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## Preface

Despite being known and studied for years, peptides have never before attracted enough attention to necessitate the invention of the term “Peptidomics” in order to specify the study of the complement of peptides from a cell, organelle, tissue or organism. This volume presents a comprehensive range of analytical techniques for analysis of the peptide contents of complex biological samples. The emphasis is often on higher throughput techniques, suitable for the analysis of large numbers of peptides typically present in the *peptidomes* or other complex biological samples. A wide range of methods is presented, covering all stages of peptidomic research including, where applicable, organism handling, tissue and organ dissection, cellular and subcellular fractionation, peptide extraction, fractionation and purification, structural characterisation, molecular cloning and sequence analysis. In addition to this, a selection of methods suitable for quantification, display, immunochemical and functional analysis of peptides and proteins are presented. The methods and techniques covered in this volume encompass a number of species ranging from bacteria to man and include model organisms such as *Caenorhabditis elegans*, *Drosophila melanogaster* and *Mus musculus*. Strong emphasis is placed on data analysis, including mass spectra interpretation and in silico peptide prediction algorithms. Where relevant, the *peptidomic* approaches are compared to the *proteomic* methods. Here is a snapshot of the practical information, peptidomic methods and other related protocols included in this volume:

*Target organisms and samples covered:* Bacteria (Chapter 2), hydra (Chapter 21), nematode (Chapter 3), mollusc (Chapter 4), crab (Chapter 5), spider venoms (Chapters 6 and 7), insects (Chapters 8, 9, 10, 11, 25), amphibians (Chapters 12, 13, 14), rodents (Chapters 15, 16, 17, 18), samples of human origin (Chapters 19, 20, 22, 23) and plants (Chapter 26).

*Peptide extraction and Liquid chromatography fractionation* methods (mostly size exclusion, ion exchange, reverse-phase modes or their combinations) can be found in Chapters 2, 3, 4, 5, 6, 7, 8, 12, 14, 15, 16, 17, 18, 19, 20, 21, 22). These include OFF-line and ON-line techniques. The former are often used with MALDI-MS detection (e.g. Chapters 3, 4, 5, 6, 7, 8, 12, 15, 16, 19) whilst the latter more generally with single or multidimensional hyphenated LC<sup>N</sup>-MS<sup>N</sup> techniques (e.g. Chapters 2, 3, 15, 17, 18, 21).

*Other separation and fractionation methods* covered include microdialysis of live animals (Chapter 5), SDS-PAGE (Chapters 6, 18), magnetic bead based purification (Chapter 20) and solid-phase extraction (Chapters 2, 6, 12, 19, 22).

*Affinity peptide detection* including anti-peptide antibody development and characterisation, Affinity peptidomics, ELISA and microarray affinity assays are covered in Chapters 22, 23 and 24.

*Mass spectrometry* techniques include MALDI-TOF MS (e.g. Chapters 3, 6, 7, 8, 12, 16, 19, 20), MALDI-TOF with PSD (Chapter 8), MALDI-TOF MS/MS (e.g. Chapters 4, 6, 15, 21); ESI-MS/MS techniques (Chapters 3, 6, 16, 17, 18) or high-resolution FTMS (Chapter 2). Direct MALDI-MS peptide profiling from cells and tissues is described in Chapters 9, 10 and 11.

The description of *functional assays* can be found in Chapters 7, 14 and 21. Of particular interest in this respect is Chapter 21, where functional activity of the peptides is assessed through the analysis of mRNA transcription levels changes in response to the peptide application. That chapter contains a selection of protocols for peptide extraction, fractionation and functional testing using a combination of molecular biology techniques, cellular and morphological assays.

*Molecular cloning of peptide cDNAs* and the associated techniques are described in Chapters 13 and 14.

Issues related to peptide *sequence analysis* are addressed in many chapters dealing with MS spectra interpretation, but of special interest in this respect are Chapters 25 and 26, dealing with *in silico peptide prediction* techniques and Chapter 20 which includes a section on bioinformatics analysis of *peptide expression profiling data*. *Differential peptide expression* issues are also covered in Chapter 2.

Peptidomics is 10-years old. My congratulations go to all scientists who have created and developed the science of Peptidomics through their research and especially those who found time to contribute their invaluable know-how in the form of methods and protocols for inclusion in this volume. *Peptidomics: Methods and Protocols* is designed to complement previously published titles in the *Methods in Molecular Biology*<sup>TM</sup> series, which focused on *protein* analysis. This volume will help the beginner to become familiar with this fascinating field of research and will provide scientists at all levels of expertise with easy-to-follow practical advice needed to set up and carry out analysis of the peptide contents of complex biological samples.

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