

Glycobiology Protocols

Edited by
Inka Brockhausen

Glycobiology Protocols Methods In Molecular Biology

Manfred P. Schneider



Glycobiology Protocols Methods In Molecular Biology:

Glycobiology Protocols Inka Brockhausen, 2008-02-04 Glycobiology involves studies of complex carbohydrates and posttranslational modifications of proteins and has become an important interdisciplinary field encompassing chemistry, biochemistry, biology, physiology, and pathology. Although initial research was directed toward elucidation of the different carbohydrate structures and the enzymes synthesizing them, the field has now moved toward identifying the functions of carbohydrates. The protocols described in *Glycobiology Protocols* form a solid basis for investigations of glycan functions in health and disease. The cloning of many of the genes participating in glycosylation processes has helped to enhance our knowledge of how glycosylation is controlled but has also added another dimension of complexity to the great heterogeneous variety of the structures of the oligosaccharides of glycoproteins, proteoglycans, and glycolipids. A family of similar enzyme proteins exists for each glycosylation step. Glycosyltransferases are extremely specific for both the nucleotide sugar donor and the acceptor substrate but many other factors control sugar transfer, including the localization and topology of enzymes, cofactors, possible chaperone proteins, and the availability of sugar acceptor substrates. The analysis of the intracellular organization of glycosylation and of the factors controlling the activities of the participating enzymes in the cell are important areas that need more research efforts. Another challenge for future research is to understand the glycodynamics of a cell, that is, how the cell responds to stimuli leading to biological and pathological changes in terms of alterations in glycosylation and how this affects the biology of the cell. **Arabidopsis Protocols, 2nd Edition** Julio Salinas, Jose J.

Sanchez-Serrano, 2008-02-04 For several decades *Arabidopsis thaliana* has been the organism of choice in the laboratories of many plant geneticists, physiologists, developmental biologists, and biochemists around the world. During this time a huge amount of knowledge has been acquired on the biology of this plant species, which has resulted in the development of molecular tools that account for much more efficient research. The significance that *Arabidopsis* would attain in biological research may have been difficult to foresee in the 1980s when its use in the laboratory started. In the meantime it has become the model plant organism, much the same way as *Drosophila*, *Caenorhabditis*, or mouse have for animal systems. Today it is difficult to envision research at the cutting edge of plant biology without the use of *Arabidopsis*. Since the first edition of *Arabidopsis Protocols* appeared, new developments have fostered an impressive advance in plant biology that prompted us to prepare *Arabidopsis Protocols*, Second Edition. Completion of the *Arabidopsis* genome sequence offered for the first time the opportunity to have in hand all of the genetic information required for studying plant function. In addition, the development of whole systems approaches that allow global analysis of gene expression and protein and metabolite dynamics has encouraged scientists to explore new scenarios that are extending the limits of our knowledge. *The Art of Carbohydrate Analysis* Gerrit J. Gerwig, 2021-10-23 The growing importance of glycobiology and carbohydrate chemistry in modern biotechnology and the pharmaceutical industry makes accurate carbohydrate analysis indispensable. This book provides the

