



Bruker's Novel *maXis ETD* Sets Dramatic New Records for Intact Protein Characterization and Top-down Sequencing at ASMS

SALT LAKE CITY, Utah – May 23rd, 2010 – At the 58th ASMS Conference, Bruker and several collaborating scientists will present a number of milestone achievements in the analysis of intact proteins, including the direct sequencing and characterization using Bruker's new *maXis ETD* system. The high mass accuracy, resolving power and dynamic range which are essential to dissect complex patterns of product ions in protein fragmentation allowed, for the first time, performing ETD-based tandem mass spectrometry on biomolecular ions above 60 kDa routinely. These results represent a new record for the mass spectrometric sequencing of intact proteins and unequivocally demonstrate the dramatic advantages of *maXis ETD* technology in ETD-based top-down protein structural analysis.

“An increasing proportion of new therapies in pharmaceutical development are proteins. At the same time, many first-generation biotherapeutics will soon come off patent protection, and thus the need for rapid and reliable total protein characterization has never been higher,” commented Dr. Michael Schubert, Executive Vice President at Bruker Daltonics. “We believe that the new *maXis ETD* has unique and unprecedented capabilities that far exceed what's feasible with intact protein ETD on ion trap/orbitrap hybrid instruments.”

Since the launch of the novel ultra-high resolution (UHR) QqTOF instrument *maXis*TM at ASMS 2008, a number of leading scientists have taken the opportunity to explore the potential of the unique combination of high mass range, resolution and speed in the direct LCMS examination of recombinant proteins. “The results are extraordinary, and *maXis* stands alone in this type of analysis,” commented Bruker's Head of LCMS Applications Development Dr. Carsten Baessmann. “Isotopic definition of proteins over 30kDa and at part-per million mass accuracy under LC conditions are straight-forward now on our *maXis ETD*, making the confirmation of correct expression unequivocal.”

Several examples will be demonstrated at Bruker's Users Meeting on Sunday and during the ASMS scientific program. The recent transfer of Bruker's leading ETD technology to *maXis* has allowed precise intact protein analysis as well as comprehensive direct protein gas-phase sequencing. An example of particular note is the direct ETD sequence analysis of intact proteins like serotransferrin and monoclonal antibodies up to a MW of 150 kDa featured by Professor Yury Tsybin of the EPFL (Swiss Federal Institute of Technology Lausanne) in his Thursday 8:30 AM oral presentation at ASMS. Further examples of top-down intact protein identification and characterization will be presented in various poster sessions at ASMS.



The *maXis ETD* will be highlighted at Bruker's Users Meeting on Sunday, May 23rd, 2010 before the 58th ASMS Conference on Mass Spectrometry in Salt Lake City, Utah (USA). For more information on Bruker's User Meeting and other ASMS activities, please visit www.bdal.com/asms2010.

For More Information:

For more information on *maXis ETD*, please visit www.bdal.com/maXis

For information about Bruker Daltonics and Bruker Corporation (NASDAQ: BRKR), please visit www.bruker.com

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