

In silico prediction of B-cell epitopes for twenty-five mite allergens: The therapeutic potentials for immunotherapy

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ARTICLE INFO

Keywords:

Allergen
B-cell epitope
House dust mite
Immunotherapy
In silico prediction
Storage mite

ABSTRACT

Mite allergens are one of the major allergens; however, their structures and epitopes have not been thoroughly studied. In the present study, we predicted the tertiary structures of several mite allergens and also identified the B-cell epitopes, which can be suggested as potential epitopes for allergen immunotherapy. Twenty-five mite allergens, from six mite allergen groups, were investigated; homology modeling and structure refinement were performed for seventeen allergens with unknown structures. Furthermore, various servers were employed to predict linear and conformational B-cell epitopes and consensus B-cell epitopes were identified (172 linear and 64 conformational epitopes). Conservation and epitope identity were also determined among the allergens of the same group and some conserved epitopes were identified. Some regions of the predicted epitopes were identified as novel epitope regions. The predicted consensus epitopes can be applied as suitable candidates to design immunotherapeutic vaccines.

1. Introduction

Mite allergens are the main causes of allergic diseases such as asthma, allergic rhinitis and atopic dermatitis. House dust mite allergy is prevalent in 1–2% of the world population and affecting 50% of the asthmatic patients [1]. *Dermatophagoides farinae* and *Dermatophagoides pteronyssinus* are the predominant house dust mite allergen species which stimulate allergic reactions [2]. Along with house dust mites, storage mites may result in similar allergic reactions, particularly in Asia. Due to the low cross reactivity between house dust mites and storage mites, the study of storage mite allergens (such as *Lepidoglyphus destructor*, *Blomia tropicalis*) should be also taken into consideration for immunotherapy [3].

Different groups of mite allergens have been identified so far and cross reactivity has been observed between some of these groups. Groups 1 and 2 of mite allergens -the major groups in allergy induction- have been extensively investigated so far [4]. Although the structures of a large number of mite allergens have been solved using NMR and X-ray crystallography [5], most of the structures are still unknown.

Immunotherapy is an effective treatment for dust mite induced allergic reactions. Protein engineering and recombinant protein production suggest new insights into characterization and preparation of wild-type allergens, hypoallergens and allergy vaccines [6]. Multi epitope allergy vaccines are based on the immunodominant B-cell and T-cell epitopes which are involved in the incitation of early and late phase reactions of allergy, respectively [7]. Knowledge about the sequence and structure of allergens is crucial to select appropriate T or B-cell epitopes, which subsequently determine the type of the induced immune response [8].

Various experimental methods are employed to predict B-cell epitopes such as: crystallography, mass spectroscopy, nuclear magnetic resonance (NMR), surface plasmon resonance (SPR), surface display and pepscan methods, binding assay and mutagenesis [9]. In recent years, aforesaid methods have been broadly used for identifying new epitopes of mite allergens [10].

The immunoinformatics methods are the advantageous techniques to identify and screen immunodominant epitopes prior to experimental studies, in order to save cost and time [11,12].

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In the present work, we studied different features of the major groups (groups 1, 2, 3, 5, 6 and 7) of three house dust mites' allergens (*Dermatophagoides farinae*, *Dermatophagoides pteronyssinus*, *Euroglyphus maynei*) and 2 storage mites' allergens (*Lepidoglyphus destructor*, *Blomia tropicalis*). We used the protein data bank (PDB) to retrieve the allergens with known structures (Der p 1, Der p 2, Der p 5, Der f 1, Der f 2, Der f 7, Blo t 1, Blo t 5); and modeled the remaining with unknown structure using the prediction servers. B-cell epitopes were identified bioinformatically, to provide information for further studies of hypoallergens and designing recombinant allergy vaccine against mites' allergens.

2. Material and methods

2.1. Sequence retrieval

Twenty-five mite allergen sequences were retrieved from the structural database of allergenic proteins (SDAP) [13], GenBank [14], international union of immunological societies (IUIS) [15] and UniProt [16]. Allergens were selected based on the predominant mite allergens (Der p, Der f, Blo t, Lep d, Eur m), predominant allergen groups (groups 1, 2, 3, 5, 6 and 7) and the availability of the sequence data.

2.2. Evaluating the physiochemical characteristics of allergens

Physiochemical characteristics of allergens such as molecular weight, isoelectric point and molar extinction coefficient, were determined using Pepstats [17]. Some of the disulfide bonds were identified based on UniProt, the remaining was predicted by Cyscon server [18].

2.3. Evaluating secondary structures and post translation modifications

Post translation modifications (PTM) were obtained from UniProt. The unknown secondary structures were predicted using PSIPRED V3.3 [19]. PSIPRED is a user-friendly and accurate secondary structure prediction method, incorporating two feed-forward neural networks that perform an analysis on output obtained from PSI-BLAST (Position Specific Iterated – BLAST). The three-state accuracy (Q3) of server is about 81.6%.

2.4. Homology modeling and structure refinement of allergens

The tertiary structures of eight allergens were retrieved from PDB. Tertiary structures of the other allergens (17 allergens) were modeled using RaptorX [20]. The server predicts 3D structures for protein sequences without close homologs in PDB. RaptorX also predicts the secondary and tertiary structures, contacts, solvent accessibility, disordered regions and binding sites of input sequences. The server assigns some confidence scores to indicate the quality of a predicted 3D model: P-value for the relative global quality, GDT (global distance test) and uGDT (un-normalized GDT) for the absolute global quality; and modeling error at each residue. Based on the confidence scores, the server suggests the best predicted structure.

Afterward, these models were refined using GalaxyRefine server, which works based on side chain repacking, followed by structure perturbation and relaxation with molecular dynamics simulation [21].

2.5. Validation of the predicted structures

The predicted tertiary structures (using RaptorX server) were evaluated using the following servers: 1) Verify 3D, which compares the atomic model of the protein (3D profile) with its own amino acid sequence (1D), scores the compatibility and calculates 3D-1D score. The 3D profile is computed based on the proteins with correct structures that are highly matched with their own amino acid sequences [22]. 2) RAMPAGE, which uses Ramachandran plot in which outlines of favored

and allowed conformational regions for amino acid residues (based on ϕ and ψ angles), which are theoretically defined and also based on the identified high resolution protein structures, are shown [23]. The predicted structures are validated by assessing the distribution of end-points in favored regions of the plot. 3) ProSA-web, which calculates the overall quality scores (Z-score) of the protein and compare it with the Z-scores of the native proteins of the same size, deposited in PDB (based on X-ray and NMR models). Positive values are indicative of problematic parts of the predicted structure [24]. 4) ERRAT, which compares the predicted structures with highly refined crystal structures and calculates the error values, based on the statistics of non-bonded atomic interactions. Overall quality factors are defined based on the calculated error values and the structures with the highest overall quality factors are selected [25].

The structures were re-evaluated by Verify 3D, RAMPAGE, ProSA, and ERRAT servers, following structure refinement (using GalaxyRefine server). Finally, comparing the evaluation results, the best structures which were suggested by GalaxyRefine server were selected for further analyses.

For further validation of the modeling strategies, modeling was performed for the structures of allergens which are available in database, as well. The modeled structures were compared with the available structures in database, using TM-align server [26].

2.6. Linear and conformational B-cell epitope prediction

In this study, two servers were applied to predict B-cell epitopes: ElliPro (antibody epitope prediction) [27] and DiscoTope 2 [28]. ElliPro predicts both linear and conformational B-cell epitopes in which a protrusion index is calculated based on the ellipsoid method. The ElliPro pipeline is based on three algorithms. (1) Initially the protein shape is approximated as an ellipsoid. (2) Then, residue protrusion index (PI) is calculated and (3) finally the neighboring residue clustering algorithm is applied based on the calculated PI to predict the epitopes [29].

DiscoTope 2 server predicts conformational B-cell epitopes based on solvent accessibility, hydrophilicity and amino acid propensity. Surface measure is based on half sphere exposure; the propensity scores are calculated and a new spatial neighborhood method is incorporated. The threshold for epitope identification in DiscoTope 2 server is -3.7 which provides the sensitivity of 0.47 and specificity of 0.75.

To map linear B-cell epitopes, Bcepred server was also applied [30], in which physiochemical properties are taking into account [31]. Bcepred applies Bcipep database for B-cell epitopes and Swiss-Prot database for non-epitopes. Epitopes are predicted based on accessibility, polarity, hydrophilicity and flexibility, with 58.7% of accuracy.

2.7. Identification of consensus B-cell epitopes

Combining the results of the predicted linear epitopes, as well as conformational epitopes, consensus regions were selected as potential epitope sequences. To present the identified epitopes regarding each allergen group, the epitopes are depicted in the aligned sequences, comparable with other allergens in the same group.

3. Results

3.1. Physiochemical characteristics and secondary structure evaluation

Table S1 (Online Resource) summarizes the general information of the selected mite allergens. The molecular weights of allergens are within the range of 11.24–25.61 kDa. The number of α -helix, β -strand and turn are also presented. α -helix structures are dominant among group 5 of allergens, while, β -sheets are prevalent among group 2. Glycosylation sites and disulfide bonds have been previously defined for some of the allergens and some of the disulfide bonds are presented

in this study. Some of the allergens such as Der p 5, Lep d5, Der f 5, Blo t 5, Blo t 7, Der f 7, Der p 7 and Lep d 7 had no disulfide bond.

3.2. Homology modeling, refinement and validation

RaptorX predicted tertiary structures. The server provided information about the best template, which was used for modeling and suggested the best model based on the confidence scores (P-value and unnormalized global distance (uGDT) or GDT) (Table S2, Online Resource). In this regard, uGDT > 50 and GDT > 50 are desired for proteins with > 100 and < 100 residues, respectively. P-value < 10^{-3} and P-value < 10^{-4} are desired for α -proteins and for β -proteins, respectively.

GalaxyRefine refined the predicted structures and selected top 5 structures. Furthermore, four servers (RAMPAGE, ERRAT, ProSA and Verify 3D) evaluated the quality of the predicted structures prior to the refinement and after the refinement (Table S3 and S4, Online Resource). The results showed that following refinement processes the quality of the initial 3D model improved remarkably. We selected the best structure for each allergen (Fig. 3), by comparing the results of pre-refinement and post-refinement evaluations (Table S4, Online Resource). To select the best structure, we considered improvements in the percent of residues in the favored regions (in RAMPAGE results), overall quality factor (ERRAT), overall model quality Z-score (ProSA) and percent of the residues had an averaged 3D-1D score ≥ 0.2 (Verify 3D).

Superimposition of the predicted structures with the available structures in database, showed RMSD values of 0.31, 2.17, 0.31, 0.49, 0.40, 0.73, 0.42 and 0.33 for Blo t 1, Blo t 5, Der f 1, Der f 2, Der f 7, Der p 1, Der p 2 and Der p 5, respectively.

3.3. Prediction of linear and conformational B-cell epitopes

Both linear and conformational B-cell epitopes are involved in the early phase reactions of allergy; however, conformational epitopes are dominant. The predicted linear B-cell epitopes with ElliPro (with the minimum score of 0.5 and maximum score of 6) and Bcepred (based on hydrophilicity, flexibility, accessibility and turns) servers are shown in Table S5 and S6 (Online Resource), respectively.

The predicted conformational B-cell epitopes, based on ElliPro and DiscoTope 2 servers, are presented in Table S7 and S8 (Online Resource), respectively.

3.4. Consensus B-cell epitopes

More accuracy is achieved with the determination of overlapping epitopes in prediction results. In this regards, we identified 172 consensus linear B-cell epitopes, based on the ElliPro and Bcepred results (Table S9, Online Resource).

In addition, sixty four consensus conformational B-cell epitopes were predicted, based on the results of ElliPro and DiscoTope 2 servers (Table S10, Online Resource). For some allergens (Blo t 2, Eur m 2, Lep d 2, Der p 3, Lep d 3), no consensus conformational epitope was found. Our results show that the determination of overlapping epitopes leads to more accurate predictions.

Furthermore, sequence identity results show that various allergens of the same group shared common epitopes. These regions are presented in Figs. 1 and 2 (a-c) which depicts the sequence alignment of allergens in groups 1, 2, 3 and groups 5, 6 and 7, respectively. Some of the predicted epitopes were found in the conserved regions.

4. Discussion

In the present work, six groups of mite allergens as major allergy contributors were studied. It has been previously reported that groups 1, 2, 3 and 7 of allergens belong to cysteine proteases, lipid binding

proteins and serine proteases classes [5]. Several of mite allergens in above-mentioned groups have unknown structures; and due to the diversity of epitopes, it is crucial to identify and select appropriate epitopes to design immunotherapeutic agents such as allergy vaccines.

Epitope specific immunotherapy with peptide vaccines is of great interest in the treatment of allergic reactions, as it precludes the drawbacks of allergen extracts [32]. In addition, peptide based multi epitope vaccines are more advantageous than traditional vaccines; because they have the high degree of safety, specificity, and stability [33]. The most important prerequisites for designing multi epitope vaccine include the identification of allergen structures and immunodominant epitopes. Moreover, hypoallergen therapeutics could be designed based on the modification of the identified epitopes.

In the previous studies, Li et al. [12] identified some novel epitopes of Der f 25 using *in silico* approaches; and epitope based vaccines were designed for Der p 1 allergen, based on T-cell epitopes [34]. For Der f 3 allergen, epitope vaccine was designed based on T-cell and B-cell epitopes [35]. Furthermore, Chen et al. [36] developed a carrier bound Der p 2 peptide vaccine. Synthetic peptides, with eliminated IgE reactivity and reduced T-cell response, were applied and upon coupling to carrier (KLH-conjugated), could induce specific IgG antibody production in animals.

B-cell epitope based allergy vaccines are the new generation of allergy vaccines having several advantages over T-cell epitope based vaccines, for instance T-cell mediated late phase allergic reactions are not elicited by B-cell epitope based vaccines [37]. Ten percent of B-cell epitopes are linear and the rests are conformational; however, the linear epitopes might be involved in conformational epitopes [38]. Linear B-cell epitopes are also applicable for epitope based vaccine design. Accordingly, in the present work, we studied both linear and conformational B-cell epitopes. Identification of the allergens' tertiary structures is an essential step to predict conformational B-cell epitopes. For this reason, homology modeling was conducted to predict the tertiary structures of the allergens.

Conformational epitopes are important structures for IgE binding; additionally the disruption of these epitopes is an efficient way to design hypoallergen vaccine [39]. As disulfide bonds play an important role in the formation of the tertiary structures, the involved cysteines could be a target of designing hypoallergens [40]. The predicted disulfide bonds of allergens, as well as the previously identified disulfide bonds are presented in Table S1 (Online Resource).

Along with the experimental approaches, different servers are available as valuable complementary methods to predict epitopes. Computational methods should be validated by experimental methods; however, consensus results reduce the possibility of false positives [38]. In the present study, we used four servers with different algorithms to select consensus epitopes, presented in Figs. 1 and 2; and Tables S9 and S10 (Online Resource), as well.

For further validation, the predicted epitopes were compared with experimentally identified mite allergen epitopes. To the best of our knowledge, some of the allergens have not been studied before and the predicted structures and epitopes are shown here for the first time. Experimentally identified epitopes in earlier studies are marked with * in Figs. 1 and 2.

