

impact II

- Get the full picture the first time

Sensational Capabilities of impact II



Optimize your LC-MS methods without compromising performance: impact II delivers the full range of specified performance parameters simultaneously to solve your analytical challenges. The Ultra-High Resolution (UHR) QTOF technology pioneered by Bruker once again defines the standards of what can be achieved using accurate mass LC-MS/MS.

New innovations in time-of-flight instrumentation are now available in a robust and market-leading benchtop system.

Your Success with impact II

Outstanding Hardware Performance

- **Enhanced dynamic range**
- **50 Gbit/sec data sampling technology**
- **10 bit ADC technology**
- **New TOF with improved resolving power**

Instant Expertise™ Software

- **IDAS™**
Intensity Dependent Acquisition Speed
- **RT²™**
RealTime Re-Think
- **SmartFormula 3D™**

Market Leading Sensitivity

- **Dual ion funnel**
- **IonBooster Source**
- **CaptiveSpray nanoBooster**
- **New collision cell with broad mass transfer**

Deepest insight into your sample

Easy-to-use

Robust & Quantitative

Robustness And Simplicity – All Day, Every Day

Dynamic range – five orders of magnitude

50 GBit/sec sampling technology enables high Dynamic range acquisition on an LC timescale

Greatly increased robustness to sample variation allowing reduced sample pretreatment especially desirable in high throughput quantitative applications. Definitive trace analysis from complex, high-background matrices makes your analytical work more productive. Increased dynamic range, excellent robustness, and full sensitivity gives you the deepest insight into your sample and what might be hiding underneath.

Sensitivity

One shot plug & play acquisition with market leading standard sensitivity

Ensuring qualitative and quantitative results in one LC run delivers fastest possible time-to-success. Whether running with standard ESI, ionBooster or even nano-flow separation coupled with the patented CaptiveSpray nano-Booster the impact II with its dual ion funnel delivers extreme sensitivity for best qualitative and quantitative results in one run.

Full sensitivity resolution

Having to choose between resolution and sensitivity on other instruments restricts the depth to which you can understand your sample. Instead of beam shaping, the impact II features a new time-of-flight tube with improved resolving power for optimized detection.

Instant Expertise™

Intelligent self-optimizing MS/MS routines deliver expert-caliber results first time from your complex biomarker discovery or small molecule unknown screening experiments where spectral fidelity is key. This also includes *de novo* molecular formula determination.

Let the impact II achieve your goals in:

- Biomarker discovery and validation in proteomics and metabolomics
- Drug metabolite, degradant and impurity identification and quantitation
- Synthetic chemistry support
- Intact protein analysis and characterization of biopharmaceuticals
- Forensic and doping control
- Food and water testing

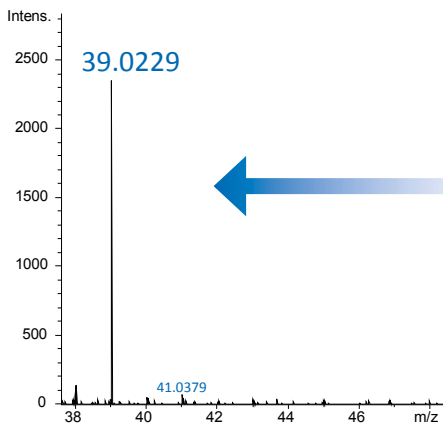
And all in an economical and benchtop design.



