# Characterization Of Proteins

*Computational methods for protein function prediction are required to bridge the gap between the number of sequenced genes and the number of experimentally characterized proteins. In this thesis I present a new framework for the organization of protein sequence, structure, and functional information that facilitates computational function prediction. In Chapter II present a semi-automated method for the collection and functional annotation of human transporter genes. Annotation of these genes is performed by placing them within the context of a characterized family, and leveraging existing information about family-specific structure-function relationships to infer their function, in a preliminary application of the Superfamily analysis method that is further explored in subsequent chapters. Streamlining the Superfamily analysis strategy requires a platform that presents Superfamily structure-function data in an easily accessible format. Chapter II describes the development of a Structure-Function Linkage Database (SFLD) to fulfill this purpose. The issues involved in database design are discussed, and an overview of the database functionality is given. The use of the database to address several types of real scientific problems is discussed. Without data, the SFLD schema is of limited use to the research community. Chapter III describes the development of a set of gold standard superfamilies that provide a preliminary dataset for the SFLD and a test set for automated methods that aim to cluster proteins based on sequence, structure, and function. The properties differentiating the gold standard set from existing datasets, as well as the difficulties involved in clustering enzymes in mechanistically diverse superfamilies are discussed. The SFLD may be used for several different purposes. Chapter IV presents two detailed scenarios for using the SFLD--the functional annotation of an uncharacterized protein and analysis of a previously annotated protein to detect misannotation. Chapter V presents some additional contributions that I have made to the SFLD. Development of the database schema is discussed in terms of the requirements for representing structure-function relationships in mechanistically diverse enzyme superfamilies. The automated update protocol for the SFLD is also presented.*

*Approaches to the Purification, Analysis and Characterization of Antibody-Based Therapeutics provides the interested and informed reader with an overview of current approaches, strategies and considerations relating to the purification, analytics and characterization of therapeutic antibodies and related molecules. While there are obviously other books published in and around this subject area, they seem to be either older (c.a. year 2000 publication date) or are more limited in scope. The book will include an extensive bibliography of the published literature in the respective areas covered. It is not, however, intended to be a how-to methods book. Covers the vital new area of R&D on therapeutic antibodies Written by leading scientists and researchers Up-to-date coverage and includes a detailed bibliography*

*Leading scientists offer detailed profiles of ten protein drugs currently in development. The case histories of these important new compounds are described from the perspective of their formulation, characterization, and stability. This ready reference also features recent data and an abundance of previously unpublished information. The in-depth coverage includes a highly useful compendium of degradation sites occurring in over 70 proteins. An invaluable aid in the rapid identification of potential `hot spots' in proteins, this accessible compilation allows for inspection of the protein's primary structure and preparation of a hydroflex plot.*

*This book is dedicated to the characterization of peptides and their applications for the study of biochemical systems. The contributing authors are all leaders in the field of peptide research. Part I, Characterization, presents the most recent advances in select analytical techniques. Part II, Application, presents a variety of specific applications for synthetic peptides. This book is an indispensable aid in the pursuit of new directions in peptide research.*

*Characterization of Protein Therapeutics using Mass Spectrometry*

*PEGylated Protein Drugs: Basic Science and Clinical Applications*

*Strategies for Protein Purification and Characterization*

*Standard Test Method for Characterization of Proteins by Electrophoretic Mobility*

*Isolation and Characterization*

*Methods and Protocols*

In this present volume, different approaches are detailed to produce membrane proteins, purify them, study their function, determine their structure, and model them in membrane. Since every membrane protein behaves mostly in a unique way /fashion, knowledge of guidelines and tricks may help to increase chances to express, purify and characterize a peculiar membrane protein. Production of correctly folded protein remains a challenge. Moreover, getting a functional and stable protein requires to optimize membrane mimicking environments that can be detergent or artificial membranes. In some cases, the finding of the correct ligand which will stabilize the desired conformation is needed. In other cases, stabilization can be obtained using specific antibodies. This volume also presents different techniques to analyze the functional status of membrane proteins. Written in the highly successful Methods in Molecular Biology series format, chapters in Membrane Protein Structure and Function Characterization: Methods and Protocols provide different techniques to analyze the functional and structural status of membrane proteins. Chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Authoritative and practical, Membrane Protein Structure and Function Characterization: Methods and Protocols aims to ensure successful results in the further study of this vital field.

