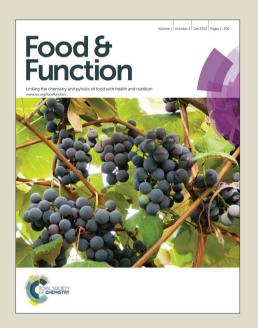
# Food & Function

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## 1 Identification of IgE and IgG epitopes on native

## 2 Bos d 4 allergen specific to allergic children

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# ABSTRACT:

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16	Alpha-lactalbumin (ALA) is one of the major allergens in cow's
17	milk. However, research on its conformational epitopes have been
18	relatively limited. In our study, specific antibodies against cow's milk
19	ALA were purified from eight children by two-step affinity
20	chromatography. Subsequently, mimotopes against IgG and IgE were
21	biopanned from Ph.D12 and Ph.DC7C, respectively. Based on the
22	mimotopes, linear epitopes were defined with UniProt alignment tool.
23	Conformational epitopes were computed using the Pepitope Server.
24	Six IgE and seven IgG linear epitopes were identified. Meanwhile,
25	five IgE and three IgG conformational epitopes were revealed with
26	PyMOL. The results showed that common residues were identified in
27	both IgE and IgG epitopes and some residues of conformational
28	epitopes were composed of linear epitopes on bovine $\alpha$ -lactalbumin.
29	The results indicated that the data could be used for developing of
30	hypoallergenic dairy products on the basis of epitopes and providing
31	a diagnostic tool for the assessment of patients who are allergic to
32	cow's milk.

# INTRODUCTION

34	Food allergy is a type of adverse reaction and it has been reported
35	that approximately 3% of adults and up to 8% of children suffer from
36	food allergies in develop countries. There are about 160 foods
37	causing allergy and 90% of allergies are caused by eight kinds
38	including milk, peanuts, egg, wheat, soybeans, crustacean, fish and
39	tree nuts. <sup>2-4</sup> Among them, cow's milk is the leading cause of food
40	allergy for infant and children. Recently, the prevalence of cow's
41	milk allergies in preschoolers, older children and adults were reported
42	to be 0-2.5%, 0.3% and less than 0.5%, respectively. <sup>5</sup>
43	There are more than 25 different types of proteins in milk, and the
44	most important allergens are casein, $\alpha$ -lactalbumin (ALA, Bos d 4)
45	and $\beta$ -lactoglobulin. <sup>6, 7</sup> ALA belongs to the lysozyme family and its
46	molecular weight is 14.2 kDa with 123 amino acid residues. It is a
47	monomeric, calcium-binding, globular protein with four disulfide
48	bonds. <sup>8,9</sup> Cow's milk ALA is secreted by mammary epithelial cells,
49	and one of its important functions is to regulate the synthesis of
50	lactose by the galactosyltransferase system. The amino acid
51	sequences of bovine and human ALA share 74% identity and 6%
52	similarity.9 In the food industry, ALA is an important additive in
53	infant formula due to the fact that it contains many essential amino

acids and performs various physiological functions. 10 such as 54 55 inhibiting colon carcinogenesis and anti-inflammatory activity and so on. 11, 12 56 57 An epitope is a specific region on the surface of an antigen that is 58 part of a macromolecule (usually a protein) recognized by antibody of the immune system. <sup>13</sup> There are two types of epitopes: linear 59 (sequential and continuous) and conformational (discontinuous). 13-16 60 Until now, linear epitopes have been detected on cow's milk 61 allergens.<sup>9, 17-20</sup> However, relatively limited research has been 62 performed to explore conformational epitopes of cow's milk allergy, 63 despite the finding that 90% of the epitopes on protein antigens are 64 65 conformational, with antibody-binding abilities that are dependent on their structures.<sup>20</sup> 66 Random peptide libraries displayed on filamentous phages is a 67 68 unification of the gene and its corresponding protein in vitro and it 69 has been widely used in many fields such as life sciences, medication and so on. <sup>21, 22</sup> It is a robust method for epitope mapping since this 70 71 technique is based on the interaction of antibody and mimic peptides. 72 The aim of work is to explore the information on epitopes of ALA and characterization of linear and conformational epitopes, which is 73 74 expected that the results of epitopes can be used for developing of

- hypoallergenic dairy products on the basis of epitopes. In our work, linear and conformational mimotopes on cow's milk ALA were
- 77 biopanned from phage display peptide libraries(Ph.D.-12 and
- 78 Ph.D.-C7C) and then IgG and IgE epitopes were identified by
- 79 bioinformatics tools.

### MATERIALS AND METHODS

#### 81 Materials

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- Purified cow's milk ALA were purchased from Sigma Co. (St.
- 83 Louis, MO) with purity of higher than 85%. Phage display libraries
- 84 (Ph.D.-C7C and Ph.D.-12) were purchased from New England
- 85 Biolabs (Beverly, MA, USA). CNBr-activated Sepharose 4B and
- 86 HiTrap Protein G columns were obtained from GE (Fairfield city,
- 87 State of Connecticut-CT, USA). All other chemicals were purchased
- 88 from Sangon Co. (Shanghai, China).
- Sera collection for diagnosis was performed by staff members of
- 90 the First Affiliated Hospital of Guangxi Medical University and the
- 91 Children's Hospital of Zhejiang University. None of the authors were
- 92 involved in the sample collection. Verbal informed consent was
- obtained from the children's parents, who agreed that their children's
- sera could be used for research on epitope mapping as long as their
- 95 private information was protected.