Some of the predicted epitopes of Der p 1, Der p 2, Lep d 2 and Blo t 5 partially or completely overlapped with the previously reported epitopes [10]. Chruszcz et al. [41] identified D57, L58, E60 and E92 residues as a common epitope for group 1 allergens. In our study, it was shown that D57, L58 and E92 residues are also part of epitopes. Jeannin et al. [42] have mentioned in their study that ¹¹⁸CQIYPPNVNKIREA-LAQ¹³³ sequences might correspond to B-cell epitopes of Der p 1 which partially overlaps with the predicted epitope in our study (Y121–N126). They have also reported ¹⁸⁸VRNSWTNWGDNGY²⁰¹ as Der p 1 epitope. L147–Q160 sequence was assigned as Der f 1 IgE epitope [43]. It is observed that F150 and G155 are conserved in all the studied allergens in group 1; while L147, A149, H152–I158 and Q160 are conserved in

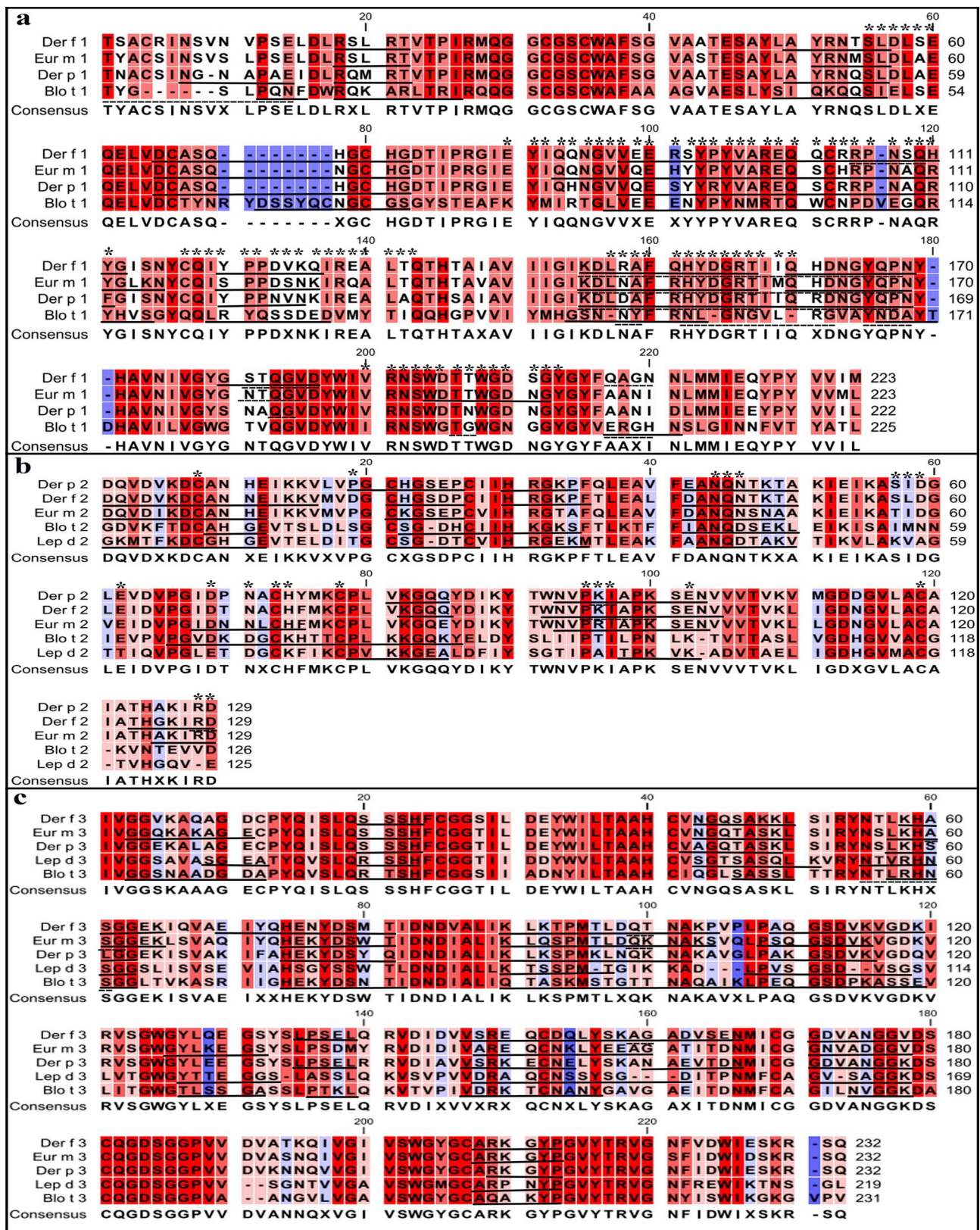


Fig. 1. Multiple sequence alignment of allergens in groups 1 (a), 2 (b) and 3 (c), based on CLC protein bench work software. Identified consensus linear B-cell epitopes are underlined and conformational B-cell epitopes are marked with dashed lines. Amino acid residues which were identified in the previous studies, as described in discussion, are marked with *.

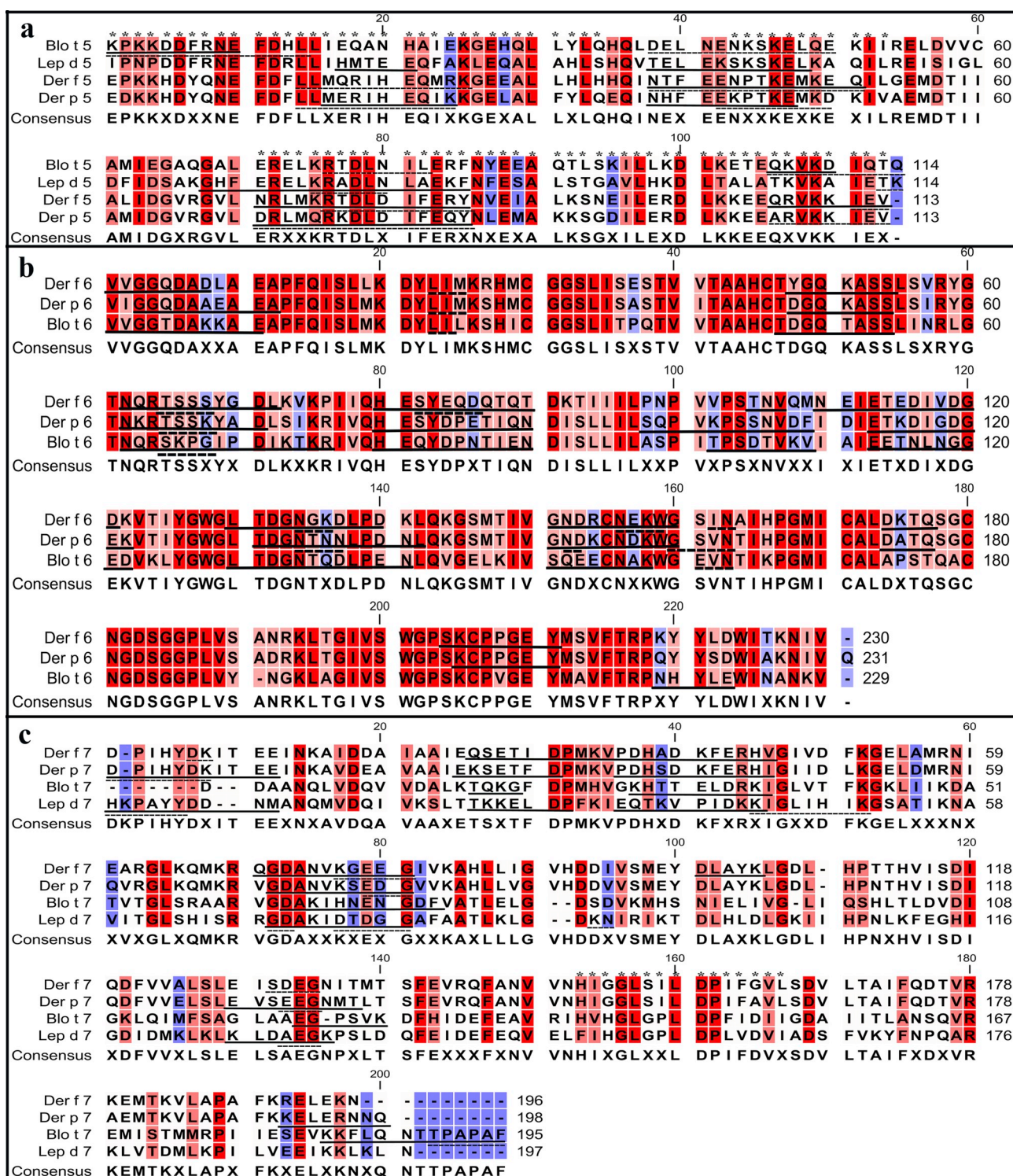


Fig. 2. Multiple sequence alignment of allergens in groups 5 (a), 6 (b) and 7 (c), based on CLC protein bench work software. Identified consensus linear B-cell epitopes are underlined and conformational B-cell epitopes are marked with dashed lines. Amino acid residues which were identified in the previous studies, as described in discussion, are marked with *.

Der f 1, Eur m 1 and Der p 1. So, the predicted conformational epitope in the present work (K145–P167) might be also considered for Eur m1 and Der p 1; as for Der f 1. In the studies by Greene et al. [44,45], regions 81–94 and 101–111 were determined as IgE binding regions in Der p 1. In this work, also, V90–Q110 residues with eight conserved amino acids were predicted as linear epitopes. In this regard, these regions can be potential targets for all the allergens in group 1 for future work. In this study, Q181–D184 residues, conserved in all the studied

allergens, were also predicted as conformational epitopes.

Reginald et al. [46] have reported cross reactivity between Blo t 2 and Der f 2. KI (96–97) residues of Der p 2 were identified as a part of the predicted epitopes in the present study. Mueller et al. [47] also studied these residues and Reginald and Chew [48] introduced K96A mutant as a candidate for hypoallergen production. On the other hand, I97 residue is conserved in all allergens of group 2, so it might be a target for further investigations for other allergens in this group, as

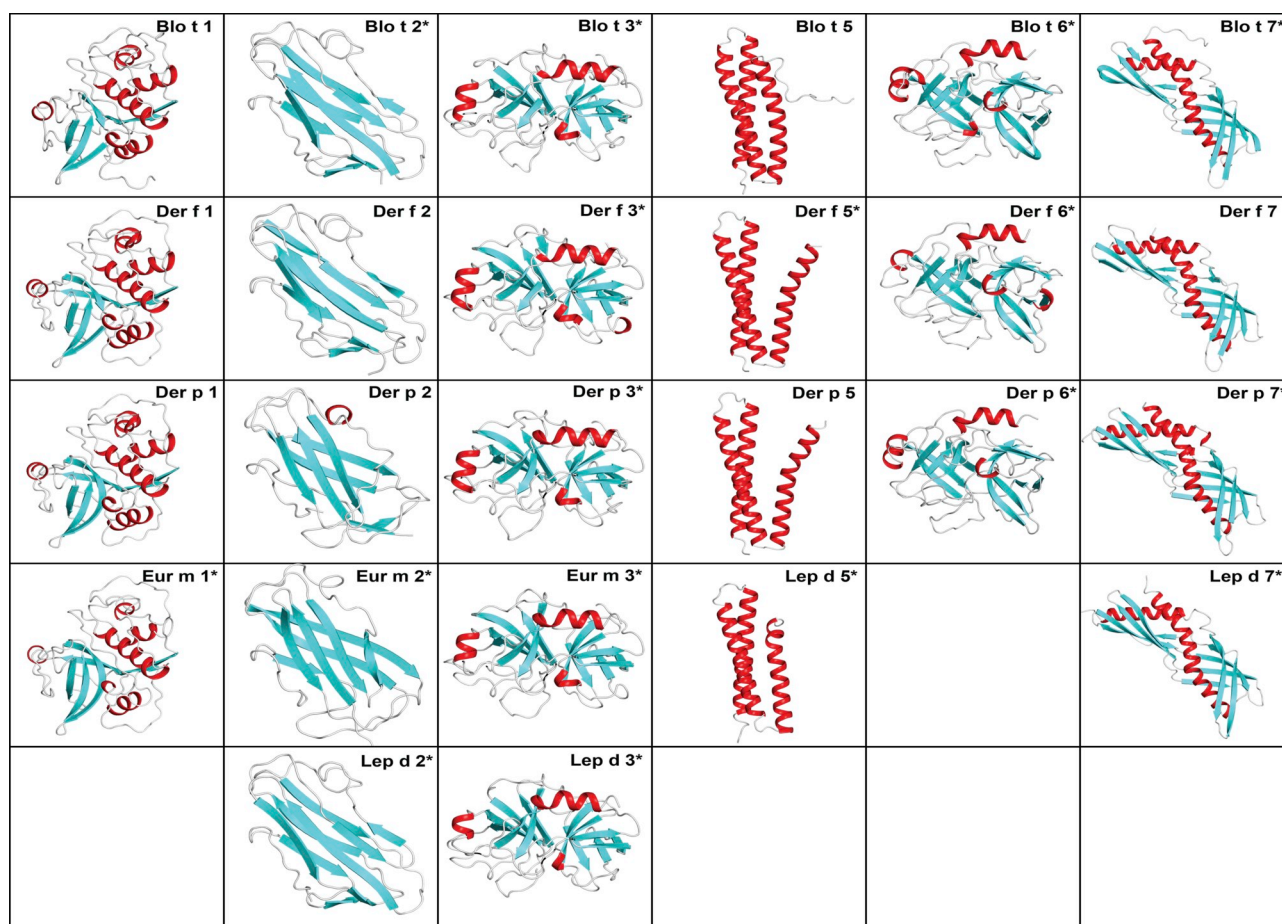


Fig. 3. Tertiary structures of the allergens. The structures which were predicted using RaptorX server and refined with GalaxyRefine server are assigned with *. Other structures were retrieved from PDB: Blo t 1 (5jt8), Der f 1 (3d6s), Der p 1 (2as8), Der f 2 (1ahk), Der p 2 (1ktj), Blo t 5 (2mey), Der p 5 (3mq1), Der f 7 (3uv1).

well. We identified NQN residues (44–46) as Der p 2 epitope, which is in consistent with Smith and Chapman report [49]. Previous studies identified E102 as an IgE binding site in Der p 2 [47,48]. This residue is a part of our predicted epitopes and is conserved in Eur m 2, Der p 2 and Der f 2. Other predicted regions in the present study, which are conserved in group 2, might be candidates for experimental studies. These regions include: V82-Q86 in which K83 and G84 are conserved in the entire group 2 allergens; and residues C21–P26 and A98–N103 which are conserved in Der p 2, Der f2 and Eur m 2.

There are limited studies about allergens of group 3 and the predicted epitopes here, might be targeted for further studies. In this group, S48–H51, G205–G211 and A242–P247 regions, which are conserved in Der f 3, Eur m 3 and Der p 3, were predicted as epitopes in this study. L85–G91 region was also predicted as epitope. H87, G90–G91, K118, A130 and G145–D147 are the conserved epitope residues in all of the allergens of this group. Additionally, H102–S107 epitope region is conserved in Der f 3, Eur m 3, Der p 3 and Blo t 3.

As mentioned above, the highest conservation in epitope regions in groups 1, 2 and 3 is observed in Der f 3, Eur m 3 and Der p 3 allergens.

Lahiani et al. [50] have studied the cross reactivity between group 5 of allergens (Blo t 5, Der f 5, Der p 5 and Sui m 5). Also, similarities in 3-D structures and cross reactivity between Blo t 5 and Der p 5 have been reported in the study by Curin et al. [51]. It was also mentioned that Blo t 5 and Der p 5 share common conformational epitopes with Blo t 21 and Der p 21, respectively. However, cross reactivity was not observed between group 5 and 21 of mite allergens. Moreover, in the study by Reginald et al. [46], cross reactivity was found between Sui m 5, Blo t 5 and Der f 5 allergens. A conformational epitope was reported for Blo t 5 with N62, K65, K70 and R73 as the main residues of this epitope. This

region was predicted as epitope for group 5 allergens in this report, as well. However, it was not very conserved in this group. Additionally, Lahiani et al. [50] have reported a linear epitope (E90–E108) with E92, D97, E102 and E107 as the main residues in Blo t 5 allergen in consistent with this study and studies by Chan et al. [52] and Tsai et al. [53] (residues Q70–Q117). In all of the evaluated allergens in group 5, there are seven conserved residues in this epitope region. The linear epitope (ERELKRTDLNIERFNYEE) was suggested for immunotherapeutic design of the group 5 mite allergens. Curin et al. [51], have identified two conformational epitopes in Der p 5: DYQNEFDL-LMERIHEQIKKGELALFYLYQ and EQYNLEMAKSGDILERDLKKEEARV-KKIEV, in consistent with the present study with three conformational epitopes in this region. Peptides for vaccine design were selected from ARVKKIEV region. Another region which was predicted as conformational epitope for Der p 5 in this study is: EKPTKEMKD, which was not mentioned in the study by Curin et al.. The aforementioned epitope regions for Der p 5 were predicted for Der f 5, as well. In the study by Lahiani et al. [54], L92–S112 amino acids were reported as linear epitope of Der p 5 and Blo t 5, reacting with IgE and IgG antibodies. L92–Y104 residues were identified as linear and conformational epitopes in our study, as well. This area was reported as a target for vaccine design.