Principles and Reactions of Protein Extraction, Purification, and Characterization provides the mechanisms and experimental procedures for classic to cutting-edge techniques used in protein extraction, purification, and characterization. The author presents the principles and reactions behind each procedure and uses tables to compare the different methods. The book also discusses the development of antibodies and immunochemical techniques as tools for characterizing proteins and modified proteins such as glycoproteins. Helpful illustrations, diagrams, and tables effectively transform theoretical concepts into practical knowledge. Along with methodical working procedures for most techniques,

the book also offers useful advice on which technique to use and when to apply a particular method. Presenting the advantages and disadvantages of the various protein techniques, Principles and Reactions of Protein Extraction, Purification, and Characterization enables students and researchers to master the mechanisms behind the protocols and choose the best method for their purposes.

Principles and Reactions of Protein Extraction, Purification, and Characterization provides the mechanisms and experimental procedures for classic to cutting-edge techniques used in protein extraction, purification, and characterization. The author presents the principles and reactions behind each procedure and uses tables to compare the different

The incorporation of proteins in artificial materials such as membranes offers great opportunities to avail oneself the miscellaneous qualities of proteins and enzymes perfected by nature over millions of years. One possibility to leverage proteins is the modification with artificial polymers. To obtain such protein-polymer conjugates, either a polymer can be grown from the protein surface (grafting-from) or a pre-synthesized polymer attached to the protein (grafting-to). Both techniques were used to synthesize conjugates of different proteins with thermo-responsive polymers in this thesis. First, conjugates were analyzed by protein NMR spectroscopy. Typical characterization techniques for conjugates can verify the successful conjugation and give hints on the secondary structure of the protein. However, the 3-dimensional structure, being highly important for the protein function, cannot be probed by standard techniques. NMR spectroscopy is a unique method allowing to follow even small alterations in the protein structure. A mutant ...

Glass Transition and Phase Transitions in Food and Biological Materials

Identification and Characterization of Proteins Secreted from Axons During Neurogenesis

Characterization of Proteins and Peptides Via Enhanced 266 Nm Ultraviolet Photodissociation Mass Spectrometry Utilizing a Selenium Based Chromophore

Computational and Experimental Characterization of Proteins With Respect to Protein-Solvent Interactions

Characterization of Proteins and Protein Complexes by Online Chromatographic Separations and Direct Infusion Native Mass Spectrometry

Membrane Protein Protocols

This book highlights current approaches and future trends in the use of mass spectrometry to characterize protein therapies. As one of the most frequently utilized analytical techniques in pharmaceutical research and development, mass spectrometry has been widely used in the characterization of protein therapeutics due to its analytical sensitivity, selectivity, and specificity. This book begins with an overview of mass spectrometry techniques as related to the analysis of protein therapeutics, structural identification strategies, quantitative approaches, followed by studies involving characterization of process related protein drug impurities/degradants, metabolites, higher order structures of protein therapeutics. Both general practitioners in pharmaceutical research and specialists in analytical sciences will benefit from this book that details step-by-step approaches and new strategies to solve challenging problems related to protein therapeutics research and development.

This text is devoted to the characterization of recombinant DNA-derived proteins by peptide mapping. It describes new technological procedures including capillary electrophoresis, analysis of glycopeptides and the use of electrospray and matrix-assisted laser desorption mass spectrometry. The book presents practical procedures for preparing a protein sample, the enzyme digestion, choice of separation method and procedures for the structural analysis of the separated species. Many figures of peptide maps illustrate typical results. Tables of summary information about digestion, separation conditions, and analyses of important protein samples are also presented.