#### Pooling of sera from patients with allergy to cow's milk

Serum samples from 19 children with allergy to cow's milk were tested in this study. Among them, 14 are boys and 5 are girls, which accounts for about 75% and 25%, respectively. Serum-specific IgE (S-IgE) antibodies specific to ALA were analyzed using an ImmunoCAP 100E (Phadia AB, Uppsala, Sweden). All selected serum samples with S-IgE values greater than or equal to 0.35 kU<sub>A</sub>/L were pooled.

#### Purification of IgG and IgE antibodies to cow's milk ALA

According to the instruction of 4B CNBr-Sepharose, 0.6g CNBr-activated Sepharose 4B powder has been washed with 1 mM HCl and transferred to 2 mL column. After that, 15mg ALA was added to the column for coupling and the concentration of protein in the supernatant was monitored for every half hour.

According to the instructions of CNBr-activated Sepharose 4B, 10 mL of PBS was used for equilibration firstly. Then 1ml of sera samples were diluted to 2ml with PBS and then were loaded onto the CNBr-activated Sepharose 4B column and the column medium was washed with a 10-fold volume of 20 mM PBS (pH 7.4) in order to remove the unbound material. Finally, specific antibody consisting of

117	both IgG and IgE were eluted with 10 medium volumes of 3 mol/L
118	MgCl <sub>2</sub> and excess salts in solution were removed by centrifugation
119	with cut-off molecular weight of 5KDa Millipore tube.

In a second step, 1ml of concentrated solution from the previous step were separated using the HiTrap Protein G column. 2 ml specific antibodies obtained from the previous step were loaded slowly onto the activated HiTrap Protein G and IgE antibodies have been flowed through by 10 column volumes of binding buffer washing. After that, specific IgG antibodies were eluted by 5 volumes of 0.1 M glycine-HCl (pH 2.7) and neutralized with 1M Tris-Cl (pH9.0). The purities of IgG and IgE were calculated by software Quantity One from Bio-Rad which based on bands in SDS-PAGE gel.

## Epitope mapping by phage display

## ALA mimotope selection from random peptide libraries

Ph.D.-12<sup>TM</sup> and Ph.D.-C7C<sup>TM</sup> phage display peptide libraries were subjected to three cycles of panning to select sequential and conformational epitopes of ALA, respectively. The biopanning protocol was conducted as described by Li et al with minor modification.<sup>20</sup> Briefly, microplate wells were coated with purified IgE and IgG antibody in 0.1 mol/L NaHCO<sub>3</sub> (pH 8.6) overnight at 4°C. Subsequently, 200 μL of 3% (w/v) BSA (or OVA) in TBS (50

mmol/L Tris-HCl [pH 7.5] and 150 mmol/L NaCl) was dispensed into the wells to block nonspecific binding, and the plate was incubated at 37°C for 2 h. Then, the wells were washed three times with TBST (TBS containing 0.1% Tween 20), and 100 µL of phage solution (2.0×10<sup>11</sup> pfu) from the random peptide library was added to each well and incubated at 37°C for 1 h. After washing with TBST to remove unbound phages, 100 uL of elution buffer (0.2 mol/L glycine-HCl, pH 2.2) was added and immediately neutralized with 1 mol/L Tris-HCl (pH 9.1). The eluted phages were used to infect Escherichia coli ER 2738 for amplification purposes, which was followed by a further round of biopanning. After the third round of biopanning, individual colonies were selected randomly from the titre culture plates (LB medium) and amplified for identification by phage ELISA.

## **Phage ELISA**

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We firstly used a sterile toothpick to stab one of the blue plaques (< 100 plaques) resulting from the third round of random panning. The phage was then transferred to an *ER2738* cell culture in log phase, and the cells were incubated at 37°C with shaking for 4.5-5 h. The cultures were then centrifuged at 10,000 rpm for 1 min, and the supernatants were assessed by a titre test.

## DNA purification and peptide alignment

Single-stranded DNA was purified from the bacteria infected with specific phage by precipitation with 20% PEG/2.5 M NaCl, resuspended in iodide buffer (10mM Tris-HCl (pH 8.0), 1 mM EDTA and 4M NaI), precipitated again with absolute ethyl alcohol and

resuspended in TE buffer. Ten microliters of the resuspended template was sent for DNA sequencing, which was carried out by Jinsirui (Nanjing, China) using the primer 5'-CCC TCA TAG TTA GCG TAA CG-3'. Sequence of the mimetic peptide and cow's milk ALA were aligned using the UniProt alignment tool.