More Dynamic Range, More Accuracy, More Confidence

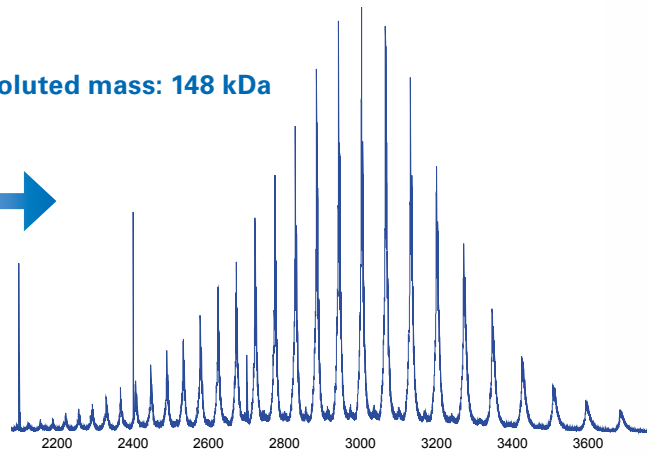
Versatility

Sensitive mass transfer from smallest fragment ions to monoclonal antibodies

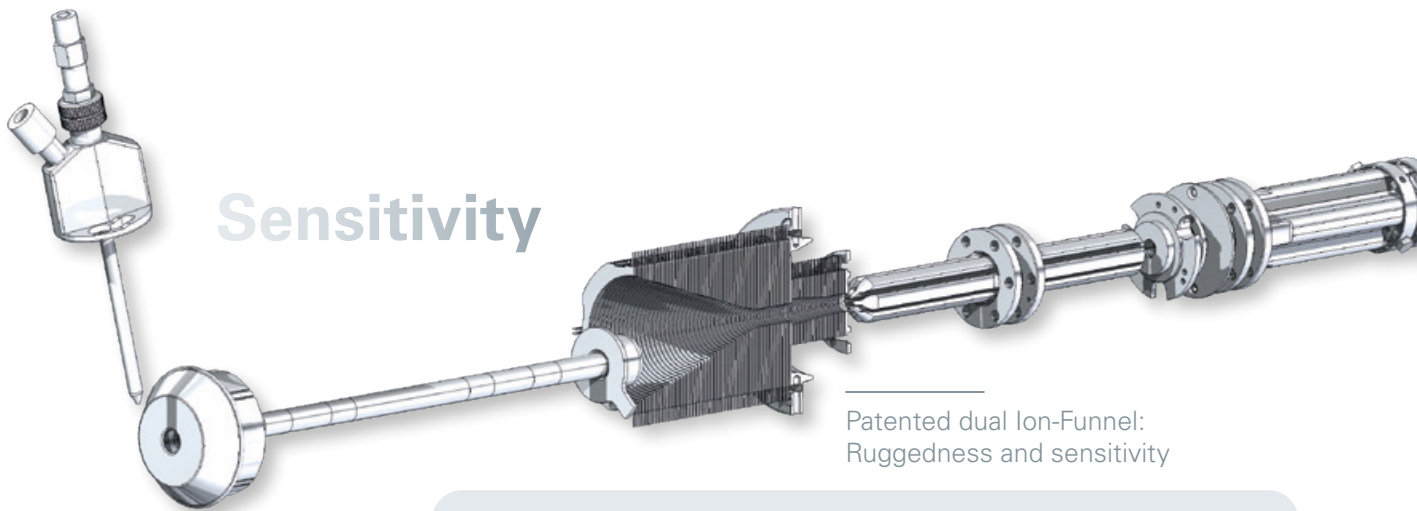


Low mass fragment ion of vanillic acid precursor at 0.1mDa Mass accuracy

Deconvoluted mass: 148 kDa



Mass Spectrum obtained from intact Adalimumab which has a molecule weight of 148k Da



Sensitivity

Patented dual Ion-Funnel:
Ruggedness and sensitivity

Choice of rugged and sensitive ion sources

*"The robustness, sensitivity and spectral accuracy of the impact QTOF-MS has accelerated the process to identify unknown compounds. This is an integral part of long-term goal to 'sequence' the *Medicago truncatula* metabolome"*

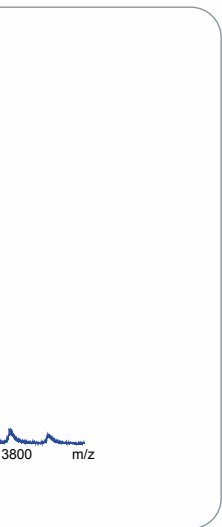
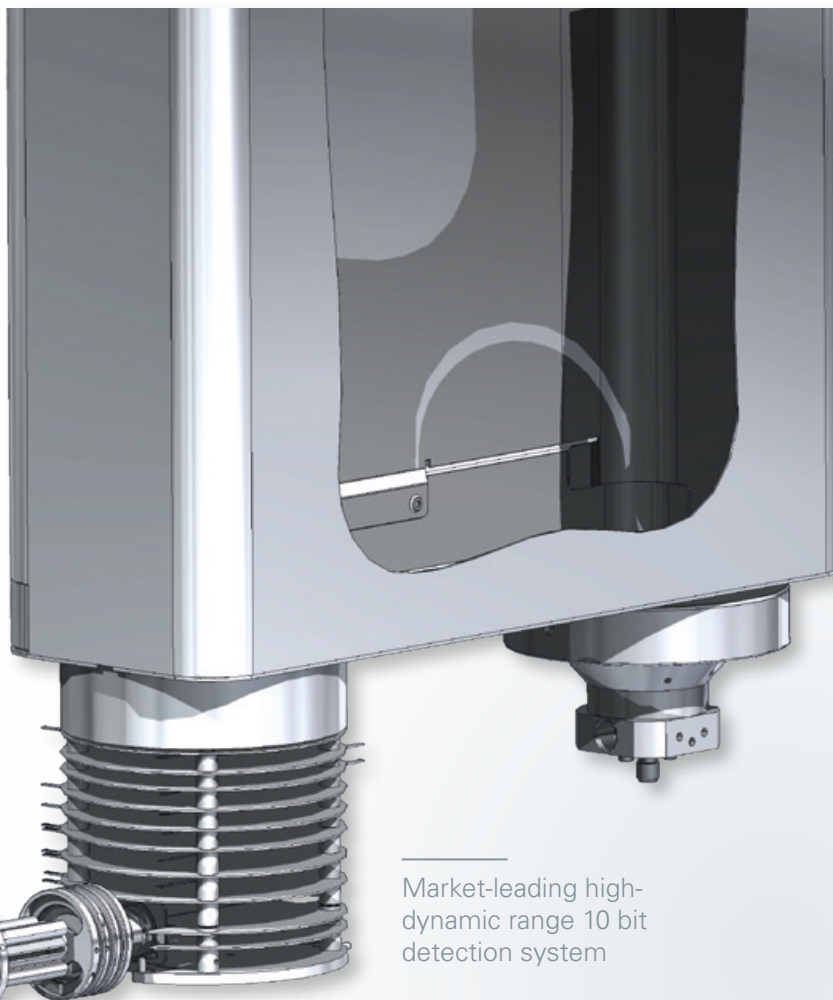
Professor Lloyd W. Sumner, Analytical Biochemistry Plant Biology Division, The Samuel Roberts Noble Foundation Ardmore, OK, USA



