

CONTENTS

Preface		ix
Section 1	Protein Analysis	1
Chapter 1	Investigation of a Calmodulin / Peptide Complex by Chemical Cross-Linking and High-Resolution Mass Spectrometry <i>Sabine Schaks, Daniel Maucher, Christian H. Ihling and Andrea Sinz</i>	3
Chapter 2	Avoiding Pitfalls in Proteomics Sample Preparation <i>Robert L. J. Graham, Anastasia Kalli, Geoffrey T. Smith, Michael J. Sweredoski and Sonja Hess</i>	19
Chapter 3	Hands-on Phosphoproteomics <i>Filip Sucharski and Jerzy Silberring</i>	35
Chapter 4	Using Native Gel Electrophoresis or Isoelectric Focusing as Experimental "Clock" for the (Iso)aspartate Formation Process of tTF-NGR Fusion Proteins <i>Christian Schwöppe, Heike Hintelmann, Rolf M. Mesters, Wolfgang E. Berdel and Simone König</i>	51

Chapter 5	ETD Reactions in Peptides Sequencing <i>Piotr Suder, Anna Drabik and Anna Bodzon-Kulakowska</i>	65
Chapter 6	Peptide Cleavage and Oxidation Using ROXY™ EC System with On-line Mass Spectrometry Detection <i>Przemysław Mielczarek, Hana Raoof and Jerzy Silberring</i>	77
Chapter 7	Separation of Rat Brain Proteins for Gel-based Expression Analysis <i>Anna-Maria Mehlich, Andreas Rogalewski, Wolf-Rüdiger Schäbitz and Simone König</i>	85
Chapter 8	Serum Proteomics of Cancer Patients: Protein Preparation <i>Anna Drabik, Przemysław Mielczarek, Marek Sierżęga and Jan Kulig</i>	95
Chapter 9	Gel-strip Sandwich Technique for Comparative Fluorescence Gel Electrophoresis <i>Wei-qun Wang, Doreen Ackermann and Simone König</i>	109
Section 2	Small Molecule Analysis	125
Chapter 10	Distribution of Cholesterol in the Brain Tissue as an Example of TOF-SIMS Analysis <i>Anna Bodzon-Kulakowska, András Kiss, Kamila Chughtai and Ron M. A. Heeren</i>	127
Chapter 11	Drug Metabolism Simulation Using TiO ₂ /UV System <i>Hana Raoof, Katarzyna A. Michalow and Jerzy Silberring</i>	139

Chapter 12	Development of a Novel Ambient Glow Discharge Plasma Source for Direct Analysis of Organic Compounds	153
	<i>Marek Smoluch, Edward Reszke, Andrzej Ramsza and Jerzy Silberring</i>	
Index		163

PREFACE

Mass spectrometry has become an analytical tool in many fields of the natural sciences extending to basic scientific research applications. With constantly improved sensitivity, the mass spectrometrists increasingly encounters sample-related difficulties in the course of work and needs to collaborate tightly with the scientists of the laboratory which submitted the sample. Since mass spectrometry is more or less a black box for the majority of the analysts, who still regarding the analyses are formed in a wrong knowledge that in many instances the instrument and hardware is perfect and sometimes that sample type is accompanied by some difficulties. The mass spectrometry is a rapidly developing science. Scientists can become quite distracted from the analytical work due to the need to identify and remove contaminants and to test new reaction products and analyze recovery.

For this book, I have asked researchers to share protocols, handling tips and tricks of routine with other fellow scientists. Often, small tricks make a difference for the success of an experiment and these are mostly not published. The book contains an extensive details in our work done in proteomics and small molecule analysis. This could be the starting point to achieve specific sample purity, comparisons of methods and tools, new testing techniques, advice on sensitivity increasing methodology. Authors contributed an extensive collection of new sample which reflect the current progress in the mass spectrometry field in order to expand our knowledge in this field. All these things it helps to find new strategies for the investigation of organic molecules and metabolites (Chapter 11-12).

Chapter 1 starts with a practical guideline in the combination of chemical derivatization and high-resolution mass spectrometry for beginners as well as for those who are already working in the field of protein mass spectrometry.