#### Location of mimotopes on ALA

The Pepitope Server is a web-based tool for predicting discontinuous epitopes based on a set of peptides that have been affinity-selected against an antibody of interest. <sup>20</sup> Chain A of the X-ray structure of ALA (Bos d4; PDB code 2G4N) was submitted to the Pepitope Server. This server implements the following three algorithms for epitope mapping: PepSurf, Mapitope, and a combined algorithm incorporating the first and second algorithms, which were used to identify conformational epitopes with mimotope sequences. <sup>23</sup> The parameters included a substitution matrix, gap penalty and the probability of obtaining the best path. Finally, conformational epitopes on ALA were modelled using PyMOL, which is an open-source, user-sponsored, molecular visualization system created by Warren Lyford DeLano. <sup>24</sup>

#### **RESULTS**

201	Preparation of pooled patient serum samples
202	S-IgE levels in serum samples collected from 19 patients who were
203	allergic to cow's milk were measured by ImmunoCAP, as shown in
204	Table 1. Equal volumes of eight samples (sample patient nos. 2, 4, 6,
205	7, 8, 9, 10, and 15) were pooled since their S-IgE levels were greater
206	than $0.35\ kU_A/L$ , which is regarded as the cut-off value for food
207	allergy. <sup>25</sup>
208	Affinity purification of IgG and IgE antibodies to cow's milk
209	ALA
210	Specific antibodies against ALA binding onto the column
211	medium were eluted with 3 M MgCl <sub>2</sub> . As shown in Figure 1A, the
212	fractions with a high concentration of specific antibody against ALA
213	(from the sixth milliliter to the tenth milliliter) were collected,
214	centrifuged, concentrated and desalinated through ultrafiltration tubes
215	with a cut-off of 5 kDa (Millipore). The highest concentration of IgE
216	reached in the ninth millilitre with 0.580 mg/mL. The specificity and
217	purity of antibody are shown in Figure 1B, and these values indicated
218	that the antibody can be used in the next step.
219	During non-specific elution for IgG antibodies using Protein G
220	(Figure 2A), we found that most of the protein had been eluted in the

first three milliliters. Most of this protein was IgE as shown in

222	SDS-PAGE pattern (Figure 2C) according to the molecular weight of
223	IgE (190 kDa, including two heavy chains and two light chains) and
224	similar studies about affinity purification of IgG and IgE antibodies.
225	<sup>26-30</sup> The protein concentration of eluent was sharply reduced until the
226	ninth millilitre, in which the protein concentration was as low as
227	0.010 mg/mL. Purified IgG was collected from the first to the sixth
228	milliliter (Figure 2B) during the specific elution. In total, $630~\mu l$ of
229	$0.153~mg/mL~ALA~S\mbox{-}IgE$ and $840~\mu l$ of $0.158~mg/ml~ALA~S\mbox{-}IgG$
230	were obtained and the purities of ALA S-IgE and S-IgG were 93.8%
231	and 85.3%.

#### IgE- and IgG-binding linear epitopes of cow's milk ALA

After three rounds of biopanning, 48 clones against IgG and IgE respectively were obtained from the phage random library Ph.D.-12. Among them, included 39 positive clones against anti-ALA IgE and 43 positive clones positive clones against anti-ALA IgE have been identified by ELISA, respectively (Table 2 A and B). Six amino acid sequences (RKQTRQKRIQSR, IKTMIRMNTIKL, NIRRNLTIRSRI, HNRKRS SSIRIT, LNNRIRSSINSL and RTRLRRKRRSLI) were identical with different frequencies among the IgE-binding mimotopes. While for IgG mimotopes, four amino acid sequences (HHQNLTQRSRRR, RRLPPLPKIPMH, HRSKQITHTRRH and

	KQN1KRIIKRRS) have been identified more than once from
244	positive clones, which were regarded as candidate epitope sequences.
245	The UniProt alignment tool was used to align the sequences of
246	mimotopes with the cow's milk ALA amino acid sequence (Locus
247	AAF63624.1) to identify linear epitope candidates with three or more
248	similar or identical amino acids. As shown in Figure 3, linear
249	IgE-binding epitopes were found at AA 41-46, AA 55-60, AA 62-72
250	AA 74-76, AA 85-90 and AA 92-99, and linear IgG-binding epitopes
251	were detected at AA 37-46, AA 52-54, AA 56-59, AA 63-72, AA
252	74-76, AA 81-90 and AA 92-99.
253	Locations of conformational IgE and IgC hinding enitones of
233	Locations of conformational IgE- and IgG-binding epitopes of
254	cow's milk ALA
254	cow's milk ALA
<ul><li>254</li><li>255</li></ul>	cow's milk ALA  After three rounds of biopanning, 96 clones were obtained from the
<ul><li>254</li><li>255</li><li>256</li></ul>	cow's milk ALA  After three rounds of biopanning, 96 clones were obtained from the phage random library Ph.DC7C, 73 of which were determined to be
<ul><li>254</li><li>255</li><li>256</li><li>257</li></ul>	cow's milk ALA  After three rounds of biopanning, 96 clones were obtained from the phage random library Ph.DC7C, 73 of which were determined to be positive by phage indirect ELISA (Table 3), including 39 IgE-binding
<ul><li>254</li><li>255</li><li>256</li><li>257</li><li>258</li></ul>	cow's milk ALA  After three rounds of biopanning, 96 clones were obtained from the phage random library Ph.DC7C, 73 of which were determined to be positive by phage indirect ELISA (Table 3), including 39 IgE-binding (Table 3 A) and 34 IgG-binding mimotopes (Table 3 B). Moreover,
254 255 256 257 258 259	cow's milk ALA  After three rounds of biopanning, 96 clones were obtained from the phage random library Ph.DC7C, 73 of which were determined to be positive by phage indirect ELISA (Table 3), including 39 IgE-binding (Table 3 A) and 34 IgG-binding mimotopes (Table 3 B). Moreover, six amino acid sequences appeared to be repetitive among the 39 IgE

