

## **SAMPLE AND DATA HANDLING FOR MALDI-TOF-BASED PROTEOME ANALYSIS**

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High Throughput proteome analysis on the multi-1000-analysis-per-day level with MALDI TOF depends on a whole sequence of critical abilities, including sample preparation and bioinformatics.

Sample preparation using hydrophobically coated targets containing 200-600  $\mu\text{m}$  hydrophilic anchor patches increase the sensitivity of the analysis by a factor of 10-100. The increased sensitivity and the confined sample area on the target enhance speed and performance of the automated spectra acquisition significantly. Furthermore, the overall information flow and software for Proteome and protein analysis is described, which combines automated procedures with very detailed and interactive procedures.

As a new approach to functional proteomics (protein structure factory), chemical crosslinking is combined with crosslink analyses in protein digests and bioinformatics. It is capable to establish 3D protein structures on the 2-5 Å level, based solely on mass spectrometric experimental data.

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