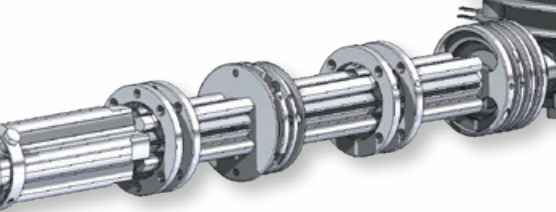


TOF with improved
Full Sensitivity
Resolution (FSR)

Spectral accuracy



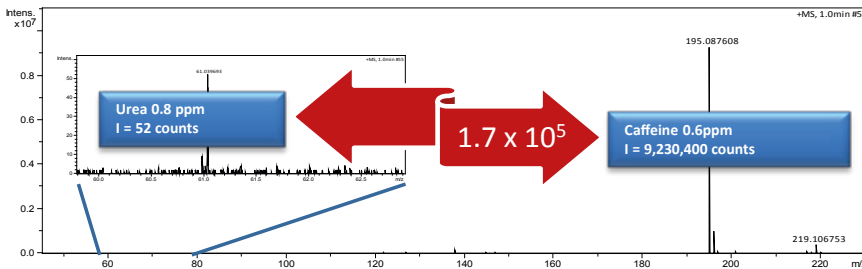
Robustness



Market-leading high-
dynamic range 10 bit
detection system

New broad mass transfer
Quadrupole CID cell with
DC gradient

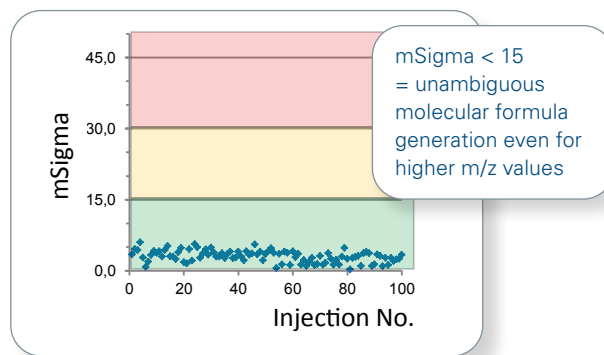
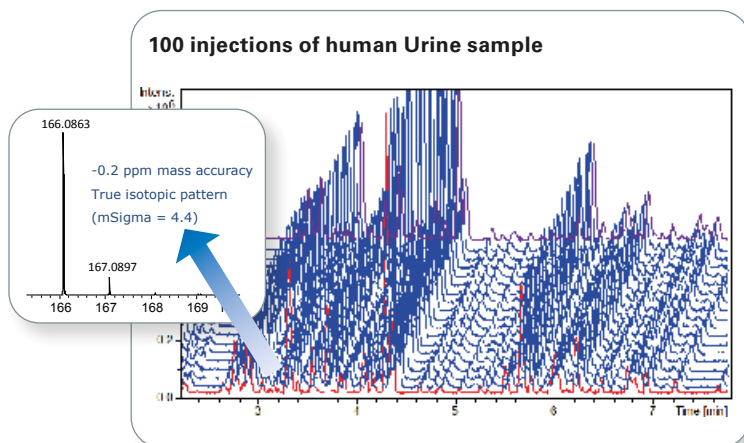
Much higher dynamic range in concentration reachable



In-spectrum dynamic range @ real LC speed – don't miss low abundant peaks.

