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## Preface

Over the past decade, we have witnessed an explosive development of research dedicated to intrinsically disordered proteins (IDPs), which are also known as natively unfolded proteins among various other names. The existence of biologically active but extremely flexible proteins is challenging the century-old structure-to-function paradigm according to which a rigid well-folded 3D structure is required for protein function. Many structural biologists now recognize that the functional diversity provided by disordered regions complements the functional repertoire of ordered protein regions. The high abundance of IDPs in various organisms, their unique structural features, numerous functions, and crucial associations with different diseases show that there are enough grounds to conclude that these proteins should be considered as a unique entity, an unfoldome.

In comparison with “normal” globular proteins, IDPs possess increased amounts of disorder that can be detected by many physico-chemical methods that were originally developed to characterize protein self-organization. On the other hand, due to the highly dynamic nature of IDPs, new and existing experimental methods need to be developed and extended, respectively, for the structural and functional analysis of these IDPs. These methods represent an instrumental foundation for experimental unfoldomics.

Information based on modern protocols is provided herein on virtually every experimental method used both to identify IDPs and to analyze their structural and functional properties. Hence, this book will be of interest to all scientists and students studying IDPs, whether the focus is on an IDP’s (lack of) structure or on its function.

The general audience for this book includes scientists working in the fields of biochemistry, biophysics, molecular medicine, biotechnology, pharmacology and drug discovery, molecular and cellular biology; Students of Medical Schools, departments of Biochemistry, Biophysics, Molecular Biology, Biotechnology, and Cell Biology, to name a few. We are aware that many scientists have encountered IDPs in their research, but have shied away from deeper studies due to the lack of knowledge of what to try next. By collecting the current methods for the analysis of IDPs in one place, our goal is to help such scientists further their investigations of these fascinating, dynamic molecules.

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