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Images in Allergy and Immunology

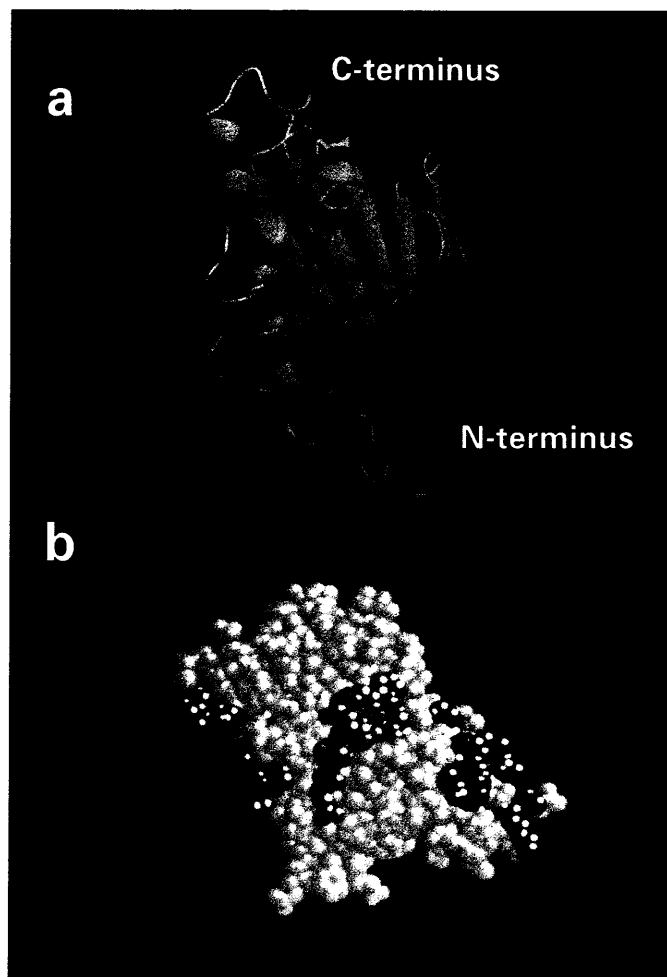
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Structure and Epitopes of Bet v 1

The binding of human IgE to a foreign allergen represents a crucial step in the development of clinical symptoms of type I allergy. The binding of IgE occurs to B-cell epitopes composed of amino acid residues located on the molecular surface of the allergen. Detailed knowledge on the three-dimensional structure of the allergen is thus essential in order to identify and characterize its IgE-binding B-cell epitopes.

a Ribbon representation of the three-dimensional molecular structure of Bet v 1, the major allergen of birch pollen, which has recently been solved both in solution by NMR spectroscopy and in the crystalline state by X-ray crystallography [1, 2]. The main feature of the structure is a seven-stranded anti-parallel β -sheet (orange) that wraps around a 25-residue-long C-terminal α -helix (red). The β -sheet and the C-terminal part of the long helix are separated by two consecutive α -helices. The structure reveals a most unusual feature, a large cavity that penetrates the entire protein with three openings on the molecular surface [2]. **b** The molecular surface of Bet v 1 is visualized by a space-filling model with surface-exposed amino acid residues in color. The areas in green, blue and red represent regions of exposed amino acid residues that are conserved among the major tree pollen allergens of *Fagales*. These areas are likely to harbor cross-reactive B-cell epitopes and provide a structural basis for the clinically observed allergic symptoms that birch-pollen-allergic patients experience when they encounter pollens from related trees such as hazel, alder and hornbeam. The structural determination represents a new and major step towards identifying and modifying IgE-binding B-cell epitopes of the major tree pollen allergens and will be invaluable to the future development of therapy and diagnosis of allergic diseases.



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