2026 ASMS Regulated Bioanalysis Interest Group (RBIG) Workshop Report

1. Meeting Details

Session Title: Advantages of Using Mass Spectrometry Assays rather than Ligand Binding Assays for the Quantitation of Protein and Peptide Biomarkers

Event: Regulated Bioanalysis Interest Group Workshop, 74th ASMS Conference on Mass Spectrometry and Allied Topics

Date and Time: Wednesday, June 3, 2026, 5:45–7:00 pm

Location: Ballroom 20D, San Diego Convention Center, San Diego, California

Estimated Attendance: Approximately 200 participants

Presiding / Chairs: Dr. Fabio Garofolo; Dr. Jian Wang; Dr. Jessica McGregor; Dr. Wenkui Li (as listed in the workshop agenda)

2. Executive Summary

The Regulated Bioanalysis Interest Group workshop, "Advantages of Using Mass Spectrometry Assays rather than Ligand Binding Assays for the Quantitation of Protein and Peptide Biomarkers," took place on June 3, 2026, at the 74th ASMS Conference in San Diego, California. The session drew approximately 150–200 bioanalytical scientists from pharmaceutical companies, contract research organizations, and the broader mass spectrometry community.

The workshop explored the expanding use of LC-MS/MS and hybrid enrichment–LC-MS/MS workflows in regulated protein and peptide biomarker analysis. Speakers emphasized applications in which mass spectrometry can outperform traditional ligand binding assays (LBA), particularly when molecular specificity, selectivity, multiplexing, or differentiation of closely related analyte forms is critical.

The presentations and panel discussion positioned mass spectrometry as a fit-for-purpose tool that complements—and, in selected applications, can replace—ligand binding assays. Successful use in regulated settings requires appropriate assay design and enrichment, robust validation, and rigorous control of clinical sample collection and processing.

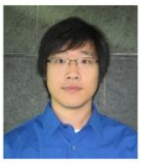
3. Workshop Objectives and Scope

The workshop compared mass spectrometry–based and ligand binding assays for regulated quantitation of protein and peptide biomarkers. Rather than positioning mass spectrometry as a universal replacement for LBA, the session identified practical applications in which LC-MS/MS, immunocapture LC-MS/MS, peptide immunoaffinity LC-MS/MS, or hybrid immunoprecipitation LC-MS offers distinct analytical advantages.

Topics included assay selectivity, endogenous analyte challenges, species specificity, surrogate peptide selection, immunoaffinity enrichment, target occupancy analysis, clinical sample handling, and fit-for-purpose validation.

4. Program Overview

Dr. Fabio Garofolo opened the workshop, followed by six brief presentations from Johnson & Johnson, Pfizer, Novartis, Frontage, Merck, and Bristol Myers Squibb, and a concluding panel discussion. Together, the presentations balanced broad bioanalytical principles with practical case studies.



Dr. Weixuan Chen (Johnson & Johnson) Associate director in the Bioanalytical Discovery & Development Sciences department of Johnson & Johnson at San Diego, CA (2015-present). Postdoc fellow at Georgia Institute of Technology. PhD in organic chemistry from Georgia State University. MS, BSc in organic chemistry from Tsinghua University. Experience in proteomics, lipidomics, small molecule and protein quantitation in several species and matrices using various LCMS platforms. Responsible for supporting discovery and development studies for PKPD and biomarkers.



Dr. Vahid Farrokhi is a Senior Principal Scientist and Team Lead in the Biomarker and Biomeasures group within Pfizer's PDM organization, based in Andover, Massachusetts. His work focuses on the development of mass spectrometry–based assays and advanced proteomics approaches to address questions around targets, and biotherapeutics target engagement to inform translational PK/PD modeling of biotherapeutics. Vahid earned his PhD in Chemistry from the University of Connecticut, where he developed quantitative and structural mass spectrometry techniques for the analysis of complex proteins and molecules.



