



Analysis of Post-Translational Modifications and Proteolysis in Neuroscience [

Grant, Jennifer Elizabeth.,
editor
Li, Hong.,
editor

Springer New York :
Imprint: Humana Press,
2016

Monografía

This volume highlights proteomics studies of quantitative PTM changes in both peripheral and central nervous system proteomes utilizing the most recent advances in mass spectrometry. Chapters include practical information pertaining to the fundamentals of sample preparation, liquid chromatography, and tandem mass spectrometry instrumental analysis and will elucidate best practices in the interpretation of data using modern bioinformatics approaches. Written for the popular Neuromethods series, chapters include the kind of detail and key implementation advice that ensures successful results in the laboratory. Authoritative and practical, Analysis of Post-Translational Modifications and Proteolysis in Neuroscience aims to ensure successful results in the further study of this vital field

<https://rebiunoda.pro.baratznet.cloud:28443/OpacDiscovery/public/catalog/detail/b2FpOmNlbGVicmF0aW9uOmVzLmJhcmF0ei5yZW4vMTgwNzAxMDI>

Título: Analysis of Post-Translational Modifications and Proteolysis in Neuroscience Recurso electrónico-En línea] edited by Jennifer Elizabeth Grant, Hong Li

Edición: 1st ed. 2016

Editorial: New York, NY Springer New York Imprint: Humana Press 2016

Descripción física: XV, 290 p. 49 illus., 29 illus. in color. online resource

Tipo Audiovisual: Medicine Neurosciences Biomedicine Neurosciences

Mención de serie: Neuromethods 0893-2336 114

Documento fuente: Springer eBooks

Nota general: Springer Protocols (Springer-12345)

Contenido: Proteomic Analysis of Post-Translational Modifications in Neurobiology -- A Boronic Acid-based Enrichment for Site-specific Identification of the N-glycoproteome using MS-based Proteomics -- Site-specific

Localization of D-Amino Acids in Bioactive Peptides by Ion Mobility Spectrometry -- Quantitative Profiling of Reversible Cysteine Modification under Nitrosative Stress -- Label-free LC-MS/MS Comparative Analysis of Protein S-nitrosylation in Synaptosomes from Wild Type and APP Transgenic Mice -- Proteomics Identification of Redox-Sensitive Nuclear Protein Targets Of Human Thioredoxin 1 from SHSY-5Y Neuroblastoma Cell Line -- Identification and Quantification of K63-Ubiquitinated Proteins in Neuronal Cells by High-Resolution Mass Spectrometry -- Phosphorylation Site Profiling of NG108 Cells Using Quadrupole/Orbitrap Mass Spectrometry -- Phosphoproteomics of Tyrosine Kinases in the Nervous System -- Analysis of PINK1 and CaMKII Substrates Using Mass Spectrometry-Based Proteomics -- Liquid Chromatography-Tandem Mass Spectrometry Analysis of Tau Phosphorylation -- Identification of Protease Substrates in Complex Proteomes by iTRAQ-TAILS -- Proteolytic Processing of Neuropeptides -- Isotope Dilution Analysis of Myelin Basic Protein Degradation after Brain Injury -- Identification and Characterization of Protein Post-Translational Modifications by Differential Fluorescent Labeling -- Mass Spectrometric Detection of Detyrosination and Polyglutamylation on the C-Terminal Region of Brain Tubulin -- Determination of polyhydroxybutyrate (PHB) Post-Translational Modifications of Proteins Using Mass Spectrometry. .

Restricciones de acceso: Accesible sólo para usuarios de la UPV

Tipo recurso electrónico: Recurso a texto completo

Detalles del sistema: Forma de acceso: Web

ISBN: 9781493934720

Autores: Grant, Jennifer Elizabeth., editor Li, Hong., editor

Entidades: SpringerLink (Servicio en línea)

Enlace a formato físico adicional: Printed edition 9781493934706

Punto acceso adicional serie-Título: Neuromethods 0893-2336 114

Baratz Innovación Documental

- Gran Vía, 59 28013 Madrid
- (+34) 91 456 03 60
- informa@baratz.es