Productivity and....

Robust profiling of large batches of complex biological samples



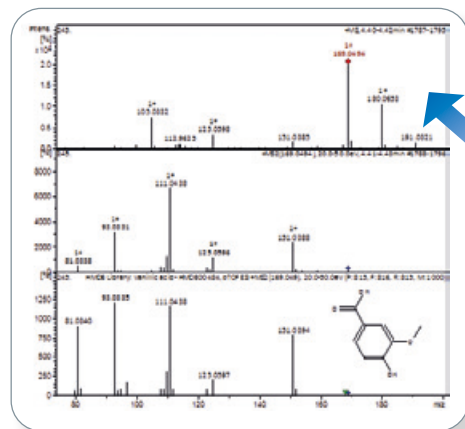
mSigma Value for phenylalanine in 100 urine samples measured

Peak shapes in urine sample remain constant:

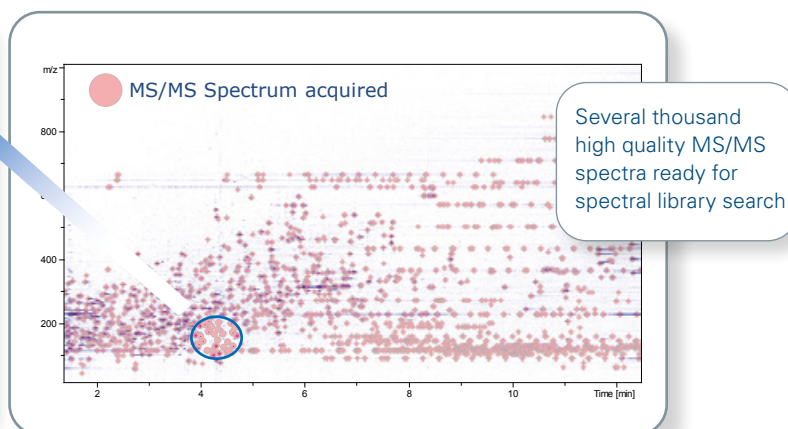
Instrument robustness enables comprehensive metabolic profiling studies of large sample sets.

Looking at a selected compound: Phenylalanine. SmartFormula provides the correct molecular formula based on accurate mass and isotopic pattern fit: $C_9H_{12}N_1O_2$. Fully reproducible isotopic fidelity for phenylalanine across 100 samples injected – unambiguous molecular formula generation also for higher m/z values all day, every day.

Simplicity: Fast and accurate acquisition of fragment spectra



impact II enables up to 50 Hz instrument scan speed combined with Instant Expertise™ software: All precursor ions fragmented in “one shot” acquisition of human urine sample spiked with vanillic acid.



The low abundant target mass 169.0495 m/z of the vanillic acid precursor was fragmented successfully. Query in custom human metabolite MS/MS Library, provides correct identification. The library was generated in a different laboratory on a different impact QTOF instrument.

...Versatility for OMICS research

Intact Protein Profiling

The combination of Isotopic fidelity and mass accuracy that makes the impact II capable of delivering molecular formulae for metabolites is preserved over the mass range. Consequently, even proteins out of a complex mixture (here : overlapping compounds resolved with the Dissect™ algorithm in an *E. coli* extract) can be extracted and measured with an unrivalled mass accuracy and an exact isotopic pattern.