This book covers the latest developments in capillary electrophoresis-mass spectrometry for the analysis of therapeutic proteins. The application of capillary electrophoresis-mass spectrometry (CE-MS) coupling technology in the analysis of recombinant therapeutic proteins is detailed thoroughly. Specific topics include recent developments in coupling capillary electrophoresis with mass spectrometry for the quality control of monoclonal antibody therapeutics, top-down analysis of monoclonal antibody using the CE-MS platform, and detection of host cell protein impurities. Comprehensive characterization of antibody-drug conjugates (ADCs) by coupling capillary electrophoresis with mass spectrometry is also covered. This is an ideal book for scientists in the life science and biopharmaceutical industry who are working on characterizing the PTMs of monoclonal antibodies, as well as graduate students and researchers in the separation science and biological mass spectrometry fields.

Protein chemistry has entered a revolutionary era due to the introduction of genetic engineering for modifying protein structure, as well as the application of advanced computer technology to the study of proteins. By supplementing the traditional ways of studying protein behavior with these newer methods, food processors will be able to resolve difficult problems without using the costly trial-and-error-method so common in the past. This book gives the reader a good foundation in the basics of modern protein chemistry and to show how applications of these concepts to food proteins helps explain their roles in food processing.

Capillary Electrophoresis-Mass Spectrometry

Benchtop Techniques

Case Histories

Recovery and Characterization of Proteins from Plants
New Methods in Peptide Mapping for the Characterization of Proteins
Synthesis and Characterization of Protein-polymer Conjugates on the Way to Biohybrid Membrane Materials

*Because the functions of proteins and protein complexes are linked to their structures, structural characterization is important to understand the underlying function. Current structural biology techniques provide high-resolution structures, but have well-known challenges that limit the structural characterization of the protein complexes. These challenges inspire the development of native mass spectrometry (MS), coupled to ion mobility (IM) and integrated separations approaches, as an alternative or complementary structural biology tool.*

*The Plasma Proteins, Volume I: Isolation, Characterization, and Function focuses on the reactions, properties, characteristics, and transformations of plasma proteins. The selection first offers information on the fractionation and isolation of purified components by precipitation methods and electrophoretic and ultracentrifugal analysis of normal human serum. Discussions focus on correlation of electrophoretic and ultracentrifugal results, electrophoretic analytical methodology and results, parameters influencing protein solubility, and techniques for the separation of proteins by precipitation methods. The text then ponders on the chromatography of plasma proteins and chemical composition and molecular parameters of purified plasma proteins. The manuscript elaborates on plasma albumin and macroglobulins and high molecular weight antibodies. Topics include immunological properties, physical and chemical properties of normal and pathological macroglobulins, purity, homogeneity, and variability, denaturation behavior, and sulfhydryl groups, mercaptalbumin, and the mercury dimer. The book then examines glycoproteins and metal-binding plasma proteins and cation transport. The selection is a highly recommended reference for biochemists and clinicians interested in plasma proteins.*

*Biophysical Characterization of Proteins in Developing Biopharmaceuticals, Second Edition, presents the latest on the analysis and characterization of the higher-order structure (HOS) or conformation of protein based drugs. Starting from the very basics of protein structure, this book explains the best way to achieve this goal using key methods commonly employed in the biopharmaceutical industry. This book will help today's industrial scientists plan a career in this industry and successfully implement these biophysical methodologies. This updated edition has been fully revised, with new chapters focusing on the use of chromatography and electrophoresis and the biophysical characterization of very large biopharmaceuticals. In addition, best practices of applying statistical analysis to biophysical characterization data is included, along with practical issues associated with the concept of a biopharmaceutical's developability and the technical decision-making process needed when dealing with biophysical characterization data. Presents basic protein characterization methods and tools applicable to (bio)pharmaceutical research and development Highlights the capabilities and limitations of each technique Discusses the underlining science of each tool Empowers industrial biophysical chemists by providing a roadmap for applying biophysical tools Outlines the needs for new characterization and analytical tools in the biopharmaceutical industry*

