



● **Q-TOF Newsletter**

impact HD™ – sensational new capabilities in shotgun proteomics

Identification of more than 4500-5000 proteins in a single LC-MS/MS run, more than 8400 from a combined 2D experiment.

(Minneapolis, June 2013) At the ASMS 2013 conference Bruker introduces exciting new High-Definition capabilities in complex-sample proteomics and biomarker research. Latest generation ion optics, record high-speed digitization and patented nano-flow ionization technology work in concert to define your sample more sharply than ever before. Analyzing your HD data using Bruker’s exceptional proprietary Protein and Glycoprotein Characterization software gives you unique insights into your research challenges.

Figure 1

- 50 cm LC column
- Separation with 4 hour gradient
- impact HD UHR-TOF with CaptiveSpray™ nanoBooster™
- Instant Expertise™ software
- ProteinScape™

Figure 2

- POLYWAX LP; A: 90% ACN, 0.1% acetic acid; B: 30% ACN, 0.1% formic acid
- MS: impact HD
- Source: CaptiveSpray nanoBooster
- 8444 proteins identified with FDR of < 1.0%

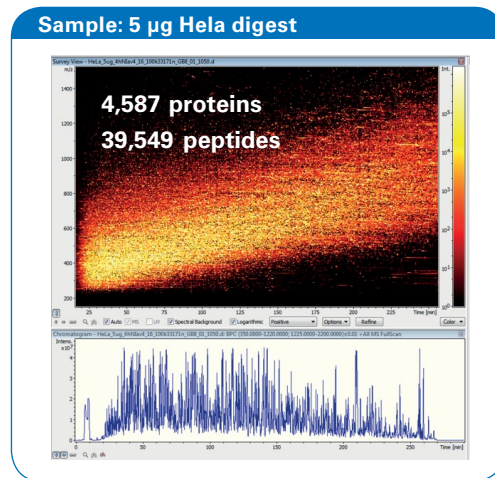


Figure 1

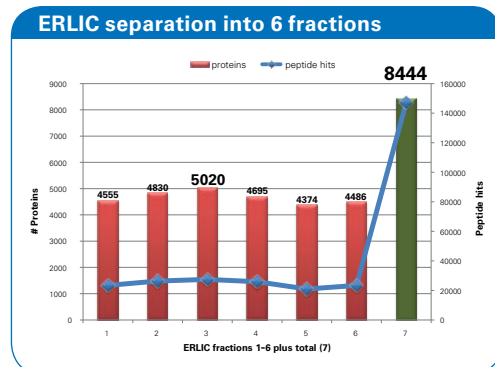


Figure 2

See poster MP24, 491 and MP24, 486 for more details.

Introducing High-Definition, Instant Expertise™ and CaptiveSpray nanoBooster™ in ultra-high resolution LC-MS/MS in a research-performance bench-top Q-TOF

- **50 GBit/sec sampling technology** maintaining full specification resolution even during ultrafast chromatography. **5 orders of magnitude dynamic range in one second** for definitive trace analysis from complex, high-background matrices
- **CaptiveSpray nanoBooster** with enhanced peptide sensitivity matching best shot-gun proteomics identifications
- **Intelligent self-optimizing** MSMS routines for expert-caliber results first time