Accurate Bottom-up proteomics quantitation

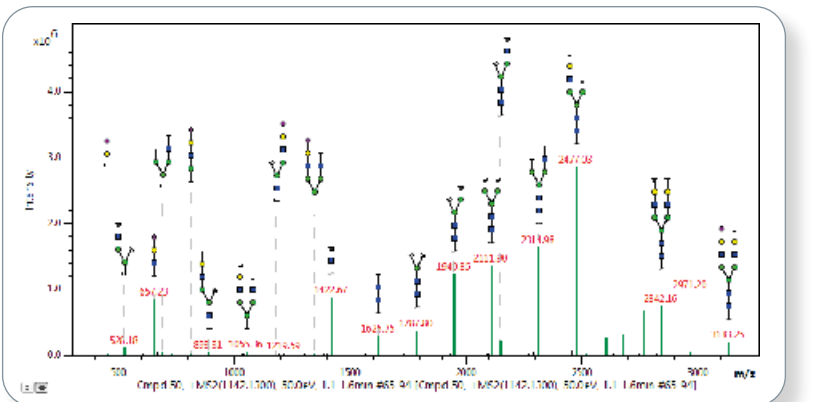
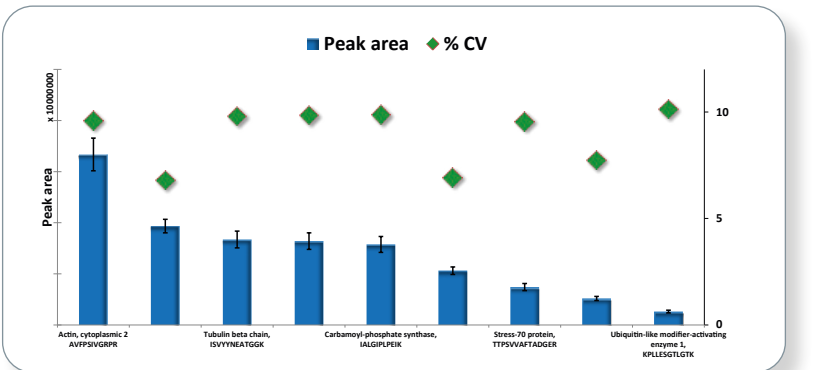
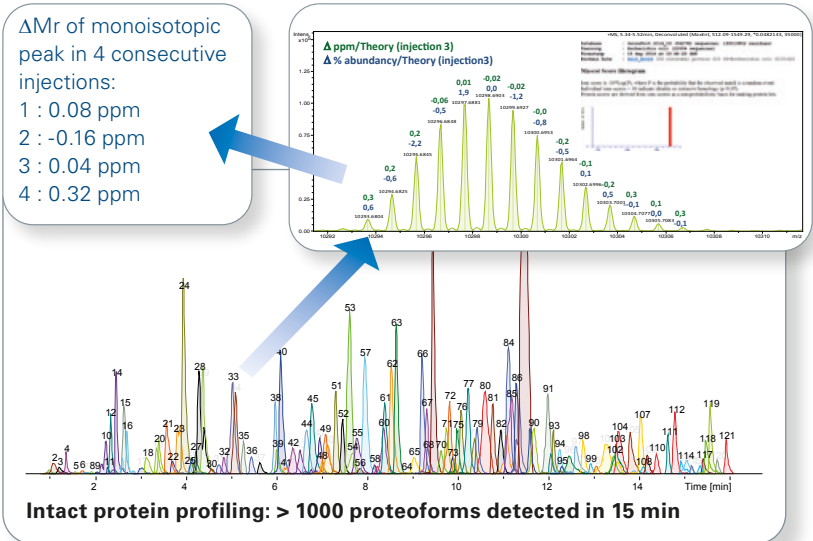
The robustness of the impact II with its impressive dynamic range enables accurate quantitation. As an example the CV's obtained for a selected subset of 10 proteins out of 55 consecutive injections of an Hela Cell digest, separated with a 90 min gradient and acquired with the Instant Expertise™ ID/Quant method: that illustrates the capabilities of the instrument for label-free discovery approaches.

Read more in Application Notes

- LCMS-81: "Introducing New Proteomics Acquisition Strategies with the compact™ – Towards the Universal Proteomics Acquisition Method"
- LCMS-89: "High quantification efficiency in plasma targeted proteomics with a full-capability discovery Q-TOF platform"

Glycomics and Glycoproteomics

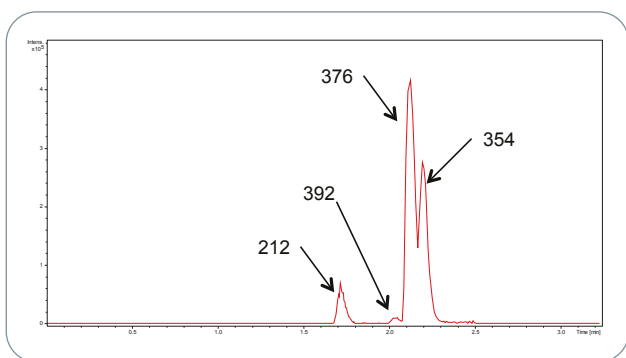
An illustration of versatility. The impact II accurate mass and data for glycans and glycopeptide can be fully exploited in Protein Scape for screening, identification and characterization operations.



