Preface

The human genome and other large-scale genome sequencing projects have inevitably led to a focus on the proteins encoded by genes. The field of proteomics has grown enormously as a result and a number of high-throughput technologies have now been developed allowing discovery-led investigations of protein populations rather than more traditional hypothesis-led studies on single proteins. These high-throughput technologies include gene and protein microarrays, the yeast two-hybrid system, and various mass spectrometry methodologies. However, despite developments and improvements in these technologies, two-dimensional electrophoresis (2DE) remains one of the most widely used approaches. This technique was revolutionised by the development of immobilised pH gradient strips which are now commercially available. This has made possible highly reproducible separations of matched samples. Developments in staining, mass spectrometry, and bioinformatics supported these developments and have led to a measure of standardisation in design, execution, and analysis of proteomics experiments.

This book began life as a proposed update of the excellent volume 2DE Protocols edited by Andrew Link of the University of Washington at Seattle. However, we realised that 2DE has undergone major development in aspects of its technology in recent years and we were anxious to reflect these in the present volume. We are also conscious that many researchers have now begun to apply proteomics methodologies to a growing range of biological material and we were anxious to include contributions to reflect the challenges posed in sample preparation in less widely used organisms. As with all of this series, the emphasis in this volume is on the presentation of clear protocols suitable for a newcomer to the field. We felt, however, that some aspects merited inclusion of overview review-type articles and a number of these are included at the beginning of the book. The protocols reflect the key steps in a 2DE experiment which include sample preparation, staining, post-translational modification, spot identification, and bioinformatics. We hope especially that newcomers to 2DE will find this volume useful and be encouraged to apply some of the powerful techniques described here to their own research. The editors would like to thank especially the series editor, Prof. John Walker, for his endless patience, enthusiasm, and encouragement throughout this project. We would also like to thank our contributors for their excellent cooperation and generosity in sharing their expertise in this book.

Cork, Ireland

David Sheehan
Raymond Tyther
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Contributors

Khosrow Adeli • Molecular Structure and Function, The Hospital for Sick Children Research Institute, and the Department of Biochemistry, University of Toronto, Toronto, ON, Canada

Kelly Andringa • Department of Environmental Health Sciences and The Center for Free Radical Biology, University of Alabama at Birmingham, Birmingham, AL, USA

Ron Appel • Proteome Informatics Group, Swiss Institute of Bioinformatics and Computer Science Department, Geneva University, Geneva, Switzerland

Shannon Bailey • Department of Environmental Health Sciences and The Center for Free Radical Biology, University of Alabama at Birmingham, Birmingham, AL, USA

James W. Baty • Department of Pathology, Christchurch School of Medicine & Health Sciences, University of Otago, Christchurch, New Zealand

Maria Bebiano • Department of Marine Science, University of the Algarve, Faro, Portugal

Sarka Beranova-Giorgianni • Department of Pharmaceutical Sciences, Charles B. Stout Neuroscience Mass Spectrometry Laboratory and Department of Neurology, The University of Tennessee Health Science Center, Memphis, TN, USA

Brian Bradley • Department of Biological Sciences, University of Maryland, Baltimore County, Baltimore, MD, USA

Kristin K. Brown • Department of Pathology, Christchurch School of Medicine & Health Sciences, University of Otago, Christchurch, New Zealand

Allan Butterfield • Department of Chemistry, Sanders-Brown Center on Aging and Center of Membrane Sciences, University of Kentucky, Lexington, KY, USA

Philip Cash • Department of Medical Microbiology, University of Aberdeen, Aberdeen, Scotland, UK

Mireille Chevallet • CEA-DSV-iRTSV/LBBSI and UMR CNRS, CEA Grenoble, Grenoble, France

David Chitwood • Nematology Laboratory, USDA, ARS, BARC-West, Beltsville, MD, USA

Suze Chora Rose • University of Nice Sophia-Antipolis, Nice, France

Department of Marine Science, University of the Algarve, Faro, Portugal

Sarah L. Cuddihy • Department of Pathology, Christchurch School of Medicine & Health Sciences, University of Otago, Christchurch, New Zealand

Dominic Desiderio • Charles B. Stout Neuroscience Mass Spectrometry Laboratory and Department of Neurology, The University of Tennessee Health Science Center, Memphis, TN, USA
Contributors

