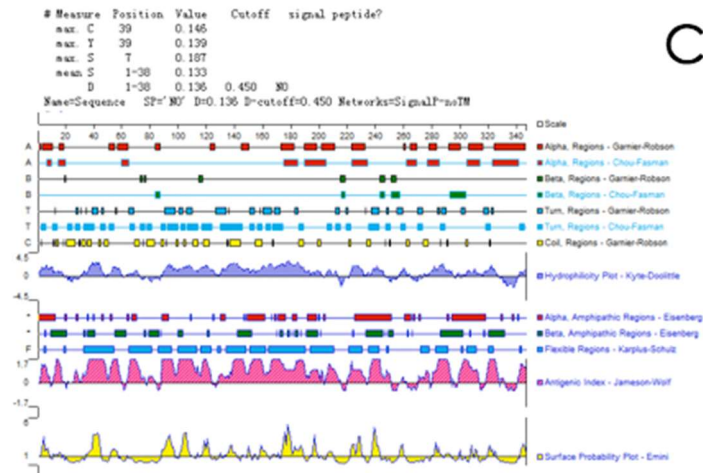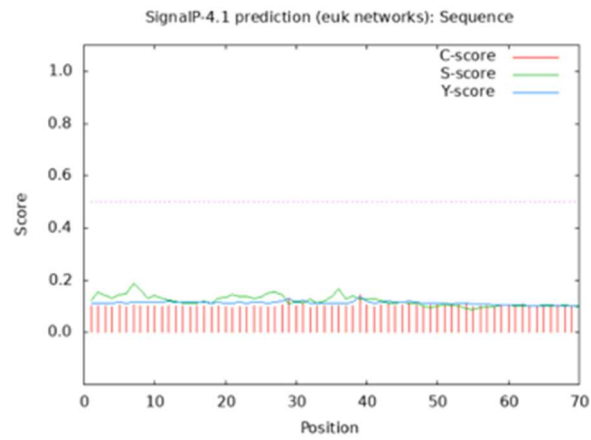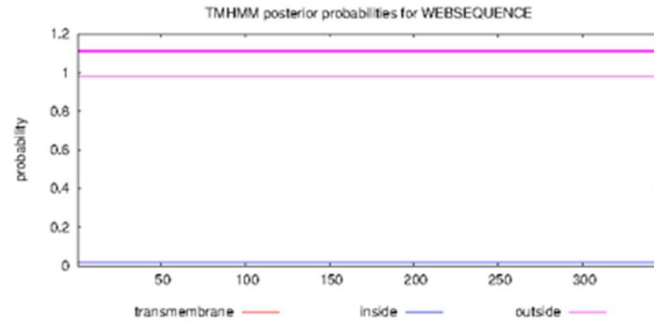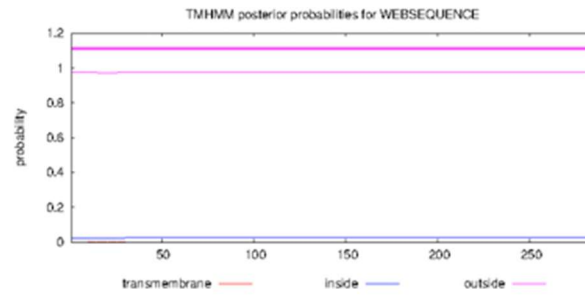
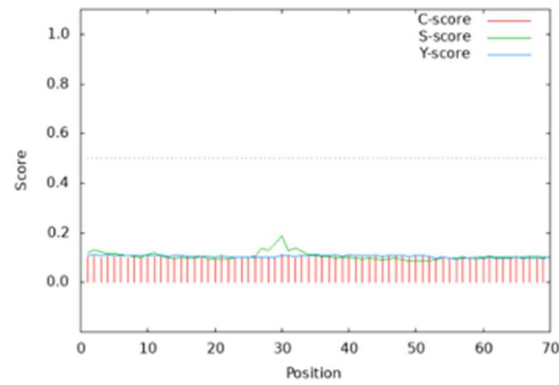**Figure S5.** Analysis of transmembrane region, signal peptide and hydrophilicity of effector B2 sequence