Qualitative and Quantitative Drug Metabolism Characterization

Metabolite Detection

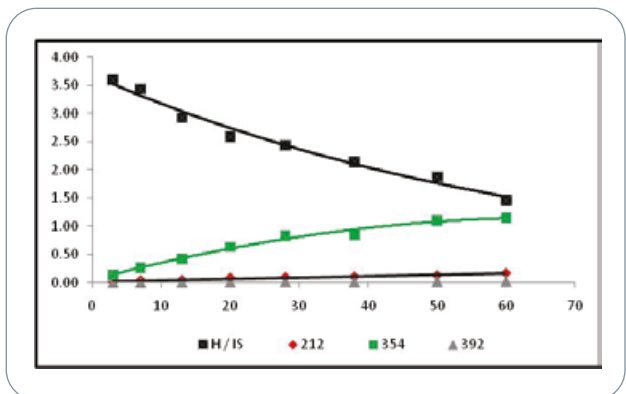
Metabolite Detect software compares the data file for the drug (in this case t_{60}) with the corresponding control sample.



A base peak chromatogram of the difference is created allowing metabolites m/z 354, 212 and even 392 to be easily observed.

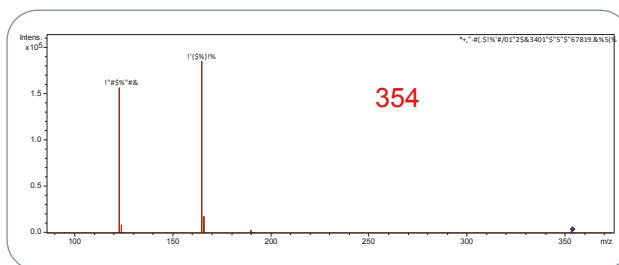
Drug and Metabolite Profiles

Integration is carried out on the EIC for the measured m/z of each metabolite ± 0.005 Da. Plotting the ratio of metabolite to internal standard (MIS) vs. time produces the metabolite profiles. Half-life and clearance values are determined from the natural log (ln) of the drug profile vs time plot.

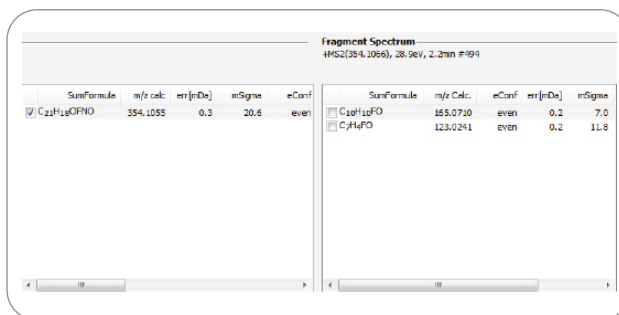


Metabolite ID

Auto MS/MS Spectrum

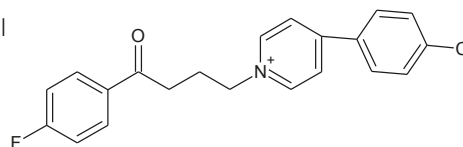


SmartFormula3D



Formula and Structure

C₂₁H₁₈NOFCI



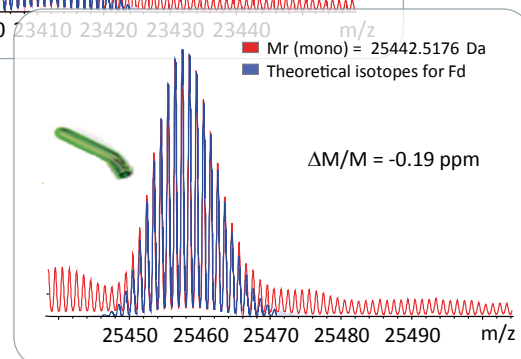
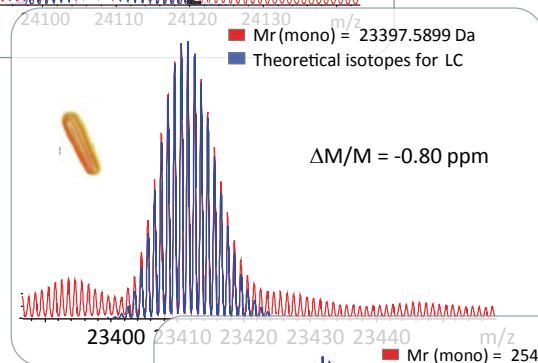
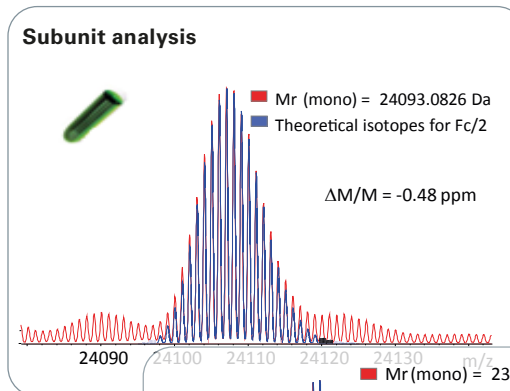
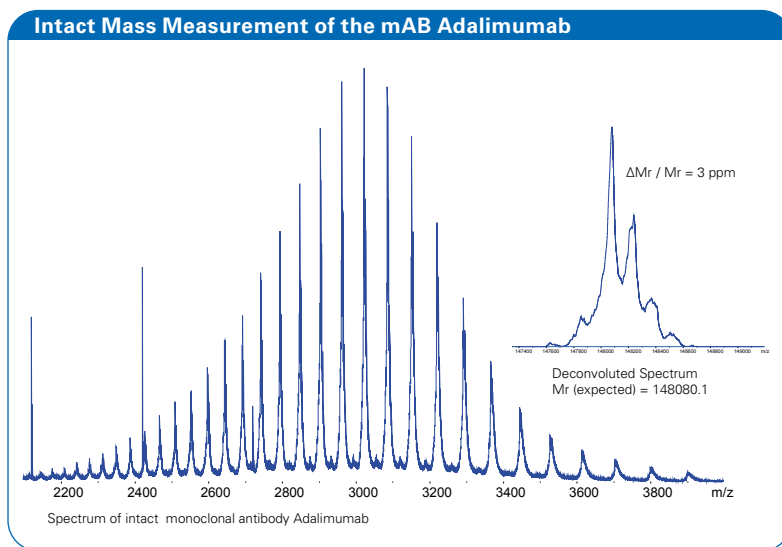
Your Partner in Biopharmaceutical Analysis

