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# Perspectives for Imaging Mass Spectrometry in the Proteomics Landscape

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Proteomics, 2009, 9 (4), 819-834

A number of techniques are used in the field of proteomics that can be combined to get the most molecular information from a specific biological sample, fluid or tissue. Imaging techniques are often used to obtain local information from tissue samples. However, imaging experiments are often staining experiments, which rely on specific or aspecific interactions between fluorescent markers and pre-defined (families of) peptide or protein. Therefore, imaging is often used as a screening or validation tool for the local presence of proteins that have been identified by other means. Imaging mass spectrometry (IMS) combines the advantages of MS and microscopy in a single experiment. It is a technique that does not require any labeling of the analytes and provides a high multiplexing capability combined with the potential for analyte identification. It enables simultaneous detection of potentially all peptides and proteins present at a tissue surface and is used for the determination and identification of tissue-specific disease markers. The workflows of IMS experiments closely resemble those of conventional proteomics. In this review, we describe IMS experiments step-by-step to position and evaluate the role of IMS in a comparative proteomics landscape. We illustrate in a concise review that IMS is a true discovery oriented tool for proteomics that seamlessly integrates in conventional proteomics workflows and can be perceived as either an alternative or complementary proteomics technique.

<http://dx.doi.org/10.1002/pmic.200800363>