

Driven by the widespread growth of proteomic practices in recent years, separation techniques have been refined to minimize uncertainties, optimize particular applications, and adapt to user preferences in the analysis of proteins.

Separation Methods in Proteomics provides a comprehensive examination of all major separation techniques for proteomics research. Written as a compilation of hands-on methods exemplified by the work of several recognized leaders in the field, this book may serve as a guide for selection of the optimal separation strategies to solve particular biological problems.

Recent progress in the development of robust analytical techniques and instrumentation has created the need for better-quality biological samples that are subject to analysis. Emphasizing the importance of sample preparation, the book explains how proteomes can be divided into smaller, less complicated "subproteomes" for individual analysis. It also highlights several hybrid approaches that take into account protein interactions.

Features:

- Contains a compilation of modern applied proteomics methods which cover the entire process, from sample preparation to identification of potential drug targets and biomarkers of disease.
- Demonstrates strategies for protein recovery from samples that are resistant to usual solubilization methods
- Provides practical examples of sample pre-fractionation for analysis of low abundance proteins
- Provides a good summary of recent improvements in the field of Two-Dimensional Gel Electrophoresis (2DGE)
- Describes optimized strategies for protein visualization in 2D gels
- Encompasses automated liquid phase separation methods employing High-Performance Liquid Chromatography (HPLC)
- Illustrates the use of Nuclear Magnetic Resonance (NMR) for the analysis of protein-DNA, protein-lipid, and protein-carbohydrate interactions

Including applications of the separation methods currently employed in proteomic analyses for both clinical and basic research, **Separation Methods in Proteomics** contains practical information that can enhance the current and future endeavors of scientists in proteomics, genomics, transcriptomics, biomarker discovery, and drug discovery.



Taylor & Francis

Taylor & Francis Group

A CRC PRESS BOOK

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New York, NY 10016

2 Park Square, Milton Park
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DK3068

ISBN 0-8247-2699-5

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