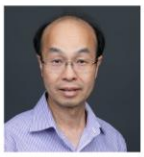
Dr. Jiekai Yin is a Senior Scientist II in the Analytics and Bioanalytics group at Novartis BioMedical Research in San Diego, California. She received her Ph.D. in Environmental Toxicology from the University of California, Riverside, where she developed expertise in mass spectrometry–based characterization of proteins, peptides, and nucleic acids, and her B.S. in Chemistry from the University of Science and Technology of China. At Novartis, her work focuses on large-molecule quantification and biotherapeutic characterization using LC–MS–based approaches, supporting pharmacokinetic, pharmacodynamic, and target engagement studies across diverse therapeutic programs.



Dr. Yong Zhou is a Principal Scientist and Subject Matter Expert in the Global Bioanalysis Services group at Frontage Laboratories in Hayward, California. He holds a Ph.D. in Biochemistry and Toxicology from Second Military Medical University in Shanghai, China, and a B.S. in Cell Biology and Genetics from Peking University in China. His expertise lies in the discovery of biomarkers using LC-MS/MS techniques for both small and large molecules, as well as in the development of laboratory-developed tests (LDTs) for human and veterinary diagnostics.



Dr. Li Sun is a Senior Principal Scientist in the Regulated Bioanalytics PK/ADA group at Merck, based in West Point, Pennsylvania. She holds a Ph.D. and M.S. in Analytical Chemistry from Rensselaer Polytechnic Institute (Troy, NY), and a B.S. in Chemistry from the University of Science and Technology of China. At Merck, Li has supported bioanalytical efforts spanning discovery, preclinical and clinical development, as well as drug submissions. Her current role focuses on cross-functional oversight of bioanalytical strategies for PK studies across diverse modalities.



Dr. Naiyu Zheng is a Scientific Associate Director in Precision Medicine, Bioanalytical & Translational Sciences (PMBATS) at Bristol Myers Squibb (BMS). He leads LC–MS-based assay development and validation to measure endogenous protein biomarkers for PK/PD and target engagement assessment in clinical studies. Since joining BMS in 2002, he has built extensive expertise in regulated LC–MS bioanalysis of small and large molecule therapeutics supporting IND, FIH, and NDA submissions. He holds a PhD from the University of Rhode Island and completed his postdoctoral training at University of Pennsylvania before joining BMS.

5. Speaker and Presentation Summaries

5.1 Introduction

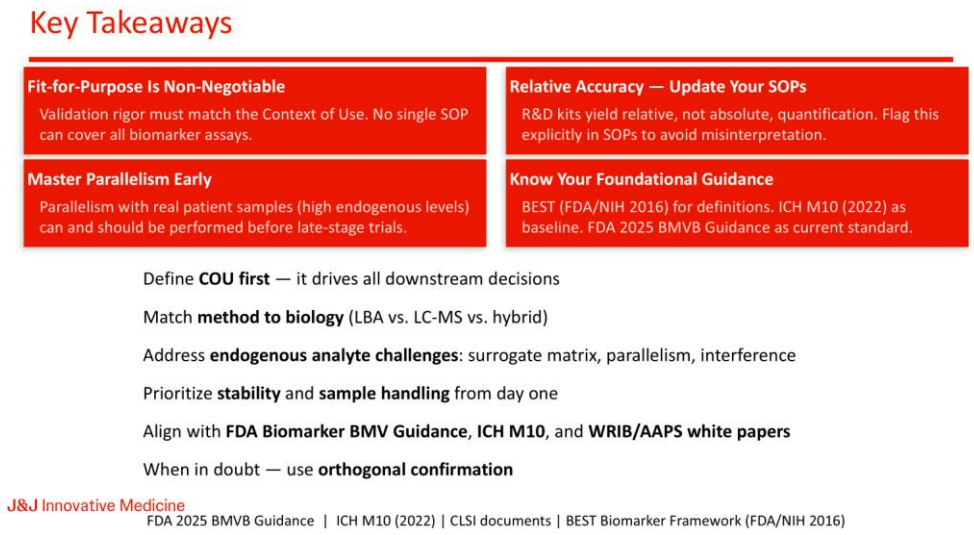
Speaker: Dr. Fabio Garofolo (BRI / Frontage)
Time: 5:45–5:48 pm

Dr. Garofolo framed the session around common challenges in quantifying protein and peptide biomarkers and highlighted how mass spectrometry can address limitations of ligand binding assays, including matrix interference, cross-reactivity, and difficulty distinguishing similar protein species.