Reports about group 6 of mite allergens are limited. In this work eight predicted epitope regions were common in group 6 allergens: G28–A32, L47–I48, G73–S78, N86–D95, H104–Y107, E137–G144, C179–N187, and T155–P163.

A previous study identified H151–L165 as an epitope for Der f 7 [55]. Although this region was predicted with ElliPro server in the present work, it was not predicted with BcePred and consequently, was not assigned as common epitope in our study. In the present research,

D30-G46 and G71-G80 regions were predicted as epitope in group 7 of allergens. E134 and G135 residues are a conserved part of epitopes in all of the studied allergens of group 7.

Due to high sequence identity, consensus epitopes that are found in one group of allergens can provide the possibility of covering different allergens. In addition, various groups of allergens might share similar epitopes. The similar residues in epitopes of various allergens might be involved in cross reactivity. These epitopes are attractive targets to design vaccines covering various species of mites and different groups of allergens. Different allergens of the same group shared some common epitopes, as shown in Figs. 1 and 2. Additionally, the predicted epitopes are dominantly located in the conserved sequences.

5. Conclusions

This study provides information for future studies about hypoallergens, allergy vaccine design and also experimental analysis of epitope mapping, by presenting consensus epitopes of mite allergens. Our results are particularly important for mite allergens with unknown structures. However, there are some other prerequisites for the selected B-cell epitopes to be applied in vaccine design: these regions should be devoid of T-cell epitopes and IgG production should be evaluated. Further experimental studies are required to confirm the accuracy of the predicted epitopes.

Author contribution

NE, NN, SA, HE, SHN and YG have contributed to the design and conception of the study. NE contributed to data collection, analysis and manuscript drafting. NN contributed to data analysis and manuscript drafting. SA, HE, YG and SHN were involved in data analysis and interpretation; and critically reading of the manuscript. All the authors have approved the final version of manuscript. The study was supervised by SA.

Declarations of interest

None.

Acknowledgments

This study was supported by Shiraz University of Medical Sciences, Shiraz, Iran.

Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.mcp.2019.05.004>.

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***In silico* prediction of B-cell epitopes for twenty-five mite allergens: the therapeutic potentials for immunotherapy**

Table S1 Physiochemical and structural characteristics of the selected allergens

Allergen	Accession number	Residue number	Mature peptide Residue	Number of α helix	Number of β strand	Disulfide bond	Glycosylation	Isoelectric point	Molecular weight (kDa)
Blo t 1. 0201	5JT8	333	225	4	7	2 (134-182; 168-214)	-	5.99	25.61
Der f 1	P16311	321	223	4	8	3 (102-216; 130-170; 164-202)	1 (151; N-linked)	6.14	25.15
Der p 1	P08176	320	222	4	8	3 (102-215; 129-169; 163-201)	1 (150; N-linked)	5.92	25.02
Eur m 1	P25780	321	223	3	9	1 (130-170)	2 (34, 151; N-linked)	6.38	25.13
Blo t 2	Q1M2P1	144	126	0	9	2 (39-44; 90-95)	-	6.33	13.46
Der f 2	Q00855	146	129	0	10	3 (25-136; 38-44; 90-95)	-	6.89	14.08
Der p 2	P49278	146	127	0	10	3 (25-136; 38-44; 90-95)	No	7.42	13.88
Eur m 2	Q9TZZ2	145	129	0	10	3 (24-135; 37-43; 89-94)	No	6.49	14.09
Lep d 2	P80384	141	125	0	9	3 (24-133; 37-42; 88-93)	-	6.49	13.11
Blo t 3	A1KXI1	266	231	2	15	3 (60-76; 187-216; 204-240)*	-	8.35	23.79

Der f 3	P49275	259	232	2	15	3 (52-68; 179-196; 208-234)	-	5.29	24.91
Der p 3	P39675	261	232	2	15	3 (54-70; 181-198; 210-236)	-	8.03	24.99
Eur m 3	O97370	261	232	2	15	3 (54-70; 181-198; 210-236)	-	6.11	25.03
Lep d 3	Q1M2L7	260	219	2	15	3 (66-82; 186-200; 211-235)*	-	7.37	22.50
Blo t 5	O96870	134	117	3	0	No	-	5.09	15.642
Der f 5	Q3LHF8	132	113	3	0	No	-	6.12	11.93
Der p 5	P14004	132	113	3	0	No	-	5.31	11.78
Lep d 5	Q9U5P2	110	110	4	0	No	-	7.09	11.24
Blo t 6	A1KXI3	275	229	2	14	3 (76-92; 201-251; 217-226)*	-	5.29	24.57
Der f 6	P49276	279	230	2	14	3 (79-95; 204-220; 229-255)	-	6.11	25.03
Der p 6	XP_027202682	281	231	3	13	3 (30-46; 155-206; 171-180)	-	5.26	24.88
Blo t 7	ASX95438	195	195	2	8	No	-	5.25	21.217
Der f 7	Q26456	213	191	2	9	No	1 (151; N-linked)	4.67	21.24
Der p 7	P49273	215	198	4	10	No	-	4.62	22.18
Lep d 7	Q1M2N1	216	197	2	8	No	-	7.95	22.09

*The prediction results of disulfide bonds by Cyscon servers. The remaining results of disulfide bonds and glycosylation patterns were retrieved from UniProt. Molecular weights and isoelectric point were obtained from Pepstats and secondary structures were predicted by PSIPRED.

Table S2 The detailed prediction results of RaptorX modeled proteins

Allergen	Best template	Overall uGDT (GDT)*	Modeled residues	Positions predicted as disordered	Solvent accessibility		
					Exposed (%)	Medium (%)	Buried (%)
Blo t 2	1ahkA	94 (74)	126 (100%)	2 (1%)	38	34	26
Blo t 3	2f91A	198 (85)	231 (100%)	17 (7%)	36	27	35
Blo t 6	5zfhA	178 (77)	229 (100%)	1 (0%)	34	28	36
Blo t 7	3uv1A	139 (71)	195 (100%)	6 (3%)	35	38	25
Der f 3	1ym0A	197 (85)	232 (100%)	3 (1%)	37	26	36
Der f 5	3mq1A	87 (87)	100 (100%)	6 (6%)	65	18	17
Der f 6	2f91A	180 (78)	230 (100%)	9 (3%)	36	28	35
Der p 3	2f91A	196 (84)	232 (100%)	3 (1%)	34	28	36
Der p 6	5zfhA	181 (78)	231 (100%)	4 (1%)	34	29	36
Der p 7	3h4zA	181 (91)	198 (100%)	7 (3%)	34	40	24
Eur m 1	1xkgA	222 (99)	223 (100%)	2 (0%)	28	32	39
Eur m 2	1a9vA	120 (93)	129 (100%)	2 (1%)	41	29	28
Eur m 3	1fn8A	197 (84)	232 (100%)	4 (1%)	34	29	36
Lep d 2	1ahkA	96 (76)	125 (100%)	1 (0%)	40	30	28
Lep d 3	1an1E	195 (89)	219 (100%)	7 (3%)	33	30	35
Lep d 5	2lm9A	88 (88)	100 (100%)	4 (4%)	68	17	15
Lep d 7	3uv1A	135 (68)	197 (100%)	6 (3%)	32	43	24

*For proteins with >100 residues, uGDT >50 is a good indicator. For proteins with <100 residues, GDT >50 is desired

Table S3 Evaluation of the initial models (predicted with RaptorX) via Verify 3D, RAMPAGE, ProSA and ERRAT servers

Allergen	Verify 3D	Ramachandran Plot Analysis			ProSA	ERRAT
	Percent of the residues had an averaged 3D-1D score ≥ 0.2	Favored (%)	Allowed (%)	Outlier (%)	Overall model quality Z-score	Overall quality factor
Blo t 2	96.03	99 (79.8)	15 (12.1)	10 (8.1)	-4.06	20.339
Blo t 3	99.13	211 (92.1)	14 (6.1)	4 (1.7)	-7.21	79.2793
Blo t 6	91.27	214 (94.3)	11 (4.8)	2 (0.9)	-8.53	57.9186
Blo t 7	98.97	183 (94.8)	7 (3.6)	3 (1.6)	-5.18	67.7596
Der f 3	99.57	215 (93.5)	8 (3.5)	7 (3.0)	-8.73	78.125
Der f 5	36.00	98 (100.0)	0 (0.0)	0 (0.0)	-3.7	90.2174
Der f 6	80.00	212 (93.0)	11 (4.8)	5 (2.2)	-6.86	54.5045
Der p 3	91.38	217 (94.3)	8 (3.5)	5 (2.2)	-8.14	59.8174
Der p 6	90.48	212 (92.6)	12 (5.2)	5 (2.2)	-7.94	70.4036
Der p 7	99.49	193 (98.5)	2 (1.0)	1 (0.5)	-5.91	93.1217
Eur m 1	99.10	212 (95.9)	7 (3.2)	2 (0.9)	-7.42	88.1517
Eur m 2	89.92	108 (85.0)	13 (10.2)	6 (4.7)	-3.83	33.0579
Eur m 3	99.14	218 (94.8)	9 (3.9)	3 (1.3)	-9.31	75.0000
Lep d 2	100.00	102 (82.9)	14 (11.4)	7 (5.7)	-3.91	17.094
Lep d 3	96.35	205 (94.5)	9 (4.1)	3 (1.4)	-7.36	80.4762
Lep d 5	55.00	92 (93.9)	4 (4.1)	2 (2.0)	-4.82	97.8261
Lep d 7	85.28	188 (96.4)	6 (3.1)	1 (0.5)	-4.52	68.0851

Table S4 Evaluation of the refined models (with GalaxyRefine) via Verify 3D, RAMPAGE, ProSA and ERRAT servers

Allergen	GalaxyRefine models	Verify 3D	Ramachandran Plot Analysis			ProSA	ERRAT
		Percent of the residues had an averaged 3D-1D score ≥ 0.2	Favored (%)	Allowed (%)	Outlier (%)	Overall model quality Z-score	Overall quality factor
Blo t 2	1	89.68	108 (87.1)	9 (7.3)	7 (5.6)	-4.66	51.6949
	2	91.27	110 (88.7)	8 (6.5)	6 (4.8)	-4.58	46.6102
	3	88.10	112 (90.3)	6 (4.8)	6 (4.8)	-4.57	50.4274
	4	91.27	110 (88.7)	8 (6.5)	6 (4.8)	-4.57	33.0508
	5*	99.21	112 (90.3)	6 (4.8)	6 (4.8)	-4.56	45.7627
Blo t 3	1	99.13	219 (95.6)	9 (3.9)	1 (0.4)	-7.09	91.1628
	2	100.00	219 (95.6)	9 (3.9)	1 (0.4)	-7.32	93.3962
	3*	100.00	221 (96.5)	7 (3.1)	1 (0.4)	-7.29	94.47
	4	100.00	219 (95.6)	8 (3.5)	2 (0.9)	-7.3	92.5581
	5	100.00	220 (96.1)	8 (3.5)	1 (0.4)	-7.25	92.0188
Blo t 6	1	83.84	221 (97.4)	6 (2.6)	0 (0.0)	-8.37	95.0226

	2	85.15	223 (98.2)	4 (1.8)	0 (0.0)	-8.42	89.1403
	3	80.79	221 (97.4)	6 (2.6)	0 (0.0)	-8.41	88.1818
	4	87.34	220 (96.9)	7 (3.1)	0 (0.0)	-8.44	89.4977
	5*	86.46	222 (97.8)	5 (2.2)	0 (0.0)	-8.31	92.7602
Blo t 7	1*	90.67	188 (97.4)	5 (2.6)	0 (0.0)	-5.56	95.90
	2	96.41	189 (97.9)	4 (2.1)	0 (0.0)	-5.5	87.0968
	3	87.69	188 (97.4)	3 (1.6)	2 (1.0)	-5.37	93.9189
	4	90.26	188 (97.4)	4 (2.1)	1 (0.5)	-5.51	87.7419
	5	90.77	187 (96.9)	5 (2.6)	1 (0.5)	-5.54	90.6475
Der f 3	1*	99.57	221 (96.1)	7 (3.0)	2 (0.9)	-9.11	91.8552
	2	98.71	219 (95.2)	9 (3.9)	2 (0.9)	-9.05	92.3767
	3	97.41	221 (96.1)	7 (3.0)	2 (0.9)	-9.02	91.8919
	4	98.28	219 (95.2)	9 (3.9)	2 (0.9)	-8.86	92.8571
	5	99.14	219 (95.2)	8 (3.5)	3 (1.3)	-8.94	91.0314
Der f 5	1	38.00	98 (100.0)	0 (0.0)	0 (0.0)	-4.19	90.2174
	2	35.00	98 (100.0)	0 (0.0)	0 (0.0)	-3.91	100
	3	35.00	98 (100.0)	0 (0.0)	0 (0.0)	-3.99	97.8261
	4*	41.00	98 (100.0)	0 (0.0)	0 (0.0)	-3.98	100

	5	36.00	98 (100.0)	0 (0.0)	0 (0.0)	-4.01	100
Der f 6	1*	80.00	220 (96.5)	4 (1.8)	4 (1.8)	-7.00	82.4324
	2	79.57	220 (96.5)	4 (1.8)	4 (1.8)	-7.02	71.9457
	3	79.57	220 (96.5)	4 (1.8)	4 (1.8)	-6.76	83.2579
	4	79.13	219 (96.1)	5 (2.2)	4 (1.8)	-7.12	83.6364
	5	79.57	219 (96.1)	5 (2.2)	4 (1.8)	-6.96	78.2805
Der p 3	1	90.09	221 (96.1)	9 (3.9)	0 (0.0)	-8.58	84.8624
	2	89.22	221 (96.1)	9 (3.9)	0 (0.0)	-8.45	92.093
	3	90.95	220 (95.7)	9 (3.9)	1 (0.4)	-8.6	88.785
	4	91.81	221 (96.1)	9 (3.9)	0 (0.0)	-8.64	86.9767
	5*	90.09	222 (96.5)	8 (3.5)	0 (0.0)	-8.6	89.8618
Der p 6	1*	97.40	226 (98.7)	2 (0.9)	1 (0.4)	-7.79	84.6847
	2	96.10	223 (97.4)	5 (2.2)	1 (0.4)	-7.74	85.6502
	3	96.54	224 (97.8)	4 (1.7)	1 (0.4)	-7.81	87.8378
	4	96.54	225 (98.3)	3 (1.3)	1 (0.4)	-7.75	82.0628
	5	96.54	223 (97.4)	5 (2.2)	1 (0.4)	-7.65	82.3529
Der p 7	1	100.00	192 (98.0)	3 (1.5)	1 (0.5)	-6.19	92.5287
	2	99.49	193 (98.5)	2 (1.0)	1 (0.5)	-6.13	93.7853

