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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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