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""; ""1.4.6 Orbitrap Mass Analyzer	""
""1.4.7 Ion Detection Spectrometry	""""1.5 Tandem Mass Spectrometry
""; ""1.5.2 Ion Dissociation Techniques	""; ""1.5.1 Introduction: ""Tandem-in-Time"" and ""Tandem-in-Space""
""1.5.3 Tandem Quadrupole MS-MS Instruments	"";
""; ""1.5.4 Ion-Trap MS n Instruments	""; ""1.5.5 Tandem TOF (TOF-TOF) Instruments
""1.5.6 Hybrid Instruments (Q-TOF, Q-LIT, IT-TOF)	""
""""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