263	While among the 34 IgG-binding mimotopes, the sequences of
264	IPMRRIR, SHRRTR, KPSLPNL and LTNSSIQ appeared twice.
265	Six mimic peptides recognized by IgE and four mimic peptides
266	recognized by IgG and a PDB file of bovine ALA were put into the
267	Pepitope Server. High algorithm scores and lower P values were
268	judged as the standard of optimal epitopes (Table 4). Thus, we
269	determined that the most probable bovine $\alpha$ -lactalbumin
270	conformational IgE-binding epitopes were ME 1 (K62-N71-I75
271	-S76-K79 and K62-I75-S76-K79-L81), ME 2 (P24-E25-K114- L115-
272	Q117-L119), ME 3 (L105-H107-K108-L110), ME 4 (V42-Q43-S47-
273	T48-Q65-P67), and ME5(N44-S47-T48-E49-Y50-K79-L81) as
274	shown in Figure 4 and conformational IgG-binding epitopes on
275	bovine α-lactalbumin were MG 1 (F9-R10-K13-K16-L23-P24-
276	L119), MG 2 (I59-Q65-P67-S69-N71-I75), and MG 3
277	(Q39-I41-N44-S47- T48) in Figure 5.

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## **DISCUSSION**

We isolated specific anti-ALA IgE and IgG antibodies from the sera of patients with an allergy to cow's milk by two-step affinity chromatography using CNBr-activated Sepharose 4B and HiTrap Protein G columns<sup>31,32</sup> and high-purity IgG (purity = 93.8%) and IgE

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(purity = 85.3%) were obtained for epitope mapping. A small number of additional miscellaneous bands were observed which might be IgA and IgM since they existed in the form of dimmer and pentamer and could not totally reduced by  $\beta$ -mercaptoethanol.

As we know, X-ray is an accurate method for epitope mapping.<sup>33</sup> However, the main limitation of X-ray based approach for B cell epitope mapping is the lack of natural IgE mAb in milligram amount required for X-ray crystallography studies, resulting in limiting the broad use of X-ray for epitope mapping. 13 Therefore, it was concluded that the mimotope identification strategy can be an alternative way for epitope mapping of different food allergen, and until now several conformational epitopes were identified by biopanning phage libraries. In 2006, one conformational IgE epitope of Bet v1 has been identified which was also the cross-reacting basis with other three allergens homologues Gly m 4 (soybean), Ara h 8 (peanut) and Pru av 1 (cherry) <sup>34</sup>. In the same year, conformational epitopes of parvalbumin recognized by both IgE and IgG antibody were obtained by screening of a constrained decamer phage library<sup>35</sup>. Following this approach, two relevant conformational IgE-binding epitopes of peach Pru p 3 have been identified.<sup>36</sup> Krisztina et al mapped a conformational epitopes

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of house dust mite allergens Der p 1 and Der p 2 with human monoclonal antibody<sup>37</sup>. The phage display technique is used to assess large sets of random peptides to select those with high binding affinity to an antibody of interest, and it has been used in many fields as well, including drug discovery, enzymatic substrate and inhibitor discovery, vaccine design, analysis of protein-protein interactions, identification and engineering of polypeptides and mapping of allergen epitopes. 21, 22, 38-40 In 2012, Bøgh et al. conducted competitive immunoscreening of a phage-displayed random peptide library to map IgE epitopes on intact and digested Ara h 1 with both human and rat sera. The identified epitopes were similar for intact and digested proteins: therefore, the IgE epitopes can be considered to be informative epitopes.<sup>41</sup> Untersmayr et al. have determined three major specific IgE epitope regions on the parvalbumin molecule and have confirmed these epitope regions using two independent matching algorithms. 42 A recent study has the utility of phage-display technology demonstrated distinguishing between the epitope patterns of IgE and IgG4. providing detailed information on fine specificity and affinity.<sup>43</sup> Knowledge about antigen epitopes can reveal the nature of antigen-antibody reactions and contributes improved to