	3	95.45	195 (99.5)	0 (0.0)	1 (0.5)	-6.05	95.4023
	4	100.00	194 (99.0)	1 (0.5)	1 (0.5)	-6.18	96.5318
	5*	100.00	195 (99.5)	0 (0.0)	1 (0.5)	-6.24	95.0276
Eur m 1	1	90.13	216 (97.7)	4 (1.8)	1 (0.5)	-7.24	91.9598
	2	93.27	216 (97.7)	4 (1.8)	1 (0.5)	-7.38	97.9899
	3	98.65	214 (96.8)	5 (2.3)	2 (0.9)	-7.06	86.2944
	4*	96.41	216 (97.7)	4 (1.8)	1 (0.5)	-7.17	89.8477
	5	92.38	215 (97.3)	5 (2.3)	1 (0.5)	-7.37	96.4286
Eur m 2	1	79.84	116 (91.3)	8 (6.3)	3 (2.4)	-4.45	66.6667
	2	92.25	116 (91.3)	7 (5.5)	4 (3.1)	-4.17	83.7838
	3	88.37	114 (89.8)	9 (7.1)	4 (3.1)	-4.33	74.3119
	4*	97.67	117 (92.1)	6 (4.7)	4 (3.1)	-4.14	91.7431
	5	85.27	114 (89.8)	9 (7.1)	4 (3.1)	-4.29	85.1485
Eur m 3	1	97.41	222 (96.5)	6 (2.6)	2 (0.9)	-9.45	86.2385
	2	99.14	221 (96.1)	7 (3.0)	2 (0.9)	-9.31	77.5701
	3	96.12	221 (96.1)	7 (3.0)	2 (0.9)	-9.34	82.6484
	4*	99.57	221 (96.1)	7 (3.0)	2 (0.9)	-9.51	87.0968
	5	99.14	222 (96.5)	6 (2.6)	2 (0.9)	-9.4	85.3211

Lep d 2	1	86.40	109 (88.6)	9 (7.3)	5 (4.1)	-4.34	50.8772
	2*	99.20	110 (89.4)	10 (8.1)	3 (2.4)	-4.69	61.4035
	3	89.60	108 (87.8)	11 (8.9)	4 (3.3)	-4.44	64.9123
	4	90.40	111 (90.2)	7 (5.7)	5 (4.1)	-4.49	61.6071
	5	86.40	110 (89.4)	10 (8.1)	3 (2.4)	-4.55	46.9027
Lep d 3	1	94.98	210 (96.8)	7 (3.2)	0 (0.0)	-7.59	88.0000
	2*	96.35	210 (96.8)	7 (3.2)	0 (0.0)	-7.49	87.5622
	3	97.72	208 (95.9)	9 (4.1)	0 (0.0)	-7.21	88.1188
	4	96.35	209 (96.3)	8 (3.7)	0 (0.0)	-7.34	92.8934
	5	92.24	209 (96.3)	8 (3.7)	0 (0.0)	-7.67	90.9091
Lep d 5	1	57.00	95 (96.9)	3 (3.1)	0 (0.0)	-5.17	100
	2*	77.00	95 (96.9)	3 (3.1)	0 (0.0)	-5.35	100
	3	73.00	95 (96.9)	3 (3.1)	0 (0.0)	-5.13	100
	4	57.00	96 (98.0)	2 (2.0)	0 (0.0)	-5.23	100
	5	52.00	95 (96.9)	2 (2.0)	1 (1.0)	-5.21	98.913
Lep d 7	1	96.45	189 (96.9)	5 (2.6)	1 (0.5)	-5.22	90.1235
	2	95.94	191 (97.9)	3 (1.5)	1 (0.5)	-5.14	93.9759
	3*	99.49	188 (96.4)	6 (3.1)	1 (0.5)	-5.03	94.6746

	4	92.39	189 (96.9)	5 (2.6)	1 (0.5)	-5.14	94.1176
	5	87.31	189 (96.9)	5 (2.6)	1 (0.5)	-5.25	97.619

The final selected structures are marked with *, they were selected based on the comparison of the results of before and after the refinement process

Table S5 The predicted linear B-cell epitopes by ElliPro server

Allergen	No.	Start	End	Peptide	Number of residues	Score*
Blo t 1	1	91	99	TYGSLPQNF	9	0.833
	2	133	140	SIQKQCSI	8	0.692
	3	177	208	IRTGLVEERNYPYNMRTQWCDPDVEGQRYHVS	32	0.682
	4	236	261	MHGSNNYFRNLGNGVLRGVAYNDAYT	26	0.667
	5	149	166	DCTYNRYDPSYQCNGCGS	18	0.645
	6	213	221	LRYHSSDED	9	0.613
	7	298	302	ERGHN	5	0.561
	8	286	293	GTGWGNGG	8	0.539
	9	102	110	RQKARLTRI	9	0.509
Blo t 2	1	91	101	LIPTILPNLK	11	0.763
	2	110	113	GDHG	4	0.639
	3	1	5	GDVKF	5	0.624
	4	57	85	MNNIEVPVPGVDKDGCKHTTCPLKKGQKY	29	0.613
	5	41	49	IANQDSEKL	9	0.609

	6	22	33	SGDHCIIHKGKS	12	0.585
	7	9	15	AHGEVTS	7	0.58
Blo t 3	1	43	50	QGLSASSL	8	0.724
	2	55	70	NTLRHNSGGLTVKASR	16	0.709
	3	147	166	VDRKTCNANYGAVGAEITDN	20	0.697
	4	127	139	TLSSGASSLPTKL	13	0.676
	5	171	178	GILNVGGK	8	0.659
	6	90	119	QTASKMSTGTTNAQAIKLPEQGSDPKASSE	30	0.641
	7	74	82	HEKYDSNTI	9	0.634
	8	20	23	RTSH	4	0.58
	9	1	12	IVGGSNAADGDA	12	0.55
	10	202	211	GYGCAQAKYP	10	0.548
Blo t 6	1	20	27	KDYLILKS	8	0.809
	2	151	168	SQEECNAKWGEVNTIKPG	18	0.742
	3	47	54	TDGQTASS	8	0.698
	4	130	141	LTDGNTQDLPEN	12	0.674
	5	96	109	ILASPITPSDTVKV	14	0.672
	6	62	76	NQRSKPGIPDIKTKR	15	0.661

	7	112	122	IEETNLNGGED	11	0.647
	8	218	229	NHYLEWINANKV	12	0.635
	9	174	177	APST	4	0.629
	10	202	211	PSKCPVGEYM	10	0.619
	11	80	90	HEQYDPNTIEN	11	0.614
	12	1	11	VVGGTDAKKAE	11	0.575
Blot 7		183	195	KKFLQNTTPAPAF	13	0.841
		58	75	RAARVGDAKIHNENGDFV	18	0.725
		142	153	HGLGPLDPFIDI	12	0.709
		27	50	GKHTTELD RKIGLVTFKGKLIKD	24	0.706
		92	103	ELIVGLIQSHLT	12	0.655
		118	127	GLAAEGPSVK	10	0.647
		17	20	TQKG	4	0.577
Der f 3	1	43	50	NGQSAKKL	8	0.73
	2	90	104	KLKTPMTLDQTNAP	15	0.716
	3	147	166	VSREQCDQLYSKAGADVSEN	20	0.692
	4	56	72	TLKHASGGEKIQVAEIY	17	0.668
	5	171	178	GDVANGGV	8	0.66

	6	126	139	GYLQEGSYSLPSEL	14	0.658
	7	108	119	PAQGSVDKVGDK	12	0.643
	8	20	23	SSSH	4	0.636
	9	74	82	HENYDSMTI	9	0.631
	10	192	195	VATK	4	0.585
	11	204	213	GYGCARKGYP	10	0.536
Der f 5	1	58	72	NRLMKRTDLDFERY	15	0.759
	2	93	100	QRVKKIEV	8	0.653
	3	25	38	NTFEENPTKEMKEQ	14	0.644
Der f 6	1	20	27	KDYLMKR	8	0.8
	2	48	54	YGQKASS	7	0.733
	3	151	168	GNDRCNEKWGSINAIHPG	18	0.725
	4	96	107	ILPNPVVPSTNV	12	0.711
	5	174	177	DKTQ	4	0.671
	6	203	212	PSKCPPGEYM	10	0.635
	7	62	78	NQRTSSSYGDLKVKPII	17	0.634
	8	110	122	NEIETEDIVDGDK	13	0.632
	9	130	142	LTDGNGKDLDPKL	13	0.621

	10	80	90	HESYEQDQTQT	11	0.619
	11	1	11	VVGGQDADLAE	11	0.562
Der p 3	1	90	102	KLKSPMKLNQKNA	13	0.724
	2	42	50	VAGQTASKL	9	0.712
	3	147	166	VSRKECNELYSKANAETDN	20	0.685
	4	56	72	SLKHSLGGEKISVAKIF	17	0.681
	5	126	139	GYLEEGSYSLPSEL	14	0.653
	6	171	178	GDVANGGK	8	0.654
	7	74	82	HEKYDSYQI	9	0.639
	8	108	119	PAKGSDEVKVGDP	12	0.639
	9	192	195	VKNN	4	0.621
	10	20	23	SSSH	4	0.613
	11	1	11	IVGGEKALAGE	11	0.576
	12	204	213	GYGCARKGYP	10	0.534
Der p 6	1	20	26	KDYLMK	7	0.839
	2	151	168	GNDKCNDKWGSVNTIHPG	18	0.736
	3	48	54	DGQKASS	7	0.724
	4	98	110	SQPVKPSSNVDFI	13	0.69

	5	113	122	ETKDIGDGEK	10	0.687
	6	62	76	NKRTSSKYADLSIKR	15	0.659
	7	130	142	LTDGNTNNLPDNL	13	0.637
	8	174	177	DATQ	4	0.623
	9	203	212	PSKCPPGEYM	10	0.623
	10	80	90	HESYDPETIQN	11	0.62
	11	1	12	VIGGQDAAEAEA	12	0.536
Der p 7	1	1	11	DPIHYDKITEE	11	0.806
	2	71	83	GDANVKSEDGVVK	13	0.751
	3	153	164	GGLSILDPIFAV	12	0.705
	4	35	58	PDHSDKFERHIGIIDLKGELDMRN	24	0.698
	5	128	136	EVSEEGNMT	9	0.697
	6	191	198	KELERNNQ	8	0.655
	7	91	94	HDDV	4	0.574
	8	21	33	AAIEKSETFDPMK	13	0.57
Eur m 1	1	1	15	TYACSINSVSLPSEL	15	0.779
	2	146	169	KDLNAFRHYDGRTIMQHDNGYQPN	24	0.761

	3	85	116	QQNGVVQEHYYPYVAREQSCHRPNAQRYGLKN	32	0.705
	4	50	56	AYRNMSL	7	0.65
	5	65	74	DCASQNGCHG	10	0.623
	6	120	127	ISPPDSNK	8	0.584
	7	18	22	RSLRT	5	0.555
	8	193	201	WDTTWGDNG	9	0.552
	9	207	210	ANIN	4	0.534
Eur m 2	1	93	103	NVPRIAPKSEN	11	0.735
	2	125	129	AKIRD	5	0.71
	3	68	85	IDNNLCHFMKCPLVKGQE	18	0.672
	4	59	66	DGVEIDVP	8	0.671
	5	21	33	CKGSEPCVIHRGT	13	0.657
	6	42	49	DANQNSNA	8	0.618
	7	112	116	GDNGV	5	0.54
	8	1	12	DQVDIKDCANHE	12	0.514
Lep d 2	1	91	101	GTIPAITPKVK	11	0.785
	2	110	113	GDHG	4	0.666
	3	9	15	GHGEVTE	7	0.625

	4	57	84	VAGTTIQVPGLETDGCKFIKCPVKKGEA	28	0.611
	5	42	49	ANQDTAKV	8	0.6
	6	21	34	CSGDTCVIHRGEKM	14	0.535
	7	1	7	GKMTFKD	7	0.53
Lep d 3	1	43	51	SGTSASQLK	9	0.732
	2	55	70	NTVRHNSGGSLISVSE	16	0.714
	3	140	156	VDRAQCNSSYSGDITPN	17	0.699
	4	161	167	GVSAGGK	7	0.653
	5	121	132	YTTEGGSLASSL	12	0.651
	6	90	112	KTSSPMTGIKKADLPVSGSDVSG	23	0.636
	7	74	84	HSGYSSWTLDN	11	0.603
	8	20	23	RSSH	4	0.59
	9	191	200	GMGCARPKNYP	10	0.585
	10	1	12	IVGGSASVASGEA	12	0.564
Lep d 5	1	24	34	TELEKSKSKEL	11	0.735
	2	92	100	TKVKAIETK	9	0.708
	3	1	7	LIHMTEE	7	0.704
	4	54	71	GHFERELKRADLNLAKEF	18	0.703

Lep d 7	1	1	10	HKPAYYDDNM	10	0.811
	2	34	52	EQTKVPIDKKIGLIHIKGS	19	0.777
	3	126	132	KLDAEGK	7	0.772
	4	70	82	GDAKIDTDGGAFA	13	0.753
	5	149	161	FIHGLGPLDPLVD	13	0.712
	6	99	111	HLDLGKIIHPNLK	13	0.646
	7	24	30	TKKELDP	7	0.603
Blo t 5	1	1	17	QEHKPKKDDFRNEFDHL	17	0.781
	2	75	88	RELKRTDLNILERF	14	0.759
	3	109	117	QKVKDIQTQ	9	0.673
Der f 1	1	1	15	TSACRINSVNPSEL	15	0.784
	2	179	185	GSTQGDD	7	0.772
	3	146	169	KDLRAFQHYDGRTIIQHDNGYQPN	24	0.764
	4	85	116	QQNGVVEERSYPYVAREQRCRRPNSQHYGISN	32	0.699
	5	50	56	AYRNTSL	7	0.643
	6	65	74	DCASQHGCHG	10	0.611
	7	120	127	IYPPDVKQ	8	0.608
	8	18	22	RSLRT	5	0.542

	9	206	210	QAGNN	5	0.538
Der f 2	1	92	104	WNVPKIAPKSENV	13	0.713
	2	112	115	GDNG	4	0.638
	3	65	85	VPIDTNACHFVKPLVKGQQ	21	0.63
	4	123	129	THGKIRD	7	0.621
	5	42	50	DANQNTKTA	9	0.607
	6	30	35	HRGKPF	6	0.58
	7	9	16	ANNEIKKV	8	0.567
	8	58	63	LDGLEI	6	0.559
	9	21	26	CHGSDP	6	0.525
	10	1	7	DQVDVKD	7	0.505
Der f 7	1	70	83	QGDANVKGEEGIVK	14	0.787
	2	35	53	PDHADKFERHVGILDFKGE	19	0.754
	3	128	138	EIPDEGNITMT	11	0.724
	4	153	163	GGLSILDPIFG	11	0.704
	5	100	113	DLAYKLGD LHPTTH	14	0.664
	6	91	94	HDDI	4	0.576
	7	25	33	QSETIDPMK	9	0.56

Der p 1	1	145	168	KDLDAFRHYDGRTIIQRDNGYQPN	24	0.77
	2	1	14	TNACSINGNAPAEI	14	0.751
	3	84	115	QHNGVVQESYYRYVAREQSCRRPNAQRFGISN	32	0.707
	4	49	55	AYRQQSL	7	0.654
	5	119	126	IYPPNANK	8	0.62
	6	64	73	DCASQHGCHG	10	0.591
	7	17	21	RQMRT	5	0.556
	8	206	209	ANID	4	0.535
	9	192	200	WDTNWGDNG	9	0.505
Der p 2	1	42	50	EANQNTKTA	9	0.578
	2	30	34	HRGKP	5	0.761
	3	93	103	NVPKIAPKSEN	11	0.682
	4	18	26	VPGCHGSEP	9	0.675
	5	58	65	IDGLEVDV	8	0.673
	6	70	85	PNACHYMKCPLVKGQQ	16	0.631
Der p 5	1	32	43	NSLMERIHEQIK	12	0.814
	2	90	104	DRLMQRKDLDFEQY	15	0.766
	3	57	66	NHFEEKPTKE	10	0.706

	4	125	132	ARVKKIEV	8	0.632
Eur m 3	1	43	50	NGQTASKL	8	0.759
	2	90	104	KLQSPMTLDQKNAKS	15	0.699
	3	57	72	LKHASGGEKLSVAQIY	16	0.688
	4	147	166	VAREQCNKLYEEAGATITDN	20	0.686
	5	108	119	PSQGSVDVKVGDK	12	0.654
	6	126	139	GYLKEGSYSLPSDM	14	0.651
	7	171	178	GNVADGGV	8	0.644
	8	74	82	HEKYDSWTI	9	0.638
	9	20	23	SSSH	4	0.611
	10	192	195	VASN	4	0.597
	11	1	11	IVGGQKAKAGE	11	0.565
	12	204	213	GYGCARKGYP	10	0.538

