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Preface

A Special Issue on Protein and Peptide Analysis can only give snapshots of the wide range of methodologies, techniques and applications in the fields of biopharmaceuticals, proteomics and the many other areas of research where protein analysis is crucial. I think, however, that the present volume has brought together a number of high-quality papers which highlight the various aspects of protein and peptide analysis and its eminent role in life sciences.

In line with the spirit of Journal of Chromatography, I have put the focus on some of the methodological developments that have so much influenced modern biological research with the goal of looking into the future. Starting with novel stationary phases for high-performance liquid chromatography and the miniaturization of silicon structures to continue the never-ending quest for handling smaller amounts of sample and enhancing sensitivity, the issue continues with applications from the field of biopharmaceuticals including gene therapy vectors. Another fast growing area, Proteomics, is covered by contributions that focus mainly on separation methods that do not rely on two-dimensional gel electrophoresis, the workhorse of today's proteomics laboratory, but which may one day replace this labor-intensive technique. Finally, applications from different areas give a flavor of protein and peptide analysis in

modern life sciences research ranging from the important field of post-translational modifications to the isolation of peptide antibiotics from human milk.

When it comes to separation technologies both high-performance liquid chromatography and capillary electrophoresis are well-represented in this issue. This bias towards instrumental analytical methods is wanted in order to emphasize the increasing need for automatable and highly reproducible separation methods to cope with the ever increasing demand for on-line protein identification all the way from sample preparation to database searching. Whether these methods will come in the form of integrated chromatographic or capillary electrophoretic systems or in the form of microchips remains to be seen but all of them will most likely have a role to play. At any rate they will in most instances be coupled to mass spectrometry as the method of choice for protein and peptide identification and this issue makes no exception in emphasizing the importance of MS.

I would like to take this occasion to thank all the contributors that helped to make this a successful and forward looking Special Issue.

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