TMHMM result
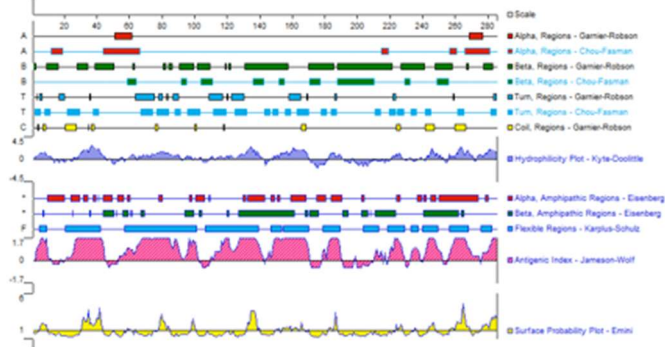
Figure S6. Analysis of transmembrane region, signal peptide and hydrophilicity of effector ChaJA6 sequence
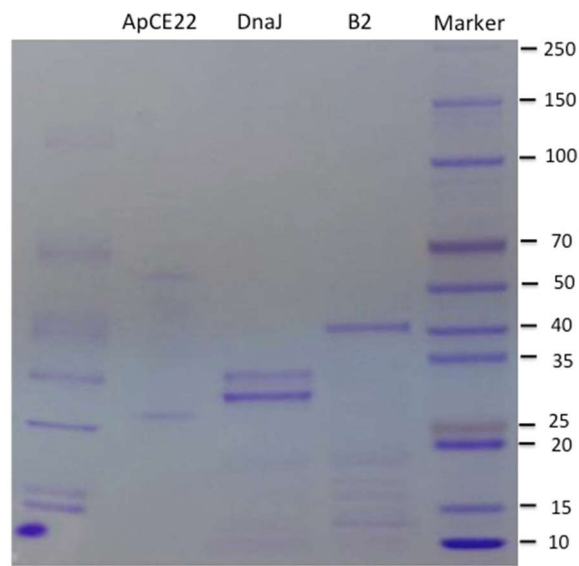
Figure S7. Electrophoresis results of the purified protein of the effector ApCE22, and the target proteins B2 and DnaJ. M: DL250KD protein marker, 1: ApCE22 protein; 2: DnaJ protein; 3: B2 protein.
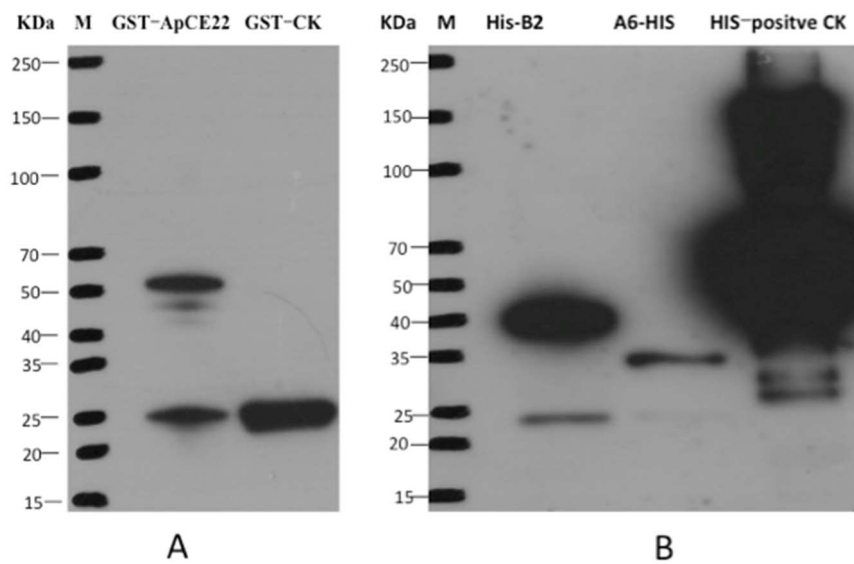
Figure S8. Western blot results of the effector ApCE22, the B2 protein and the DnaJ protein. Note: A: ApCE22 protein. B: B2 protein and DnaJ protein. M: DL250KD protein marker.