A powerful benchtop solution with comprehensive capabilities for biological therapeutics screening, characterization and confirmation

Rapidly and routinely acquire monoisotopic antibody subunit data, with resolved isotopes and superb mass accuracy. This yields greater confidence in sequence confirmation and easy detection of heterogeneities.

Acquire high coverage peptide maps and confidently detect and identify low-level sequence variants with increased MS/MS acquisition speed and wider dynamic range.

Effective screening and quantitation of released glycans and small molecule impurities due to broadband transmission and wide dynamic range.



Peptide Maps

- Annotated BPC
- Multiple enzymes
- Library matching

Intact Mass Analysis

- Comparison with reference material
- Glycoform ratio calculation



**BioPharma
Compass**

Subunit analysis

- Comparison with reference material

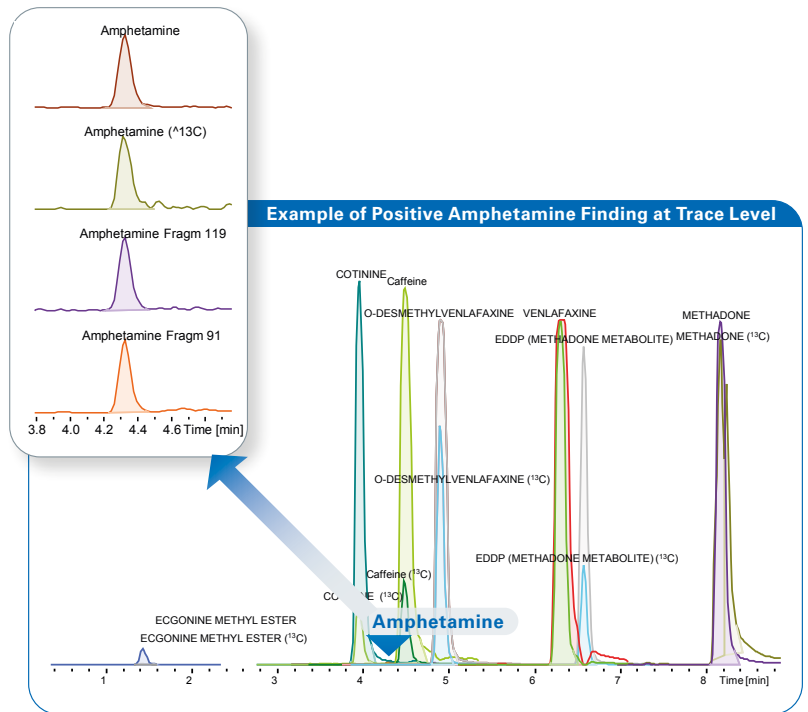
Screening

- impurities
- released glycans

... for Rapid Profiling and Screening of Unknowns

Comprehensive forensic drug screening with maximum confidence in the results with impact II. Accurate mass measurement of 'diagnostic ions', including the pseudo-molecular ion, adducts, isotopes as well as broad band CID (bbCID) fragment ions reduces or eliminates false positive findings, even in complex matrices such as serum. At trace levels, 'buried in the grass' at RT=4.3 minutes, diagnostic fragment ions m/z 119 and m/z 91 and the ^{13}C isotope for amphetamine are observed. Amphetamine is truly detected as positive finding from the screening result.