*Minimum score was set as 0.5

Table S6 The predicted linear epitopes by Bcepred server

Allergen	Hydrophilicity	Flexibility	Accessibility	Turns
Blo t 1	a. RQQGSCGSC b. DSSYQCNGCGSGYSTE c. NPDVEGQR d. RYQSSDEDVM e. NDAYTDH	a. TRIRQQGSC b. YQCNGCG c. LRYQSSD d. GYVERGH	a. PQNFDWRQKARLTRIRQQGS b. LYSIQKQQSIELSEQEL c. DCTYNRYDSSYQ d. YSTEAFKY e. LVEEENYPYNMRTQWCNPDVEGQRYHVSGYQQLRYQSSDEDV f. GSNNYFRNL g. AYNDAYTDH h. YVERGHNSL	a. MHGSNNYFR b. RGHNSLG
Der f 1	a. QGGCGSC b. DCASQHGCHGDT c. AREQQCRRPNSQH d. QHYDGRT e. QHDNGYQPN f. GYGSTQGVD g. DTTWGDS	a. EQQCRRPN	a. DLRSLRT b. YLAYRNTSLD c. EYIQQNG d. VEERSYPYVAREQQCRRPNSQHYG e. YPPDVKQIREALTQT f. KDLRAFQHYDGRT g. QHDNGYQPNYHA	a. RPNSQHY b. IQHDNGYQ

			h. RNSWDTT	
Der p 1	a. NGNAPAE b. QGGCGSC c. DCASQHGCHGDT d. AREQSCRRPN e. QRDNGYQPN f. SNAQGVD g. DTNWGDN	a. YVAREQSCRR	a. DLRQMRTVTP b. YLAYRNQSLDL c. VQESYYRYVAREQSCRRPNAQRF d. YPPNVNKIREAL e. KDLDAFRHYDGRTIIQRDNGYQPNYHA f. RNSWDTNWGDN	-
Eur m 1	a. QGGCGSC b. DCASQNGCHGDT c. REQSCR d. SPPDSNKIRQ e. QHDNGYQPN f. GYGNTQGVD g. DTTWGDN	a. CQISPPDSNKI	a. DLRLRT b. YRNMSLD c. EYIQQNG d. VQEHYYPYVAREQSCHRPNAQRYGLKNY e. SPPDSNKIRQALTQT f. KDLNAFRHYDGRT g. MQHDNGYQPNYHA h. RNSWDTT i. RNSWDTT	a. SPPDSNK b. MQHDNGYQ
Blo t 2	a. TDCAHGE b. SGCSGDHC c. IANQDSEKLE	a. LDLSGCS b. IIHKGKS	a. HKGKSFTLKT b. ANQDSEKLEIK	-

	d. PGVDKDGCKHTT e. KKGQKYE	c. FIANQDS d. PGVDKDG e. TCPLKKG	c. DKDGCKHT d. PLKKGQKYELDYS	
Der f 2	a. DQVDVKDCANNE b. DGCHGSDP c. DANQNTKTAK	a. FDANQNT	a. DQVDVKDCANNEIKKV b. HRGKPFT d. FDANQNTKTAKIE e. VKGQQYDIKYTWNVPKIAPKSENV f. THGKIRD	a. DANQNTK
Der p 2	a. DVKDCANHE b. PGCHGSEP c. EANQNTKTAK	a. FEANQNT	a. KDCANHEIKKV b. HRGKPFQL c. FEANQNTKTAKIE d. VKGQQYDIKYTWNVPKIAPKSENV e. THAKIRD	-
Eur m 2	a. KDCANHE b. PGCKGSEP c. DANQNSNAAK	a. VMVPGCKGSE	a. DQVDIKDCANHEIKKV b. FDANQNSNAAK c. VKGQEYDIKYTWNVPRIAPKSENV d. THAKIRD	a. FDANQNSNA A b. GIDNNLCHF
Lep d 2	a. KDCGHGE b. TGCSGDTC	-	a. GKMTFKD b. HRGEKMTLEAKFAANQDTAKVT	-

	c. AANQDTAKV		c. PVKKGEALD d. TPKVKAD	
Blot 3	a. GGSNAADGDAPYQ b. GHEKYDSNTIDND c. STGTTNAQA d. PEQGSDPKASSE e. DRKTCNAN f. NVGGKDACQGDSGGPV	a. YQVSLQR b. LSASSLT c. NTLRHNS d. QTASKMSTGT e. IKLPEQGSDPKAS f. GTLSSGA g. PIVDRKT h. DACQGDSG	a. DGDAPYQVSLQRTSH b. SSLTTRYNTRLRHNS c. IGHEKYDSNTIDND d. QTASKMS e. KLPEQGSDPKASSE f. LPTKLQKVT g. PIVDRKTCNANY h. AQAKYPGVYTRVGNY	a. LRHNSGG
Derf 3	a. KAGAGDC b. NGQSAKK c. KHASGGEK d. QHENYDS e. DQTNAP f. AQGSDVK g. VSREQCDQ h. GADVSEN	a. YQISLQS b. HCVNGQSA c. LKHASGG d. DVVSREQ e. GVDSCQGDSG f. VDWIESKRSQ	a. NGQSAKKLSIRYNTLKHA b. EIYQHENVDSMT c. KLKTPMTLDQTNAPVP d. KVGDKIR e. LPSELQRVD f. DVVSREQCDQLYSKA g. ARKGYPG h. DWIESKRSQ	a. QSSSHFCG

	i. GGDVANGGVDSCQGDSG GPV j. ESKRSQ			
Der p 3	a. AGQTASK b. AHEKYDSYQ c. NQKNAKA d. AKGSDVK e. SRKECNE f. NAEVTDN g. GGDVANGGKDSCQGDSG GPV h. ESKRSQ	a. YQISLQS b. CVAGQTA c. LKHSLGG d. MKLNQKN e. LPAKGSD f. AVVSRKEC g. DVANGGKDSCQ GDSG h. IDWIESKRSQ	a. KLSIRYNSLKHS b. FAHEKYDSYQIDND c. KLKSPMKLNQKNAKAV d. LPSELRRVD e. VSRKECNELYSKANAETVDN f. VDVKNQV g. ARKGYPG h. DWIESKRSQ	a. QSSSHFCG
Eur m 3	a. GGQKAKAGE b. NGQTASK c. KHASGGEK d. QHEKYDS e. DQKNAKS f. PSQGSDVK g. AREQCNK	a. IVGGQK b. YQISLQS c. CVNGQTA d. LKHASGGEK e. MTLQKNA f. VQLPSQG	a. QKAKAGE b. NGQTASKLSIRYNSLKH c. QIQHEKYDSWT d. KLQSPMTLDQKNAKSVQ e. KVGDKVR f. YLKEGSY	a. QSSSHFCG

	h. GGNVADGGVDSCQGDSG GPV i. DSKRSQ	g. GYLKEGS h. IVAREQC i. GVDSCQGDSG j. IDWIDSKRSQ	g. AREQCNKLYEEAG h. ARKGYPG i. DWIDSKRSQ	
Lep d 3	a. SGEATYQ b. SGTSASQ c. RHNSGGS d. SGSDVSGS e. GYTTEGGS f. DRAQCNSYSYSGD g. VSAGGKDSCQGDSGGPV	a. YQVSLQR b. HCVSGTSA c. NTVRHNSGG d. ALLKTSS e. LPVSGSDVS f. WGYTTEG g. AQCNSYSY h. AGVSAGGKDSC QGDSG	a. YQVSLQRSSH b. SQLKVRYNTVRHNS c. KTSSPMT d. DRAQCNSYSYSGD e. ARPNYPGV f. RVGNFREWIKTNS	a. VRHNSGG b. AQCNSYSY
Blo t 5	a. GSQEHKPKKDDFRNE b. DELNENKSKEL c. NYEEAQT d. KDLKETEQKVVD	-	-	-
Der f 5	a. EQMRKGEE b. EENPTKEMKEQ c. ERDLKKEEQRVKK	a. HEQMRKGE b. NTFEENPT	a. MQRIHEQMRKGEEAL b. QINTFEENPTKEMKEQI	-

		c. EILERDLKKEEQ RV	c. LNRLMKRTDLDIFERYNVEI d. KSNEILERDLKKEEQRVKKIEV	
Der p 5	a. EEKPTKEMKDK b. MAKKSGD c. ERDLKKEE	a. NHFEEKPTKEMK b. LEMAKKSGDILE RDLKKEE	a. MERIHEQIKKGEL b. YLQEQINHFEKPTKEMKDKI c. LDRLMQRKDLDFEQYNLEMAKKSGD d. LERDLKKEEARVKKIEV	-
Lep d 5	a. EKSKSKE	a. QVTELEKSKSKE b. GHFEREL	a. HMTEEQFAKLEQ b. QVTELEKSKSKELKAQILRE c. AKGHFERELKRADLNLAKEFNFES	-
Blo t 6	a. GGTDAKKAEA b. AHCTDGQTASS c. GTNQRSKPG d. QHEQYDPNT e. EETNLNGGEDVK f. TDGNTQDL g. VSQEECNAK h. STQACNGDSGGP	a. VVGGTDA b. CTDGQTA c. NRLGTNQRSK d. GLTDGNT e. TQACNGDSG	a. GGTDAKKAEAPFQ b. NRLGTNQRSKPGIPDIKTKRIVQHEQYDPNTIEND c. TPSDTVK d. EETNLNG e. TDGNTQDLPENLQ f. KIVSQEECNAK g. FTRPNHYLE	-
Der f 6	a. VGGQDAD b. YGTNQRTSSSYGD c. QHESYEQDQTQTDKT	a. CTYGQKA	a. TYGQKASS b. VRYGTNQRTSSSYG	-

	d. NEIETEDIVDGD e. TDGNGKDLPD f. VGNDRCNEK g. DKTQSGCNGDSGGP h. SKCPPGE	b. VRYGTNQRSSS Y c. EQDQTQTD d. WGLTDGNG e. LPDKLQK f. VGNDRCN g. CALDKTQSGCN GDSG	c. IQHESYEQDQTQTDKTI d. TNVQMNEIETED e. TDGNGKDLDPDKLQKGSM f. GNDRCNEKWG g. ALDKTQSG h. SANRKL TG i. KCPPGEY j. SVFTRPKYYLDW	
Der p 6	a. GGQDAAEAEA b. AHCTDGQKASS c. GTNKRTSSKYAD d. QHESYDPET e. KPSSNVD f. ETKDIGDGEKVT g. TDGNTNNL h. DNLQKGS i. VGNDKCNDK j. DATQSGCNGDSGGP k. SKCPPGE	a. HCTDGQKA b. IRYGTNKRSS c. SQPVKPSS d. WGLTDGNT e. VGNDKCN f. ATQSGCNGDSG	a. TDGQKASS b. IRYGTNKRSSKYAD c. KRIVQHESYDPETIQND d. SQPVKPSSNVD e. ETKDIGD f. TDGNTNNLPDNLQKGS g. GNDKCNDKWG h. SADRKL T i. KCPPGEY j. VFTRPQYYSDW	a. KPSSNVDF b. TDGNTNNLPD N
Blo t 7	a. DDAANQ b. IHNENGD c. EGPSVKD	a. LELGDSD b. PIIESEV	a. DALKTQKGFDP b. KHTTELD RKI c. DAKIHNENGDF d. EGPSVKDFHIDE e. ANSQVREM	a. IHNENGD

			f. IESEVKKFLQNTTPAP	
Der f 7	a. EQSETID b. QMKRQGDANVKGEEG c. EISDEGNIT d. QDTVRKE	a. RGLKQMKRQG b. DTVRKEM c. PAFKREL	a. DKITEEINKA b. EQSETIDPMKVPDHADKFERHV c. MRNIEARGLKQMKRQGDANVKGEEG d. EYDLAYK e. FQDTVRKEMTKV f. APAFKRELEKN	-
Der p 7	a. EKSETFD b. KVPDHSDKFE c. GDANVKSEDG d. EVSEEGNMT e. QDTVRAE f. ERNNQ	a. PDHSDKF b. GDANVKSED c. PAFKKELENN	a. DPIHYDKITEEINKA b. AIEKSETFDPMKVPDHSDKFERHI c. KGELDMR d. QVRGLKQMKRVGDANVKSEDG e. EYDLAYK f. EVSEEGNMT g. QDTVRAEMTKV h. APAFKKELENNQ	a. VPDHSDKF b. DLHPNTHVI
Lep d 7	a. DDNMANQ b. SRRGDAKIDTDGG c. DAEGKPS	a. QIVKSLTT b. LSHISRRGD	a. HKPAYYDDNMANQ b. KSLTTKELDPFKIEQTKVPIDKK c. HISRRGDAKIDTD d. LKLGDKNIRIKTDLH	-

			e. HPNLKFE f. DMKLKLKLD AEGKPSLDQFEIDFEQVE g. VKYFNPQARKL h. EEIKKLKLN	
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Minimum score of 0.5 was set for the results

Table S7 The predicted conformational B-cell epitopes based on Ellipro server

Allergen	Discontinuous epitope	Number of residues	Score*
Blo t 1	_:T91, _:Y92, _:G93, _:S94, _:L95, _:P96, _:Q97, _:N98, _:Y224, _:Q227, _:Q228, _:G271, _:T272, _:V273, _:Q274, _:G275, _:V276, _:D277, _:R299	19	0.785
	_:Q112, _:Q113, _:G114, _:S115, _:C116, _:G117, _:S143, _:D149, _:C150, _:T151, _:Y152, _:N153, _:R154, _:Y155, _:D156, _:P157, _:S158, _:Y159, _:Q160, _:C161, _:N162, _:G163, _:C164, _:G165, _:S166, _:I177, _:R178, _:T179, _:G180, _:L181, _:V182, _:E183, _:R185, _:N186, _:Y187, _:P188, _:Y189, _:N190, _:M191, _:R192, _:T193, _:Q194, _:C196, _:D197, _:P198, _:D199, _:V200, _:E201, _:G202, _:Q203, _:R204, _:Y205, _:H206, _:V207, _:S208	55	0.631
	_:W101, _:K104, _:A105, _:R106, _:L107, _:S133, _:I134, _:Q135, _:K136, _:Q137, _:Q138, _:S139, _:I140	13	0.63
	_:T108, _:R109, _:I110, _:M236, _:H237, _:G238, _:S239, _:N240, _:N241, _:Y242, _:R244, _:N245, _:L246, _:G247, _:N248, _:G249, _:V250, _:L251, _:R252, _:G253, _:V254, _:A255, _:Y256, _:N257, _:D258, _:A259, _:Y260, _:T261, _:D262, _:G286, _:T287, _:G288, _:W289, _:G290, _:N291, _:G292, _:G293, _:E298, _:G300, _:H301, _:N302	41	0.614
	_:L213, _:R214, _:Y215, _:H216, _:S217, _:S218, _:E220, _:D221, _:N307, _:N308	10	0.572
Blo t 2	_:G1, _:D2, _:V3, _:K4, _:F5, _:S22, _:G23, _:D24, _:H25, _:I27, _:H29, _:K30, _:G31, _:K32, _:S33, _:M57, _:N58, _:L91, _:I92, _:I93, _:P94, _:T95, _:I96, _:L97, _:P98, _:N99, _:L100, _:K101, _:N121, _:T122, _:V124, _:V125, _:D126	33	0.671
	_:A9, _:G11, _:E12, _:V13, _:T14, _:S15, _:I41, _:A42, _:N43, _:Q44, _:D45, _:S46, _:E47, _:K48, _:L49, _:E61, _:V62, _:P63, _:V64, _:P65, _:G66, _:V67, _:D68, _:K69, _:D70, _:G71, _:C72, _:K73, _:T75, _:T76, _:C77, _:P78, _:L79, _:K80, _:K81, _:G82, _:Q83, _:K84, _:Y85, _:G110, _:D111, _:H112, _:G113	43	0.619
Blo t 3	_:I1, _:V2, _:G3, _:G4, _:S5, _:N6, _:A7, _:A8, _:D9, _:G10, _:D11, _:A12, _:P13, _:R20, _:F24, _:A31, _:D32, _:N33, _:Q43, _:G44, _:L45, _:S46, _:A47, _:S48, _:S49, _:L50, _:N55, _:T56, _:L57, _:R58, _:H59, _:N60, _:S61, _:G62, _:G63, _:L64, _:T65, _:V66, _:K67, _:A68, _:S69, _:R70, _:Q90, _:A92, _:S93, _:K94, _:M95, _:S96, _:T97, _:G98, _:T99, _:T100, _:N101, _:A102, _:Q103, _:A104, _:P108, _:E109, _:Q110, _:G111, _:S112, _:D113, _:P114, _:K115, _:A116, _:S117, _:S118, _:E119, _:W125, _:G126, _:T127, _:L128, _:S129, _:S130, _:G131, _:A132, _:S133, _:S134, _:L135, _:P136, _:T137, _:K138, _:L139, _:I146, _:V147, _:D148, _:R149, _:K150, _:T151, _:N153, _:A154, _:N155, _:Y156, _:G157, _:A158, _:V159, _:G160, _:A161, _:E162, _:I163, _:G171, _:I172, _:L173, _:N174, _:V175,	126	0.655

