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Titolo	Mass Spectrometry: Developmental Approaches to Answer Biological Questions // by Gwenael Pottiez
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Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references.
Nota di contenuto	General and most usual proteomics methods based on mass spectrometry analysis: Protein identification and protein quantification -- Direct analysis of tissues and body fluids -- Mass spectrometry in archaeology -- Determination and quantification of post-translational modifications -- Protein-Protein interaction determined by mass spectrometry -- Protein structure analysis -- Determination of protein function by mass spectrometry -- Computer-assisted data analysis and data mining for new applications.
Sommario/riassunto	The understanding of the events taking place in a cell, a biological fluid or in any biological system is the main goal of biology research. Many fields of research use different technology to assess those events. Mass spectrometry is one of those techniques and this undergoes constant evolution and adaptation to always enhance the accuracy of the information provided. Proteomics provides a large panel of data

on protein identity and protein expression that were made possible by mass spectrometry. For several years now mass spectrometry has become central to performing proteomic research, however this powerful tool is under constant evolution to be more sensitive and more resolute. More importantly mass spectrometry became a field of research focusing on new applications. Indeed, the complexity in biological systems relies on the changes of expression of transcription of proteins but also on the post-translational modification of proteins, the structure of proteins and the interaction between proteins, amongst others. As of now, several investigations tried to improve the quantification of proteins by mass spectrometry, the determination of post-translational modifications, the protein-protein and protein-nucleic acids interaction or the proteins structures. This book is structured as follows: after a brief introduction of the usual and most popular applications for mass spectrometry in proteomics, the most recent research and developments in mass spectrometry-based methodologies will be explored.
