



Bruker Daltonics Inc.

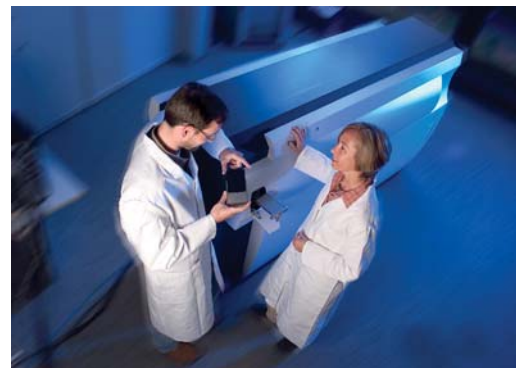
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FOR IMMEDIATE RELEASE

Bruker Daltonics Introduces Revolutionary *Edmass*™ MALDI-TOF Solutions for Rapid Protein Sequencing as an Edman Alternative

Edmass is a Novel Solution for Rapid Top-Down Protein Analysis to Map C- and N-Terminal Sequences of Intact Proteins

CHICAGO, Illinois -- March 9, 2009 – At Pittcon® 2009, Bruker Daltonics today announced the launch of two novel and revolutionary solutions for rapid protein sequence validation. These unique, and truly novel *Edmass* solutions are rapid top-down protein sequencing methods based on high-performance MALDI-TOF mass spectrometry and unique software algorithms. The *Edmass* solutions specifically employ rapid MALDI-ISD (In-Source Decay) to fragment intact proteins across a wide mass range in fractions of a second, and without prior protein digestion. The *Edmass* solution is now available in two versions, *Edmass Ultra* and *Edmass Micro*. The *Edmass*™ *Ultra* solution can even identify and validate C- and N-terminal sequence information directly in a mass spectrometer – very rapidly and again without prior protein digestion.



Edman sequencing has been indispensable for N-terminal protein sequencing in a number of applications for decades. Its major application today is sequence validation in recombinant protein production. The availability of both N- and C-terminal sequences is very desirable, an important aspect that cannot be addressed by classical Edman sequencing. Moreover, Edman sequencing, whilst powerful, is very time-consuming and requires expensive consumables.

The discontinuation of Edman sequencers in 2008 by the market leading manufacturer has prompted the protein sequencing community to search for and assess alternative, next generation protein sequencing technologies. So-called bottom-up proteomics methods, which are excellent for identifying and quantifying proteins, are not suitable for complete protein sequence determination and validation, which also requires N- and C-terminal mapping.

The *Edmass Ultra* solution is based on an *ultraFlex*™ *III* 200 Hz *smartBeam*™ laser MALDI-TOF/TOF. The high mass resolution, excellent mass accuracy and outstanding a.a. sequence coverage of the

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protein fragments up to several kDa allows *de novo* protein sequencing, as well as reliable database searches on the complete MS/MS dataset. MALDI-MSD can be combined with Bruker's proprietary *T³-Sequencing*[™] for the confident determination of N- and C-termini. The *Edmass Ultra* solution is intended for any protein research laboratory, and will be an essential new tool for any pharma, biotech or CRO companies developing biologics.

The *Edmass Micro* solution is based on a cost-effective, bench-top, linear *microFlex*[™] *LT* MALDI-TOF. Using push-button methods suitable for walk-up use and operation by lab technicians, it provides a compact, efficient and easy-to-use solution for top-down sequence validation in protein research and QC of recombinant proteins.

The effectiveness of the *Edmass Ultra* solution was impressively confirmed by the research study 2009 of the ABRF-ESRG (Edman Sequencing Research Group of the Association of Biomolecular Research Facilities). The objective of this study was to obtain the N-terminal sequence of two test proteins. Bruker's *Edmass Ultra* solution provided straight-forward and reliable identification of N- and C-terminal sequences of the isolated proteins in this study.

The *Edmass* solutions provide significant additional analytical benefits:

- longer sequence calls of up to ~80 a.a. residues
- total analysis time for protein QC is just a few minutes
- consumables costs are minimal
- *Edmass Ultra* can assign both N- and C-termini using proprietary *T³-Sequencing*
- works even for N-term modified (blocked) proteins, and
- *Edmass Ultra* permits the direct characterization of modified termini using *T³-Sequencing*;

Mr. Ralf Schäfer, MALDI-TOF Product Manager at Bruker Daltonics, commented: "At ABRF 2009, top-down sequencing using our unique *Edmass* solution clearly demonstrated its enormous potential to become the preferred next-generation protein sequencing method for purified or recombinant proteins due to its performance, speed, reliability and low cost."

For Further Information:

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