320	understanding of the fole of food affergens in affergic feactions. Prior
327	to this study, some studies investigated IgE-binding linear epitopes
328	on ALA. Jarvinen et al. described four IgE epitopes at AA 1-16, AA
329	13-26, AA 47-58, and AA 93-102 of native bovine ALA.9 Maynard
330	et al. showed that AA 17-58 and one large tryptic peptide containing
331	this sequence were the most strongly and frequently recognized by
332	IgE. 18 Adams et al. used the RAST assay to show that a synthetic
333	peptide comprising AA 5-18 contains an IgE-binding epitope. 19
334	Hochwallner et al. identified sequential epitopes on ALA using 8
335	synthetic overlapping peptides spanning the ALA sequence. <sup>44</sup>
336	In the current study, six linear IgE-binding epitopes on bovine
337	ALA were identified, including AA 41-46, AA 55-60, AA 62-72, AA
338	74-76, AA 85-90 and AA 92-99. The linear IgE-binding epitopes AA
339	41-46, AA 55-60, and AA 92-99 overlap with those reported in
340	Maynard's study, <sup>18</sup> which included AA 17-58, and with those
341	reported in Jarvinen's study,9 which included AA 47-58 and AA
342	93-102. Epitope AA93-102 reported by Jarvinen contained an
343	additional epitope AA92-99.9 Although exact comparisons are
344	difficult to perform, these findings may be related to patients' living
345	environments, including geographical factors, and concentrations of
346	specific IgE antibodies. More importantly, three new linear

347	IgE-binding epitopes on bovine ALA—AA 62-72, AA 74-76, and
348	AA 85-90—were identified. However, the carboxy terminus (AA
349	109-123) was not found to be identical to that of the IgE from our
350	cow's milk-allergic patients. <sup>9, 18, 19</sup>
351	Regarding linear IgG epitopes on ALA, only one study has
352	identified three IgG-binding sequences—AA 7-18, AA 53-62, and
353	AA 89-108—in human sera from CMA patients. <sup>9</sup> In the present study,
354	seven linear IgG-binding epitopes were found: AA 37-46, AA 52-54,
355	AA 56-59, AA 63-72, AA 74-76, AA 81-90 and AA 92-99. Among
356	these, five epitopes—AA 37-46, AA 52-54, AA 56-59, AA 81-90 and
357	AA92-99—overlapped with epitopes previously reported by Jarvinen
358	et al. Moreover, epitopes AA 52-54 and AA 56-59 are included
359	within AA 53-62, while AA 92-99 is included within AA 89-108,
360	which was reported by Jarvinen et al.9
361	In addition, the current study revealed that the linear IgE-binding
362	epitopes AA 74-76 and AA 92-99 were exactly the same as the linear
363	IgG-binding epitopes AA 74-76 and AA 92-99 and that the linear
364	IgE-binding epitopes AA 55-60 and AA 62-72 were exactly the same
365	as the linear IgG-binding epitopes AA 56-59 and AA 63-72 on ALA.
366	Other epitopes contained large numbers of shared amino acids. Thus,
367	the sequences and position of linear IgE- and IgG-binding epitopes

368	on cow's milk ALA were very similar since both of them were
369	located in AA 37-99. Even some of linear epitopes were the same
370	such as AA 74-76 and 92-99. Based on their overlap position, it was
371	indicated that common residues could with different frequencies be
372	regarded as informative maker for detecting and diagnosis of milk
373	allergy in further.
374	With respect to linear IgE epitopes from figure 3A, the highest
375	frequency of residue is Asparagine in the position of 66 since there
376	were 12 positive clones containing this residue. The second highest
377	frequency was Lysine which appeared ten repetitions at the position
378	of 93, 94 and 98, respectively. Based on full sequence of bovine
379	ALA, we found that the highest frequency of amino acids identified
380	as the composition of epitopes were Asparagine (50 times), Lysine
381	(47 times), Isoleucine (45 times), Aspartic acid (28 times), Glutamine
382	(22 times), successively. Moreover, the characterization of IgG
383	epitopes showed the same results, which means the same residues
384	such as Aspartic acid, Lysine acid, Asparagine, Isoleucine and
385	Glutamine showed the highest frequencies as shown in figure 3B.
386	Related studies have indicated that more than 90% of epitopes
387	involved in allergic reactions were conformational epitopes and that
388	some linear epitopes were components of conformational epitopes. <sup>20</sup>

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Maynard et al. concluded that conformational epitopes are 'more important' because the majority of patients (60%) respond to native ALA and larger peptides. 18 IgG antibodies from patients with cow's milk allergy also showed marked preferences for conformational epitopes. 45 These findings further confirm that the epitopes on the milk-based allergen ALA are conformational epitopes. However, ALA conformational epitopes have not been identified before our study. In our study, we identified five IgE-binding conformational epitopes (ME 1, ME 2, ME 3, ME 4, and ME 5) in addition to three IgG-binding conformational epitopes (MG 1, MG 2, and MG 3) on bovine ALA. We found that most of these residues of these epitopes also appeared in linear epitopes in Figure 3. A total of 61% of the amino acids in the IgE-binding conformational epitopes and 94% of the amino acids in the IgG-binding conformational epitopes identified in this study have been previously reported as linear epitope sequences. In particular, the amino acids of the two conformational epitopes MG 2 and MG 3 have been reported as IgG-binding linear epitopes. These findings also support those of a previous study by Aalberse, who found that some linear epitopes are components of conformational epitopes.46

In conclusion, B cell epitopes including linear and conformational
epitopes have been identified successfully by phage display technique
at the same time. Common residues were found in IgG and IgE
epitopes. Some Asparagine (50 times), Lysine (47 times), Isoleucine
(45 times), Aspartic acid (28 times), Glutamine (22 times) were more
be the composition of residues. It is the first time to identify
conformational epitopes of ALA which could provided a diagnostic
tool for the assessment of patients who are allergic to cow's milk.
These findings also indicate that some residues of conformational
epitopes are composed of linear epitopes on bovine $\alpha$ -lactalbumin.

