Pharmaceuticals Interest Group Workshop at the 74th ASMS (San Diego, CA)

Title of the workshop: The peptide renaissance: emerging modalities and analytical challenges

Date of the Workshop: Tuesday, June 2nd, 2026

Organizers/Presiders list: Josh Johnson (Eli Lilly), Mack Shih (FDA) and Valeria Guidolin (Pfizer)

Participants: ~70

Peptide therapeutics are undergoing a significant resurgence within the pharmaceutical industry, driven in part by the clinical success of peptide drug products such as GLP-1 receptor agonists and by advances in peptide engineering. Modern therapeutic peptides are increasingly moving beyond conventional linear sequences toward more complex structures incorporating non-native amino acids, cyclization, peptide stapling, conjugation, and other structural modifications. These advances expand the therapeutic potential of peptides while simultaneously introducing new analytical challenges for mass spectrometry.

The 2026 Pharmaceuticals Interest Group workshop, "The Peptide Renaissance: Emerging Modalities and Analytical Challenges," was organized as an interactive panel discussion rather than a series of traditional presentations. Following introductory remarks and brief introductions from the panelists, most of the session was dedicated to discussion between the panelists, presiders, and audience.

The panel brought together scientists with perspectives spanning pharmaceutical research and development and later-stage/GMP analytical activities. The panelists included Joomi Ahn (Eli Lilly), Iain Campuzano (Amgen), Jessica Hoskins (AbbVie), Jiaxuan Yan (Merck), and Ping Jiang (PPD).

The discussion was framed around a central question: How is mass spectrometry evolving to address the analytical challenges created by increasingly complex peptide and peptide-conjugate therapeutics? A second major theme considered how the MS strategy changes as a peptide progresses from early discovery through development and ultimately into commercial manufacturing.

Several analytical challenges were explored. Modern peptide structures can create difficulties for sequence confirmation and structure elucidation, including incomplete fragmentation, near-isobaric variants, amino-acid isomerism, complex charge-state distributions, and interpretation of deconvoluted data. The planned discussion also considered how intact, middle-down, and bottom-up MS strategies can provide complementary structural information for increasingly modified peptide therapeutics

Attention was given to the role of advanced MS approaches in structure characterization. The discussion questions covered the application of alternative fragmentation techniques such as ETD and UVPD, as well as ion mobility, for characterization of active pharmaceutical ingredients and related impurities. Strategies for characterizing low-level or coeluting impurities and distinguishing amino-acid isomers were also included among the key discussion areas.

Another major theme was the evolution of analytical strategies across the pharmaceutical development lifecycle. The panel was asked to consider the transition from high-resolution, deep-characterization approaches used during discovery and development toward robust, validated, and QC-compatible methods suitable for GMP release and stability testing. Related topics included method transfer, implementation of MS in GMP environments.

Data processing was also identified as an important challenge for peptide characterization. The workshop materials highlighted automated sequencing, impurity assignment, confidence scoring, and predictive or machine-learning-based approaches as areas of growing interest. The panel discussion specifically considered what an ideal software platform for synthetic peptide analysis would look like and how software requirements differ between exploratory/non-GMP characterization and regulated GMP applications.

Overall, the workshop provided a forum for discussing how the rapid evolution of peptide therapeutics is challenging conventional analytical paradigms. The breadth of the discussion, from fundamental structure elucidation and fragmentation strategies to impurity characterization, software, method transfer, and GMP implementation, highlighted the increasingly important role of mass spectrometry throughout the peptide pharmaceutical development lifecycle.