
Preface

Proteins are essential constituents of all organisms, and they participate in virtually every process within cells. These macromolecules are found in roles that are enzymatic, regulatory, structural, and immunological, to name but a few. In order to elucidate the structure and function of any protein, it is first necessary to purify it, and consequently many purification schemes and chromatographic methods for the isolation of native proteins from complex sources have been developed over the years. Every protein has its own particular sequence of amino acids which is determined by the nucleotide sequence of a corresponding gene. The last 30 years or so has witnessed revolutionary changes in experimental biology and specifically in the way that we identify, isolate, and manipulate individual genes and proteins. Thus, the emergence of recombinant DNA technology, genomics, and bioinformatics, in particular, means that now theoretically any protein can be expressed in a “tagged” and rapidly purifiable recombinant form from a heterologous host cell.

As in any *Methods in Molecular Biology*TM volume, the emphasis here is on the provision of clear protocol-style chapters that are suitable for newcomers to the field. We first felt that it was important to include contributions that dealt with generic topics in protein biochemistry, addressing such areas as protein stability and storage, avoiding proteolysis during chromatography, protein quantitation methods including immuno-qPCR, and the contrasting challenges that microfluidics and scale-up production pose to the investigator.

At a glance, it is clear that more than one third of the chapters concern the generation and purification of recombinant proteins, reflecting the major contribution of molecular biology to the field. These largely deal with topics such as recombinant antibody production and the tagging of proteins as a means to enhance their solubility and simplify their purification on an individual scale or in high-throughput systems. Of course, it is also expected that a compilation such as this would include the more “classical” purification methods that are based on exploiting the physico-chemical properties of the target protein. The reader will therefore find protocol-style chapters on many of the more commonly used methodologies, including proteomic/mass spectrometric techniques. We also felt that some topics necessitated treatment in an overview-style format due to the need to encompass a great number of variations that have evolved within these areas (e.g., ion-exchange and immunoaffinity chromatography as well as the tagging of recombinant proteins), often in addition to individual methods-style chapters on those subjects. However, this compendium of methods in protein chromatography does not pretend to be comprehensive, and we plead that an attempt to cover the entire potential menu in one volume would have been futile.

We are indebted to all the authors who have generously given their expertise here. Our aims were to assemble contributions from experienced scientists who have hands-on expertise in the field of protein chromatography and to place particular emphasis on the production of clearly presented step-by-step methodologies, tips, and associated

explanatory notes. We hope that those who use these methods will succeed in establishing them in their own laboratories and in troubleshooting any issues that arise. We wish to extend a particular thanks to the series editor, Prof. John Walker, for his patience, advice, and encouragement throughout.

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