



Analyzing Biomolecular Interactions by Mass Spectrometry

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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 proteomics and interactomics. The third and final part discusses other important technologies frequently employed in interaction studies, such as biosensors and microarrays. For pharmaceutical, analytical, protein, environmental and biochemists, as well as those working in pharmaceutical and analytical laboratories.

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Editorial Review

Review

"Illustrated with beautiful artwork, the book presents a combination of topics that will be useful to inspire new work." (Analytical and Bioanalytical Chemistry 2016)

From the Back Cover

This monograph reviews all relevant technologies based on mass spectrometry that are used to study or screen biological interactions in general. Different distinct areas for analysis of bioaffinity interactions can be recognized in this regard. These areas include pre-column based ligand trapping followed by MS analysis, affinity chromatography following MS and post column on-line affinity profiling. Other methodologies relate to separately performed bioassays and (LC) MS analysis. Besides these, direct approaches are nowadays also used in several research areas and include direct MS based bioassays and native MS studies in which the latter looks at intact protein complexes in the gas phase.

About the Author

Jeroen Kool focused on the integration of chemical and biochemical detection after separation methodologies during his PhD study at the VU University Amsterdam. Following his PhD, he was responsible for target evaluation, hit screening and identification, and lead optimization processes at Kiadis Pharma. He continued his academic career in 2005 as a postdoc in the Biomolecular Mass Spectrometry group in Utrecht working on proteomics and biomarker discovery. From 2007 to present, he is responsible for the research line Bioanalytical Screening Methodologies at the VU University Amsterdam with a particular focus on hyphenated analytical techniques combining mass spectrometry and chromatography with novel bioassay techniques for bioactive mixture analysis. He published over 50 peer reviewed articles and one book chapter.

Wilfried M.A. Niessen studied chemistry at the VU University Amsterdam. After his PhD, he worked for 9 years as an analytical chemist within the Leiden/ Amsterdam Center for Drug Research at Leiden University. After leaving the university in 1996, he started the company hyphen MassSpec, providing independent consultancy and training in the field of analytical mass spectrometry. In parallel to this, he was extraordinary professor in bioanalytical mass spectrometry at the Faculty of Science of the VU University Amsterdam between 2002 and 2014. There, he was involved in high-resolution screening and the role of MS therein. His main research interests involve principles, instrumentation and applications of liquid chromatography-mass spectrometry as well as interpretation of small-molecule MS-MS mass spectra. He is (co)author of more than 200 peer reviewed publications in the field of LC-MS and more than 40 book chapters. Wilfried Niessen authored and edited five books, and was guest editor on several special journal issues.

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