5.2 Bioanalytical Method Considerations for Protein and Peptide Biomarker Analysis

Speaker: Dr. Weixuan Chen (Johnson & Johnson)
Time: 5:48–5:55 pm

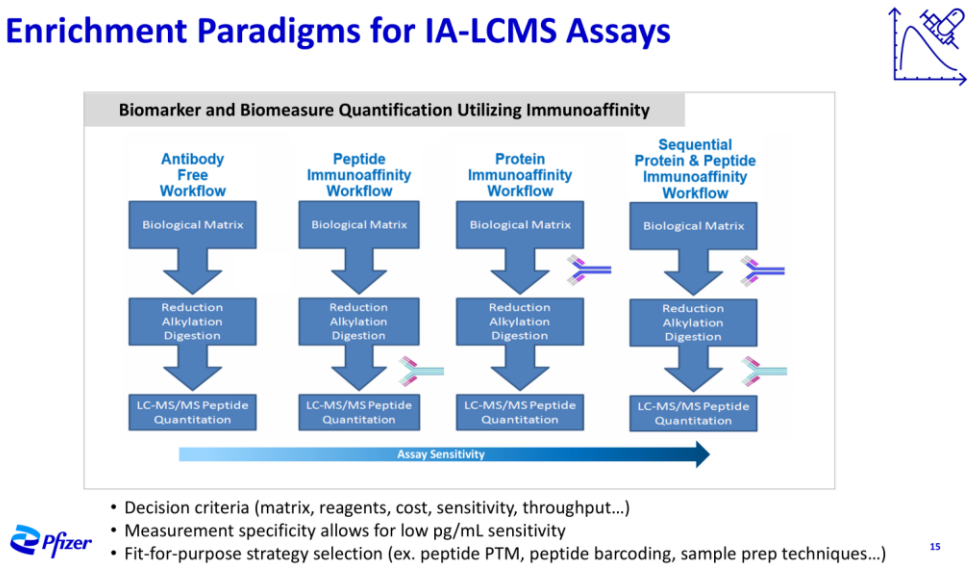
Dr. Chen of Johnson & Johnson outlined a framework for selecting and developing bioanalytical methods for protein and peptide biomarkers. The fit-for-purpose approach aligns assay selection with biomarker biology, sample matrix, sensitivity requirements, study objectives, and regulatory expectations. Key performance criteria include specificity, sensitivity, precision, accuracy, matrix effects, endogenous analyte interference, stability, reproducibility, and robustness.



5.3 Opportunities with Peptide Immunoaffinity Enrichments in Hybrid Mass Spectrometry Assays

Speaker: Dr. Vahid Farrokhi (Pfizer)
Time: 5:55–6:02 pm

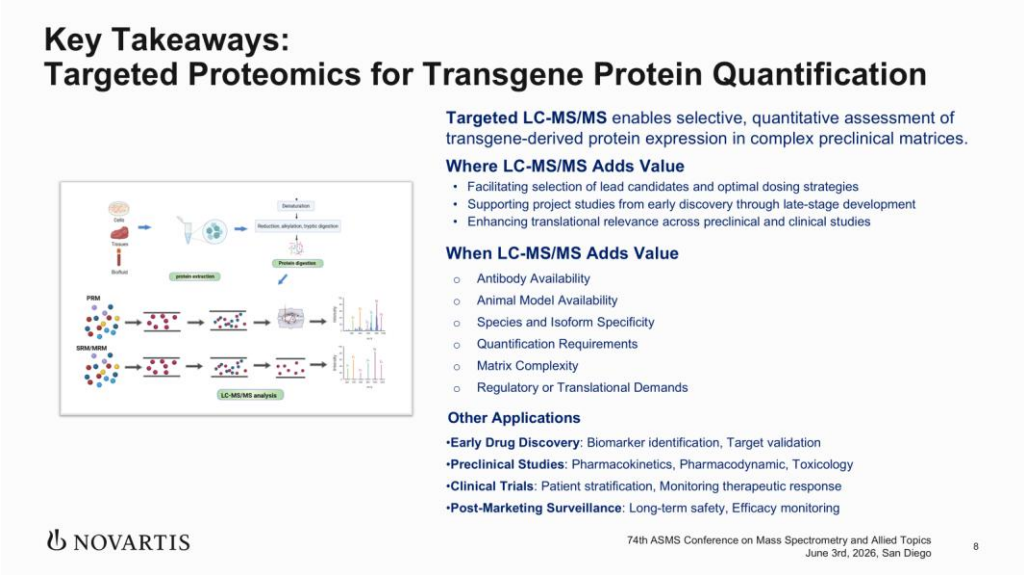
Dr. Farrokhi described peptide immunoaffinity enrichment as a means of increasing the sensitivity and selectivity of hybrid LC-MS/MS assays. Applications included measuring post-translational modification isoforms—nonphosphorylated, monophosphorylated, and diphosphorylated peptides—and multiplexed peptide barcode variants. The central message was that immunoaffinity enrichment enhances capture sensitivity, while LC-MS/MS provides the molecular resolution required for variant-specific quantitation.