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- 431
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## Figure captions

- **Fig. 1.** Affinity chromatography by CNBr-Sepharose 4B. (A) Specific elution curve with 3 mol/L MgCl<sub>2</sub>. (B) SDS-PAGE patterns of solutions during CNBr-Sepharose 4B affinity chromatography (M, protein marker; 1, serum pool (diluted to 1:10); 2, solution from the first non-specific elution; 3, specific concentrated elution).
- **Fig. 2.** Affinity chromatography by protein G. (A) The concentration change during non-specific elution. (B) The concentration change during specific elution. (C) SDS-PAGE patterns of different solutions (M, Marker; 1, IgE; 2, IgG).
- **Fig. 3.** Positions of linear epitopes located in amino acid sequence of ALA. (A) IgE binding epitopes. (B) IgG binding epitopes.
- **Fig. 4.** Ribbon (A) and globular (B) presentations of cow's milk α-lactalbumin mimic peptides to IgE binding composition epitopes. ME 1-5 from Table 4A are marked in green, blue, yellow, magenta and hotpink, respectively. Overlapping amino acids (K79, L81) in ME 1 and 5 are marked in orange, while overlapping amino acids (S47, T48) in ME 4 and 5 are marked in red.

Fig. 5. Ribbon (A) and globular (B) presentations of cow's milk  $\alpha$ -lactalbumin mimic peptides to IgG binding composition epitopes. MG 1,2 and 3 in Table 4B are marked in green, blue and yellow, respectively.

**Table 1.** Demographic, clinical and serologic characterization of bovine milk allergic children

Patient no.	Age range	Milk-related symptoms	α-La S-IgE(kU <sub>A</sub> /L)
1	1-5 years	asthma	0.11
2	1-5 years	asthma	4.14
3	less than 1 year	bronchial asthma	0.19
4	less than 1 year	bronchial asthma	0.45
5	1-5 years	eczema	ND
<u>6</u> 7	1-5 years	cough variant asthma	12
7	1-5 years	asthma	2.42
8	1-5 years	NK	0.75
9	less than 1 year	leukocytosis	1.09
10	NK	NK	25.3
11	less than 1 year	NK	0.15
12	less than 1 year	urticaria	0.22
13	less than 1 year	NK	0.11
14	1-5 years	urticaria	0.31
15	1-5 years	rhinoconjunctivitis	3.18
16	6-10 years	rhinoconjunctivitis	0.04
17	5-10 years	rhinoconjunctivitis	0.25
18	1-5 years	pneumonia	0.27
19	5-10 years	rhinoconjunctivitis	0.02

NK, not known; ND, not done.

**Table 2.** Mimotope sequences from the phage display random peptide libraries Ph.D.-12

A: Target molecule is anti-ALA IgE

Phage	Peptide sequence	Times	Phage	Peptide sequence	Times
Ph 5, Ph 6, Ph 29, Ph 43, Ph 45	RKQTRQKRIQSR	5	Ph 32, Ph 41, Ph 42	IKTMIRMNTIKL	3
Ph 11, Ph 37, Ph 39	NIRRNLTIRSRI	3	Ph 9, Ph 14	HNRKRSSSIRIT	2
Ph 17, Ph 31	LNNRIRSSINSL	2	Ph 1, Ph 46	RTRLRRKRRSLI	2
Ph 18	HKRNRRPPRLLN	1	Ph 19	NIPRITIRLHMP	1
Ph 15	HRIRSPSSLRKP	1	Ph 10	NRPKKRIKQIQL	1
Ph 36	HRRPRHRKRRRL	1	Ph 25	NTRIRRRTNRTI	1
Ph 23	IHKRQQKRIKPI	1	Ph 4	PRQLQRRNHRHH	1
Ph 34	ILHNPRRIKRHI	1	Ph 7	QKQRINLILTNR	1
Ph 24	IPRTIRTKRKLI	1	Ph 3	QQLTITRKLLPK	1
Ph 8	KSKQKRIKTRIT	1	Ph 47	QQQRMKKRIKRT	1
Ph 35	KSMRSSIKSINI	1	Ph 22	RHNTIRSRIMRI	1
Ph 16	LIIRRLLQKPMT	1	Ph 13	RHRNNSIRSSHI	1
Ph 21	LNNHRKRRRPRL	1	Ph 44	SPWSPKFPGDPT	1
Ph 30	MLPIIRNLIHTT	1	Ph 20	TNLRRTTTHRLN	1

