NEWS RELEASE

Bruker Introduces Novel Mass Spectrometry Solutions for MALDI Imaging, Metabolomics, Proteoform Profiling and Toxicology at ASMS 2017

6/5/2017

INDIANAPOLIS, June 5, 2017 /PRNewswire/ -- Bruker is show-casing several new and innovative, high-performance mass spectrometry solutions for metabolomics, proteoform profiling and toxicology at ASMS 2017 (**www.asms.org**). Bruker is also celebrating 25 years of MALDI innovation with an emphasis on robust, high-throughput MALDI analytical, clinical and imaging solutions.

Frank H. Laukien, Ph.D., Bruker's President and CEO, commented: "At ASMS 2017, we are introducing novel and performance-leading mass spectrometry solutions for life-science and translational research markets, as well as for pharmaceutical and applied markets. Our advanced MALDI Imaging solutions now integrate the industry-leading SCiLS mass-spec imaging software with the rapifleX high-throughput MALDI-TOF/TOF system, or the novel MALDI-Magnetic Resonance Mass Spectrometry (MRMS) extreme resolution system for drug and metabolite tissue imaging. We are also show-casing our unique timsTOF research system, novel Metabolomics research and Phenomics translational research solutions, a breakthrough Proteoform Profiling solution, and a new robust, routine forensic Toxicology platform. In 2017, we are also celebrating 25 years of MALDI innovation, an ionization technique that has enabled pioneering breakthroughs in proteomics, microbiology, imaging and high-throughput screening for drug discovery."

A. Pharmaceutical and Translational Mass Spectrometry Imaging

The new SCiLS Cloud and SCiLS Lab software solutions, now with MultiVendor Support (MVS), bring innovative software features to mass spectrometry imaging (MSI) applications. MALDI Imaging has rapidly developed as a label-free technique for spatially resolved molecular analysis of proteins, glycans, lipids, as well as drugs and their metabolites. MALDI Imaging is finding rapidly increasing use in pharmaceutical drug development, in tissue-

resolved biomarker research (e.g. glycans on cell surfaces as cancer markers), as well as in translational pathology research to complement immunohistochemistry (IHC).

The new SCiLS Cloud software offers web-based tools to facilitate distributed workflows, where data and analysis results can be shared, viewed and manipulated with a web browser through secure access. SCiLS Lab provides advanced and user-friendly solutions for data handling, visualization and computational analysis for Bruker MALDI imaging data sets, and now also offers support for data acquired from non-Bruker mass spectrometers.

Dr. Ron Heeren, Professor at the University of Maastricht and scientific director of the Maastricht MultiModal Molecular Imaging Institute (M4I), commented: "We use mass spectrometry imaging techniques at M4I with the aim to develop and apply mass spectrometry as a diagnostic and prognostic tool for personalized medicine in oncology, neurology and cardiovascular medicine. Powerful and user-friendly software is essential for mining the huge amount of data which is generated in MSI experiments. At M4I we already used SCiLS Lab for our Bruker MALDI Imaging system for years. We are now looking forward to expand SCiLS deployment to the entire lab and to our portfolio of mass-spec equipment." **More...**

B. Metabolomics and Proteoform Profiling for Life-Science and Translational Research

Bruker introduces its third-generation metabolomics research and validation solution, **MetaboScape® 3.0**, which has powerful new features essential for discovery metabolomics, including support for direct-injection (DI) or MALDI Magnetic Resonance Mass Spectrometry (MRMS) for high-throughput phenomics translational research and validation. Innovations include a novel algorithm called Time-aligned-Region-complete-eXtraction ('T-ReX'), which automatically extracts all relevant information in sample cohorts in a "region complete" manner. Included in MetaboScape 3.0 are workflows that support evaluating high-throughput, chromatography-free DI-MRMS or MALDI-MRMS data, enabling two powerful extreme mass resolution techniques that enable higher sample throughput for profiling complex metabolic extracts. The speed and high throughput of these MRMS methods yields advantages for validating larger sample cohorts, and enabling larger-scale longitudinal studies.