5.4 Advantages of Mass Spectrometry over Ligand Binding Assays: Selective Quantitation of Transgene Proteins via LC-MS/MS

Speaker: Dr. Jiekai Yin (Novartis)
Time: 6:02–6:09 pm

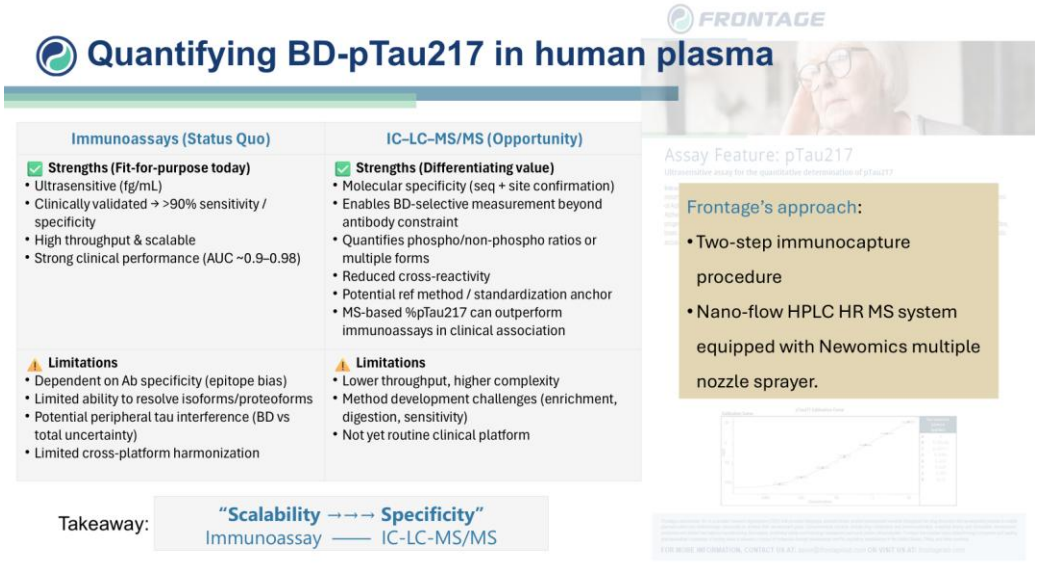
Dr. Yin of Novartis presented case studies showing how LC-MS/MS can selectively quantify transgene proteins and distinguish them from endogenous homologs. In a transgenic mouse model, sequence alignment enabled selection of surrogate peptides unique to human, mouse, non-human primate, or conserved protein regions, supporting species-specific and total quantitation. A second case involving an autocleaved protein used peptides from the N-terminal, middle, and C-terminal regions to separately measure intact protein, cleavage fragments, and total protein-related signal.



