

Scientific presence at ASMS 2021

In addition to our booth, we are also
excited to promote all these abstracts



MP 001	SPIN – Species by Proteome INvestigation
MP 024	Evaluation of dia-PASEF for short gradient using library and library free approaches
MP 035	Opportunities and challenges for scaling quantitative proteomics studies with high-throughput DIA-MS
MP 038	Achieving high performance with EvoSep One using optimized analytical column configurations for Data-Independent Acquisition (DIA) using the Bruker timsTOF-MS instrument
MP 039	Rapid proteome analysis using DIA and super-resolution Orbitrap mass spectrometry
MP 162	Validation of an Automated Platform for In Cell Footprinting Studies
MP 176	Inference of Collisional Cross-Sections of peptides in an Orbitrap Mass Analyzer
MP 257	LiDIA-PASEF: A framework using experimental libraries for optimal acquisition of (phospho)proteomes by diaPASEF
TP 021	Deep and high-throughput urine proteomics profiling for the classification of Parkinson's disease patients
TP 050	Validation of an Automated Platform for In Cell Footprinting Studies
TOG pm	A complete and automated sample preparation strategy for high throughput and standardized proteomics
WP 028	Ultrafast bacterial detection in Urine using high-throughput proteomics and artificial intelligence
WP 171	Implementation of Data-independent Acquisition Parallel Accumulation-serial Fragmentation (dia-PASEF) to Investigate Accurate and Quantitative Biomarker Discovery in Human Myocardia-Demand Ischemia
WP 289	Detection of SARS-CoV-2 antigen and its variants from clinical specimens using mass spectrometry-based targeted assays
WP 299	High Throughput Plasma Glycated Proteome Profiling to Discover Cardiovascular Disease Biomarkers from the Epidemiology of Diabetes Interventions and Complications Study
WP 330	Beyond TurboTMT: Phi-SDM Super-resolution Methods for Next-generation Highly-multiplexed Quantitative Ultrasensitive and Single-Cell Proteomics via TMTPro Complement Ion Deconvolution
ThP 006	New LC-MS Platforms for Primary and High-Order Structural Characterization of a Biotherapeutic Immunocaptured from Serum
ThOE am	Pre-formed gradients for high-throughput and robust nanoflow lipidomics with trapped ion mobility and PASEF
ThOB pm	Biomarkers: Quantitative Analysis – PRM-Studio: Improved data extraction and quality control of peptide PRM data for complex clinical samples
FP 101	Evaluation of LC-MS/MS Instrumentation for Targeted Analysis of SARS-CoV-2 Peptides
FP 110	Leveraging a Higher Duty Cycle DIA Acquisition On a Novel QTOF for Enhanced Proteomics Analysis
FP 111	In-depth proteome analysis of bronchoalveolar lavage fluid from a chronic obstructive pulmonary disease model using high throughput 4D-diaPASEF
FP 112	Using state of the art data independent acquisition (DIA) methods for protein identification in complex mixtures
FP 265	DeGlyPHER: an ultrasensitive method for analysis of viral spike N-glycoforms
FP 425	Ultra-sensitive proteome quantification on the timsTOF SCP mass spectrometer
FP 686	Advantages of a dynamic polygon for MHC class I and II immunopeptides
FP 706	Label-free quantification of oxidized peptides in eHAP cell lines via a high-throughput dia-PASEF workflow