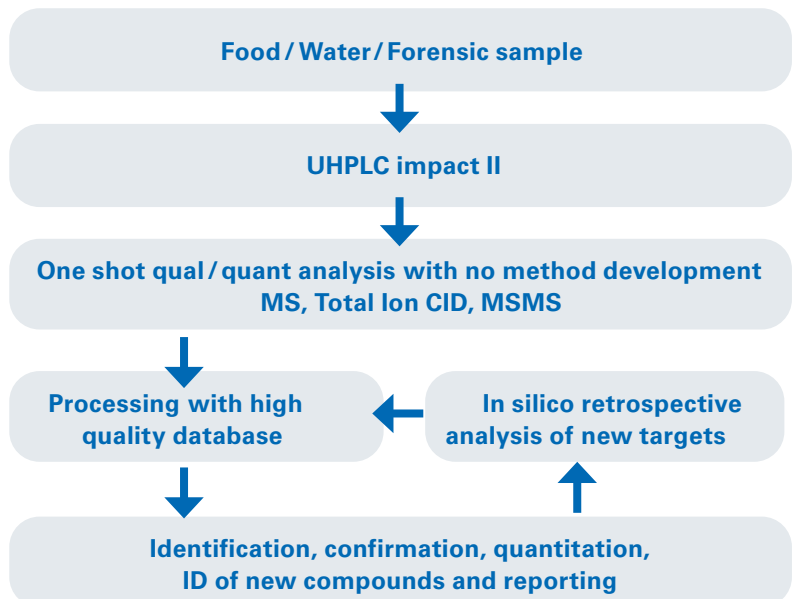
To facilitate comprehensive screening for hundreds of target compounds, the Bruker Toxtyper and TargetScreener solutions are supported by high quality accurate mass databases, enabling users to readily process the data and obtain accurate, reliable screening results.



"We use the Bruker impact QTOF with bbCID to attain enhanced sensitivity for drugs-of-abuse and designer drug screening in a forensic setting, covering critical low concentration compounds like THC acid, buprenorphine, LSD, and synthetic cannabinoids. The bbCID workflow has been carefully validated against spectral library comparison, and it has proven to deliver equal confidence, but with a much higher efficiency, significantly increasing our productivity. Our forensic screening method has now been accredited by the Finnish Accreditation Service"

Dr. Anna Pelander, Laboratory of Forensic Toxicology at the University of Helsinki

- High resolution, accurate mass MS and bbCID MS/MS data acquisition enables rapid reaction to emerging challenges in food safety and doping even before reference standards are available
- Facilitates retrospective *in-silico* analysis for post-hoc identification of true unknown contaminants
- Accurate mass screening databases for Food Testing and Forensic Toxicology



Dynamic Source Configuration

In addition to ESI sources, Bruker life science MS systems support a wide range of source options from Bruker and third-party vendors, all switchable within seconds.

CaptiveSpray™ nanoBooster

CaptiveSpray nanoBooster is the proteomics ion source that brings your MS to the next performance level – The operation is as easy as electrospray can be. The nanoBooster enables Glycoanalysis, supercharging and pushes up ID rates.

ionBooster

The ionBooster offers a 5–100x gain in sensitivity for many compounds of interest in the fields of environmental analysis, food testing and therapeutic drug monitoring.

APCI

Atmospheric Pressure Chemical Ionization is used in metabolomics as well as for drug or pesticide screening for less polar molecules where ESI fails to deliver reasonable quantities of ions.

APPI

Atmospheric Pressure Photo Ionization is used for less polar or non-polar molecules that can not be ionized in either ESI or APCI.

DIP

The DirectProbe add-on for the Bruker APCI II and APPI II ion sources allows direct analysis of liquid and solid samples without tedious sample preparation.

GC-APCI II

The GC-APCI II source with unique flexible, heated transfer line and calibrant delivery enables GC coupling to any Bruker TOF or QTOF, trap or FTMS system originally designed for LC coupling.



GC-APCI II



APPI



APCI with DIP



CaptiveSpray nanoBooster

"We have been using the impact since almost a year for routine shotgun bottom up proteomics. In association with the CaptiveSpray nanoBooster, the instrument has provided an excellent level of sustainable performances, being capable of delivering untouched performances for over 6-8 weeks of 24/7 use. This is of tremendous importance for the success of our label-free measurement campaigns"
Prof. Alain Van Dorsselaer, LSMBO, Strasbourg



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● Bruker Switzerland AG

Fällanden · Switzerland
Phone +41 44 825 91 11

Bruker Scientific LLC

Billerica, MA · USA
Phone +1 (978) 663-3660

www.bruker.com