	_:G176, _:G177, _:K178, _:D179, _:G202, _:Y203, _:G204, _:C205, _:A206, _:Q207, _:A208, _:K209, _:Y210, _:P211, _:K225, _:G226, _:K227, _:G228, _:V229, _:P230, _:V231		
	_:H74, _:E75, _:K76, _:N84	4	0.613
	_:T21, _:S22, _:H23	3	0.574
	_:Y77, _:D78, _:S79, _:N80, _:T81, _:I82, _:D83	7	0.573
Blo t 6	_:K20, _:D21, _:Y22, _:L23, _:I24, _:L25, _:K26, _:S27, _:A44, _:T47, _:D48, _:G49, _:Q50, _:T51, _:A52, _:S53, _:S54	17	0.721
	_:V1, _:V2, _:G3, _:G4, _:T5, _:D6, _:A7, _:K8, _:K9, _:A10, _:E11, _:A12, _:P13, _:T36, _:P37, _:Q38, _:G60, _:T61, _:N62, _:Q63, _:R64, _:S65, _:K66, _:P67, _:G68, _:I69, _:P70, _:D71, _:K75, _:R76, _:H80, _:E81, _:Q82, _:Y83, _:D84, _:P85, _:N86, _:T87, _:I88, _:E89, _:N90, _:I96, _:A98, _:S99, _:P100, _:I101, _:T102, _:P103, _:S104, _:D105, _:T106, _:V107, _:K108, _:V109, _:I112, _:E113, _:E114, _:T115, _:N116, _:L117, _:N118, _:G119, _:G120, _:E121, _:G129, _:L130, _:T131, _:D132, _:G133, _:N134, _:T135, _:Q136, _:D137, _:L138, _:P139, _:E140, _:N141, _:L142, _:K148, _:S151, _:Q152, _:E153, _:E154, _:C155, _:N156, _:A157, _:K158, _:W159, _:G160, _:E161, _:V162, _:N163, _:T164, _:I165, _:K166, _:P167, _:G168, _:A174, _:P175, _:S176, _:T177, _:Q178, _:Y190, _:N191, _:G192, _:K193, _:P202, _:S203, _:K204, _:C205, _:P206, _:V207, _:G208, _:E209, _:Y210, _:M211, _:R216, _:N218, _:H219, _:Y220, _:L221, _:E222, _:W223, _:N225, _:A226, _:N227, _:K228, _:V229	128	0.632
Blo t 7	_:D1, _:D2, _:A3, _:N5, _:Q6, _:A60, _:R61, _:V62, _:G63, _:D64, _:A65, _:K66, _:I67, _:H68, _:N69, _:E70, _:N71, _:G72, _:D73, _:F74, _:V75, _:G118, _:L119, _:A120, _:A121, _:E122, _:G123, _:P124, _:S125, _:K183, _:K184, _:F185, _:L186, _:Q187, _:N188, _:T189, _:T190, _:P191, _:A192, _:P193, _:A194, _:F195	42	0.768
	_:G27, _:K28, _:T30, _:T31, _:E32, _:L33, _:D34, _:R35, _:K36, _:I37, _:G38, _:L39, _:V40, _:T41, _:F42, _:K43, _:G44, _:K45, _:I47, _:K49, _:D50, _:E92, _:I94, _:V95, _:G96, _:L97, _:I98, _:Q99, _:S100, _:H101, _:L102, _:T103, _:H142, _:G143, _:L144, _:G145, _:P146, _:L147, _:D148, _:P149, _:F150, _:I151, _:D152, _:I153	44	0.725
	_:S83, _:D84, _:V85	3	0.627
	_:K19, _:G20, _:D22	3	0.53
Der f 3	_:V2, _:G3, _:G4, _:V5, _:K6, _:A7, _:Q8, _:A9, _:G10, _:D11, _:P13, _:S20, _:S21, _:S22, _:H23, _:D31, _:E32, _:Y33, _:N43, _:G44, _:Q45, _:S46, _:A47, _:K48, _:K49, _:L50, _:N55, _:T56, _:L57, _:K58, _:H59, _:A60, _:S61, _:G62, _:G63, _:E64, _:K65, _:I66, _:Q67, _:V68, _:A69, _:E70, _:Y72, _:K90, _:K92, _:T93, _:P94, _:M95, _:T96, _:L97, _:D98, _:Q99, _:T100, _:N101, _:A102, _:K103, _:P104, _:P108, _:A109, _:Q110, _:G111, _:S112, _:D113, _:V114, _:K115, _:V116, _:G117, _:D118, _:K119, _:G126, _:Y127, _:L128, _:Q129,	126	0.667

	_:E130, _:G131, _:S132, _:Y133, _:S134, _:L135, _:P136, _:S137, _:E138, _:L139, _:V146, _:V147, _:S148, _:R149, _:E150, _:Q151, _:D153, _:Q154, _:L155, _:Y156, _:S157, _:K158, _:A159, _:G160, _:A161, _:D162, _:V163, _:G171, _:D172, _:V173, _:A174, _:N175, _:G176, _:G177, _:V178, _:D179, _:G204, _:Y205, _:G206, _:C207, _:A208, _:R209, _:K210, _:G211, _:Y212, _:P213, _:D224, _:E227, _:S228, _:K229, _:R230, _:S231, _:Q232		
	_:H74, _:E75, _:N76, _:N84	4	0.614
	_:V192, _:A193, _:T194, _:K195	4	0.585
	_:Y77, _:D78, _:S79, _:M80, _:T81, _:I82, _:D83	7	0.565
Der f 5	_:L1, _:L2, _:M3, _:Q4, _:R5, _:I6, _:H7, _:E8, _:Q9, _:R11, _:K12, _:E15	12	0.816
	_:L60, _:M61, _:R63, _:T64, _:D65, _:L66, _:D67, _:I68, _:F69, _:E70, _:R71, _:Y72, _:E75	13	0.755
	_:N30, _:P31, _:T32, _:K33, _:E34, _:K36, _:E37, _:Q38, _:I98, _:E99, _:V100	11	0.713
	_:H22, _:N25, _:T26, _:E28, _:E29	5	0.648
	_:G55, _:N58, _:R59	3	0.597
Der f 6	_:E113, _:T114, _:E115, _:D116, _:I117, _:V118, _:D119, _:G120, _:D121, _:K122, _:K219	11	0.681
	_:V1, _:V2, _:G3, _:G4, _:Q5, _:D6, _:A7, _:D8, _:L9, _:A10, _:E11, _:A12, _:P13, _:K20, _:D21, _:Y22, _:L23, _:I24, _:M25, _:K26, _:R27, _:S36, _:E37, _:S38, _:Y48, _:G49, _:Q50, _:K51, _:A52, _:S53, _:S54, _:G60, _:T61, _:N62, _:Q63, _:R64, _:T65, _:S66, _:S67, _:S68, _:Y69, _:D71, _:V74, _:K75, _:P76, _:I77, _:I78, _:I96, _:P98, _:N99, _:P100, _:V101, _:V102, _:P103, _:S104, _:T105, _:N106, _:V107, _:L130, _:T131, _:D132, _:G133, _:N134, _:G135, _:K136, _:D137, _:L138, _:P139, _:D140, _:K141, _:L142, _:G151, _:N152, _:D153, _:R154, _:C155, _:N156, _:K158, _:W159, _:G160, _:S161, _:I162, _:N163, _:A164, _:I165, _:D174, _:K175, _:T176, _:Q177, _:S178, _:P203, _:S204, _:K205, _:C206, _:P207, _:P208, _:G209, _:E210, _:Y211, _:M212, _:D223, _:W224, _:T226, _:K227, _:N228, _:I229, _:V230	107	0.671
	_:H80, _:E81, _:S82, _:Y83, _:E84, _:Q85, _:D86, _:Q87, _:T88, _:Q89, _:T90, _:H166, _:P167, _:G168	14	0.581
	_:N110, _:E111, _:I112, _:A191, _:N192, _:K194	6	0.515

Der p 3	_:I1, _:V2, _:G3, _:G4, _:E5, _:K6, _:A7, _:L8, _:A9, _:G10, _:E11, _:C12, _:P13, _:D31, _:E32, _:Y33, _:A39, _:V42, _:A43, _:G44, _:Q45, _:T46, _:A47, _:S48, _:K49, _:L50, _:N55, _:S56, _:L57, _:K58, _:H59, _:S60, _:L61, _:G62, _:G63, _:E64, _:I66, _:S67, _:V68, _:A69, _:K70, _:F72, _:Y77, _:D78, _:S79, _:Y80, _:Q81, _:I82, _:D83, _:K90, _:K92, _:S93, _:P94, _:M95, _:K96, _:L97, _:N98, _:K100, _:N101, _:A102, _:P108, _:A109, _:K110, _:G111, _:S112, _:D113, _:V114, _:K115, _:V116, _:G117, _:D118, _:W125, _:G126, _:Y127, _:L128, _:E129, _:E130, _:G131, _:S132, _:Y133, _:S134, _:L135, _:P136, _:S137, _:E138, _:L139, _:V146, _:N153, _:E154, _:L155, _:Y156, _:S157, _:K158, _:A159, _:N160, _:A161, _:E162, _:V163, _:G171, _:D172, _:V173, _:A174, _:N175, _:G176, _:G177, _:K178, _:D179, _:Q182, _:V192, _:K193, _:N194, _:N195, _:G204, _:Y205, _:G206, _:C207, _:A208, _:R209, _:K210, _:G211, _:Y212, _:P213, _:G220, _:I223, _:D224, _:E227, _:S228, _:K229, _:R230, _:S231, _:Q232	131	0.641
	_:H74, _:E75, _:K76, _:N84	4	0.621
	_:V147, _:S148, _:R149, _:K150, _:E151, _:T164, _:D165, _:N166	8	0.58
	_:S20, _:S21, _:S22, _:H23, _:F24	5	0.566
Der p 6	_:K20, _:D21, _:Y22, _:L23, _:I24, _:M25, _:K26, _:D48, _:G49, _:Q50, _:K51, _:A52, _:S53, _:S54	14	0.781
	_:A191, _:D192, _:K194	3	0.665
	_:V1, _:I2, _:G3, _:G4, _:Q5, _:D6, _:A7, _:A8, _:E9, _:A10, _:E11, _:A12, _:P13, _:S36, _:A37, _:S38, _:G60, _:T61, _:N62, _:K63, _:R64, _:T65, _:S66, _:S67, _:K68, _:Y69, _:S73, _:K75, _:R76, _:H80, _:E81, _:S82, _:Y83, _:D84, _:P85, _:E86, _:T87, _:I88, _:Q89, _:N90, _:S98, _:Q99, _:P100, _:V101, _:K102, _:P103, _:S104, _:S105, _:N106, _:V107, _:E113, _:T114, _:K115, _:D116, _:I117, _:G118, _:D119, _:G120, _:E121, _:K122, _:G129, _:L130, _:T131, _:D132, _:G133, _:N134, _:T135, _:N136, _:N137, _:L138, _:P139, _:D140, _:N141, _:L142, _:G151, _:N152, _:D153, _:K154, _:C155, _:N156, _:D157, _:K158, _:W159, _:G160, _:S161, _:V162, _:N163, _:T164, _:I165, _:H166, _:P167, _:G168, _:D174, _:A175, _:T176, _:Q177, _:P203, _:S204, _:K205, _:C206, _:P207, _:P208, _:G209, _:E210, _:Y211, _:M212, _:R217, _:P218, _:Q219, _:Y220, _:S222, _:D223, _:A226, _:K227, _:N228, _:I229, _:V230, _:Q231	118	0.649
Der p 7	_:D1, _:P2, _:I3, _:H4, _:Y5, _:D6, _:K7, _:I8, _:T9, _:E10, _:E11, _:K14, _:G71, _:D72, _:A73, _:N74, _:V75, _:K76, _:S77, _:E78, _:D79, _:G80, _:V81, _:V82, _:K83, _:E128, _:V129, _:S130, _:E131, _:E132, _:G133, _:N134, _:T136, _:K191, _:E192, _:E194, _:R195, _:N196, _:N197, _:Q198	40	0.753
	_:P35, _:D36, _:S38, _:K40, _:F41, _:E42, _:R43, _:H44, _:I45, _:G46, _:I47, _:I48, _:D49, _:L50, _:K51, _:G52, _:E53, _:D55, _:R57, _:N58, _:D100, _:K104, _:L105, _:G106, _:D107, _:L108, _:H109, _:P110, _:N111, _:T112, _:H113, _:G153, _:G154, _:L155, _:S156, _:I157, _:L158, _:D159, _:P160, _:I161, _:F162, _:A163, _:V164	43	0.735
	_:A21, _:A22, _:E24, _:K25, _:S26, _:E27, _:T28, _:F29, _:D30, _:P31, _:G63, _:K65, _:Q66, _:H91, _:D92, _:D93, _:V94	17	0.587

Eur m 1	_:K146, _:D147, _:L148, _:N149, _:A150, _:R152, _:H153, _:D163, _:N164, _:G165, _:Y166, _:Q167, _:P168, _:N169	14	0.824
	_:T1, _:Y2, _:A3, _:C4, _:S5, _:I6, _:N7, _:S8, _:V9, _:S10, _:L11, _:P12, _:S13, _:E14, _:I120, _:S121, _:P122, _:P123, _:D124, _:N126, _:K127, _:Q130, _:G179, _:N180, _:T181, _:Q182, _:G183, _:V184, _:D185, _:A207, _:N208, _:I209, _:N210, _:Q216	34	0.716
	_:R52, _:N53, _:M54, _:S55, _:L56	5	0.689
	_:M28, _:Q29, _:G30, _:G31, _:C32, _:G33, _:S34, _:D65, _:C66, _:A67, _:S68, _:Q69, _:N70, _:G71, _:C72, _:H73, _:G74, _:Y97, _:V98, _:A99, _:R100, _:E101, _:Q102, _:S103, _:C104, _:H105, _:Y154, _:D155, _:G156, _:R157, _:T158, _:I159, _:Q161, _:H162, _:D194, _:T195, _:T196, _:W197, _:G198, _:D199, _:N200, _:G201	42	0.64
	_:A50, _:Y51, _:D57, _:L58, _:A59, _:E82, _:Q85, _:Q86, _:N87, _:G88, _:V89, _:V90, _:Q91, _:E92, _:H93, _:Y94, _:Y95, _:P96, _:R106, _:P107, _:N108, _:A109, _:Q110, _:R111, _:Y112, _:L114, _:L223	27	0.618
	_:T133, _:Q134, _:H136	3	0.541
Eur m 2	_:D1, _:Q2, _:V3, _:D4, _:I5, _:K6, _:G20, _:C21, _:K22, _:G23, _:S24, _:E25, _:P26, _:C27, _:V28, _:I29, _:H30, _:R31, _:G32, _:T33, _:D59, _:G60, _:V61, _:E62, _:I63, _:D64, _:V65, _:P66, _:N93, _:V94, _:P95, _:R96, _:I97, _:A98, _:P99, _:K100, _:S101, _:E102, _:N103, _:H124, _:A125, _:K126, _:I127	43	0.639
	_:D7, _:C8, _:A9, _:N10, _:H11, _:E12, _:D42, _:A43, _:N44, _:Q45, _:N46, _:S47, _:N48, _:A49, _:A50, _:I68, _:D69, _:N70, _:N71, _:L72, _:C73, _:H74, _:F75, _:M76, _:K77, _:C78, _:P79, _:L80, _:V81, _:K82, _:G83, _:Q84, _:E85, _:G112, _:D113, _:N114, _:G115, _:V116	38	0.605
Eur m 3	_:V2, _:G3, _:G4, _:Q5, _:K6, _:A7, _:K8, _:A9, _:G10, _:E11, _:P13, _:D31, _:E32, _:Y33, _:N43, _:G44, _:Q45, _:T46, _:A47, _:S48, _:K49, _:L50, _:N55, _:L57, _:K58, _:H59, _:A60, _:S61, _:G62, _:G63, _:E64, _:K65, _:L66, _:S67, _:V68, _:A69, _:Q70, _:Y72, _:H74, _:E75, _:K76, _:N84, _:K90, _:Q92, _:S93, _:P94, _:M95, _:T96, _:L97, _:D98, _:Q99, _:K100, _:N101, _:A102, _:K103, _:S104, _:W125, _:G126, _:Y127, _:L128, _:K129, _:E130, _:G131, _:S132, _:Y133, _:S134, _:L135, _:P136, _:S137, _:D138, _:M139, _:N153, _:K154, _:L155, _:E157, _:E158, _:A159, _:G160, _:A161, _:T162, _:I163, _:G171, _:N172, _:V173, _:A174, _:D175, _:G176, _:G177, _:V178, _:D179, _:G204, _:Y205, _:G206, _:C207, _:A208, _:R209, _:K210, _:G211, _:Y212, _:P213, _:D224, _:W225, _:D227, _:S228, _:K229, _:R230, _:S231, _:Q232	108	0.669
	_:P108, _:S109, _:Q110, _:G111, _:S112, _:D113, _:V114, _:K115, _:V116, _:G117, _:D118, _:K119, _:I146, _:V192, _:A193, _:S194, _:N195	17	0.62