5.5 Advancing Bioanalysis with Immunocapture LC-MS/MS: From ADCs to Biomarkers and Therapeutic Antibodies

Speaker: Dr. Yong Zhou (Frontage)
Time: 6:09–6:16 pm

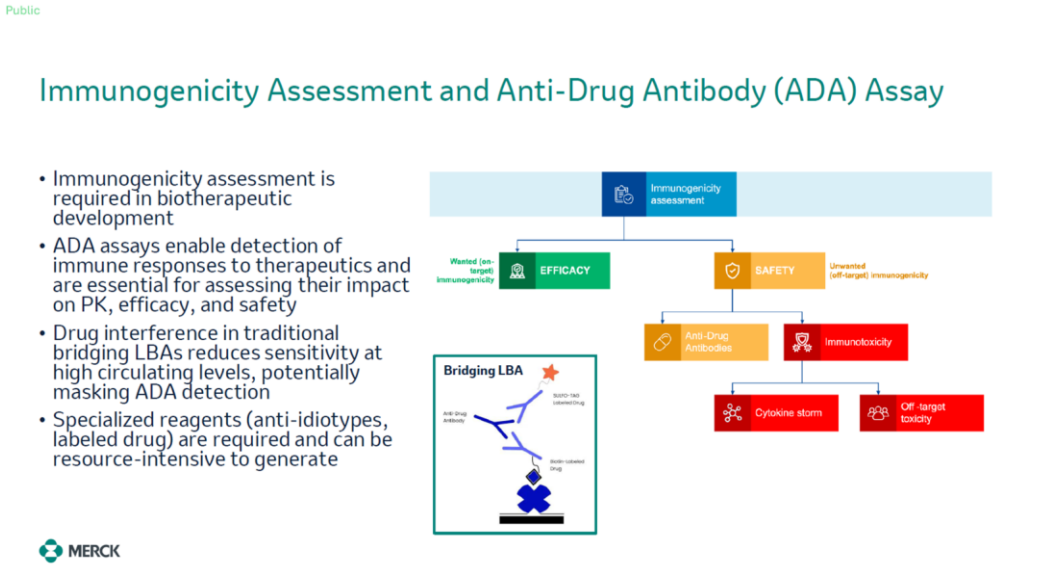
Dr. Zhou of Frontage reviewed immunocapture LC-MS/MS as a hybrid approach for analyzing antibody–drug conjugates, protein biomarkers, and therapeutic antibodies. Immunocapture enriches targets from complex matrices and reduces interference, while LC-MS/MS enables specific detection through unique peptide or molecular signatures. This approach is particularly valuable when ligand binding assays are constrained by cross-reactivity, reagent specificity, or limited ability to distinguish analyte forms.



5.6 Hybrid IP-LC-MS for Anti-Drug Antibody Assessment: Expanding Beyond Traditional Ligand-Binding Assays

Speaker: Dr. Li Sun (Merck)
Time: 6:16–6:23 pm

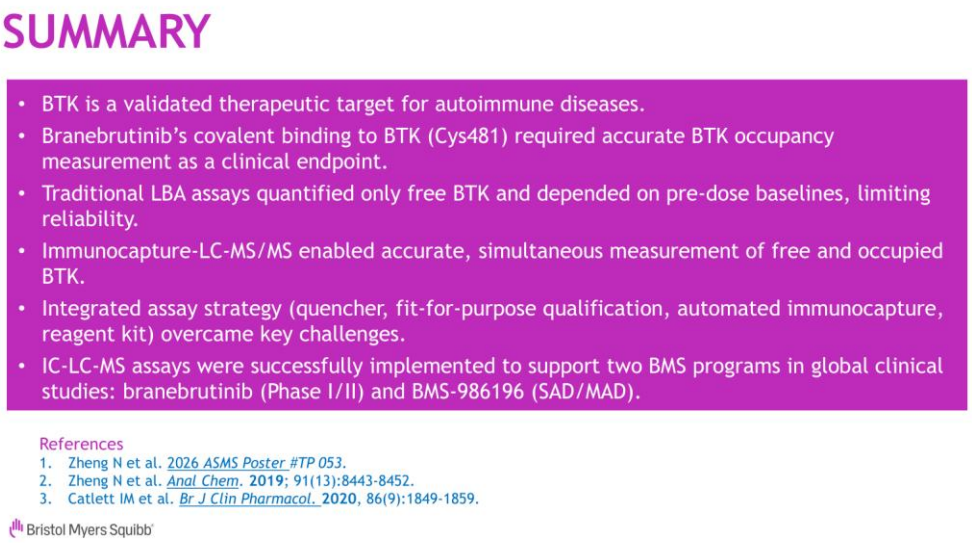
Dr. Sun of Merck presented hybrid immunoprecipitation LC-MS (IP-LC-MS) as a complementary method for anti-drug antibody (ADA) assessment. Unlike traditional ligand-binding ADA assays, which may be affected by drug interference, matrix effects, and limited specificity, hybrid IP-LC-MS enriches antibody-related species or immune complexes and uses MS for more specific detection. This approach can provide orthogonal confirmation and more detailed molecular characterization of the ADA response.



