NEUROMETHODS

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Current Proteomic Approaches Applied to Brain Function

Edited by

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Preface to the Series

Experimental life sciences have two basic foundations: concepts and tools. The *Neuromethods* series focuses on the tools and techniques unique to the investigation of the nervous system and excitable cells. It will not, however, shortchange the concept side of things as care has been taken to integrate these tools within the context of the concepts and questions under investigation. In this way, the series is unique in that it not only collects protocols but also includes theoretical background information and critiques which led to the methods and their development. Thus it gives the reader a better understanding of the origin of the techniques and their potential future development. The *Neuromethods* publishing program strikes a balance between recent and exciting developments like those concerning new animal models of disease, imaging, in vivo methods, and more established techniques, including, for example, immunocytochemistry and electrophysiological technologies. New trainees in neurosciences still need a sound footing in these older methods in order to apply a critical approach to their results.

Under the guidance of its founders, Alan Boulton and Glen Baker, the *Neuromethods* series has been a success since its first volume published through Humana Press in 1985. The series continues to flourish through many changes over the years. It is now published under the umbrella of Springer Protocols. While methods involving brain research have changed a lot since the series started, the publishing environment and technology have changed even more radically. Neuromethods has the distinct layout and style of the Springer Protocols program, designed specifically for readability and ease of reference in a laboratory setting.

The careful application of methods is potentially the most important step in the process of scientific inquiry. In the past, new methodologies led the way in developing new disciplines in the biological and medical sciences. For example, Physiology emerged out of Anatomy in the nineteenth century by harnessing new methods based on the newly discovered phenomenon of electricity. Nowadays, the relationships between disciplines and methods are more complex. Methods are now widely shared between disciplines and research areas. New developments in electronic publishing make it possible for scientists that encounter new methods to quickly find sources of information electronically. The design of individual volumes and chapters in this series takes this new access technology into account. Springer Protocols makes it possible to download single protocols separately. In addition, Springer makes its print-on-demand technology available globally. A print copy can therefore be acquired quickly and for a competitive price anywhere in the world.

Wolfgang Walz

Preface

Genome-wide analyses of the brain transcriptome have revealed specific regional transcriptional signatures that are regulated in a spatiotemporal manner. In particular, translational and post-translational regulatory events are localized to specific neuronal cell lineages and subcellular organelles, leading to specific activities based on discrete profiles of protein expression. Due to the complexity of the structural and molecular organization of the brain, characterization of protein profiles within specific regions and cellular structures forms an essential part of unearthing the molecular basis for structure specialization and perturbation associated with neuropsychiatric disorders and neurodegenerative diseases.

During the last years, the application of mass spectrometry-based quantitative proteomics to the central nervous system has emerged as a powerful strategy to profile neuronal proteomes in normal and pathological states, increasing our understanding of human brain biology. The themes discussed within this book (*Current Proteomic Approaches Applied to Brain Function*) will be mainly focused on protein analysis, encompassing a wide spectrum of the utility of mass spectrometry within neurobiological disciplines. Specifically, this book will bring a collection of detailed protocols written by experienced professionals around the world to cover a variety of mass spectrometry-based approaches used in neuroproteomics. Chapters will include label (iTRAQ, TMT, protein arrays) and label-free workflows (SWATH, MALDI imaging, and label-free quantitation). Moreover, additional chapters will focus on experimental strategies targeted to the identification and quantitation of specific lipids, and post-translational modifications (phosphorylation, glycosylation, ubiquitination, sumoylation, and nitrosylation) as well as proteomic workflows focused on the characterization of subcellular proteomes in order to achieve finer cellular and subcellular resolution in proteomic studies of neural tissues. All these approaches useful to quantify neuroproteomes, identify post-translational modifications, and characterize protein networks and interactomes are beginning to shed new light on the metabolic regulation that occurs in neurological disorders at cerebral level. Finally, several chapters will describe different bioinformatic pipelines useful to analyze and integrate the molecular information derived from high-throughput transcriptomic and proteomic experiments performed in brain tissue.

We consider that this book will be a useful resource for graduate students or junior postdoctoral fellows interested in starting a journey in neuroproteomics, as well as established researchers seeking valuable insight into the growing utility of mass spectrometry in neuroscience.

Pamplona, Spain

Enrique Santamaría
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