	_:V147, _:A148, _:R149, _:E150, _:Q151, _:T164, _:D165, _:N166	8	0.568
	_:Y77, _:D78, _:S79, _:W80, _:T81, _:I82, _:D83	7	0.566
	_:S20, _:S21, _:S22, _:H23, _:F24	5	0.559
Lep d 2	_:G9, _:H10, _:G11, _:E12, _:V13, _:T14, _:E15, _:A42, _:N43, _:Q44, _:D45, _:T46, _:A47, _:K48, _:V49, _:V57, _:A58, _:G59, _:T60, _:T61, _:Q63, _:V64, _:P65, _:G66, _:L67, _:E68, _:T69, _:D70, _:G71, _:C72, _:K73, _:I75, _:K76, _:C77, _:P78, _:V79, _:K80, _:K81, _:G82, _:E83, _:A84, _:G110, _:D111, _:H112, _:G113	45	0.634
	_:G1, _:K2, _:M3, _:T4, _:F5, _:G20, _:C21, _:S22, _:G23, _:D24, _:T25, _:C26, _:V27, _:I28, _:H29, _:R30, _:G31, _:E32, _:K33, _:T35, _:G91, _:T92, _:I93, _:P94, _:A95, _:I96, _:T97, _:P98, _:K99, _:V100, _:K101, _:V124, _:E125	33	0.622
Lep d 3	_:A101, _:D102, _:L103, _:P104, _:V105, _:S106, _:G107, _:S108, _:D109, _:V110, _:S111, _:G112, _:V139, _:G181, _:N182, _:R210, _:E211, _:K214, _:T215, _:N216, _:S217, _:G218, _:L219	23	0.679
	_:V2, _:G3, _:G4, _:S5, _:A6, _:V7, _:A8, _:S9, _:G10, _:E11, _:A12, _:T13, _:D31, _:D32, _:Y33, _:S43, _:G44, _:T45, _:S46, _:A47, _:S48, _:Q49, _:L50, _:K51, _:N55, _:T56, _:V57, _:R58, _:H59, _:N60, _:S61, _:G62, _:G63, _:S64, _:L65, _:I66, _:S67, _:S69, _:E70, _:K90, _:S92, _:S93, _:P94, _:M95, _:T96, _:G97, _:I98, _:K99, _:G120, _:Y121, _:T122, _:T123, _:E124, _:G125, _:G126, _:S127, _:L128, _:A129, _:S130, _:S131, _:L132, _:V140, _:D141, _:R142, _:A143, _:Q144, _:C145, _:N146, _:S147, _:S148, _:Y149, _:S150, _:G151, _:D152, _:I153, _:T154, _:P155, _:N156, _:G161, _:V162, _:S163, _:A164, _:G165, _:G166, _:K167, _:D168, _:G191, _:M192, _:G193, _:C194, _:A195, _:R196, _:P197, _:N198, _:Y199, _:P200	96	0.656
	_:S21, _:S22, _:H23	3	0.616
	_:H74, _:S75, _:G76, _:Y77, _:S78, _:S79, _:W80, _:T81, _:L82, _:D83, _:N84	11	0.603
Lep d 5	_:E98, _:T99, _:K100	3	0.857
	_:L1, _:I2, _:H3, _:M4, _:E6, _:E7	6	0.78
	_:H21, _:T24, _:E25, _:L26, _:E27, _:K28, _:S29, _:K30, _:S31, _:K32, _:E33, _:L34	12	0.74
	_:G54, _:H55, _:E57, _:R58, _:E59, _:L60, _:K61, _:R62, _:A63, _:D64, _:L65, _:N66, _:L67, _:A68, _:E69, _:K70, _:F71, _:E74	18	0.723

	_:T92, _:K93, _:K95	3	0.643
Lep d 7	_:P39, _:I40, _:D41, _:K42, _:K43, _:I44, _:G45, _:L46, _:I47, _:H48, _:I49, _:K50, _:G51, _:S52, _:D101, _:G103, _:K104, _:I105, _:I106, _:H107, _:P108, _:N109	22	0.82
	_:H1, _:K2, _:P3, _:A4, _:Y5, _:Y6, _:D7, _:D8, _:N9, _:M10, _:G70, _:D71, _:A72, _:I74, _:D75, _:T76, _:D77, _:G78, _:G79, _:A80, _:F81, _:A82, _:K126, _:L127, _:D128, _:A129, _:E130, _:G131, _:K132, _:K192, _:K195, _:L196, _:N197	33	0.786
	_:K111, _:H151, _:G152, _:L153, _:G154, _:P155, _:L156, _:D157, _:P158, _:L159, _:D161	11	0.76
	_:K20, _:S21, _:T24, _:K25	4	0.668
	_:Q35, _:K56, _:N57, _:H99	4	0.603
	_:K26, _:E27, _:L28, _:D29, _:P30	5	0.552
	_:G62, _:H65, _:K90, _:N91, _:I92	5	0.537
Blo t 5	_:F10, _:R11, _:N12, _:F14	4	0.833
	_:K4, _:P5, _:K6, _:K7, _:D8, _:D9	6	0.792
	_:E76, _:L77, _:K78, _:R79, _:T80, _:D81, _:L82, _:N83, _:I84, _:L85, _:E86, _:F88	12	0.747
	_:D41, _:E42, _:L43, _:N44, _:E45, _:N46, _:K47, _:S48, _:K49, _:E50, _:L51, _:Q52, _:E53, _:Q109, _:K110, _:K112, _:D113, _:I114, _:Q115, _:T116, _:Q117	21	0.701
	_:E13, _:D15, _:H16, _:L17	4	0.643
Der f 1	_:K146, _:D147, _:L148, _:A150, _:Q152, _:H153, _:H162, _:D163, _:N164, _:G165, _:Y166, _:Q167, _:P168, _:N169	14	0.822
	_:T1, _:S2, _:A3, _:C4, _:R5, _:I6, _:N7, _:S8, _:V9, _:N10, _:V11, _:P12, _:S13, _:E14, _:I120, _:Y121, _:P122, _:P123, _:D124, _:K126, _:Q127, _:E130	22	0.752
	_:N53, _:T54, _:S55, _:L56	4	0.65

	_:D16, _:L17, _:R18, _:S19, _:L20, _:T22, _:I26, _:M28, _:Q29, _:G30, _:G31, _:C32, _:G33, _:A50, _:Y51, _:D57, _:L58, _:S59, _:D65, _:C66, _:A67, _:S68, _:Q69, _:H70, _:G71, _:C72, _:H73, _:G74, _:D75, _:Q85, _:Q86, _:N87, _:G88, _:V89, _:V90, _:E91, _:E92, _:R93, _:S94, _:Y95, _:P96, _:Y97, _:V98, _:A99, _:R100, _:E101, _:Q102, _:C104, _:R105, _:R106, _:P107, _:N108, _:S109, _:Q110, _:H111, _:Y112, _:I114, _:S115, _:N116, _:H136, _:Y154, _:D155, _:G156, _:R157, _:T158, _:I159, _:I160, _:Q161, _:G179, _:S180, _:T181, _:Q182, _:G183, _:D184, _:D185, _:D194, _:T195, _:T196, _:W197, _:G198, _:D199, _:S200, _:G201, _:Q206, _:A207, _:G208, _:N209, _:M223	88	0.602
Der f 2	_:A9, _:N10, _:N11, _:E12	4	0.682
	_:D19, _:G20, _:H30, _:R31, _:G32, _:K33, _:P34, _:T36, _:S57, _:L58, _:D59, _:G60, _:L61, _:N93, _:V94, _:P95, _:K96, _:I97, _:A98, _:P99, _:K100, _:S101, _:E102, _:N103, _:V104, _:K126, _:R128, _:D129	28	0.662
	_:D42, _:N44, _:Q45, _:N46, _:T47, _:K48, _:T49, _:A50, _:K51, _:D64, _:V65, _:P66, _:G67, _:I68, _:D69, _:T70, _:N71, _:A72, _:C73, _:H74, _:F75, _:V76, _:K77, _:C78, _:P79, _:L80, _:V81, _:K82, _:G83, _:Q84, _:Q85, _:G112, _:D113, _:N114, _:G115	35	0.619
Der f 7	_:P35, _:D36, _:K40, _:F41, _:E42, _:R43, _:H44, _:V45, _:G46, _:I47, _:L48, _:D49, _:F50, _:K51, _:G52, _:E53, _:R57, _:N58, _:D100, _:K104, _:L105, _:G106, _:D107, _:L108, _:H109, _:P110, _:T111, _:T112, _:H113, _:G153, _:G154, _:L155, _:S156, _:I157, _:L158, _:D159, _:P160, _:I161	38	0.765
	_:D6, _:K7, _:I8, _:T9, _:E10, _:E11, _:N13, _:Q70, _:G71, _:D72, _:A73, _:N74, _:V75, _:K76, _:G77, _:E78, _:E79, _:G80, _:I81, _:V82, _:K83, _:E128, _:I129, _:P130, _:D131, _:E132, _:G133, _:N134, _:I135, _:T136, _:T138, _:K190, _:R191, _:E192, _:E194	35	0.753
	_:A21, _:A22, _:Q25, _:S26, _:E27, _:T28, _:I29, _:D30, _:P31, _:G63, _:K65, _:Q66, _:H91, _:D92, _:D93, _:I94	16	0.586
Der p 1	_:T1, _:N2, _:A3, _:C4, _:S5, _:I6, _:N7, _:G8, _:N9, _:A10, _:P11, _:A12, _:E13, _:I14, _:I119, _:Y120, _:P121, _:P122, _:N123, _:N125, _:K126, _:E129, _:S178, _:N179, _:A180, _:Q181, _:G182, _:V183, _:D184, _:A206, _:N207, _:I208, _:D209, _:E214, _:E215	35	0.691
	_:I25, _:M27, _:K145, _:D146, _:L147, _:D148, _:A149, _:R151, _:H152, _:Y153, _:D154, _:G155, _:R156, _:T157, _:I158, _:I159, _:Q160, _:R161, _:D162, _:N163, _:G164, _:Y165, _:Q166, _:P167, _:N168, _:W192, _:D193, _:T194, _:N195, _:W196, _:G197, _:D198, _:N199, _:G200	34	0.685
	_:R51, _:Q53, _:S54, _:L55	4	0.632

	_:G29, _:G30, _:C31, _:G32, _:D56, _:L57, _:A58, _:D64, _:C65, _:A66, _:S67, _:Q68, _:H69, _:G70, _:C71, _:H72, _:G73, _:D74, _:T75, _:R78, _:Q84, _:H85, _:N86, _:G87, _:V88, _:V89, _:Q90, _:E91, _:S92, _:Y93, _:Y94, _:Y96, _:V97, _:A98, _:R99, _:E100, _:Q101, _:S102, _:C103, _:R104, _:R105, _:P106, _:N107, _:A108, _:Q109, _:R110, _:F111, _:G112, _:I113, _:S114, _:N115, _:L222	52	0.613
	_:D15, _:R17, _:Q18, _:R20	4	0.58
	_:L16, _:M19, _:T21, _:A49, _:Y50, _:A132, _:Q133, _:H135	8	0.5
Der p 2	_:I58, _:D59, _:G60, _:L61, _:S101, _:E102, _:N103	7	0.737
	_:H30, _:R31, _:G32, _:K33, _:P34, _:V94, _:P95, _:K96, _:I97, _:A98, _:P99, _:K100, _:D129	13	0.73
	_:V3, _:D4, _:V5, _:K6, _:D7, _:C8, _:A9, _:N10, _:H11, _:E12, _:V18, _:P19, _:G20, _:C21, _:H22, _:G23, _:S24, _:E25, _:P26, _:E42, _:A43, _:N44, _:Q45, _:N46, _:T47, _:K48, _:T49, _:A50, _:D69, _:P70, _:N71, _:C73, _:H74, _:Y75, _:M76, _:K77, _:C78, _:P79, _:L80, _:V81, _:K82, _:G83, _:Q84, _:Q85, _:G112, _:D113, _:D114, _:G115, _:H124	49	0.609
	_:E62, _:V63, _:D64, _:V65, _:P66	5	0.553
Der p 5	_:N32, _:S33, _:L34, _:M35, _:E36, _:R37, _:I38, _:H39, _:E40, _:Q41, _:K43	11	0.852
	_:H58, _:E61, _:K62, _:P63, _:T64, _:K65, _:E66, _:D69, _:K129, _:I130, _:E131, _:V132	12	0.755
	_:G87, _:D90, _:R91, _:L92, _:M93, _:R95, _:K96, _:D97, _:L98, _:D99, _:I100, _:F101, _:E102, _:Q103, _:Y104, _:E107	16	0.735
	_:A125, _:R126, _:K128	3	0.535

*Minimum score was set as 0.5 and maximum distance as 6 (angstrom)

Table S8 The predicted conformational B-cell epitopes based on DiscoTope 2 server

Allergen	Position	Residue
Blo t 1	a. 91-98	a. THR TYR GLY SER LEU PRO GLN ASN
	b. 103	b. GLN
	c. 137	c. GLN
	d. 199	d. ASP
	e. 201	e. GLU
	f. 216	f. HIS
	g. 218	g. SER
	h. 220	h. GLU
	i. 241-242	i. ASN TYR
	j. 245	j. ASN
	k. 247-250	k. GLY ASN GLY VAL
	l. 252-253	l. ARG GLY
	m. 256-257	m. TYR ASN
	n. 259	n. ALA
	o. 272-277	o. THR VAL GLN GLY VAL ASP
	p. 287-288	p. THR GLY
	q. 291	q. ASN
	r. 298-301	r. GLU ARG GLY HIS
Der f 1	a. 103	a. ARG
	b. 106	b. ARG
	c. 108-110	c. ASN SER GLN
	d. 146-150	d. LYS ASP LEU ARG ALA
	e. 152-168	e. GLN HIS TYR ASP GLY ARG THR ILE ILE GLN HIS ASP ASN GLY
	f. 180-185	TYR GLN PRO
	g. 206	f. SER THR GLN GLY ASP ASP
	h. 208-210	g. GLN

		h. GLY ASN ASN
Der p 1	a. 107 b. 145-149 c. 151-152 d. 154-157 e. 160-167 f. 181-182 g. 195	a. ASN b. LYS ASP LEU ASP ALA c. ARG HIS d. ASP GLY ARG THR e. GLN ARG ASP ASN GLY TYR GLN PRO f. GLN GLY g. ASN
Eur m 1	a. 108 b. 146-150 c. 152-153 d. 155-159 e. 161-168 f. 180-184 g. 196 h. 199 i. 209	a. ASN b. LYS ASP LEU ASN ALA c. ARG HIS d. ASP GLY ARG THR ILE e. GLN HIS ASP ASN GLY TYR GLN PRO f. ASN THR GLN GLY VAL g. THR h. ASP i. ILE
Blo t 2	-	-
Der f 2	a. 32 b. 95-96 c. 98-100 d. 128-129	a. GLY b. PRO LYS c. ALA PRO LYS d. ARG ASP
Der p 2	a. 32 b. 96-97 c. 129	a. GLY b. LYS ILE c. ASP
Eur m 2	a. 129	a. ASP
Lep d 2	-	-