#### **B:** Target molecule is anti-ALA IgG.

Phage	Peptide sequence	Times	Phage	Peptide sequence	Times
Ph 24, Ph 30, Ph 36	HHQNLTQRSRRR	3	Ph 20, Ph 33, Ph 47	RRLPPLPKIPMH	3
Ph 5, Ph 19	HRSKQITHTRRH	2	Ph 26, Ph 29	KQNTKRIIKRRS	2
Ph 22	IKTPSLMHQSNI	1	Ph 7	NIIKNRLRITPL	1
Ph 9	ITTLLIKRMTKI	1	Ph 42	NKSKPLIQRLIN	1
Ph 4	KKHRKQLIKRLI	1	Ph 10	NRRQQLRNSRRT	1
Ph 17	KMRMNHRRISNN	1	Ph 48	PIIHIILNMTHS	1
Ph 12	KQSPQLRKIQRI	1	Ph 43	PRNHNLLQKNRR	1
Ph 6	KRPLIHRRNRLR	1	Ph 14	PSKMLIQTRITI	1
Ph 39	LLKSTTKSSNIR	1	Ph 35	PTIRHSKRLHQN	1
Ph 46	LMKPNNLLKISI	1	Ph 31	QKQNIIIRNLLN	1
Ph 23	MNQRTKKIRSRR	1	Ph 45	QQHINSRRRIMK	1
Ph 16	MQTKMTKKKMPI	1	Ph 2	RIKIRLNRIKPH	1

Ph 34	MRRSSHQSLKKR	1	Ph 13	RIRTIITNTIMK	1
Ph 41	NHKHPIKNKIHI	1	Ph 21	RKHRTQSTQIIR	1
Ph 1	RMIRRINPTIII	1	Ph 44	STRVVVPDGNLP	1
Ph 25	RNKHLSHQRRMS	1	Ph 15	TLIHRHKKLNIN	1
Ph 8	RRKRIHRRNPLR	1	Ph 38	TNRNISKIRIRR	1
Ph 37	SRKRSHMRRRNQ	1	Ph 28	TTSTIPPTLRMT	1
Ph 32	SSIMNSKSLHKH	1			

**Table 3.** Mimotope sequences from the phage display random peptide libraries Ph.D.-C7C

A: Target molecule is anti-ALA IgE.

Phage	Peptide sequence	Times	Phage	Peptide sequence	Times
Ph 7, Ph 10, Ph 12, Ph 14, Ph 18, Ph 20, Ph 21, Ph 24, Ph 30, Ph 32, Ph 37, Ph 39, Ph 44	RIRSRRN	13	Ph 6, Ph 15, Ph 16, Ph 29, Ph 36, Ph 38, Ph 40, Ph 42	LRSLKRP	8
Ph 19, Ph 22, Ph 45	LRKLKRP	3	Ph 31, Ph 35	LRHLKRP	2
Ph 25, Ph 26	LSSLQRP	2	Ph 5, Ph 9	NTTKHIK	2
Ph 41	ILKRRPI	1	Ph 3	LTRKLRS	1
Ph 23	IPRKLPN	1	Ph 13	RRLTRIQ	1
Ph 48	LIRRTSI	1	Ph 27	RRTQLHL	1
Ph 2	LPRKRHS	1	Ph 33	TLKRRPN	1
Ph 43	LRPLKRP	1			

#### **B**: Target molecule is anti-ALA IgG.

Phag	e Peptide sequence	Times	Phage	Peptide sequence	Times
Ph 4	· IPWIKKIK	2	Ph 47, Ph 48	ISHRRTR	2
Ph 3 Ph 3	KPSLPNI	2	Ph 17, Ph 18	LTNSSIQ	2
Ph 2:	5 HIQRTTP	1	Ph 13	LRHTIMN	1
Ph 1	4 HIRIMIP	1	Ph 2	MSHNTRR	1
Ph 2	4 HLRRRHT	1	Ph 39	NPLRKRR	1
Ph 1	1 ILLKRPR	1	Ph 26	PLRLRRP	1
Ph 3	8 ILQRRPS	1	Ph 29	QQITRRP	1
Ph 9	KIRMLRR	1	Ph 35	RHSLMPM	1
Ph 7	LHPPLTL	1	Ph 32	RIRMRRL	1
Ph 4	LITQMMP	1	Ph 15	RLHRRIH	1

Ph 36	LLHKLRQ	1	Ph 21	RMSRHLN	1
Ph 41	LLKRRPT	1	Ph 30	RRPLRIR	1
Ph 42	LLLLRNL	1	Ph 20	RTKLRKL	1
Ph 12	LLLRPMT	1	Ph 16	RTTMQQI	1
Ph 37	LLRRLRL	1	Ph 23	TLRKRRP	1