Table S1. Primer sequences of various expression vectors

Primer name	Primer sequence 5'-3'
pGBKT7-B2-F	<u>AGGCCGAATTCCCGGGGATCC</u> ATGGAGGGATACGACCGCGAGT
pGBKT7-B2-R	<u>CCGCTGCAGGTCGACGGATCC</u> TCAGGCATCATCCTTGTCTGCAAAGAT
pGBKT7- DnaJ-F	<u>AGGCCGAATTCCCGGGGATCC</u> ATGGGCACAGGAGATTACTCAAACCCGT
pGBKT7- DnaJ -R	<u>CCGCTGCAGGTCGACGGATCC</u> TCATCTCCTGCTATTGGCTGTTTGAGCCT
pGBKT7-MRH1-F	<u>AGGCCGAATTCCCGGGGATCC</u> ATGTCCCCGAGCTGGCCGG
pGBKT7-MEH1-R	<u>CCGCTGCAGGTCGACGGATCC</u> TCAGGTAGCTTCAGCAGACATGATC
pGBKT7-myb-F	<u>AGGCCGAATTCCCGGGGATCC</u> ATGGGGAGGGCGCCGTGCT
pGBKT7-myb-R	<u>CCGCTGCAGGTCGACGGATCC</u> TTAGCACGCGTCAGACAGGAGCCA
pGBKT7-ApCE22-F	<u>AGGCCGAATTCCCGGGGATCC</u>ATGAAGTACACCGCGATCGC
pGBKT7-ApCE22-R	<u>CCGCTGCAGGTCGACGGATCC</u>TTAAAGGACCATAGCCATAAGACC
pGADT7-ApCE22-F	<u>TGGGCATCGATACGGGATCC</u> ATGAAGTACACCGCGATCGC
pGADT7-ApCE22-R	<u>AGCTCGAGCTCGATGGATCC</u> TTAAAGGACCATAGCCATAAGACC
pGADT7-B2-F	<u>TGGGCATCGATACGGGATCC</u> ATGGAGGGATACGACCGCGAGT
pGADT7-B2-R	<u>AGCTCGAGCTCGATGGATCC</u> TCAGGCATCATCCTTGTCTGCAAAGAT
pGADT7-DnaJ-F	<u>TGGGCATCGATACGGGATCC</u> ATGGGCACAGGAGATTACTCAAACCCGT
pGADT7- DnaJ 6-R	<u>AGCTCGAGCTCGATGGATCC</u> TCATCTCCTGCTATTGGCTGTTTGAGCCT
pGADT7-MRH1-F	<u>TGGGCATCGATACGGGATCC</u> ATGTCCCCGAGCTGGCCGG
pGADT7-MRH1-R	<u>AGCTCGAGCTCGATGGATCC</u> TCAGGTAGCTTCAGCAGACATGATC
pGADT7-myb-F	<u>TGGGCATCGATACGGGATCC</u> ATGGGGAGGGCGCCGTGCT
pGADT7-myb-R	<u>AGCTCGAGCTCGATGGATCC</u> TTAGCACGCGTCAGACAGGAGCCA
pSPYNE(R)173-ApCE22-F	GGGCCC<u>AGGCCTACTAGTGGATCC</u>ATGAAGTACACCGCGATCGC
pSPYNE(R)173- ApCE22-R	GGTACCCTCGAGGTCGAC<u>GGATCC</u>TTAAAGGACCATAGCCATAAGACC
pSPYCE(M)-B2-F	GCCTGGCGCGCC<u>ACTAGTGGATCC</u>ATGGAGGGATACGACCGCGAGT
pSPYCE(M)-B2-R	GTCGACAGTACTATCGATGGATCCTCAGGCATCATCCTTGTCTGCAAAGAT
pSPYCE(M)-DnaJ-F	GCCTGGCGCGCC<u>ACTAGTGGATCC</u>ATGGGCACAGGAGATTACTCAAACCCGT
pSPYCE(M)-DnaJ-R	GTCGACAGTACTATCGATGGATCCTCATCTCCTGCTATTGGCTGTTTGAGCCT
PGEX-6P-1-*ApCE22*-F	<u>CAGGGGCCCCTGGGATCC</u>ATGAAGTACACCGCGATCGC
PGEX-6P-1- *ApCE22*-R	<u>CGGGAATTCCGGGGATCC</u>TTAAAGGACCATAGCCATAAGACC
pET28a-B2-F	<u>CAAATGGGTCGCGGATCC</u> ATGGAGGGATACGACCGCGAGT
pET28a-B2-R	<u>GAGCTCGAATTCGGATCC</u>TCAGGCATCATCCTTGTCTGCAAAGAT
pET28a-DnaJ-F	<u>CAAATGGGTCGCGGATCC</u> ATGGGCACAGGAGATTACTCAAACCCGT
pET28a-DnaJ-R	<u>GAGCTCGAATTCGGATCC</u>TCATCTCCTGCTATTGGCTGTTTGAGCCT

Note: the underline represents the upstream and downstream complementary sequence at the BamHI digestion site on the pGBKT7vector; the dashed underline represents the downstream complementary sequence at the upper and lower BamHI digestion sites of the pSPYNE(R)173 vector; the wavy lines represent the upstream and downstream complementary sequences at the BamHI digestion site on the pSPYCE(M) vector; the dot-dash underline represents the upstream and downstream complementary sequence at the BamHI digestion site on the PGEX-6P-1 vector; The bold underline represents the upstream and downstream complementary sequence at the BamHI digestion site on the pET28a vector. Double underscores represents the upstream and downstream complementary sequence at the BamHI digestion site on the pGADT7 vector.

Table S2. List of different plasmid ingredients in the self-activation and toxicity test.

Plasmid 1(100ng)	Plasmid 2（200ng）	Culture medium
pGBKT7-53	pGAT7-T	SD/-Trp/-Leu/X-a-gal
pGBKT7-Lam	pGAT7-T	SD/-Trp/-Leu/X-a-gal
pGBKT7–	pGAT7-T	SD/-Trp/-Leu/X-a-gal
ApCE12/ApCE22		SD/-Trp/-Leu/-His/X-a-gal
		SD/-Trp/-Leu/-His/-Ade/X-a-gal/AbA
pGBKT7		SD/-Trp