

**EU-Projekt:
New Microfluidic Mass Spectrometry Technologies
for High Performance Proteomics**

Projektleiter: Prof. Dr. Michael Przybylski

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This project aims at providing high performance proteome analysis by developing a fully automated system based on integrated microfluidics. Biological fluids will be prefractionated by protein isoelectric points using mini-segmented focusing chambers. Proteins will then be automatically driven into a microchip to be separated according to mass and affinity in micro sieving matrices, and injected into a high resolution mass spectrometer by a microchip-nanoelectrospray interface. This platform includes innovations in prefractionation, protein microseparation, matrices, microfluidics and MS interface; it will increase range and selectivity of proteome analysis, and improve analysis speed, sample economy and cost effectiveness. Initial applications will be assessed as model tasks. In the longer term, these technologies will also lead to improved miniaturized tools for protein-based diagnostics.

The objective of the project is to provide a novel analytical platform enabling the rapid and automated analysis of proteins from a complex biological matrix. The project is aimed at: 1/ increasing the efficiency of proteome analysis by miniaturization, automation and integration; 2/ extend the range of proteins amenable to analysis by novel solubilizing cocktails and multidimensional separation strategies; 3/ increase the information content by new separation criteria and direct hyphenation to ultra-high resolution FT-ICR mass spectrometry. Proteins with any isoelectric point, or high hydrophobicity, will be amenable to analysis. Analytical challenges such as differentiation of protein isoforms, correlation of protein structure and post-translational modifications, and of immunogenic activity with pathological properties will be addressed.