

Mass Spectrometry in Proteomics: Technologies, Methods, and Research Applications for the Life Sciences

Paolo Nanni, Peter Gehrig, Ralph Schlapbach

Functional Genomics Center Zurich, University of Zurich / ETH Zurich
Winterthurerstrasse 190, 8057 Zurich, Switzerland
paolo.nanni@fgcz.uzh.ch

Mass spectrometry (MS) has evolved from a technology to characterize small chemical molecules to an indispensable tool in the hands of researchers in all life sciences. Thanks to their analytical power and versatility, MS-based methods enable the investigation of proteins, peptides, metabolites, lipids, glycans, and biomolecules in general. Many life science studies involve MS at some step, either to check the quality of molecules (i.e., identity of a protein), to characterize them in detail (i.e., glycan profiling of an antibody), to discover new markers for biological processes (i.e., metabolites involved in a specific disease), or to validate findings obtained by other analytical means (i.e., increased level of specific protein post-translational modifications). Mass spectrometry is increasingly relevant also in the biopharmaceutical sector, where the filing of new biotechnological products follows detailed characterization procedures.

Given its broad range of applications, MS is a field of research and technology development on its own, with branches concentrating on different life science disciplines, and more specifically on distinct types of biomolecules and applications. Examples of these disciplines are proteomics, metabolomics, lipidomics and glycomics, which focus on the large-scale studies of proteins, metabolites, lipids and glycans, respectively. The analysis of these classes of biomolecules requires different analytical workflows and instrument capabilities, but also distinct technical and scientific expertise.

In this lecture^[1], we will discuss the most important technological and analytical developments that shaped the field of life science mass spectrometry, with a particular focus on the field of proteomics. We will provide examples on how proteomics is applied to unravel cellular mechanisms, to analyze protein interaction networks, or to characterize protein structures. We will also comment on the importance of data analysis and bioinformatics.

[1] P. Nanni, P. Gehrig, R. Schlapbach *Chimia*, **2022**, 76, 73