*Knowledge of the three-dimensional structure of a protein is absolutely required for the complete understanding of its function. The spatial orientation of amino acids in the active site of an enzyme demonstrates how substrate specificity is defined, and assists the medicinal chemist in the design of s- cific, tight-binding inhibitors. The shape and contour of a protein surface hints at its interaction with other proteins and with its environment. Structural ana- sis of multiprotein complexes helps to define the role and interaction of each individual component, and can predict the consequences of protein mutation or conditions that promote dissociation and rearrangement of the complex. Determining the three-dimensional structure of a protein requires milligram quantities of pure material. Such quantities are required to refine crystallization conditions for X-ray analysis, or to overcome the sensitivity limitations of NMR spectroscopy. Historically, structural determination of proteins was limited to those expressed naturally in large amounts, or derived from a tissue or cell source inexpensive enough to warrant the use of large quantities of cells. H- ever, with the advent of the techniques of modern gene expression, many p- teins that are constitutively expressed in minute amounts can become accessible to large-scale purification and structural analysis.*

*Membrane Proteins*
*Characterization of Proteins*
*Membrane Proteins - Production and Function Characterization*
*Aqueous Two-phase System-based Bioengineering Strategies*
*Total Chemical Synthesis of Proteins*
*Approaches to the Purification, Analysis and Characterization of Antibody-Based Therapeutics*

This test method describes a procedure for determining the electrophoretic mobility of proteins of molecular weight greater than 10, 000 Daltons.

Characterization of ProteinsSpringer

The main drawback for general acceptance of plants as economically viable production systems is the lack of efficient initial concentration and separation procedures. In order to facilitate the general acceptance of plants as bioreactors, the establishment of efficient downstream operations is critical. It has been established that with the general knowledge of the molecular properties of contaminant proteins, the selection and design of suitable downstream strategies for recombinant proteins can be improved. The present dissertation addresses the potential use of quantitative 2D electrophoresis (2-DE) coupled with hydrophobic partitioning in aqueous two-phase systems (ATPS) for three-dimensional characterization of proteins from plant extracts. The application of this experimental approach to soybean proteins resulted in molecular characterization of proteins. Molecular weight (MW), isoelectric point (pI) and

hydrophobicity were measured simultaneously and demonstrated that this technique can be a valuable tool for predictive design of recovery steps for recombinant proteins from plants. The extension of this experimental approach in alfalfa green tissue extracts containing a model recombinant protein provided additional information on the molecular properties of the main host proteins that will allow the design of pre-fractionation and purification methods to facilitate its recovery from alfalfa extracts. As a result of the application of this three-dimensional characterization technique to soybean and alfalfa protein extracts, more efficient downstream strategies could be designed for recovery of recombinant proteins, facilitating the future adoption of plants as a production system.

Proteins are the servants of life. They occur in all com- nent parts of living organisms and are staggering in their fu- tional variety, despite their chemical similarity. Even the simplest single-cell organism contains a thousand different p- teins, fulfilling a wide range of life-supporting roles. Additions to the total number of known proteins are being made on an increasing scale through the discovery of mutant strains or their production by genetic manipulation. The total international protein literature could fill a medi- sized building and is growing at an ever-increasing rate. The reader might be forgiven for asking whether yet another book on proteins, their properties, and functions can serve a useful purpose. An explanation of the origin of this book may serve as justification. The authors form the tutorial team for an int- sive postexperience course on protein characterization or- nized by the Center for Professional Advancement, East Brunswick, New Jersey, an educational foundation. The course was first mounted in Amsterdam in 1982 and has since been repeated several times, in both Amsterdam and the US, with participants from North America and most European countries. In a predecessor to this book, emphasis was placed on the role of protein isolation in the food industry, because at the time this reflected the interests of most of the participants at the course. Today, isolated proteins for food use are extracted from yeasts, fungal sources, legumes, oilseeds, cereals, and leaves.