Professor Philippe Schmitt-Kopplin at the Helmholtz Zentrum for Analytical BioGeoChemistry in Munich, Germany, elaborated: "We set up new discovery approaches to describe the compositional space of any complex system in biology and geochemistry. The eXtreme Resolution of Magnetic Resonance Mass Spectrometry (MRMS) enables us to address next-generation "metabotyping", i.e. simultaneous rapid description of hundreds of known and thousands of new metabolites relevant for dynamic biological/chemical processes. MRMS in combination with MetaboScape will also enable other researchers to shed light onto this new and exciting research field of exploring the yet 'dark metabolome'." **More...**

Bruker's novel Proteoform Profiling™ 1.0 solution enables a powerful new life-science research and translational research workflow, i.e. the systematic, large-scale, label-free study of all expressed proteoforms, including protein mutations, splice variants, post-translational modifications, as well as protein processing or degradation products. Detailed proteoform characterization is of tremendous importance in cell biology and in clinical proteomics research, where traditional bottom-up proteomics analysis of digested proteins scrambles key biological information. While the human genome only has about 25-30,000 coding sequences, or 'genes', for transcription and translation into protein families, the human body may have up to 1 billion different proteoforms expressed.

Bruker's new nanoElute® nano-flow UHPLC system, together with the new Proteoform Profiling™ 1.0 solution, aims to bring enhanced ease-of-use to nano-spray mass spectrometry, which is essential for label-free discovery workflows on intact protein mixtures.

Professor Leonard Foster at the Department of Biochemistry & Molecular Biology of the University of British Columbia in Vancouver, Canada, stated: "LC-MS experts and biologists alike require trouble-free operation and ease-of-use, along with top performance. Our experience has shown that the nanoElute system readily meets those high demands."

Both innovations take advantage of the superior performance of Bruker's impact II and ETD-enabled maXis II UHR-QTOFs, which deliver accurate and reproducible proteoform profiles from complex intact, undigested protein mixtures. Unlike common Top-Down approaches, these UHR-QTOFs deliver information from proteoform mixtures with a reduced level of pre-fractionation, enabling the analysis of large sample sets from clinically relevant cohorts, or for longitudinal studies. The Proteoform Profiling 1.0 workflow automates the use of Bruker's proprietary Dissect™ and SNAP™ algorithms, together with advanced molecular filtering functions, to generate a non-redundant list of monoisotopic masses, intensities and retention time from the isotopically resolved proteins.
More...

C. Applied Toxicology and Forensics

Bruker announces the release of TargetScreener 3.0HR (high-resolution), which includes TASQ™ 1.4 (Target Analysis for Screening and Quantitation) software to provide a unified software platform for automated screening and quantitative applications in forensic, food and environmental safety markets. Bruker also launches the ToxTyper 2.0E solution for routine, high-throughput forensic toxicology with further improved capabilities and database updates, to enhance customer productivity.

George W. Hime, M.S., Assistant Laboratory Director at the Miami-Dade Medical Examiner's Toxicology Labora-

tory in Miami, Florida, said: "The Toxtyper has been our go-to instrument for post-mortem casework containing novel substances, substances that are otherwise undetectable via GC-MS, and unknown substances we have not yet seen in the lab. This instrument has been a blessing to our laboratory over the last few years of dealing with the flood of new illegal drugs in Miami. From synthetic cathinones to synthetic fentanyls, we have detected and identified them all reliably and with high confidence."

Further improvements in the new ToxTyper 2.0E solution for automated toxicology integrates Bruker's newly launched line of Elute UHPLC liquid chromatography systems. With an expanded curated toxicology screening database and new automated software for LIMS sample table I/O, automated parallel processing with TASQ, and automated reporting of results, these solutions enable increased throughput while minimizing false positives and increasing confidence for routine 'push-button' forensic toxicology. **More...**

Please join us at Bruker's ASMS Booth #518 throughout the conference, and at our press conference on Monday, June 5, 2017, at 9:30 am EDT at the JW Marriott Indianapolis, 3rd floor, JW Grand Ballroom. For more information: **www.bruker.com/events/2017/mass-spectrometry/asms-2017**

About Bruker Corporation (NASDAQ: BRKR)

For more than 55 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 instruments and high-value analytical and diagnostic 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, and in microscopy, nano-analysis and industrial applications. In recent years, Bruker has also become a provider of high-performance systems for cell biology, preclinical imaging, clinical phenomics and proteomics research, clinical microbiology, and for molecular pathology research. For more information, please visit: **www.bruker.com**

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