
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 Tytther***

Two-Dimensional Electrophoresis Protocols

Sheehan, D.; Tyther, R. (Eds.)

2009, XIV, 546 p. 100 illus., 1 illus. in color., Hardcover

ISBN: 978-1-58829-937-6

A product of Humana Press