Peptide Characterization and Application Protocols

Comparison and Characterization of Proteins in Scrapie-infected Cell Membrane Fractions

Light Scattering, Size Exclusion Chromatography and Asymmetric Flow Field Flow Fractionation

Membrane Protein Structure and Function Characterization

Toward an Automated Strategy for Superfamily Analysis and Characterization of Proteins

*Glass and State Transitions in Food and Biological Materials describes how glass transition has been applied to food micro-structure, food processing, product development, storage studies, packaging development and other areas. This book has been structured so that readers can initially grasp the basic principles and instrumentation, before moving through the various applications. In summary, the book will provide the “missing link” between food science and material science/polymer engineering. This will allow food scientists to better understand the concept and applications of thermal properties.*

*This volume is the third of a series on Membrane Proteins and, like the pre ceding manuals, is the result of an International Advanced Course entitled Isolation and Characterization of Membrane Proteins: Biochemical and Bio physical Aspects sponsored by the Federation of European Biochemical So cieties (FEBS) and the Italian Research Council (CNR). The success of the course and the continuous development in the field of membrane biology has prompted me to publish also in this case the protocols of the experiments which were carried out by the students. The students have been able not only to perform the experiments pub lished in this manual without help from the instructors, but also to suggest improvements, which have been incorporated in the published version. Care has been taken in making the planning and the execution of the ex periments as simple as possible, by listing in detail all the necessary pieces of equipment, test tubes, pipettes, chemicals, etc. At the same time the intro duction and the "philosophy" have been limited to the essential, as also the references, only those having been listed which may help in a better under standing of the principles and of the biological background of a given experi ment.*

*PEGylation technology and key applications are introduced by this topical volume. Basic physical and chemical properties of PEG as basis for altering/improving in vivo behaviour of PEG-conjugates such as increased stability, improved PK/PD, and decreased immunogenicity, are discussed. Furthermore, chemical and enzymatic strategies for the coupling and the conjugate characterization are reported. Following chapters describe approved and marketed PEG-proteins and PEG-oligonucleotides as well as conjugates in various stages of clinical development.*

*Mass spectrometry and chemical derivatization have been used as tools for the identification of proteins in both top-down and bottom-up studies. Cysteine is the rarest and most nucleophilic amino acid thus making it a popular target for chemical tagging strategies. Ultraviolet photodissociation (UVPD) is a versatile activation technique for fragmentation of peptides and proteins. For successful photodissociation, ions of interest must contain a suitable chromophore that matches the wavelength of irradiation. N-(Phenylseleno)phthalimide (NPSP) is a fast reacting reagent which attaches a selenium based chromophore that absorbs at 266 nm light to free thiols. In the studies presented in this thesis, NPSP was used to derivatize free cysteine residues in both intact proteins and tryptic peptides. Activation with 266 nm photons causes a dominant neutral loss of the benzeneselenol groups on the tagged protein or peptide ions. This diagnostic neutral loss allows the determination of the number of free versus bound cysteine residues in intact proteins. Additionally, tagging peptides with benzeneselenol provides a means to target only the cysteine-containing peptides in bottom-up proteomics experiments. Both of these methods provide a significantly reduced search space for identification of cysteine-containing proteins. Counting the number of cysteine residues also provides an effective way to restrict the number of protein candidates for database searches. Moreover, cysteine peptides are inherently more unique than other peptides created upon enzymatic digestion of proteins due to the low frequency of cysteine in the proteome, thus allowing these peptides to be used as surrogates for protein identification.*

*Isolation, Characterization, and Stabilization*

*Therapeutic Protein Characterization*

*Formulation, Characterization, and Stability of Protein Drugs*

*Expression, Purification, and Characterization*

*Analytical Characterization of Biotherapeutics*
*Biochemical Characterization of Proteins which Mediate Immunoglobulin Heavy Chain Enhancer Function*

