

# 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*

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## 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 post-doctoral 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  
Joaquín Fernández-Irigoyen*

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# Contents

<i>Preface to the Series</i> .....	v
<i>Preface</i> .....	vii
<i>Contributors</i> .....	xiii

## PART I INTRODUCTION

1 Brain Proteomics: Decoding Neuroproteomes Using Mass Spectrometry .....	3
<i>Joaquín Fernández-Irigoyen and Enrique Santamaría</i>	

## PART II LABELING METHODS IN NEUROPROTEOMICS

2 Applications of Amine-Reactive Tandem Mass Tags (TMT) in Human Neuroproteomics .....	11
<i>Linnéa Lagerstedt, Leire Azurmendi, and Jean-Charles Sanchez</i>	
3 Application of Isobaric Tags for Relative and Absolute Quantitation (iTRAQ) to Monitor Olfactory Proteomes During Alzheimer's Disease Progression.....	29
<i>Andrea González Morales, Mercedes Lachén-Montes, María Ibáñez-Vea, Enrique Santamaría, and Joaquín Fernández-Irigoyen</i>	
4 Protein Microarrays in Neurodegenerative Diseases .....	43
<i>Pablo San Segundo-Acosta, María Garranzo-Asensio, Ana Montero-Calle, Carmen Oeo-Santos, Mayte Villalba, Ana Guzman-Aranguez, and Rodrigo Bardeas</i>	

## PART III LABEL-FREE METHODS IN NEUROPROTEOMICS

5 Comprehensive Shotgun Proteomic Analyses of Oligodendrocytes Using Ion Mobility and Data-Independent Acquisition .....	65
<i>Juliana S. Cassoli and Daniel Martins-de-Souza</i>	
6 Nontargeted Brain Lipidomic Profiling Performed by UPLC-ESI-qToF-MS/MS .....	75
<i>Alba Naudí, Rosanna Cabré, Mariona Jové, and Reinald Pamplona</i>	
7 Methods for Human Olfactory Bulb Tissue Studies Using Peptide/Protein MALDI-TOF Imaging Mass Spectrometry (MALDI-IMS) .....	91
<i>Ibon Iloro, Joaquín Fernández-Irigoyen, Iraide Escobes, Mikel Azkargorta, Enrique Santamaría, and Felix Elortza</i>	
8 Neuroproteomics Using Short GeLC-SWATH: From the Evaluation of Proteome Changes to the Clarification of Protein Function.....	107
<i>Sandra I. Anjo, Cátia Santa, Susana C. Saraiva, Karolina Freitas, Faraj Barah, Bruno Carreira, Inês Araújo, and Bruno Manadas</i>	

PART IV MASS SPECTROMETRY-BASED NEUROPROTEOMICS TO ANALYZE  
POST-TRANSLATIONAL MODIFICATIONS

- 9 Analysis of Brain Phosphoproteome Using Titanium Dioxide  
Enrichment and High-Resolution LC-MS/MS ..... 141  
*Jeffrey M. Sifford, Haiyan Tan, Hong Wang, and Junmin Peng*
- 10 N-Glycomics and N-Glycoproteomics of Human Cerebrospinal Fluid ..... 161  
*Sophie Cholet, Arnaud Goyallon, Christophe Junot, and François Fenaille*
- 11 In Vivo Strategies to Isolate and Characterize the Neuronal  
Ubiquitinated Proteome ..... 179  
*Juanma Ramirez, Nagore Elu, Aitor Martinez, Benoit Lectez,  
and Ugo Mayor*
- 12 Characterization of the Phosphoproteome and Sialoproteome  
in Brain Tissues by Mass Spectrometry ..... 191  
*María Ibáñez-Vea, Stefan J. Kempf, and Martin R. Larsen*
- 13 Proteomic Analysis of SUMOylation in the Post-ischemic Brain ..... 207  
*J. Will Thompson, Meng Jiang, and Wei Yang*
- 14 S-Nitrosylation in Alzheimer's Disease Using Oxidized  
Cysteine-Selective cPILOT..... 225  
*Ryan R. Dyer, Liqing Gu, and Renā A.S. Robinson*

PART V SUBCELLULAR NEUROPROTEOMICS

- 15 Proteomic Analysis of Extracellular Vesicles in Neurological Diseases ..... 245  
*Matías Sáenz-Cuesta, Enrique Santamaría, Joaquin Fernández-Irigoyen,  
and David Otaegui*
- 16 Quantitative In-Depth Profiling of the Postsynaptic Density Proteome  
to Understand the Molecular Mechanisms Governing Synaptic  
Physiology and Pathology ..... 255  
*Rita Reig-Viader and Alex Bayés*
- 17 Nuclear Proteomics for Exploring MK-801-Treated Oligodendrocytes  
to Better Understand Schizophrenia..... 281  
*Aline G. Santana, Giuliana S. Zuccoli, Verónica M. Saia-Cereda,  
Juliana S. Cassoli, and Daniel Martins-de-Souza*
- 18 Localized Proteomics of Individual Neurons Isolated from  
Formalin-Fixed, Paraffin-Embedded Tissue Sections Using Laser  
Capture Microdissection ..... 289  
*Eleanor Drummond, Shrutti Nayak, Beatrix Ueberheide,  
and Thomas Wisniewski*

## PART VI BIOINFORMATICS

19	Creation of Reusable Bioinformatics Workflows for Reproducible Analysis of LC-MS Proteomics Data.....	305
	<i>Julian Uskoreit, Maike Abrens, Katalin Barkovits, Katrin Marcus, and Martin Eisenacher</i>	
20	Integration of Transcriptomic and Proteomic Data for Disease Insights .....	325
	<i>Ravi Sirdeshmukh, Savita Jayaram, Manoj Kumar Gupta, Pranali Sonpatki, Manika Singh, Raksha A. Ganesh, Chaitra B. Amaresha, and Nameeta Shah</i>	
	<i>Index</i> .....	357



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