



## Preface

The present volume represents a loosely bound continuation of the preceding volumes published in *J. Chromatogr. B* on Proteomics, in particular Proteomic Databases Part I and II (*J. Chromatogr.*, Vols. 771 and 787) as well as two additional volumes edited by C.G. Huber, D.M. Lubman and P. Oefner (*Proteomics and Genomics*, Vol. 782), and the last one in this series by M. Kaleja (*From Gene to Functional Protein*, Vol. 786).

While in the two first volumes on Proteomic databases we have focussed basically on categorization of the proteins present in different biologically relevant entities, in the first part of this volume we highlighted the advances in proteomic technology, inclusive peptide sequencing, high throughput technology and selective detection, while the second part of this volume is devoted to various aspects of proteomic profiling (inclusive the analysis of fragments created by specific proteolysis), i.e. applications. Naturally, some (but not frequent) overlaps with the previously published volumes can

be traced. On the other hand, such overlaps shed some light on the advances of this rapidly developing technology that have occurred the past two years. Besides the classical 2D separations and e.g. MALDI-MS coupling, adequate attention has been paid to the techniques of analyzing peptide maps.

Let me repeat what we have used as a conclusion to a number of previous Prefaces to this series of Topical Volumes: Nobody is perfect and if anybody of the potential readers will care to comment either on the results achieved or on the technology used, we shall certainly appreciate it.

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2 November 2004

Available online 15 December 2004