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Title (English)

Analysis of evolutionary co-variation of amino acid positions to discover features typical of allergens

Title (Swedish)

Abstract

In this study two protein families, both holding allergens and non-allergens, were investigated with regard to amino acid sequence features that may be attributed to allergenicity. With this purpose in mind, various computational biology operations were conducted, *e.g.* investigation on pair-wise co-variation of amino acids across the sequences. Intriguing patterns of co-varying pairs in and near known IgE epitopes were seen. The findings show that evolutionary co-variation analysis is a powerful method that can give valuable information on protein segments of potential importance to allergenicity.

Keywords
Allergy, Evolutionary co-variation, ELSC

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