Ivano Eberini • Dipartimento di Scienze Farmacologiche, Università degli Studi di Milano, Milan, Italy
Lutz Eichaker • Department für Biologie I, Ludwig-Maximilians-Universität, Munich, Germany
Kiichi Fukui • Department of Biotechnology, University of Osaka, Osaka, Japan
Pietro Ghezzi • Istituto di Ricerche Farmacologiche “Mario Negri”, Milan, Italy
Elisabetta Gianazza • Dipartimento di Scienze Farmacologiche, Università degli Studi di Milano, Milan, Italy
Francesco Giorgianni • Charles B. Stout Neuroscience Mass Spectrometry Laboratory and Department of Neurology, The University of Tennessee Health Science Center, Memphis, TN, USA
Bernhard Granvogl • Department für Biologie I, Ludwig-Maximilians-Universität, Munich, Germany
Wilhelm Grussem • Institute of Plant Sciences and Functional Genomics Center, ETH Zurich, Zurich, Switzerland
Mark B. Hampton • Department of Pathology, Christchurch School of Medicine & Health Sciences, University of Otago, Christchurch, New Zealand
Elizabeth Harry • Institute for the Biotechnology of Infectious Diseases, University of Technology, Sydney, NSW, Australia
Ben Herbert • Institute for the Biotechnology of Infectious Diseases, University of Technology, Sydney, NSW, Australia
Christine Hoogland • Swiss Institute of Bioinformatics, Geneva, Switzerland
Mai-Loan Huynh • Minomic Pty Ltd, Chatswood West, NSW, Australia
Kimihisa Ichikawa • Advanced Technology Research Laboratories, Daiichi Sankyo Co., Ltd., Hiromachi, Shinagawa-ku, Tokyo, Japan
Mi-Jeong Jeong • Yonsei Proteome Research Center, Biomedical Proteome Research Center and Department of Biochemistry, Yonsei University, Seoul, Korea
Pan-Young Jeong • Yonsei Proteome Research Center, Biomedical Proteome Research Center and Department of Biochemistry, Yonsei University, Seoul, Korea
Won-A Joo • The Wistar Institute, Philadelphia, PA, USA
Cornelia Joppich • Medizinisches Proteom-Center, Ruhr-Universität Bochum, Bochum, Germany
Bose Kalampanyil • Department of Biological Sciences, University of Maryland, Baltimore County, Baltimore, MD, USA
Adrienne King • Department of Environmental Health Sciences and The Center for Free Radical Biology, University of Alabama at Birmingham, Birmingham, AL, USA
Joachim Klose • Institut für Humangenetik, Universitätsklinikum Charité, Berlin, Germany
Toshiyuki Kosaka • Advanced Technology Research Laboratories, Daiichi Sankyo Co., Ltd., Hiromachi, Shinagawa-ku, Tokyo, Japan
Kazuishi Kubota • Advanced Technology Research Laboratories, Daiichi Sankyo Co., Ltd., Hiromachi, Shinagawa-ku, Tokyo, Japan
Alexander Lellner • Department of Analytical Chemistry and Food Chemistry, University of Vienna, Vienna, Austria
CÉCILE LELONG • CEA-DSV-iRTSV/LBBSI and UMR CNRS, CEA Grenoble, Grenoble, France
BETTINA LEVÄNEN • Karolinska Biomics Center and Department of Medicine, Division of Respiratory Medicine, Karolinska Institutet, Stockholm, Sweden
WOLFGANG LINDNER • Department of Analytical Chemistry and Food Chemistry, University of Vienna, Vienna, Austria
FREDÉRIQUE LISACEK • Proteome Informatics Group, Swiss Institute of Bioinformatics, Geneva, Switzerland
SYLVIE LUCHE • CEA-DSV-iRTSV/LBBSI and UMR CNRS, CEA Grenoble, Grenoble, France
KATRIN MARCUS • Medizinisches Proteom-Center, Ruhr-Universität Bochum, Bochum, Germany
AXEL MASANEK • Department für Biologie I, Ludwig-Maximilians-Universität, Munich, Germany
CAROLINE MAY • Medizinisches Proteom-Center, Ruhr-Universität Bochum, Bochum, Germany
BRIAN MCDONAGH • Department of Biochemistry, University College Cork, Cork, Ireland
HELMUT MEYER • Medizinisches Proteom-Center, Ruhr-Universität Bochum, Bochum, Germany
KHALED MOSTAGUIR • Swiss Institute of Bioinformatics, Geneva, Switzerland