Proteins are the servants of life. They occur in all component parts of living organisms and are staggering in their functional var- ty, despite their chemical similarity. Even the simplest single-cell organism contains a thousand different proteins, fulfilling a wide range of life-supporting roles. Their production is controlled by the cell ' s genetic machinery, and a malfunction of even one protein in the cell will give rise to pathological symptoms. Additions to the total number of known proteins are constantly being made on an increasing scale through the discovery of mutant strains or their production by genetic manipulation; this latter technology has become known as protein engineering. The in vivo functioning of proteins depends critically on the chemical structure of individual peptide chains, but also on the detailed folding of the chains themselves and on their assembly into larger supramolecular structures. The molecules and their fu- tional assemblies possess a limited in vitro stability. Special methods are required for their intact isolation from the source material and for their analysis, both qualitatively and quantitatively. Proteins are also increasingly used as " industrial components, " e.g., in biosensors and immobilized enzymes, because of their specificity, selectivity, and sensitivity. This requires novel and refined proce- ing methods by which the protein isolate can be converted into a form in which it can be utilized.

This book is designed to be a practical progression of experimental techniques an investigator may follow when embarking on a biochemical project. The protocols may be performed in the order laid out or may be used inde pendently. The aim of the book is to assist a wide range of researchers. from the novice to the frustrated veteran, in the choice and design of experiments that are to be performed to provide answers to specific questions. The manual describes standard techniques that have been shown to work, as well as some newer ones that are beginning to prove important. By following the promi nently numbered steps. you can work your way through any protocol. whether it's a new technique or a task you've done before for which you need a quick review or updated methodology. This manual will assist the experimentalist in designing properly controlled experiments. There will be no advice for dealing with specific pieces of equip ment other than encouragement to read the manual, if you can find it. Through out all manipulations try to be objective. Be on the lookout for unexpected findings. You will learn the most from unexpected results. and they are often the beginning of the next project. It is never possible to record too much in your lab notebook. Do not get discouraged. Remember, things will not always run smoothly.

The definitive guide to the myriad analytical techniques available to scientists involved in biotherapeutics research Analytical Characterization of Biotherapeutics covers all current and emerging analytical tools and techniques used for the characterization of therapeutic proteins and antigen reagents. From basic recombinant antigen and antibody characterization, to complex analyses for increasingly complex molecular designs, the book explores the history of the analysis techniques and offers valuable insights into the most important emerging analytical solutions. In addition, it frames critical questions warranting attention in the design and delivery of a therapeutic protein, exposes analytical challenges that may occur when characterizing these molecules, and presents a number of tested solutions. The first single-volume guide of its kind, Analytical Characterization of Biotherapeutics brings together contributions from scientists at the leading edge of biotherapeutics research and manufacturing. Key topics covered in-depth include the structural characterization of recombinant proteins and antibodies, antibody de novo sequencing, characterization of antibody drug conjugates, characterization of bi-specific or other hybrid molecules, characterization of manufacturing host-cell contaminant proteins, analytical tools for biologics molecular assessment, and more. Each chapter is written by a recognized expert or experts in their field who discuss current and cutting edge approaches to fully characterizing biotherapeutic proteins and antigen reagents Covers the full range of characterization strategies for large molecule based therapeutics Provides an up-to-date account of the latest approaches used for large molecule characterization Chapters cover the background needed to understand the challenges at hand, solutions to characterize these large molecules, and a summary of emerging options for analytical characterization Analytical Characterization of Biotherapeutics is an up-to-date resource for analytical scientists, biologists, and mass spectrometrists involved in the analysis of biomolecules, as well as scientists employed in the pharmaceuticals and biotechnology industries. Graduate students in biology and analytical science, and their instructors will find it to be fascinating and instructive supplementary reading.

