



NEWS RELEASE

Bruker Announces Unique and Comprehensive Workflows For Biopharmaceutical Characterization, Automated by Biopharma Compass 2.0

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WASHINGTON, Jan. 24, 2017 /PRNewswire/ -- At the CASSS CMC Strategy Forum and WCBP 2017 (www.casss.org), Bruker today announced the release of new Biopharma Compass 2.0 (BPC 2.0) software that automates biopharmaceutical characterization workflows for high resolution mass spectrometry. The BPC 2.0 solution is unique and more comprehensive in scope, as it unifies data acquired from the two most relevant and perfectly complementary mass spectrometry methods for the characterization of biologics, MALDI-TOF/TOF and ESI-UHR-QTOF. BPC 2.0 offers a new 3D feature finder, supports 21CFR Part 11 compliance, full integration of UV and MS data and easy-to-use wizards allow defining methods from acquisition to report generation required by the biopharmaceutical industry. Data inspection is accelerated by automatically generated and color coded analysis assessments.

Biopharma Compass 2.0 unifies the data acquisition, data analysis and result reporting of the most often used biopharma workflows:

- Intact mass analysis of large proteins, antibodies or antibody fragments to screen for and identify sequence errors or post-translational modifications (PTM) quickly. Coupled with Bruker's industry-leading SNAP-II algorithm for monoisotopic mass determination (up to the heavy chain), this workflow delivers PTM profiles quickly and with minimal experimental alteration.
- Top-down and middle-down screening of large proteins with both ESI-UHR-QTOF and MALDI-TOF/TOF for sequence confirmation, and to find protein N- or C-terminal modifications.
- Peptide screening with routine PTM and artifact quantification with highest dynamic range, fully integrating LC-UV and MS, MS/MS data in predefined report formats.

Biopharma Compass 2.0 wizard-driven workflows make it easy to highlight common facets of monoclonal antibody and antibody-drug conjugates (ADC) characterization, such as intact mass analysis, sequence errors, truncations, substitutions, and key PTMs such as glycosylation.

Dr. Rohan Thakur, Executive Vice President at Bruker Daltonics, commented: "The wide dynamic range of the maXis II ESI-UHR-QTOF system for large intact proteins and their low abundance isoforms has provided a unique benefit to our users trying to characterize mAbs. The exceptional functionality and convenience offered by BPC 2.0 is a result of co-developments with our biopharmaceutical customers to improve their workflow efficiency."

To learn more, please attend the technical seminar on Tuesday, January 24th, 2017 in the District Ballroom of the Mayflower Hotel in Washington, D.C. to listen to Dr. Jason Wood (Bruker) and Dr. Kristin Boggio's (Pfizer, Andover, MA) talk on 'Overcoming challenges of intact biotherapeutics characterization with ultra-high resolution mass spectrometers and the latest in automated biopharmaceutical software'.

About Bruker Corporation (NASDAQ: BRKR)

For more than 50 years, Bruker has enabled scientists to make breakthrough discoveries and develop new applications that improve the quality of human life. Bruker's high-performance scientific research instruments and high-value analytical solutions enable scientists to explore life and materials at molecular, cellular and microscopic levels.

In close cooperation with our customers, Bruker is enabling innovation, productivity and customer success in life science molecular research, in applied and pharma applications, in microscopy, nano-analysis and industrial applications, as well as in cell biology, preclinical imaging, clinical research, microbiology and molecular diagnostics. For more information, please visit **www.bruker.com**.

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