KEUN NA • Yonsei Proteome Research Center, Biomedical Proteome Research Center and Department of Biochemistry, Yonsei University, Seoul, Korea
MICHAEL C. O’NEILL • Department of Biological Sciences, University of Maryland, Baltimore County, Baltimore, MD, USA
YOUNG-KI PAIK • Yonsei Proteome Research Center, Biomedical Proteome Research Center and Department of Biochemistry, Yonsei University, Seoul, Korea
PATRICIA PALAGI • Proteome Informatics Group, Swiss Institute of Bioinformatics, Geneva, Switzerland
KATHY PFEIFFER • Medizinisches Proteom-Center, Ruhr-Universität Bochum, Bochum, Germany
MATTHIAS PLÖSCHER • Department für Biologie I, Ludwig-Maximilians-Universität, Munich, Germany
THIERRY RABILLOUD • Commissariat à l’Energie Atomique, Grenoble, France
TANEA REED • Department of Chemistry, Sanders-Brown Center on Aging and Center of Membrane Sciences, University of Kentucky, Lexington, KY, USA
VERONIKA REISINGER • Department für Biologie I, Ludwig-Maximilians-Universität, Munich, Germany
MICHELE ROMEO • University of Nice Sophia-Antipolis, Nice, France
PAMELA J. RUSSELL • Oncology Research Centre, Prince of Wales Hospital, Randwick, and Faculty of Medicine, University of New South Wales, Sydney, NSW, Australia
BART SAMYN • Department of Biochemistry Physiology and Microbiology, University of Ghent, Ghent, Belgium
Kjell Sergeant • Department of Biochemistry Physiology and Microbiology, University of Ghent, Ghent, Belgium
YHONG-HEE SHIM · Department of Bioscience and Biotechnology and Bio/Molecular Informatics Center, Konkuk University, Seoul, Korea
BARBARA SITEK · Medizinisches Proteom-Center, Ruhr-Universität Bochum, Bochum, Germany
RICHARD SMITH · Department of Medical Physics and Applied Radiation Sciences, McMaster University, Hamilton, ON, Canada
DAVID SPEICHER · The Wistar Institute, Philadelphia, PA, USA
MIRIELLE STARITA-GERIBALDI · Department des Sciences Biologique UFR d’Ontologie, Pôle Universitaire Saint-Jean d’Angely, Nice, France
KAI STUEHLER · Medizinisches Proteom-Center, Ruhr-Universität Bochum, Bochum, Germany
RUKNSHA SULTANA · Department of Chemistry, Sanders-Brown Center on Aging and Center of Membrane Sciences, University of Kentucky, Lexington, KY, USA
RAYMOND TYTHER · Department of Biochemistry, University College Cork, Cork, Ireland
SUSUMU UCHIYAMA · Department of Biotechnology, University of Osaka, Osaka, Japan
JOSEF VAN BEEUMEN · Department of Biochemistry Physiology and Microbiology University of Ghent, Ghent, Belgium
GERT VAN DEN BERGH · Laboratory of Neuroplasticity and Neuroproteomics, Katholieke Universiteit Leuven, Leuven, Belgium
ANNE VON ZYCHLINSKI · Department of Biochemistry, University of Otago, Dunedin, New Zealand
CHAD WALLS · Department of Biochemistry and Molecular Biology, Indiana University School of Medicine, Indianapolis, IN, USA
BRADLEY WALSH · Minomic Pty Ltd, Chatswood West, NSW, Australia
ÅSA WHEELOCK · Karolinska Biomics Center and Department of Medicine, Division of Respiratory Medicine, Karolinska Institutet, Stockholm, Sweden
CHRISTINE C. WINTERBOURN · Department of Pathology, Christchurch School of Medicine & Health Sciences, University of Otago, Christchurch, New Zealand
DIANA WONG · Molecular Structure and Function, The Hospital for Sick Children Research Institute, and the Department of Biochemistry, University of Toronto, Toronto, ON, Canada
CLAUS ZABEL · Institut für Humangenetik, Universitätsklinikum Charité, Berlin, Germany
ZHONG-YIN ZHANG · Department of Biochemistry and Molecular Biology, Indiana University School of Medicine, Indianapolis, IN, USA
ZHENJUN ZHAO · Institute for Eye Research and Vision Cooperative Research Centre, University of New South Wales, Sydney, NSW, Australia
BO ZHOU · Department of Biochemistry and Molecular Biology, Indiana University School of Medicine, Indianapolis, IN, USA