

1. Record Nr.	UNINA9910132256203321
Titolo	Analyzing biomolecular interactions by mass spectrometry // edited by Jeroen Kool and Wilfried M. A. Niessen
Pubbl/distr/stampa	Weinheim, Germany : , : Wiley-VCH Verlag GmbH & Co., , 2015 ©2015
ISBN	3-527-67341-5 3-527-67342-3 3-527-67339-3
Descrizione fisica	1 online resource (403 p.)
Disciplina	572.33
Soggetti	Biomolecules - Analysis Chemistry, Analytic - Quantitative
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	<p>             ""Analyzing Biomolecular Interactions by Mass Spectrometry"";              ""Contents""; ""List of Contributors"";              ""Preface""; ""Abbreviations""; ""Chapter 1              Introduction to Mass Spectrometry, a Tutorial              ""; ""1.1 Introduction""; ""1.2 Figures of Merit              ""; ""1.2.1 Introduction""; ""1.2.2 Resolution              ""; ""1.2.3 Mass Accuracy""              ""1.2.4 General Data Acquisition in MS              """"1.3 Analyte Ionization""; ""1.3.1 Introduction              ""; ""1.3.2 Electrospray Ionization""; ""1.3.3              Matrix-Assisted Laser Desorption Ionization              ""; ""1.3.4 Other Ionization Methods""; ""1.3.5              Solvent and Sample Compatibility Issues              ""              ""1.4 Mass Analyzer Building Blocks""""1.4.1              Introduction""; ""1.4.2 Quadrupole Mass Analyzer              ""; ""1.4.3 Ion-Trap Mass Analyzer""; ""1.4.4              Time-of-Flight Mass Analyzer""; ""1.4.5              Fourier Transform Ion Cyclotron Resonance Mass Spectrometer           </p>

""; ""1.4.6 Orbitrap Mass Analyzer	""
""1.4.7 Ion Detection Spectrometry	""""1.5 Tandem Mass Spectrometry
in-Time"" and ""Tandem-in-Space""	""; ""1.5.1 Introduction: ""Tandem-
""; ""1.5.2 Ion Dissociation Techniques	"";
""1.5.3 Tandem Quadrupole MS-MS Instruments	"";
""; ""1.5.4 Ion-Trap MS n Instruments	""; ""1.5.5
Tandem TOF (TOF-TOF) Instruments	""
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""""1.5.7 MS-MS and MSn in FT-ICR-MS	"";
""1.5.8 Orbitrap-Based Hybrid Systems	"";
""1.5.9 Ion-Mobility Spectrometry-Mass Spectrometry	"";
""; ""1.6 Data Interpretation and Analytical Strategies	"";
""; ""1.6.1 Data Acquisition in MS Revisited	""
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""1.6.2 Quantitative Bioanalysis and Residue Analysis	""

## Sommario/riassunto

This monograph reviews all relevant technologies based on mass spectrometry that are used to study or screen biological interactions in general. Arranged in three parts, the text begins by reviewing techniques nowadays almost considered classical, such as affinity chromatography and ultrafiltration, as well as the latest techniques. The second part focusses on all MS-based methods for the study of interactions of proteins with all classes of biomolecules. Besides pull down-based approaches, this section also emphasizes the use of ion mobility MS, capture-compound approaches, chemical proteomi