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Proteomics through integrated MALDI and ESI

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The proteome is far more complex than it was ever expected at the genesis of the proteomics revolution. Dynamics in time, space and concentration as well as variability due to modifications and mutations require novel and complementary approaches to generate useful, reliable and complete information. As it turns out, there is no single platform able to unravel the proteome in its full complexity.

Here we present a multi-tier approach to turn proteomic data into knowledge based on the combination of LC- MALDI-TOF and LC-ESI based technology for identification, quantification, characterization and localization of proteins combined with software tools for integration of different technology platforms allowing querying and reporting according to generally accepted guidelines.

The data presented covers top-down as well as bottom-up analysis and shows ways to increase the proteome coverage in terms of identified peptides and their inferred proteins. Further information is obtained by the characterization of the proteins regarding their posttranslational modifications such as phosphorylation or glycosylation. We will also describe new tools for the comprehensive analysis of glycans and glycopeptides parallel to unmodified peptides. We will demonstrate how quantitative information using labelfree as well as label-based approaches can be obtained and turned into comparative data for in-depth sample analysis. As MALDI-TOF also allows for obtaining spatially resolved information directly from tissue, we will show an example for a workflow where differences between different cancer types had been identified using MALDI-TOF imaging in combination with statistical analysis and subsequent identification of a protein cancer biomarker could be obtained using ETD ion trap tandem mass spectrometry.