

## Bruker Daltonics Showcasing Novel Proteomics Solutions Based on Mass Spectrometry at the 7<sup>th</sup> HUPO World Congress 2008

Amsterdam, The Netherlands -- (BUSINESS WIRE) — August 17, 2008 -- Bruker Daltonics today is showcasing several new high performance mass spectrometry products and applications for proteomics at the 7<sup>th</sup> HUPO World Congress 2008:

- **maXis™** is the world's first high speed Ultra High Resolution TOF (UHR-TOF) mass spectrometer platform, and truly represents a revolution in tandem mass spectrometry. **maXis** offers exceptional proteomics performance with sub-ppm mass accuracy, mass resolution of 40,000 to 60,000 across a broad mass range, outstanding sensitivity and five orders of dynamic range - all at the high spectral rate of 20 Hz for MS and MS/MS that is essential for quantitative proteomics and to take full advantage of ultra-high performance liquid chromatography.
- **ETD II** is the next-generation electron transfer dissociation module for Bruker's **HCTultra™** high capacity ion trap. It is based on a novel and compact nCI (negative chemical ionization) source with increased ETD/PTR reactant ion generation, resulting in rapid, confident characterization of PTMs such as phosphorylations or glycosylations at sub-fmol sensitivity. In combination with the major and fundamental ETD efficiency and sensitivity advantages of the spherical high capacity trap design, **ETD II** is designed to provide the most sensitive, fastest and most robust ETD fragmentation. Due to **HCTultra's** inherent m/z range of greater 3,000 and its superior mass resolution that can resolve 3+ and 4+ charge states of peptides on-the-fly at full analytical speed, ETD/PTR on the **HCT-Ultra** can even be used for up to 12 kDa proteins and beyond.
- **MALDI-TDS™** Top-Down Sequencing (TDS) solution provides unparalleled levels of information from undigested proteins in pharmaceutical and biotechnology applications, including C- and N-terminal assignments even in the case of N-terminally blocked proteins. **MALDI-TDS** is available on Bruker's top-of-the line **ultraflex™ III TOF/TOF** system for the characterization of PEGylation sites and other protein modifications of vital importance in fields such as recombinant protein production, biologics drug development and quality control. **MALDI-TDS** has clearly proven its usefulness in the recent ABRF Protein Research Group (PRG) 2008 Study for the identification and differentiation of various truncated proteins of the same origin and provided 100% protein sequence coverage. Bruker's unique **SmartBeam™** is the enabling technology for **MALDI-TDS**, complemented by next generation **BioTools 3.2** top-down bioinformatics.
- The high sensitivity **SmartBeam™** MALDI ion funnel source has now been coupled with the ultra-high mass resolution **apex-ultra™** FTMS, representing a 'perfect match' for MALDI small molecule tissue imaging, including drugs and metabolites from animals dosed at therapeutic levels, e.g. at or below 5 mg/kg. With mass resolution greater than 900,000 (at 7 Tesla), the cluttered spectra produced in small molecule MALDI imaging of tissue samples are readily resolved, allowing for the first time MALDI-MS imaging of small molecules *without* the requirement to use MS/MS (SRM) for chemical background suppression. The high mass accuracy combined with Bruker's **SmartFormula™** software automatically provides sum formula determination for detected molecules. This new imaging solution promises to advance areas such as drug development and delivery, clinical and pathology research, as well as other areas such as lipidomics.
- **EASY-nLC™** is a Bruker-supported nanoscale LC system with 1D and 2D separation capabilities. Due to the true split-free gradient mixing it avoids cumbersome maintenance, and guarantees robust, steady and reliable operation. **EASY-nLC** dramatically reduces total solvent consumption and enables fast separations with peak widths less than 5 sec. The control by Bruker's **Hystar™** software supports all proteomics applications on the maxis, micrOTOF-Q II, HCT ion trap, Flex MALDI and apex FTMS instrument series for complete, turn-key LC/MS/MS solutions.

The new Bruker mass spectrometry products and applications for proteomics will be presented throughout the HUPO conference with more than 30 scientific contributions. During two Bruker Daltonics' luncheon seminars on Monday and Tuesday titled "(R)evolution in Biomarker Discovery", a prestigious researcher's panel including Helmut Meyer (MPC Bochum), Andrew Pitt (Univ. Glasgow)

and Ron Heeren (FOM Amsterdam) will present talks detailing proteomics applications based on the novel developments.

Bruker Daltonics Executive Vice President Dr. Michael Schubert commented: "At this year's HUPO World Congress in Amsterdam, Bruker Daltonics is continuing its history of market leading innovations and is proudly releasing the maXis, an instrument with unprecedented, simultaneous high speed and ultra-high resolution performance across a broad mass range. In addition, Bruker Daltonics is greatly expanding the capabilities of its existing products through the release of several important enhancements, as well as new and innovative applications."

For further information on the HUPO conference, please see [www.hupo2008.org](http://www.hupo2008.org).  
For more information about Bruker Daltonics and Bruker Corporation (NASDAQ: BRKR), please visit [www.bdal.com](http://www.bdal.com) and [www.bruker.com](http://www.bruker.com).  
EASY-nLC(TM) is a trademark of Proxeon Biosystems, Denmark

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