Blo t 3	a. 52-61 b. 99	a. HIS ASN SER b. THR
Der f 3	a. 61 b. 99-100 c. 159-160	a. SER b. GLN THR c. ALA GLY
Der p 3	a. 61 b. 99 c. 159	a. LEU b. GLN c. ALA
Eur m 3	a. 60-62 b. 99-100 c. 228	a. ALA SER GLY b. GLN LYS e. SER
Lep d 3	a. 61	a. SER
Blo t 5	a. 1-16 b. 34 c. 38 d. 41-54 e. 79 f. 81-85 g. 109-110 h. 112-117	a. GLN GLU HIS LYS PRO LYS LYS ASP ASP PHE ARG ASN GLU PHE ASP HIS b. LEU c. HIS d. ASP GLU LEU ASN GLU ASN LYS SER LYS GLU LEU GLN GLU LYS e. ARG f. ASP LEU ASN ILE LEU g. GLN LYS h. LYS ASP ILE GLN THR GLN
Der f 5	a. 1-12 b. 14-45 c. 62-69 d. 71-73 e. 83 f. 86-87	a. LEU LEU MET GLN ARG ILE HIS GLU GLN MET ARG LYS b. GLU GLU ALA LEU LEU HIS LEU HIS HIS GLN ILE ASN THR PHE GLU GLU ASN PRO THR LYS GLU MET LYS GLU GLN ILE LEU GLY GLU MET ASP THR c. LYS ARG THR ASP LEU ASP ILE PHE d. GLU ARG TYR ASN

	g. 89-100	e. ILE f. ARG ASP g. LYS LYS GLU GLU GLN ARG VAL LYS LYS ILE GLU VAL
Der p 5	a. 33-43 b. 47 c. 50-51 d. 53-70 e. 72-73 f. 76 g. 87-88 h. 90-108 i. 110-111 j. 118-119 k. 121-132	a. SER LEU MET GLU ARG ILE HIS GLU GLN ILE LYS b. LEU c. PHE TYR d. GLN GLU GLN ILE ASN HIS PHE GLU GLU LYS PRO THR LYS GLU MET LYS ASP LYS e. VAL ALA f. ASP g. GLY VAL h. ASP ARG LEU MET GLN ARG LYS ASP LEU ASP ILE PHE GLU GLN TYR ASN LEU GLU MET i. LYS LYS j. ARG ASP k. LYS LYS GLU GLU ALA ARG VAL LYS LYS ILE GLU VAL
Lep d 5	a. 29 b. 32 c. 61 d. 63-64 e. 66 f. 99-100	a. SER b. LYS c. LYS d. ALA ASP e. ASN f. THY LYS
Blo t 6	a. 23-24 b. 65-68 c. 82 d. 161-163	a. LEU ILE b. SER LYS PRO GLY c. GLN d. GLU VAL ASN
Der f 6	a. 23-25 b. 65-68	a. LEU ILE MET b. THR SER SER SER

	c. 82 d. 84 e. 86 f. 134 g. 136 h. 153 i. 156-159 j. 162-163	c. SER d. GLU e. ASP f. ASN g. LYS h. ASP i. ASN GLU LYS TRP j. ILE ASN
Der p 6	a. 23-25 b. 65-68 c. 82 d. 86 e. 118 f. 134-137 g. 140 h. 153 i. 156-157 j. 160-163 k. 167	a. LEU ILE MET b. THR SER SER LYS c. SER d. GLU e. GLY f. ASN THR ASN ASN g. ASP h. ASP i. ASN ASP j. GLY SER VAL ASN k. PRO
Blo t 7	a. 71 b. 190-191 c. 193 d. 195	a. ASN b. THR PRO c. PRO d. PHE
Der f 7	a. 6-7 b. 76-80 c. 130-131 d. 133	a. ASP LYS b. LYS GLY GLU GLU GLY c. PRO ASP d. GLY
Der p 7	a. 1-7	a. ASP PRO ILE HIS TYR ASP LYS

	b. 38 c. 47 d. 78-80 e. 107 f. 131-133	b. SER c. ILE d. GLU ASP GLY e. ASP f. GLU GLU GLY
Lep d 7	a. 1-6 b. 13 c. 20 d. 26 e. 43 f. 45-48 g. 50 h. 67 i. 69-71 j. 73 k. 75 l. 77-79 m. 90-91 n. 105 o. 118 p. 129-131 q. 197	a. HIS LYS PRO ALA TYR TYR b. GLN c. LYS d. LYS e. LYS f. GLY LEU ILE HIS g. LYS h. SER i. ARG GLY ASP j. LYS k. ASP l. ASP GLY GLY m. LYS ASN n. ILE o. ASP p. ALA GLU GLY q. ASN

Epitopes with the DiscoTope scores > -3.7 are shown

Table S9 Consensus linear B-cell epitopes identified by Ellipro and Bcepred servers

Allergen	Epitope number	Sequence	Residue number
Blo t 1	1	SIQKQSI	133-140
	2	LVEEENYPYNMRTQWCNPDVEGQRYHVS	181-208
	3	GSNNYFRNL	238-246
	4	NDAYT	257-261
	5	DSSYQCNGCGS	156-166
	6	LRYSSEDED	213-221
	7	ERGHN	298-302
	8	PQNF	96-99
	9	RQKARLTRI	102-110
Der f 1	1	GSTQGVD	179-185
	2	KDLRAFQHYDGRT	146-158
	3	QHDNGYQPN	161-169
	4	VEERSYPYVAREQQCRPN SQHYG	90-113
	5	AYRNTSL	50-56
	6	DCASQHGCHG	65-74
	7	YPPDVKQ	121-127
	8	RSLRT	18-22
Der p 1	1	KLDLDAFRHYDGRTIIQRDNGYQPN	145-168
	2	NGNAPAE	7-13
	3	VQESYYRYVAREQSCRRPNAQRF	89-111
	4	DCASQHGCHG	64-73
	5	AYRNQSL	49-55
	6	RQMRT	17-21
	7	YPPNVNK	120-126

Eur m 1	1	KDLNAFRHYDGRT	146-158
	2	QHDNGYQPN	161-169
	3	QQNGVVQEHYYPYVAREQSCHRPNAQRYGLKN	85-116
	4	YRNMSL	51-56
	5	DCASQNGCHG	65-74
	6	SPPDSNK	121-127
	7	RSLRT	18-22
	8	WDTTWGDNG	193-201
Blo t 2	1	AHGE	9-12
	2	PGVDKDGCKHTTCPLKKGQKY	65-85
	3	IANQDSEKL	41-49
	4	SGDHCIHKGKS	22-33
Der f 2	1	WNVPKIAPKSENV	92-104
	2	KGQQ	82-85
	3	DANQNTKTA	42-50
	4	HRGKPF	30-35
	5	DQVDVKDCANNEIKKV	1-16
	6	CHGSDP	21-26
	7	THGKIRD	123-129
Der p 2	1	EANQNTKTA	42-50
	2	NVPKIAPKSEN	93-103
	3	VKGQQ	81-85
	4	PGCHGSEP	19-26
	5	HRGKP	30-34
Eur m 2	1	NVPRIAPKSEN	93-103
	2	AKIRD	125-129
	3	IDNNLCHF	68-75

	4	CKGSEP	21-26
	5	DANQNSNA	42-49
	6	DQVDIKDCANHE	1-12
Lep d 2	1	TPKVK	97-101
	2	GKMTFKDCGHGE	1-12
	3	PVKKGEA	78-84
	4	ANQDTAKV	42-49
	5	CSGDTC	21-26
	6	HRGEKM	29-34
	1	SASSL	46-50
	2	LRHNSGG	57-63
	3	VDRKTCNANY	147-156
	4	TLSSGA	127-132
	5	PTKL	136-139
	6	NVG GK	174-178
	7	QTASKMSTGTTNAQAIKLPEQGSDPKASSE	90-119
	8	HEKYDSNTI	74-82
	9	RTSH	20-23
	10	GGSNAADGDA	3-12
	11	AQAKYP	206-211
Der f 3	1	NGQSAKKL	43-50
	2	KLKTPMTLDQTNAP	90-104
	3	VSREQCDQLYSKAGADVSEN	147-166
	4	KHASGGEK	58-65
	5	EIYQHENYDSMT	70-81
	6	GDVANGGV	171-178
	7	LPSEL	135-139

	8	AQGSDVKVGDK	109-119
	9	SSSH	20-23
	10	ARKGYP	208-213
Der p 3	1	KLKSPMKLNQKNA	90-102
	2	VAGQTASK	42-49
	3	VSRKECNE	147-154
	4	NAEVTDN	160-166
	5	LKHS LGG	57-63
	6	LPSEL	135-139
	7	GDVANGGK	171-178
	8	HEKYDSYQ	74-81
	9	AKGSDVK	109-115
	10	SSSH	20-23
	11	RKGYP	209-213
Eur m 3	1	NGQTASKL	43-50
	2	KLQSPMTLDQKNAKS	90-104
	3	LKHASGGEK	57-65
	4	AREQCNKLYEEAG	148-160
	5	PSQGSDVK	108-115
	6	GYLKEGS	126-132
	7	GNVADGGV	171-178
	8	HEKYDSWT	74-81
	9	SSSH	20-23
	10	GGQKAKAGE	3-11
	11	ARKGYP	208-213
Lep d 3	1	SGTSASQLK	43-51
	2	NTVRHNSGG	55-63

	3	DRAQCNSSYSGD	141-152
	4	GVSAGGK	161-167
	5	YTTEGGS	121-127
	6	KTSSPMT	90-96
	7	LPVSGSDVSG	103-112
	8	RSSH	20-23
	9	ARPNYP	195-200
	10	SGEA	9-12
Blo t 5	1	QEHKPKKDDFRNE	1-13
	2	QKVKD	109-113
Der f 5	1	NRLMKRTDLDIFERY	58-72
	2	QRVKKIEV	93-100
	3	NTFEENPTKEMKEQ	25-38
Der p 5	1	MERIHEQIK	35-43
	2	DRLMQRKDLDFEQY	90-104
	3	NHFEEKPTKE	57-66
Lep d 5	1	TELEKSKSKEL	24-34
	2	HMTEE	3-7
	3	GHFERELKRADLNLAKEF	54-71
Blo t 6	1	SQEECNAK	151-158
	2	TDGQTASS	47-54
	3	LTDGNTQDLPEN	130-141
	4	TPSDTVKV	102-109
	5	NQRSKPGIPDIKTKR	62-76
	6	EETNLNGGED	113-122
	7	NHYLE	218-222

	8	HEQYDPNTIEN	80-90
	9	VVGGTDAKKAE	1-11
Der f 6	1	YGQKASS	48-54
	2	GNDRCNEKWG	151-160
	3	TNV	105-107
	4	DKTQ	174-177
	5	SKCPPGEY	204-211
	6	NQRTSSSYGDL	62-72
	7	NEIETEDIVDGD	110-121
	8	LTDGNGKDLPD	130-140
	9	HESYEQDQTQT	80-90
	10	VGGQDAD	2-8
Der p 6	1	GNDKCNDKWG	151-160
	2	DGQKASS	48-54
	3	SQPVKPSSNVDF	98-109
	4	ETKDIGDGEK	113-122
	5	NKRTSSKYAD	62-71
	6	TDGNTNNLPDNL	131-142
	7	DATQ	174-177
	8	KCPPGEY	205-211
	9	HESYDPETIQN	80-90
	10	GGQDAAEAEA	3-12
Blo t 7	1	TQKG	17-20
	2	KKFLQNTTPAPAF	183-195
	3	DAKIHNENGDF	64-74
	4	KHTTELDRKI	28-37

	5	EGPSVK	122-127
Der f 7	1	QGDANVKGEEG	70-80
	2	QSETIDPMKVDPHADKFERHV	25-45
	3	DLAYK	100-104
Der p 7	1	DPIHYDKITEE	1-11
	2	GDANVKSEDG	71-80
	3	PDHSDKFERHI	35-45
	5	EVSEEGNMT	128-136
	6	KELERNNQ	191-198
	7	EKSETFD	24-30
Lep d 7	1	HKPAYYDDNM	1-10
	2	EQTKVPIDKK	34-43
	3	KLDAEGK	126-132
	4	GDAKIDTDGG	70-79
	5	TKKELDP	24-30

Table S10 Consensus conformational B-cell epitopes determined by Ellipro and DiscoTope 2 servers

Allergen	Epitope number	Sequence	Residue number
Blo t 1	1	TYGSLPQN	91-98
	2	NY	241-242
	3	NLGNGVLRG	245-253
	4	YNDA	256-259
	5	TG	287-288
	6	ERGH	298-301
Der f 1	1	RPNSQ	106-110
	2	KDLRAFQHYDGRTIIQHDNGYQP	146-168
	3	STQGVD	180-185
	4	QAGN	206-209
Der p 1	1	KLDLAFRHYDGRT	145-157
	2	QRDNGYQP	160-167
	3	QG	181-182
Eur m 1	1	KDLNAFRHYDGRTIMQHDNGYQP	146-168
	2	NTQGV	180-184
Blo t 2	-	-	-
Der f 2	1	PKIAPK	95-100
	2	RD	128-129
Der p 2	1	KI	96-97
Eur m 2	-	-	-
Lep d 2	-	-	-
Blo t 3	1	NTLRHNS	55-61
Der f 3	1	QT	99-100
	2	AG	159-160

Der p 3	-	-	-
Eur m 3	1	ASG	60-62
	2	QK	99-100
Lep d 3	-	-	-
Blo t 5	1	KPKKDDFRNFDHL	4-16
	2	DELNENKSKELQE	41-53
	3	RTDLNIL	79-85
	4	QKVKKDIQTQ	109-117
Der f 5	1	LLMQRIHEQMRK	1-12
	2	RTDLIDIFERY	63-72
	3	NTFEENPTKEMKEQ	25-38
	4	IEV	98-100
Der p 5	1	LLMERIHEQIK	33-43
	2	EKPTKEMKD	61-69
	3	DRLMQRKDLIDIFEQY	90-104
	4	ARVKKIEV	125-132
Lep d 5	1	KRADLN	61-66
	2	TK	99-100
Blo t 6	1	LI	23-24
	2	SKPG	65-68
	3	EVN	161-163
Der f 6	1	LIM	23-25
	2	TSSS	65-68
	3	SYEQD	82-86
	4	NGK	134-136
	5	NEKW	156-159

	6	IN	162-163
Der p 6	1	LIM	23-25
	2	TSSK	65-68
	3	NTNN	134-137
	4	ND	156-157
	5	GSVN	160-163
Blo t 7	1	TPAPAF	190-195
Der f 7	1	DK	6-7
	2	KGEEG	76-80
	3	SDEG	130-133
Der p 7	1	DPIHYDK	1-7
	2	EDG	78-80
	3	EEG	131-133
Lep d 7	1	HKPAYY	1-6
	2	KIGLIHIK	43-50
	3	GD	70-71
	4	DTDGG	75-79
	5	KN	90-91
	6	AEG	129-131