Membrane Proteins - Production and Function Characterization a volume of Methods in Enzymology, encompasses chapters from the leading experts in the area of membrane protein biology. The chapters provide a brief overview of the topics covered and also outline step-by-step protocol. Illustrations and case example images are included wherever appropriate to help the readers understand the schematics and general experimental outlines. Volume of Methods In Enzymology Contains a collection of a diverse array of topics in the area of membrane protein biology ranging from recombinant expression, isolation, functional characterization, biophysical studies and crystallization

Stability and Characterization of Protein and Peptide Drugs

Food Proteins

Isolation, Characterization, and Function

The Plasma Proteins: Isolation, characterization, and function

Protein Analysis and Purification

Development of Asymmetrical Flow Field-flow Fractionation for the Characterization of Proteins, Protein Aggregation, and Nanoparticles

How to synthesize native and modified proteins in the test tube With contributions from a panel of experts representing a range of disciplines, Total Chemical Synthesis of Proteins presents a carefully curated collection of synthetic approaches and strategies for the total synthesis of native and modified proteins. Comprehensive in scope, this important reference explores the three main chemoselective ligation methods for assembling unprotected peptide segments, including native chemical ligation (NCL). It includes information on synthetic strategies for the complex polypeptides that constitute glycoproteins, sulfoproteins, and membrane proteins, as well as their characterization. In addition, important areas of application for total protein synthesis are detailed, such as protein crystallography, protein engineering, and biomedical research. The authors also discuss the synthetic challenges that remain to be addressed. This unmatched resource: Contains valuable insights from the pioneers in the field of chemical protein synthesis Presents proven synthetic approaches for a range of protein families Explores key applications of precisely controlled protein synthesis, including novel diagnostics and therapeutics Written for organic chemists, biochemists, biotechnologists, and molecular biologists, Total Chemical Synthesis of Proteins provides key knowledge for everyone venturing into the burgeoning field of protein design and synthetic biology.

This is the first volume to make available specific case histories of therapeutic proteins and peptides that have been marketed or are currently under clinical testing. The editors have selected a wide range of molecules derived from monoclonal antibodies, recombinant DNA, and natural and chemical sources to provide formulation scientists with practical examples of the deveopment of pharmaceutical products.

A comprehensive, practical approach to three powerful methods of polymer analysis and characterization This book serves as a complete compendium of three important methods widely used for the characterization of synthetic and natural polymers—light scattering, size exclusion chromatography (SEC), and asymmetric flow field flow fractionation (A4F). Featuring numerous up-to-date examples of experimental results obtained by light scattering, SEC, and A4F measurements, Light Scattering, Size Exclusion Chromatography and Asymmetric Flow Field Flow Fractionation takes an all-in-one approach to deliver a complete and thorough explanation of the principles, theories, and instrumentation needed to characterize polymers from the viewpoint of their molar mass distribution, size, branching, and aggregation. This comprehensive resource: Is the only book gathering light scattering, size exclusion chromatography, and asymmetric flow field flow fractionation into a single text Systematically compares results of size exclusion chromatography with results of asymmetric flow field flow fractionation, and how these two methods complement each other Provides in-depth guidelines for reproducible and correct determination of molar mass and molecular size of polymers using SEC or A4F coupled with a multi-angle light scattering detector Offers a detailed overview of the methodology, detection, and characterization of polymer branching Light Scattering, Size Exclusion Chromatography and Asymmetric Flow Field Flow Fractionation should be of great interest to all those engaged in the polymer analysis and characterization in industrial and university research, as well as in manufacturing quality control laboratories. Both beginners and experienced can confidently rely on this volume to confirm their own understanding or to help interpret their results.

A Laboratory Course Manual

Symposium on Characterization of Proteins

The Plasma Proteins

Structural Characterization of Proteins by Tandem Mass Spectrometry

Biophysical Characterization of Proteins in Developing Biopharmaceuticals

Powerful Tools for the Characterization of Polymers, Proteins and Nanoparticles