principles and protocols of various fundamental carbohydrate analysis methods Choice of method is entirely dependent upon the type of material being investigated biological samples food products etc and the level of structural detail required i e sugar content compositional analysis linkages between the sugar components or the total chemical structure of a given molecule Full structural characterization of carbohydrate chains requires significant time resources and skill in several methods of analysis no single technique can address all glycan analysis needs This book summarizes several existing analytical techniques both chemical and physical in an introductory volume designed for the non expert researcher or novice scientist While background in carbohydrate chemistry is assumed all information necessary to understanding the described techniques is addressed in the text *PRINS and In Situ PCR Protocols* Franck Pellestor, 2008-02-03 The in situ hybridization and PCR technologies are now well established molecular techniques for studying chromosomal aneuploidy and rearrangements gene localization and expression and genomic organization Over the last decade we have seen increasing applications in these fields By combining the high sensitivity of the PCR reaction and the cytological localization of target sequences both PRINS and in situ PCR techniques have provided highly powerful complements to FISH for in situ cellular and molecular investigations Both these approaches have several advantages in terms of sensitivity and specificity owing to the use of primers and to the fast kinetics of annealing and elongation reactions in situ In the first edition of PRINS and In Situ PCR Protocols edited by John R Gosden experts in the field presented in detail a variety of applications of PRINS and in situ PCR techniques in a wide range of clinical conditions Since the publication of this successful reference book there have been significant improvements in in situ detection techniques This completely revised and updated second edition presents a comprehensive selection of new procedures developed in the field of PRINS and in situ PCR technologies The book has two sections Part I Basic Methodology contains chapters that provide useful protocols for many variations of PRINS and in situ PCR including a new fast multicolor PRINS method and protocols for PRINS detection of unique sequences in situ YAC Protocols Alasdair MacKenzie, 2007-10-26 It is now 10 years since the first edition of YAC Protocols was published in 1996 YAC Protocols was first produced to address the huge demand within the research community for a lab based text that described in detail the wide range of uses for large insert yeast artificial chromosome YAC DNA clones In doing this the original editor David Markie and the many different contributors who provided descriptions of the protocols they used and developed did a magnificent job Indeed many of the techniques described within the first edition require little change and have stood up admirably to the test of time Since the first edition the use of YACs has proved invaluable for addressing a wide range of new biological problems ranging from those of basic biochemistry to assisting in the mapping and sequencing of the human genome The requirement for a second edition of YAC Protocols was prompted by a number of major advances in biology since the publication of the first edition These advances have included the sequencing of the human genome and the genomes of a wide variety of other organisms and the increased use of transgenic animals for understanding the

molecular basis of human and animal disease *Diagnostic Bacteriology Protocols* Louise O'Connor, 2008-02-05 The field of bacterial diagnostics has seen unprecedented advances in recent years The increased need for accurate detection and identification of bacteria in human animal food and environmental samples has fueled the development of new techniques The field has seen extensive research aided by the information from bacterial genome sequencing projects Although traditional methods of bacterial detection and identification remain in use in laboratories around the world there is now a growing trend toward the use of nucleic acid based diagnostics and alternative biochemically and immunologically based formats The ultimate goal of all diagnostic tests is the accurate detection identification or typing of microorganisms in samples of interest Although the resulting information is of obvious use in the areas of patient management animal health and quality control it is also of use in monitoring routes of infection and outlining strategies for infection control There is therefore a need to ensure that the information being provided is of the highest standard and that any new technique is capable of delivering this **Protocols for Nucleic Acid Analysis by Nonradioactive Probes** Elena Hilario, John F.

MacKay, 2008-02-02 *Protocols for Nucleic Acid Analysis by Nonradioactive Probes* Second Edition provides a firm background on the basic preparative protocols required for the analysis of nucleic acids by nonradioactive methods Presenting the methodologies using amazing new applications this volume offers guide chapters on nucleic acid extractions preparation of nucleic acid blots and labeling of nucleic acids with nonradioactive haptens New fluorescent techniques such as Real Time PCR and microarrays are also included allowing users to get a nonradioactive protocol implemented in the laboratory with minimum adaptation required and fastest time to results The protocols follow the successful *Methods in Molecular Biology*™ series format each offering step by step laboratory instructions an introduction outlining the principles behind the technique lists of the necessary equipment and reagents and tips on troubleshooting and avoiding known pitfalls

Macromolecular Crystallography Protocols, Volume 2 Sylvie Doublie, 2008-02-05 In the decade since publication of the first edition of *Crystallographic Methods and Protocols* the field has seen several major developments that have both accelerated the pace of structure determination and made crystallography accessible to a broader range of investigators Volume I *Preparation and Crystallization of Macromolecules* is dedicated to the crystallization and ways to increase the odds of obtaining crystals in macromolecules while Volume 2 *Structure Determination* covers both computational methods for characterizing crystals and solving structures **MicroRNA Protocols** Shao-Yao Ying, 2008-02-04 *MicroRNA Protocols*

provides diverse novel and useful descriptions of miRNAs in several species including plants worms flies fish chicks mice and humans These include some useful adaptations and applications that could be relevant to the wider research community who are already familiar with the identification of miRNAs This volume will stimulate the reader to explore diverse ways to understanding the mechanism in which miRNAs facilitate the molecular aspects of the biomedical research *Human Embryonic Stem Cell Protocols* Kursad Turksen, 2006 All of the electronic versions of illustrations in this book may be found