**Table 4.** Composition and position of conformational epitopes on ALA by Pepitope Server

## **A:** Mimic peptide binding to IgE

Phage	Mimic peptide	Amino acid sequence	Algorithm scores	P values	Name
Ph 5, Ph 9	NTTKHIK	N44-S47-T48-E49-	12.6053	0.0024	ME5
		Y50-K79-L81			
Ph19, Ph22,	LRKLKRP	P24-E25-K114-	10.5609	0.0027	ME2
Ph 45		L115-Q117-L119			
Ph31, Ph35	LRHLKRP	L105-H107-K108-	10.1631	0.0010	ME3
		L110			
Ph7, Ph10,	RIRSRRN	K62-N71-I75-S76	7.5717	0.0013	ME1
Ph12, Ph14,		-K79			
Ph18, Ph20,					
Ph21, Ph24,					
Ph 30, Ph 32,					
Ph 37, Ph 39,					
Ph 44					
Ph 6, Ph15,	LRSLKRP	K62-I75-S76-K79	7.4178	0.0056	ME1
Ph 16, Ph 29,		-L81			
Ph 36,					
Ph 38, Ph 40,					
Ph 42					
Ph 25, Ph 26	LSSLQRP	V42-Q43-S47-T48	6.1000	0.0040	ME4
111 23, 111 20	LooLQId	-Q65-P67	0.1000	0.0040	111111

#### B: Mimic peptide binding to IgG

Phage	Mimic peptide	Amino acid sequence	Algorithm scores	P values	Name
Ph33,	KPSLPNL	I59-Q65-P67-S69-	10.2792	0.0009	MG2
Ph 34		N71-I75			
Ph17,	LTNSSIQ	Q39-I41-N44-S47-	9.4523	0.0013	MG3
Ph 18		T48			
Ph 45,	IPMRRIR	F9-R10-K13-K16-	8.8165	0.0011	MG1
Ph 46		L23-P24-L119			

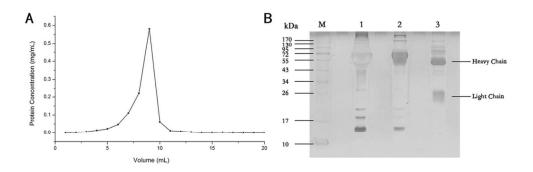


Fig. 1. Affinity chromatography by CNBr-Sepharose 4B.  $92x32mm\ (300\ x\ 300\ DPI)$ 

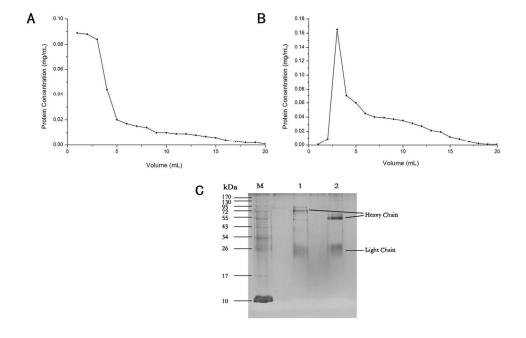


Fig. 2. Affinity chromatography by protein G. 125x81mm (300 x 300 DPI)

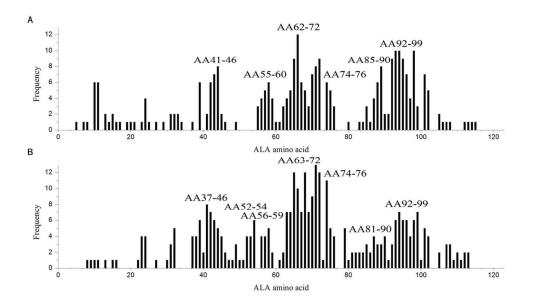


Fig. 3. Positions of linear epitopes located in amino acid sequence of ALA. 120x71mm~(300~x~300~DPI)

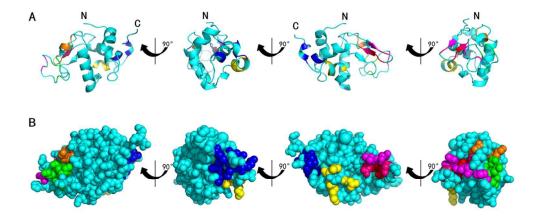


Fig. 4. Ribbon (A) and globular (B) presentations of cow's milk  $\alpha$ -lactalbumin mimic peptide to IgE binding composition epitopes. 95x43mm (300 x 300 DPI)

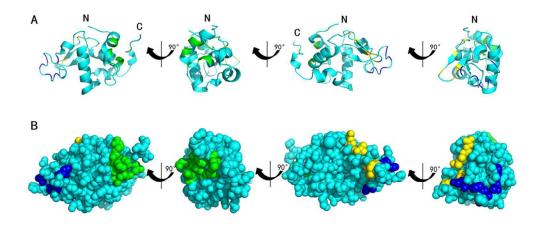
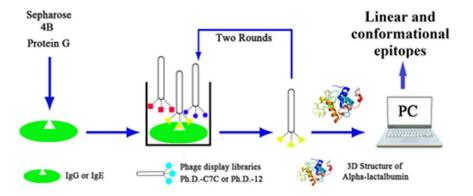


Fig. 5. Ribbon (A) and globular (B) presentations of cow's milk  $\alpha$ -lactalbumin mimic peptide to IgG binding composition epitopes. 95x43mm (300 x 300 DPI)



39x19mm (300 x 300 DPI)