Preface

Individual organisms are defined by their genetic code. During development and as a response to external stimuli the genetic information is translated into a well-defined answer resulting in the expression and modification of proteins. The processes that control protein–protein interactions (PPI) are presently mostly described in terms of individual protein–protein interactions. In vivo such interactions are part of complex molecular interaction networks that are highly dynamic in time and space. On the basis of quantitative experiments, it would be possible to understand such complex biological systems leading to an unraveling of these networks and allowing them to be caught in quantitative and predictive models.

This textbook illustrates the rise of a relatively new area of biology. The shifting of research from the structural assembly of cells and whole organisms to metabolic diversity led to the beginning of interactomics. This field has arisen from the increasing importance of molecular biology and biochemistry in basic research as well as in prognostics and prevention of diseases in connection with biomarker development.

The behavior, morphology, and response to stimuli in biological systems are predetermined by the interactions between their components. These interactions, as we observe them now, are therefore shaped by genetic variations and selective pressure. With the understanding of molecular interactions the biology is getting easier to survey. The characterization of protein interactions can contribute to the understanding of many processes in nature.

Knowledge of the different types of biological macromolecules and increasing numbers of whole genomic studies facilitate the elucidation of cellular processes. Whether it is genomics, transcriptomics, proteomics, interactomics, or metabolomics, the full complement of genomic information at different levels can be compared between different organisms to reveal similarities or differences and even to provide consensus models.

A protein's role is reflected in its interaction with others. Much of the function of novel proteins can be predicted from identifying its interaction partners, and from characterizing its localization within the cell. There is a need to employ a combination of approaches to overcome this deficit in understanding of gene function. A number of experimental strategies have been developed and applied at a large scale with the aim to decipher gene

function through identifying proteins interacting with the gene product of interest.

Protein–protein interactions are key elements for normal functioning of a living cell. A detailed description of the protein interactomics field is given in this book. We first give an introduction to the different large-scale experimental approaches used to discover protein–protein interactions. Single PPI validation techniques such as co-immunoprecipitation or fluorescence methods are then presented because they are becoming more and more integrated in a global PPI discovery strategy.

Understanding gene function at the molecular level requires characterization of protein–protein interactions. Formation of multiprotein complexes is a dynamic process, where the composition of the complex is altered to allow physiological interactions to take place. To obtain a deep understanding of such processes it is necessary to combine a number of experimental approaches. Most of these processes are driven by technologies and assays allowing automatization and parallelization of the experiments. In addition, we believe that a detailed analysis is still necessary to gain a real understanding of how proteins interact and the way they exchange their information.

Proteins are modified with a wide variety of diverse chemical groups, such as phosphate or amino groups. Stimuli of cells results in an altered modification of proteins. Every modification adds information to the proteins. That information is transformed via protein–protein interaction through the cell and results in a specific response. This means that of each protein a number of differently modified forms exist with clearly defined interaction partners and duties.

In contrast to DNA and RNA, proteins cannot be amplified to achieve sufficient amounts of material to analyze. The success of high-throughput DNA sequencing projects followed by techniques like DNA microarrays and second-generation sequencing approaches is determined by the physical and chemical behavior of DNA.

The wide spectrum of techniques dealing with protein–protein interaction provided us with the opportunity to choose the most interesting and relevant ones. Therefore, the book focuses on certain aspects ranging from sample extraction to different methods of interaction measurements. With this background we asked researchers from different universities and departments to write about their experiences in handling and achieving their aims.

In part, this book has been written as a recruiting guide as new generations of researchers are needed to move interactomics forward. An increased knowledge in this field would help in fighting the main diseases by confirmation of diagnosis and specifically targeted drug delivery.

The book owes its existence to the contributions of many people. We would like to thank Springer-Verlag for their interest in this topic and for continued support and help during the preparation of this volume, especially Dr. Marion Hertel, Chemistry Editor, and Ms. Ulrike Kreusel, Chemistry Desk Editor. We

would also like to thank the scientists who spent their time in preparing up-to-date chapters allowing an in-depth view into the individual techniques. Finally, we would like to acknowledge all colleagues who made this book possible.

Habent sua fata libelli!

In this spirit, we hope that much of what you will learn from this book will be useful in understanding many aspects of bioanalytics.

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