5.7 Immunocapture-LC-MS-Based Measurement of BTK Occupancy in Blood Lysate: Advantages, Challenges and Strategies to Support Clinical Studies

Speaker: Dr. Naiyu Zheng (Bristol Myers Squibb)
Time: 6:23–6:30 pm

Dr. Zheng of BMS presented an immunocapture LC-MS/MS assay for measuring BTK occupancy in blood lysate in support of clinical studies. Key challenges and mitigation strategies included controlling ex vivo conversion with a quencher; conducting fit-for-purpose validation using modified BTK calibrators and authentic quality controls; addressing limited sample volume and sensitivity through automated processing of larger lysate volumes with improved throughput; and reducing study variability through standardized on-site procedures for Phase I and pre-aliquoted, single-use reagent kits for global Phase II studies.



6. Panel Discussion Summary

The panel discussion (6:30–7:00 pm) integrated themes from the presentations and focused on practical decision-making around when mass spectrometry is preferred over ligand binding assays, and how MS can be used as an orthogonal or complementary technology. Panelists emphasized that MS is particularly valuable when molecular specificity is required—for example, differentiating homologous proteins, fragments, isoforms, post-translationally modified species, species-specific variants, transgene products, therapeutic antibodies, anti-drug antibodies, and target-occupancy biomarkers.

The panel also addressed implementation considerations in regulated bioanalysis, including matrix effects, endogenous background, reagent quality, assay transferability, clinical site sample handling, and fit-for-purpose validation strategies. The discussion reinforced the

importance of robust sample collection/stabilization procedures and the role of enrichment (immunocapture or peptide immunoaffinity) in achieving adequate sensitivity.

7. Key Themes and Scientific Takeaways

- Molecular specificity: LC-MS/MS can distinguish closely related forms that LBA may not resolve.
- Hybrid enrichment workflows—including immunocapture, immunoprecipitation, and peptide immunoaffinity—enhance sensitivity while retaining MS specificity.
- Fit-for-purpose development and validation are essential in regulated settings and should align with the assay's intended use.
- Successful clinical implementation requires operational controls, including standardized collection, appropriate stabilizers or quenchers, automation, and consistent quality-control strategies.
- MS provides powerful orthogonal confirmation and can clarify or refine results from ligand binding assays.

8. Conclusions

The workshop highlighted the growing role of LC-MS/MS and hybrid mass spectrometry in regulated protein and peptide biomarker analysis. Case studies showed that these methods can overcome key limitations of ligand binding assays, particularly when high specificity, species differentiation, or discrimination among fragments and isoforms is required.

Attendance of approximately 200 participants reflected strong interest in applying MS-based strategies to complex bioanalytical challenges. Speakers and panelists emphasized that MS complements LBA and offers distinct value when molecular resolution or orthogonal confirmation is needed.

9. Overall Significance

The workshop highlighted a broader shift in regulated bioanalysis toward integrated strategies rather than dependence on a single assay platform. Hybrid workflows combine affinity-based enrichment with mass spectrometric detection, leveraging the complementary strengths of ligand binding and LC-MS/MS. As biomarkers and therapeutic modalities become more complex, these approaches will play an increasingly important role in translational research, clinical development, and regulatory decision-making.