
Preface

More than 10 years have passed by since the first edition of *Epitope Mapping Protocols* edited by Glenn E. Morris was published as part of the Methods in Molecular Biology series. The success of the first edition clearly demonstrated the need for detailed descriptions of experimental protocols to determine epitopes, i.e., identify protein domains, sequences, or even amino acids, that are recognized by either antibodies or T-cell receptors. A multitude of disciplines require detailed knowledge about epitopes, and therefore state-of-the-art and reliable protocols. Not only immunologists who have an a priori interest depend on epitope mapping protocols, but also biologists using antibodies as research tools, structural biologists studying protein–protein interactions, clinicians investigating patients' immune responses, vaccine developers designing and testing immunogens, diagnostic labs developing and applying ELISAs, and last but not the least, biotech and pharmaceutical companies obliged to monitor the immunogenicity of novel therapeutic antibodies, proteins, and peptides, to mention only a few.

The development of new techniques as well as new applications demanded a new edition. Some of the protocols of the first edition were simply updated, while others were entirely overhauled in order to keep up with recent developments. An important extension of the scope of the book was not only to cover antibody or B-cell epitope mapping techniques but also to dedicate a total of eight protocols to T-cell epitope mapping in the second part of the volume.

However, the majority of the chapters deal with antibody epitope mapping. This part of the book starts out with two nonlaboratory protocol chapters describing general considerations and definitions of B-cell epitopes and the structural basis of antibody–antigen interactions. These chapters set the scene for the following protocols and are helpful if not necessary to interpret experimental epitope mapping results. The following chapters are arranged in four groups. The first group of eight protocols applies to whole native antigens and covers nuclear magnetic resonance (NMR), enzyme-linked immunosorbent assays (ELISAs), surface plasmon resonance (SPR), proteolytic fragmentation, chemical modification, and mass spectrometry as general methods. The second group of seven chapters addresses peptide library approaches with synthetic as well as phage-displayed peptides, antigen sequence-derived and randomly generated peptide sequences, collections of peptides derived from diverse human proteins, and peptide derivatives mimicking posttranslational modified proteins. The third group of four chapters represents a crucial, completely new part compared with the first edition. Peptides displayed on phages or on high-content microarrays are used to profile complex (auto)antibody signatures in biological fluids such as human or mice sera. Statistical analysis of results in comparison with control cohorts yields novel biomarkers for cancer, allergy, infectious, and autoimmune diseases. The last group of three protocols requires antigen expressed from recombinant DNA. The final single chapter describes B-cell epitope prediction tools.

The second part of the book focuses on techniques for T-cell epitope mapping. It starts with a chapter analyzing molecular recognition of T-cell epitopes presented by T-cell receptors. The following chapters summarize well-established techniques to identify

MHC class I and class II binding peptides such as EliSpot using peptides and peptide mixes, flow cytometry, and the tetrameric MHC-based iTOPIA epitope discovery system. Two novel powerful methods for MHC ligand identification such as the exchange of photolabile conditional MHC class I ligands by peptides and the use of peptide microarrays together with soluble MHC class II molecules complement the second part of the book. One chapter related to T-cell epitope processing was included to complete the picture of epitope presentation by MHC molecules for antigen recognition.

We hope that this book will become a standard reference for anybody interested in understanding and investigating the complexity of antigen processing, antigen presentation on cell surfaces by MHC molecules, and recognition of antigens or antigen–MHC complexes by antibodies or T-cell receptors. All chapters present well-established, state-of-the-art and cutting-edge techniques that are proven to be reliable and robust. The protocols are comprehensive and complete without cross references. Contributors to this book represent a broad spectrum of immunologists, biochemists, biologists, physicists, physicians, and mathematicians. Some have more than 30 years of experience, and most of them have published text books in their fields. Here, readers can find more complete coverage of techniques common in the diversifying field of epitope mapping compared with many immunological and molecular biological text books and manuals.

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