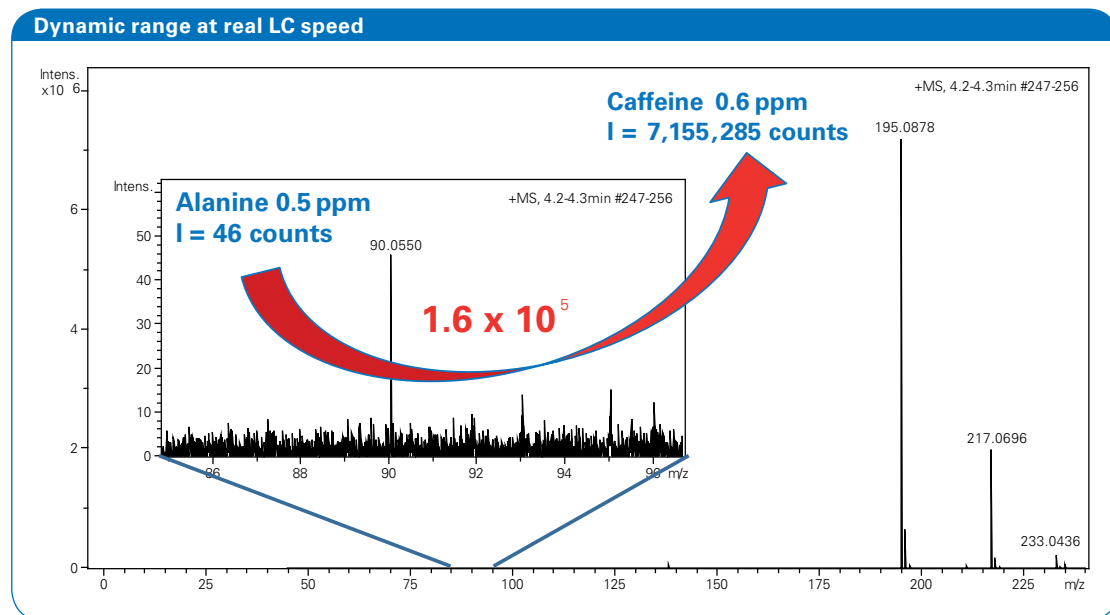
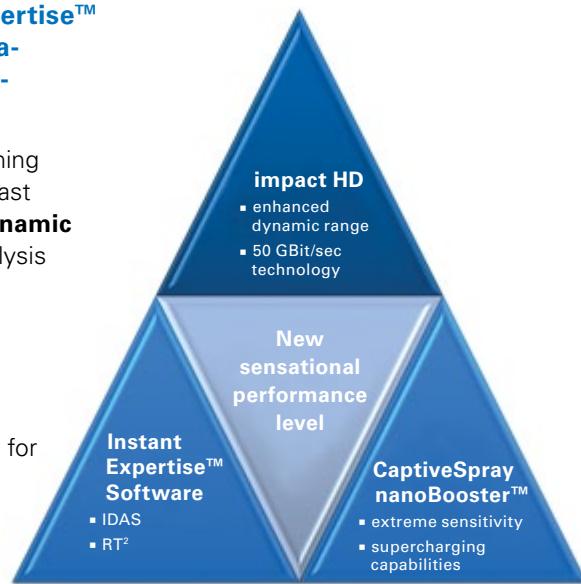
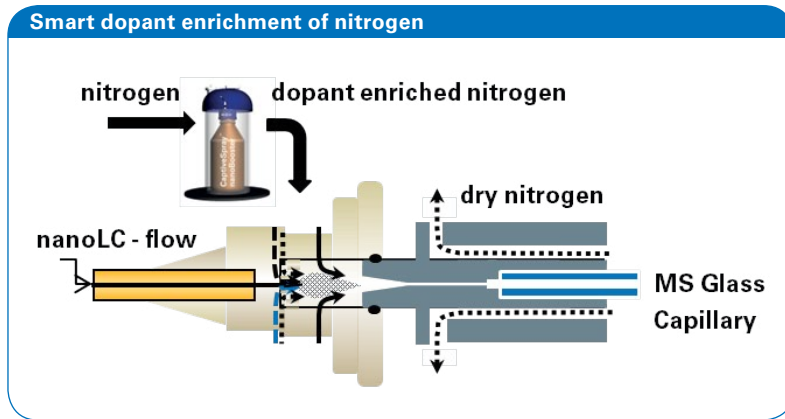


Figure 3: Five orders of magnitude dynamic range @ 1 Hz speed LC timescale

- 3 - 4 x higher dynamic range from 10 bit ADC technology
- Provides 50 GBit/sec highest sampling speeds and maintains high resolution
- Much higher dynamic range in protein concentration measurable



CaptiveSpray nanoBooster™ for ultimate proteomics performance



- Boost nanoflow sensitivity
- Enable glycoanalysis
- Supercharging capability
- Push up ID rates
- Reduce noise
- Patented technology

Figure 4: Optimized ionization condition

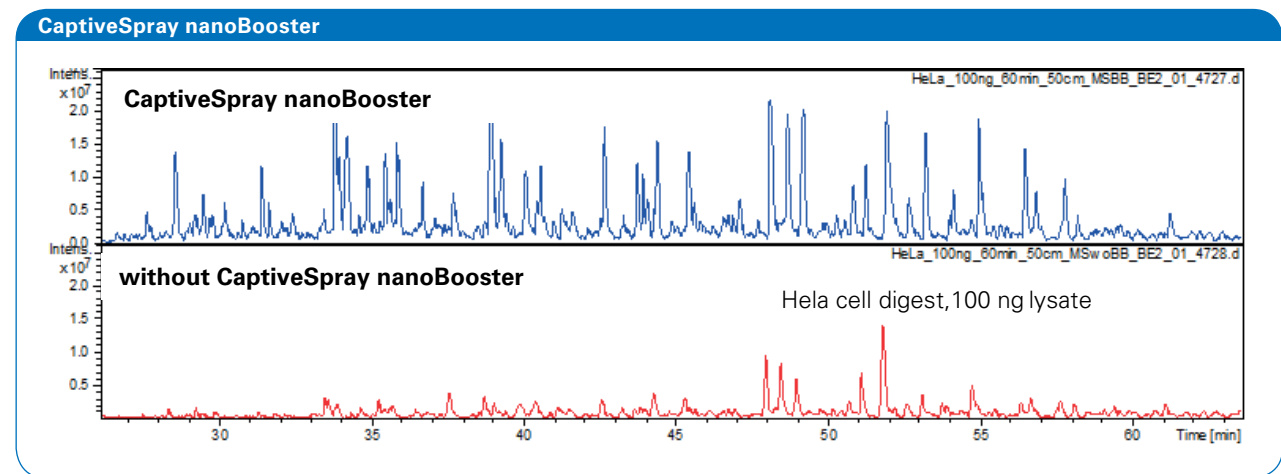
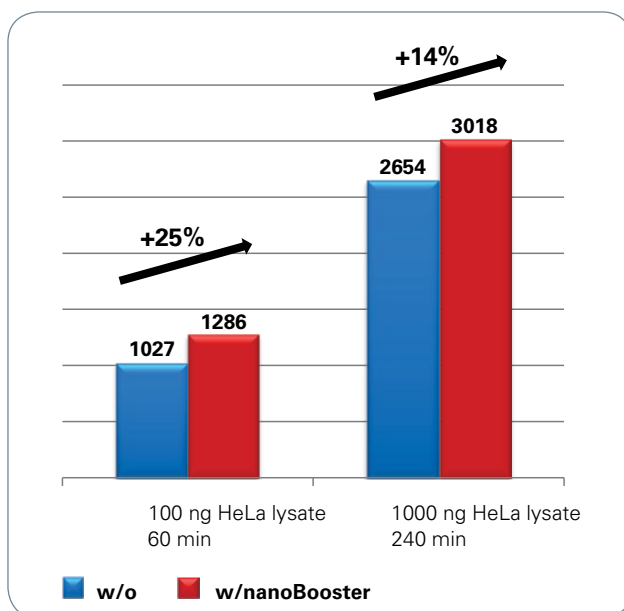


