Preface

Proteins are the most diverse group of biologically important substances. They form biological systems that are vital of molecular and cellular structure and function. The technological advances in the genomics area and the efforts in proteomics research have increased the rate of discovering many new proteins with unknown structure and function. These proteins generated from genomic approaches present enormous opportunities for research and industrial application. The key factor to elucidate their structure/function and develop applications for commercial exploitation depends on the development of an efficient and effective purification procedure. However, with thousands of proteins each displaying unique characteristics, it is important to develop a strategy for purification that delivers the correct purity needed for downstream applications. The challenge, therefore, is to separate the protein of interest from all of the other components in the cell, especially the unwanted contaminating proteins, with reasonable efficiency, speed, and yield while retaining the biological activity and chemical integrity of the polypeptide. The increasing requirement for the production of pure proteins is forcing scientists to gain a thorough understanding of protein purification methods and gain abilities and knowledge to improve current and develop new and more effective purification methods and protocols.

This volume is designed to give the laboratory worker the information needed to design and implement a successful purification strategy. It presents reliable and robust protocols in a concise form, emphasizing the critical aspects on practical problems and questions encountered at the lab bench. Written in the highly successful Methods in Molecular Biology series format, each chapter provides introductory material with an overview of the topic of interest; a description of methods, materials, and reagents; readily reproducible step-by-step protocols; a Notes section for tips on troubleshooting; and a collection of published data with a list of references for further details.

This volume consists of 38 chapters. It is divided into five parts (I–V), each of which deals with different approaches and methods. Part I starts with an overview of screening and design of purification strategies and covers initial aspects on high-throughput screening, method development, media selection, and thermodynamic analysis. Part II and III of this volume concentrate on low- and high-resolution protein purification methods that currently enjoy frequent citation in the literature with the emphasis being on affinity chromatography. Information on scale-up considerations is given where appropriate. Aside from methods related directly to purification, this volume includes a description of analytical techniques of value in protein preparation. For example, much space has been allowed in Part IV on cutting-edge analytical techniques of purified proteins. These cutting-edge techniques include not only electrophoretic techniques for analysis and characterization but also mass spectrometry, quantitative affinity chromatography, and X-ray crystallography for protein structure validation and analysis. This section also discusses methods and useful protocols for stabilization of purified proteins. The last Part V presents a number of diverse applications and case studies for the purification of high-added-value proteins and enzymes.

It is impossible for a single book volume to cover all of the different methods, techniques, and applications of protein purification in which scientists have made significant progress. Thus, I have selected key examples covering a wide range of diverge scientific disciplines and state-of-the-art experimental approaches in order to provide the reader with a representative sample of current status of the field. The success of a purification schedule is critically dependent on obtaining a good initial extract with which to work; however, chapters that concerned with procedures for the extraction of proteins from various sources were not included in the present volume. These aspects were perfectly covered by the first and second editions of Methods in Molecular Biology: Protein Purification Protocols (1996; 2004), edited by Professor Shawn Doonan and Paul Cutler, respectively. Despite the obvious omissions the material covered in this volume will allow the investigator the flexibility to adapt these methods to the varied problems which await.

The present book would definitely be an ideal source of scientific information to the advanced students, junior researchers, and scientists involved in health sciences, cellular and molecular biology, biochemistry, biotechnology, and other related areas in both academia and industry.

I sincerely hope that the readers will enjoy the information provided in this book and find its contents interesting and scientifically stimulating. I also hope that I have established a successful compilation of chapters within the exciting area of protein purification. I would like to thank all contributing authors for their enthusiasm and for the time they spent preparing the chapters for this book. I would also like to thank Dr. John Walker, the series editor, for putting forward the idea of the book and for his help and encouragement, and everybody at Springer for their helpful advice and support. I would especially like to thank my family for its understanding and patience during the editing and organization of the book chapters.

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http://www.springer.com/978-1-62703-976-5

Protein Downstream Processing
Design, Development and Application of High and Low-Resolution Methods
Labrou, N. (Ed.)
2014, XV, 555 p. 121 illus., 62 illus. in color., Hardcover
ISBN: 978-1-62703-976-5
A product of Humana Press