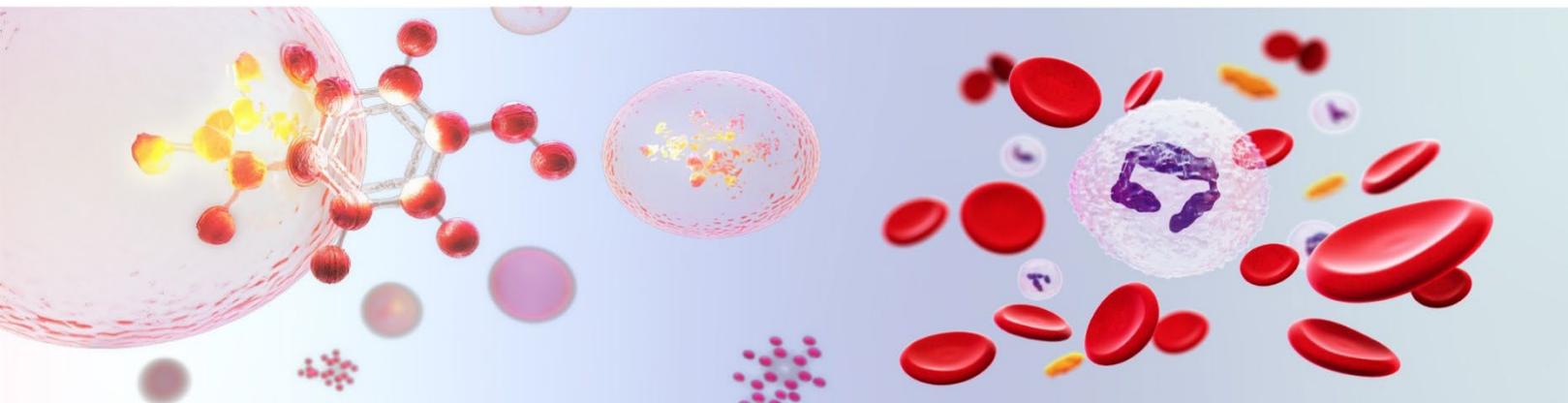


Discovery continuum seminar

Thursday, March 5, 2026 | 08:30 a.m. - 05:00 p.m.

IBBR | 9600 Gudelsky Dr. | Rockville, MD 20850



Join SCIEX and industry leaders for an in-depth seminar designed to address the most pressing challenges in drug discovery and development. This event covers the full spectrum of analytical solutions driving progress in pharma and biopharma.

Agenda:

- 8:30 a.m. Registration and breakfast
- 9:00 a.m. Welcome and introductions – Carl Schwarz and Josh Plath, SCIEX
- 9:10 a.m. Innovations in mass spectrometry and software: Unveiling the latest SCIEX advancements – Mahbod Hajivandi, SCIEX
- 9:40 a.m. Acoustic ejection mass spectrometry (AEMS) for rapid synthesis and direct-to-biology – Daniel Blair, St. Jude Children’s Research Hospital
- 10:10 a.m. Automated sample preparation and separation for high-throughput, reproducible proteomics – Banu Vignesh, Beckman Coulter
- 10:40 a.m. Coffee break
- 11:00 a.m. Drug discovery and ADME characterization through LC-MS/MS – Rana Rais, Johns Hopkins Drug Discovery
- 11:30 a.m. Nitrosamine analysis: Risk identification, characterization, and remediation – Jason Brown, ADARE Pharma Solutions
- 12:00 p.m. Validation of a direct MRM peptide panel for quantitation of cell death oncologic markers – Chelsea Boo, NIH
- 12:30 p.m. Lunch and networking
- 1:15 p.m. Quantification of oligonucleotides and GLP-1 peptides in biological matrices using QTOF HRMS - Lata Venkatarangan, QPS
- 1:45 p.m. Charge heterogeneity characterization and peak identification of complex protein therapeutics using the Intabio ZT icIEF-MS system – Mingjie Cui, Astra Zeneca
- 2:15 p.m. Evaluation of the next-generation BioPhase 8800 system with native fluorescence detection – Douglas Johnson, Astra Zeneca
- 2:45 p.m. Characterization of peptide therapeutics and conjugated protein modalities – Ramesh Indrakanti, Phenomenex
- 3:15 p.m. Closing remarks
- 3:30 p.m. Happy hour refreshments
- 5:00 p.m. Event adjourns



Register today: <https://sciex.li/discovery-continuum-MD>

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