NEWS RELEASE

Bruker Announces Unique New NMR and MS Tools at Metabolomics 2018

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- Novel High-throughput NMR and MS Solutions for Translational Phenomics Research and Biobanking
- NMR quantification of metabolites and lipoprotein subclass analysis now in one measurement

SEATTLE, June 25, 2018 /PRNewswire/ -- At Metabolomics 2018 (**metabolomics2018.org**), Bruker today announced **B.I.QUANT-PS™**, a metabolite quantification solution on its **AVANCE IVDr™** 600 MHz NMR platform, which brings cost-effective nuclear magnetic resonance (NMR) screening to high-throughput, translational phenomics research and biobank metabolic analysis. The novel B.I.QUANT-PS delivers automatic quantification of 26 disease-relevant metabolites and in the same experiment also enables lipoprotein subclass analysis. In addition, the NMR reference spectral base for pure compounds in biofluids, BBIOREFCODE, has been expanded to cover 800 compounds and >23.500 high quality NMR spectra.

The transferability and reproducibility of B.I.QUANT-PS was proven as part of an 11 instrument ring test in the International Phenome Center Network (IPCN). Metabolites providing information on liver, kidney and cardiovascular diseases are now accessible in a fast and fully validated analysis under DIN-ISO wet spiking.

B.I.QUANT-PS is also an integral part of the new **B.I.BioBankTool™** , a solution for biobanks that addresses their increasing need for standardization and quality control (QC). The B.I.BioBankTool QC procedure delivers information on pre-analytics, sample preparation and analytical performance. It gives information on matrix identity and integrity, e.g. for urine, EDTA-plasma, citrate plasma or serum, and it can flag sample degradation. It also confirms fasting/non-fasting, identifies contaminations, as well as reported or unreported medications. The B.I.BioBankTool can generate quantitative information on 150 metabolites in urine, and >140 lipoprotein and small molecule parameters in plasma/serum. Retrospective analysis of previously recorded data is feasible.

Professor Matthias Nauck, Director of the Institute for Clinical and Laboratory Medicine at Medical University of

Greifswald, commented: "We are excited about the possibilities of NMR screening in biobank quality control to deliver standardized analytical data for biobank metadata. Having multiple biobanks on the same NMR standards will create a wealth of data from all over the world for integration in support of the development of efficient epidemiological and diagnostic tools. The addition of B.I.QUANT-PS substantially enhances the value of data generated, and the IVDr platform can replace conventional analysis tools, which alleviates the cost pressures in clinical analysis. We just installed our AVANCE IVDr at Greifswald University Hospital and will rapidly expand our analytical offerings to biobanks, and for projects such as the German National Cohort."

Bruker also offers novel mass spectrometry-based tools for next-generation metabolomics and translational phenomics research and validation:

Bruker has just announced the revolutionary **scimaX™ MRMS** (magnetic resonance mass spectrometer) with extreme mass resolution exceeding twenty million, which allows the determination of isotope fine structure (IFS) to determine elemental formulae in complex mixtures without liquid chromatography. The scimaX is based on novel conduction-cooled Maxwell™ magnet technology, essentially making the magnet 'invisible' by eliminating the need for liquid cryogens. Powered by **MetaboScape 4.0®** software, the scimaX now offers a novel workflow of flow injection analysis (FIA) MRMS for large cohort, high-throughput phenomics studies, allowing analysis of ~200 samples per day.

MetaboScape 4.0 also forms an integral part of our impact-II ultra-high resolution QTOF platform. Dr. Mathew R. Lewis, COO, MRC-NIHR National Phenome Center, Faculty of Medicine at Imperial College London, stated: "The sensitivity and precision were beyond what I expected, and robustness trials have yielded encouraging results for biofluid profiling. MetaboScape and TASQ software are practical and feature-rich – well suited to the extraction and analysis of data. The total package looks like a real 'Phenomics Workhorse'."

Novel algorithms inMetaboScape 4.0 now also enable the processing of 4D TIMS-separated LC-MS/MS data from Bruker's revolutionary timsTOF™ platform. This harnesses the information derived from reproducible, accurate Collisional Cross Section (CCS) values of target compounds, allows to dig deeper into the dark metabolome. This unique CCS capability is a new parameter in the visual 'Annotation Quality Scoring' feature for confidence in compound ID, or characterization of known unknowns.

Professor Lloyd Sumner, University of Missouri in Columbia, MO, said: "The innovative technology of our **timsTOF Pro** instrument has enabled us to compile a library of CCS values for many plant metabolites. This additional CCS information can be searched and ultimately increases our final confidence in metabolite identifications."

To learn more, **please join our informative lunch symposium** at the Metabolomics Society Conference on Tuesday, June 26th, 2018. Guest speakers Dr. Lloyd Sumner of the University of Missouri and Dr. Matthew Lewis of Imperial College London will present some of their most recent research.

About Bruker Corporation (NASDAQ: BRKR)

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