on the Companion CD attached to the inside back cover compatible with both MAC and PC operating systems P xv *New and Emerging Proteomic Techniques* Dobrin Nedelkov, Randall W. Nelson, 2008-02-04 Leading researchers and innovators describe in step by step detail the latest techniques that promise to significantly impact the practice of proteomics as well as its success in developing novel clinical agents The methods span the entire spectrum of top down and bottom up approaches including microarrays gels chromatography and affinity separations and address every aspect of the human proteome both quantitatively and qualitatively The techniques of protein detection utilized are diverse and range from fluorescence and resonance light scattering to surface plasmon resonance and mass spectrometry The protocols follow the successful *Methods in Molecular Biology*TM series format each offering step by step laboratory instructions an introduction outlining the principles behind the technique lists of the necessary equipment and reagents and tips on troubleshooting and avoiding known pitfalls

Protein Design Raphael Guerois, Manuela López de la Paz, 2008-02-04 Proteins have evolved through selective pressure to accomplish specific functions The functional properties of proteins depend upon their three dimensional structures which result from particular amino acid sequences folding into tightly packed domains Thus to understand and modulate protein function rationally one definitely needs methods and algorithms to predict and decipher how amino acid sequences shape three dimensional structures Protein design aims precisely at providing the tools to achieve this goal The predictive power of rational protein design methods has dramatically increased over the past five years A broad range of studies now illustrate how the sequence of proteins and peptides can be tuned to engineer biological tools with intended properties 1 3 The extensive characterization of peptides and protein mutants has enormously benefited the understanding of protein sequence to structure relationships Synergies between computational and experimental approaches have also added momentum to the advancing limits of design methods The potential applications in fundamental biochemistry and in biotechnology justify the considerable excitement that this progress has generated within the research community The field is probably mature enough so that expert knowledge can assist researchers of diverse disciplines to rationally create or modify their favorite protein Thus the aim of *Protein Design Methods and Protocols* is to account for the most up to date protein design and engineering strategies so that readers can undertake their own projects with maximum confidence in a successful return The basic concepts underlying rational design of proteins are intimately related to their three dimensional structures

Cell'Cell Interactions Sean P. Colgan, 2008-02-04 A versatile collection of readily reproducible cell cell interaction assays for uncovering cellular interactions at the molecular level both in vitro and in vivo The protocols cover a diverse set of cell cell interaction models in both normal and pathological states are readily adaptable to nearly any cell type and organ system and include primary data and outcome analysis In addition the protocols follow the successful *Methods in Molecular Biology*TM series format each offering step by step laboratory instructions an introduction outlining the principles behind the technique lists of the necessary equipment and reagents and tips on troubleshooting and avoiding known pitfalls

Mass Spectrometry Data Analysis in Proteomics Rune Matthiesen, 2008-02-02 Mass Spectrometry Data Analysis in Proteomics is an in depth guide to the theory and practice of analyzing raw mass spectrometry MS data in proteomics As MS is a high throughput technique proteomic researchers must attend carefully to the associated field of data analysis and this volume outlines available bioinformatics programs algorithms and databases available for MS data analysis General guidelines for data analysis using search engines such as Mascot X tandem and VEMS are provided with specific attention to identifying poor quality data and optimizing search parameters Several different types of MS data are discussed followed by a description of optimal methods for conversion of raw data into peak lists for input to search engines Choosing the most accurate and complete databases is emphasized and a report of available sequence databases is included Methods for assembling expressed sequence tags ESTs into assembled nonredundant databases are provided along with protocols for further processing the sequences into a format suitable for MS data Mass Spectrometry Data Analysis in Proteomics describes publicly available applications whenever possible

