

Preface

More than a decade after the beginning of the "Proteomics Rush" the methodological and systematic approaches for the analysis of proteomes have evolved from being holistic and non-hypothesis driven to phenomenon-based, dedicated protein studies. Importantly and correctly so, it has been widely reported that it is very difficult to obtain all necessary information from one single workflow, e.g. 2-D gel-mass spectrometry; and that different workflows deliver complementary information rather than similar, overlapping results. Therefore it is necessary to make additions to the manuscript for the second edition of *Proteomics in Practice* and include a comprehensive description of chromatography methods, written mainly by Hans-Rudolf Höpker.

The objective of the second edition of *Proteomics in Practice* is to provide the reader with a comprehensive reference and practical guide for the successful analysis of proteins by 2-D electrophoresis, chromatography and mass spectrometry. The book includes a theoretical introduction into the most-applied methodologies, a practical section complete with worked examples, a unique troubleshooting section and a thorough reference list to guide the interested reader to further details.

The theoretical section introduces the fundamentals behind the techniques applied in proteomics and describes how the techniques are used for proteome analysis. However, the practical aspects of the book focus on 2D-DIGE technology and mass spectrometry. 2-D DIGE is increasingly cited for studying differential protein expression and, as such, a considerable section of the text is dedicated to this technique. The core components of 2D-DIGE, sample preparation and labeling, 2-D electrophoresis and image analysis are addressed in considerable detail. Further, the importance of mass spectrometry, sequence databases and search engines for successful protein identification are discussed.

The practical section of the book is, in principle, a course manual, which has been optimized over a number of years. The experimental

section describes how to achieve consistent, reliable and reproducible results using a single instrumental setup, instead of presenting a wide choice of techniques and instruments.

Fundamentally, the book celebrates the attention to detail that is necessary to perform proteome analysis routinely, with confidence.

As the technical developments in this field are proceeding quickly, the contents of the book will need to be updated every few months. The reader can have access to a web-site at <http://www.wiley-vch.de/books/info/3-527-31941-7/index.html/>, which will contain the updated chapters and recipes.

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