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## Preface

Food allergies, which are abnormal immune responses to food proteins (known as food allergens), have become a major public health problem due to their increasing prevalence, life-threatening potential, and enormous medical and economic impact. So far, the most common food allergens are described in few food products such as cow's milk, eggs, tree nuts, peanuts, soy, wheat, fish, and shellfish. With the recent advances in genomics, molecular biology, and immunology techniques, a complex network of interactions and cross-reactivities becomes apparent. While improved versions of traditional methods (e.g., ELISA) are still widely applied in many laboratories for food allergen studies and allergy diagnostics, novel techniques (e.g., microarray, flow cytometry, mass spectrometry) have led to new methods in the food allergy field.

*Food Allergens: Methods and Protocols* provides a collection of methodologies for both basic research and clinical diagnosis/treatment relevant to food allergens, including food allergen production, purification, characterization, detection, and quantification, together with bioinformatics approaches applied to modern food allergen studies. In addition, current developments and future trends in food allergen-related laboratory techniques are also covered.

Chapter 1 is an introductory overview chapter describing commonly used methods for food allergen production, detection, and epitope mapping. The remaining 19 chapters are divided into four parts:

Part I, Food Allergen Purification and Production, provides methods of producing recombinant food allergens in bacterial and yeast expression systems, the two most commonly used system for protein production, and the chromatographic methods in protein purification.

Part II, Food Allergen Discovery, Detection, and Quantification, can be classified into three types of methods including DNA-based methods, protein-based methods (e.g., Western blotting, ELISA), and cell-based methods (e.g., basophil activation assay). Many of these methods are also useful for food diagnostics.

Part III, Allergenic Epitope Mapping, comprises experimental methods used for mapping of B-cell epitopes (IgE epitopes) or T-cell epitopes, in silico epitope prediction method, and an overview of bioinformatics resources/tools in epitope/allergen prediction.

Part IV, Methods Currently Being Developed and Future Development, deals mainly with the new concepts of allergenicity as an outcome of protein and food matrix interaction. The particular search for NKT bioactive lipids is described as well as a review on the novel techniques in development for food allergen detection.

Over the past decades, the development of new innovations and technologies has led to great improvements in many aspects of food allergen studies (e.g., reproducibility, sensitivity, specificity, and high throughput capacity). These methods greatly facilitate identification, characterization, and quantification of food allergen and are slowly leading to a better understanding of food allergic diseases and their diagnosis and pointing toward specific therapeutics. We have tried to include in this book a set of important protocols highly relevant to food allergens studies. We hope that the protocols provided here would be valu-

able resources not only to immunologists, biochemists, molecular biologists, and medical doctors/students working in the food allergy area but also useful for the food industry, legislators, food standard agencies, allergologists, pediatricians, and clinicians/biologists working in the general field of allergic diseases and immunology.

We would like to take this opportunity to express our gratitude to all the authors for sharing their valuable expertise through the contribution of detailed protocols and notes for this book. We also want to thank Professor John Walker and the editorial staff of Springer for continuous assistance and encouragement.

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