Fluorescent Energy Transfer Nucleic Acid Probes Vladimir V. Didenko, 2008-02-04 Fluorescent nucleic acid probes which use energy transfer include such constructs as molecular beacons molecular break lights Scorpion primers TaqMan probes and others These probes signal detection of their targets by changing either the intensity or the color of their fluorescence Not surprisingly these luminous multicolored probes carry more flashy names than their counterparts in the other fields of molecular biology In recent years fluorescent probes and assays which make use of energy transfer have multiplied at a high rate and have found numerous applications However in spite of this explosive growth in the field there are no manuals summarizing different protocols and fluorescent probe designs In view of this the main objective of Fluorescent Energy Transfer Nucleic Acid Probes Designs and Protocols is to provide such a collection Oligonucleotides with one or several chromophore tags can form fluorescent probes capable of energy transfer Energy transport within the probe can occur via the resonance energy transfer mechanism also called Förster transfer or by non Förster transfer mechanisms Although the probes using Förster transfer were developed and used first the later non Förster based probes such as molecular beacons now represent an attractive and widely used option The term fluorescent energy transfer probes in the title of this book covers both Förster based fluorescence resonance energy transfer FRET probes and probes using non FRET mechanisms Energy transfer probes serve as molecule size sensors changing their fluorescence upon detection of various DNA reactions

Microarrays Jang B. Rampal, 2007-07-27 Microarray Technology Volumes 1 and 2 present information in designing and fabricating arrays and binding studies with biological analytes while providing the reader with a broad description of microarray technology tools and their potential applications The first volume deals with methods and protocols for the preparation of microarrays The second volume details applications and data analysis which is important in analyzing the enormous data coming out of microarray experiments Among the topics discussed in Volume 1 Synthesis Methods are matrices in the synthesis of microarrays array optimization processes array

based comparative genomic hybridization 60 mer oligonucleotide probes bifunctional reagents NTMTA and NTPAC and high density arrays using digital microarray synthesis platforms Other topics include multiplex ligation dependent probe amplification MLPA hybridization conditions in situ synthesized oligo arrays peptide arrays high density replication tools HDRT protocols for the quantification of oligo hybridization glyco bead arrays and an investigation into the emerging nano technology Microarray Technology Volumes 1 and 2 provide ample information to all levels of scientists from novice to those intimately familiar with array technology

Agrobacterium Protocols Kan Wang, 2008-02-05 *Agrobacterium tumefaciens* is a soil bacterium that for more than a century has been known as a pathogen causing the plant crown gall disease Unlike many other pathogens *Agrobacterium* has the ability to deliver DNA to plant cells and permanently alter the plant genome The discovery of this unique feature 30 years ago has provided plant scientists with a powerful tool to genetically transform plants for both basic research purposes and for agricultural development Compared to physical transformation methods such as particle bombardment or electroporation *Agrobacterium* mediated DNA delivery has a number of advantages One of the features is its propensity to generate single or a low copy number of integrated transgenes with defined ends Integration of a single transgene copy into the plant genome is less likely to trigger gene silencing often associated with multiple gene insertions When the first edition of *Agrobacterium Protocols* was published in 1995 only a handful of plants could be routinely transformed using *Agrobacterium* *Agrobacterium* mediated transformation is now commonly used to introduce DNA into many plant species including monocotyledon crop species that were previously considered non hosts for *Agrobacterium* Most remarkable are recent developments indicating that *Agrobacterium* can also be used to deliver DNA to non plant species including bacteria fungi and even mammalian cells

Antibody Expression and Production Mohamed Al-Rubeai, 2011-05-16 Engineered antibodies currently represent over 30% of biopharmaceuticals in clinical trials and their total worldwide sales continue to increase significantly The importance of antibody applications is reflected in their increasing clinical and industrial applications as well as in the progression of established and emerging production strategies This volume provides detailed coverage of the generation optimization characterization production and applications of antibody It provides the necessary theoretical background and description of methods for the expression of antibody in microbial and animal cell cultures and in transgenic animals and plants There is a strong focus on those issues related to the production of intrabodies bispecific antibody and antibody fragments and also to novel applications in cancer immunotherapy

Clinical Applications of PCR Y. M. Dennis Lo, 2008-02-04 In this updated second edition leading researchers apply molecular diagnostics to the many recent advances that have occurred in polymerase chain reaction PCR based technologies Highlights include real time PCR which allows the technique to be performed in a quantitative manner with improved sensitivity robustness and resilience to carryover contamination mass spectrometric analysis of nucleic acids and circulating cell free nucleic acids in plasma The authors apply these innovations to a broad spectrum of applications including gene expression methylation trace

molecule gene dosage and single cell analysis

Chemical Probes in Biology Manfred P. Schneider, 2003

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