

# METHODS IN MOLECULAR BIOLOGY

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# **High-Throughput Glycomics and Glycoproteomics**

**Methods and Protocols**

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## Preface

Carbohydrates—or glycans—are a highly abundant class of biomolecules and can be found in various shapes and sizes in all kingdoms of life. Glycans often exist in the form of oligo- or polysaccharides as well as glycoconjugates, i.e., with a covalent linkage of the glycan portion to proteins or lipids. Glycans significantly contribute to the structure and function of the majority of proteins. Interindividual variability in both glycome composition and glycome changes after environmental challenge is large, and these differences strongly affect many physiological functions. Due to chemical and biological complexity of glycans, the knowledge about glycans is lagging significantly behind the knowledge about genes and proteins. However, recent comprehensive report endorsed by the US National Academies concluded that “glycans are directly involved in the pathophysiology of every major disease” and the interest in glycomics studies is growing exponentially.

The analysis of glycans is an often challenging endeavor, due to their heterogeneity, their non-template-based synthesis, and the abundance of functionally distinct isomers which are challenging for separation and characterisation using current analytical techniques. Technological challenges in glycan analysis are generally seen as the major obstacle for revealing insights into functional relevance of glycans. In the last few years several robust methods that enable high-throughput analysis of glycans have been developed and glycomics is now ready to join genomics and other omics in genetic, epidemiological, and clinical studies.

This volume of *Methods in Molecular Biology* entitled *High-Throughput Glycomics and Glycoproteomics* brings detailed protocols for the analysis of glycosylation at the level of free glycans and glycopeptides, an essential reference for researchers planning to enter this rapidly evolving field. The importance of glycans in eukaryotic life, with a focus on mammals and particularly humans, is highlighted in Chapter 1 of this issue. The following chapters largely have a focus on recent technologies that allow the characterization of larger sets of samples, and major attention has been paid to method repeatability and robustness as well as higher throughput with respect to sample preparation, measurement, and data analysis. The chapters span a wide range of techniques, including the analysis of fluorescently labeled glycans with HPLC, LC-MS analysis of glycopeptides both for glycosylation profiling and for in-depth tandem mass spectrometric analysis of protein glycosylation, and the analysis of glycans with fluorescent labeling and capillary electrophoresis in conjunction with laser-induced fluorescence detection. The chapters also pay attention to specific sample types including brain tissues, N-glycans from in vitro cell cultures, milk oligosaccharides, invertebrate and protist N-glycans as well as plant glycans.

We thank all the contributors, who are leading researchers in analytical glycomics and developers as well as expert users of the presented methods, for sharing their protocols in this volume. We thank Dr. John Walker, the Editor-in-Chief of the *Methods in Molecular Biology* series, for his guidance and continuous support.

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## Contents

<i>Preface</i> . . . . .	<i>v</i>
<i>Contributors</i> . . . . .	<i>ix</i>
1 Ubiquitous Importance of Protein Glycosylation . . . . . <i>Jasminka Kristić and Gordan Lauc</i>	1
2 Laboratory Experimental Design for a Glycomic Study . . . . . <i>Ivo Ugrina, Harry Campbell, and Frano Vučković</i>	13
3 High-Throughput Analysis of the IgG N-Glycome by UPLC-FLR . . . . . <i>Maja Pučić-Baković</i>	21
4 High-Throughput Analysis of IgG Fc Glycopeptides by LC-MS . . . . . <i>David Falck, Bas C. Jansen, Noortje de Haan, and Manfred Wuhrer</i>	31
5 Sialic Acid Derivatization for the Rapid Subclass- and Sialic Acid Linkage-Specific MALDI-TOF-MS Analysis of IgG Fc-Glycopeptides . . . . . <i>Noortje de Haan, Karli R. Reiding, and Manfred Wuhrer</i>	49
6 The Use of Multiple Reaction Monitoring on QQQ-MS for the Analysis of Protein- and Site-Specific Glycosylation Patterns in Serum . . . . . <i>L. Renee Ruhaak</i>	63
7 Analysis of Permethylated Glycan by Liquid Chromatography (LC) and Mass Spectrometry (MS) . . . . . <i>Shiyue Zhou, Kerry M. Wooding, and Yehia Mechref</i>	83
8 High-Throughput Analysis of the Plasma N-Glycome by UHPLC . . . . . <i>Barbara Adamczyk, Henning Stöckmann, Róisín O’Flaherty, Niclas G. Karlsson, and Pauline M. Rudd</i>	97
9 Site-Specific N- and O-Glycopeptide Analysis Using an Integrated C18-PGC-LC-ESI-QTOF-MS/MS Approach . . . . . <i>Kathrin Stavenhagen, Hannes Hinneburg, Daniel Kolarich, and Manfred Wuhrer</i>	109
10 Analysis of Milk Oligosaccharides by Mass Spectrometry . . . . . <i>Lauren D. Wu, L. Renee Ruhaak, and Carlito B. Lebrilla</i>	121
11 N- and O-Glycomics from Minor Amounts of Formalin-Fixed, Paraffin-Embedded Tissue Samples . . . . . <i>Hannes Hinneburg, Falko Schirmeister, Petra Korać, and Daniel Kolarich</i>	131
12 Carbohydrate Microarray Technology Applied to High-Throughput Mapping of Plant Cell Wall Glycans Using Comprehensive Microarray Polymer Profiling (CoMPP) . . . . . <i>Stjepan Krešimir Kračun, Jonatan Ulrik Fangel, Maja Gro Rydahl, Henriette Lodberg Pedersen, Silvia Vidal-Melgosa, and William George Tycho Willats</i>	147

13	Analysis of Invertebrate and Protist <i>N</i> -Glycans . . . . .	167
	<i>Alba Hykollari, Katharina Paschinger, Barbara Eckmair,</i> <i>and Iain B.H. Wilson</i>	
14	High-Throughput and High-Sensitivity Mass Spectrometry-Based <i>N</i> -Glycomics of Mammalian Cells . . . . .	185
	<i>Stephanie Holst, Gabi W. van Pelt, Wilma E. Mesker, Rob A. Tollenaar,</i> <i>Ana I. Belo, Irma van Die, Yoann Rombouts, and Manfred Wuhrer</i>	
15	Analysis of <i>N</i> -Glycosylation of Total Membrane Proteins. . . . .	197
	<i>Tamara Pavić and Olga Gornik</i>	
16	HILIC-UPLC Analysis of Brain Tissue <i>N</i> -Glycans. . . . .	207
	<i>Thomas Klarić and Ivan Gudelj</i>	
17	Automated Integration of a UPLC Glycomic Profile . . . . .	217
	<i>Anna Agakova, Frano Vučković, Lucija Klarić, Gordan Lauc,</i> <i>and Felix Agakov</i>	
18	Databases and Associated Tools for Glycomics and Glycoproteomics . . . . .	235
	<i>Frederique Lisacek, Julien Mariethoz, Davide Alocci, Pauline M. Rudd,</i> <i>Jodie L. Abrahams, Matthew P. Campbell, Nicolle H. Packer, Jonas Stähle,</i> <i>Göran Widmalm, Elaine Mullen, Barbara Adamczyk,</i> <i>Miguel A. Rojas-Macias, Chunsheng Jin, and Niclas G. Karlsson</i>	
19	High-Throughput <i>N</i> -Glycan Analysis with Rapid Magnetic Bead-Based Sample Preparation . . . . .	265
	<i>Marton Szigeti and Andras Guttman</i>	
	<i>Index</i> . . . . .	273

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