

## **Supporting Information**

### **Supplementary Methods**

#### **The titer analysis of oyster AK polyclonal antibodies**

The oyster AK polyclonal antibody titer was measured by dot blot and ELISA, following the method of Liu et al.<sup>1</sup> The specific polyclonal antibody (1:500,000 dilution) was then recruited as the primary antibody for the subsequent experiments.

#### **Analysis of physical and chemical properties of AK**

Native PAGE analysis of AK is performed according to the method of He et al.<sup>2</sup> The isoelectric point of AK was predicted by ExPASy online server. The disulfide bonds were predicted by bioinformatics sites (<http://www.csbio.sjtu.edu.cn/bioinf/Cyscon/>).

## References

1. Y. Y. Liu, M. J. Cao, M. L. Zhang, J. W. Hu, Y. X. Zhang, L. J. Zhang, G. M. Liu, Purification, characterization and immunoreactivity of  $\beta'$ -component, a major allergen from the roe of large yellow croaker (*Pseudosciaena crocea*). *Food Chem Toxicol.* 2014, **72**, 111-121.
2. X. R. He, Y. M. Cheng, Y. Yang, J. J. Xie, K. H. Chu, Y. X. Zhang, G. X. Chen, H. Liu, M. J. Cao, G. M. Liu, Cloning, expression and comparison of the properties of Scy p 9, a *Scylla paramamosain* allergen, *Food Funct.*, 2020, **11**(4), 3006-3019.

## Supplementary Figure Legends

**Figure S1.** Determination of the oyster AK polyclonal antibody titer.

(A) ELISA analysis of the AK polyclonal antibody titers, BSA was used as a negative control. All data were presented as the mean  $\pm$  SD (n = 3).

(B) Dot blot analysis of the AK polyclonal antibody titers.  $1:10^3$  -  $1:10^6$  is the polyclonal antibody dilution.

**Figure S2.** Analysis of physicochemical properties of AK.

(A) Native PAGE analysis of AK.

(B) Western blot analysis of AK after Native PAGE using oyster AK polyclonal antibody (1:500,000).

(C) Theoretical isoelectric point prediction by ExPASy online server.

(D-E) Disulfide bonds were predicted by bioinformatics sites and displayed in 3D model.

**Table S1.** AK epitopes predicted by five immunoinformatic tools.

Software	Epitope position
DNA star	5-27, 30-42, 84-92, 96-101, 121-125, 130-145, 151-159, 165-176, 189-200, 227-234, 281-289, 307-313, 318-323
BepiPred 1.0 server	12-17, 32-39, 59-69, 86-108, 121-143, 165-174, 186-199, 228-234, 306-317
ABCpred Server	11-26, 62-109, 121-146, 157-172, 180-210, 248-263, 302-341
Immunomedicine Group	16-30, 40-54, 56-95, 110-120, 125-133, 231-266, 272-282, 310-317
NetMHC II 2.3 Server	68-82, 141-159, 219-246

**Table S2.** Ten epitopes were selected from five immunoinformatic tools.

Number	Amino acid sequence	Position	Length	Identified epitope
P1	LSEGESKSLKKHCTKE	11-27	17	-
P2	SGAGVYACDPEGYEVFKE	56-73	18	L-AK-1
P3	PVIMDYHKVDKVEHPP	77-92	16	L-AK-2
P4	CDFGPQDKLGFDPD	93-107	15	L-AK-3
P5	GRSHEGYPFPPVS	121-133	13	L-AK-4
P6	TDEQRKEMENKTI	134-146	13	L-AK-5
P7	TMTPEENQQLID	165-176	12	L-AK-6
P8	DKMLGDAGGYNGWPKA	185-200	16	L-AK-7
P9	QKGGDVGEVYKR	227-238	12	L-AK-8
P10	GEHTESVGGVYDISNKRR	306-323	18	L-AK-9

Figure S1

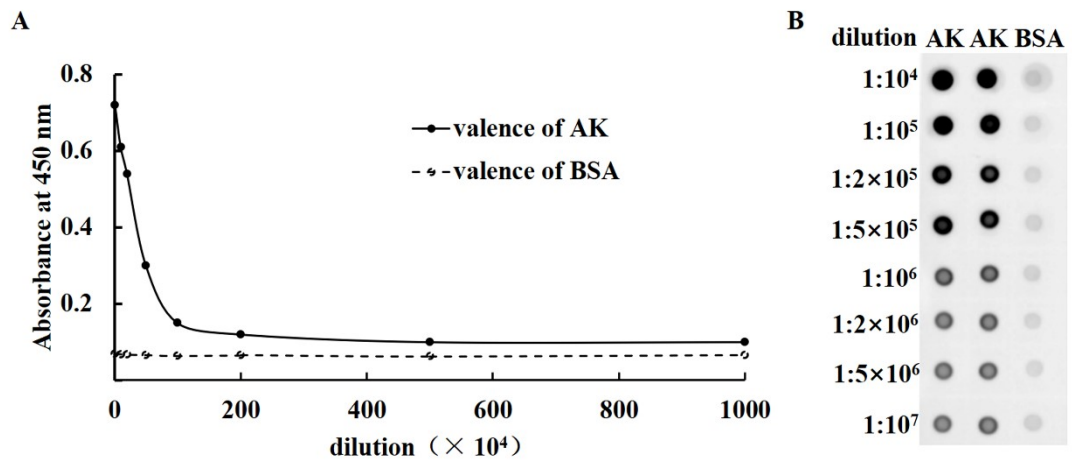


Figure S2

