

Automation in Large-scale Proteomics: From Sample to Data Without Manual Intervention

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Abstract

MS-based proteomics is used more and more widely in research and clinical applications with cohorts of 100s to 1000s of samples. As the technology matures, the focus of development is broadening from depth of analysis to scalability and reproducibility, and compatibility with regulatory requirements for clinical samples. We present an approach towards full automation, consisting of robotized sample preparation, unified MS instruments and DIA methods, and orchestrated data analysis. Data quality is ensured by rigorous QC of instrument performance and independent qualification of each data file, and integrated in a GLP-based quality management system.