Figure 5: Significant increase in signal intensities for low sample amounts



Enhance signal intensity and charge state for enhanced Protein ID capabilities. CaptiveSpray nanoBooster is particularly sensitive for low-abundance peptides, lower quantitation limits, and detection of glycosylation sites. Data measured with impact „classic“ prior to HD improvement.

Performance and ease of use

- Direct benefit for quantitation / glycosylation detection
- One method for all concentrations

Figure 6: Data measured with impact UHR-TOF prior to HD improvement

Instant Expertise™: Method for optimal quant and ID results in one acquisition

Issue: Classical Auto MS/MS strategies use basically the same pre-set conditions for fragmentation; independent of the peptide amount and chromatographic resolution – meaning that dynamic range and MS/MS quality are compromised.

Solution: Instant Expertise Software with new autoMSMS strategies:

- **IDAS (Intensity Dependent Acquisition Speed)**
MSMS acquisition time automatically derived from precursor intensity
- **RT² (RealTime Re-Think)**
RealTime Re-Think reconsiders an additional MS/MS at a higher precursor signal intensity before activating dynamic exclusion

- Higher productivity – one acquisition method for all concentration levels
- Higher yield (> 50%) of good MSMS => higher ID rates
- High accuracy for quantitation
- Always obtain optimal results, independent of sample amount or complexity

See Application Note LCMS-81 for more details.

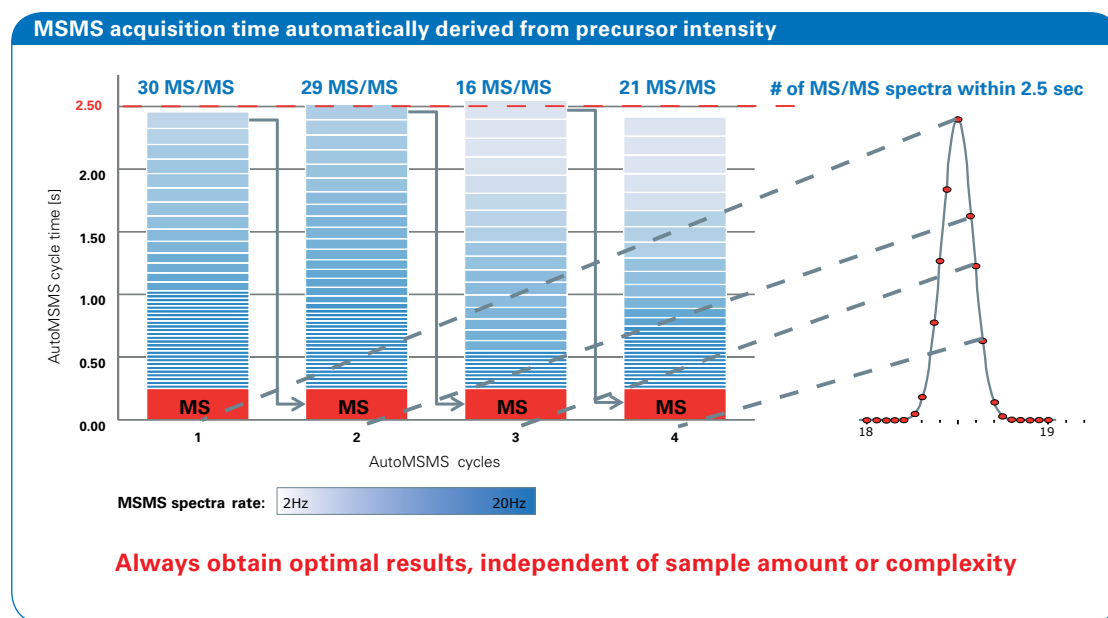


Figure 7: Sampling rate automatically derived from precursor intensity

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