BRUKER

Bruker Daltonics

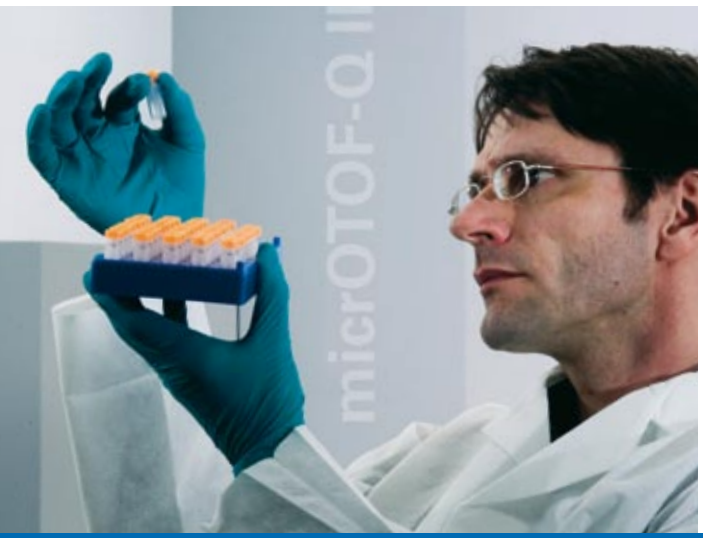
micrOTOF-Q II

- Cutting Edge Performance with Sub-ppm Confidence

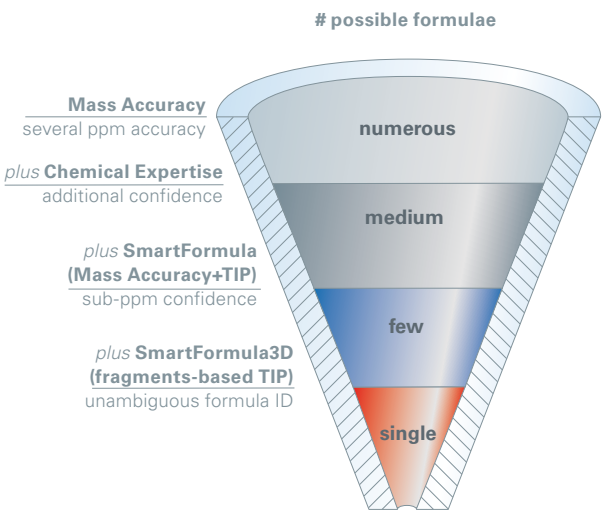
think forward

ESI-Qq-TOF

The advantage of Ultimate Confidence



Do you need maximum confidence in your analytical system?
Bruker Daltonics' new micrOTOF-Q II™ ESI-Qq-TOF mass spectrometer features the very latest technology developments to provide maximum certainty in your research in Small Molecule Identification, Metabolomics or Proteomics.



SmartFormula determination

Three dimensions of information simultaneously raise your analytical tasks to unrivaled heights of confidence:

- Measure with unequalled accurate mass
- Validate with True Isotopic Pattern (TIP) analysis
- Also benefit from accurate mass and TIP in analysis of fragments in MS/MS mode

Mass accuracy, chemical knowledge and SmartFormula 3D™ clearly limit the number of possible formulae in molecular formula generation: for confident determination of the elemental composition of a given peak.

This valuable sub-ppm confidence is available for formula determination in pharmaceutical impurity analysis, metabolite identification, pesticide screening and toxicology & doping analysis.

Unique Power³ – Simultaneously without Compromise

Cutting-edge performance has never been this easy to use:

Sensitivity

Experience market leading sensitivity with the next-generation Apollo II™ ion funnel ESI source, dramatically improving ion transmission.

Mass accuracy

Be impressed by a mass accuracy of 1 – 2 ppm over an exceptionally wide dynamic range.

Resolution

Be amazed by superb focus resolving power exceeding a resolution of 17,500 – 20,000 FWHM.

Fragment analysis

Featuring a superb quadrupole mass filter and a quadrupole collision cell for accumulation of parent and fragment ions prior to mass analysis, the micrOTOF-Q II expands the renowned micrOTOF's advanced performance in the analysis of molecule fragments, adding a third level of confidence to the two dimensions of accurate mass and True Isotopic Pattern analysis with SmartFormula 3D.

A convenient, highly stable, one-step calibration for automated data output makes this instrument your easy-to-use companion with superior performance to all other (ESI)-Q-TOF instruments.

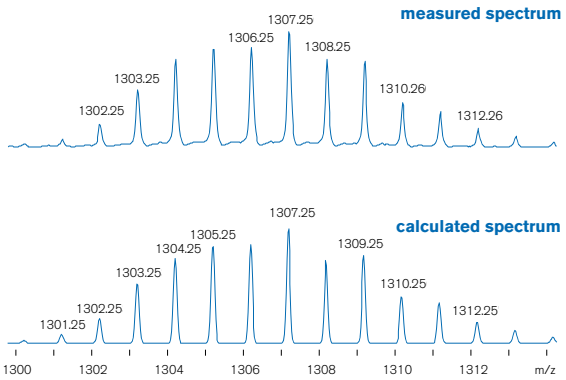
Simultaneously achieve reliable MS and MS/MS accuracy, independent of whether calibration was performed in MS or MS/MS mode.

Thus, for chemical formula determination, a detailed formula suggestion is only a keystroke away.

Raise your research to a higher power with all these capabilities available concurrently!

Unprecedented Certainty

Isotopic pattern analysis



MS analysis of Pd-Complex ($C_{61}H_{64}N_4O_{15}Pd_2$) in synthetic chemistry. Isotopic Pattern of measured spectrum and calculated spectrum show outstanding homogeneity, providing a superior SmartFormula scoring for enhanced confidence in structural analysis.

Precision in organic chemistry

Accurate mass and Bruker Daltonics' proprietary SmartFormula 3D True Isotopic Pattern analysis algorithm provide unrivalled certainty for the identification of unknowns.

Due to an extraordinarily wide dynamic range, the entire mass range is covered with a high mass accuracy – resulting in unambiguous molecular formula generation.

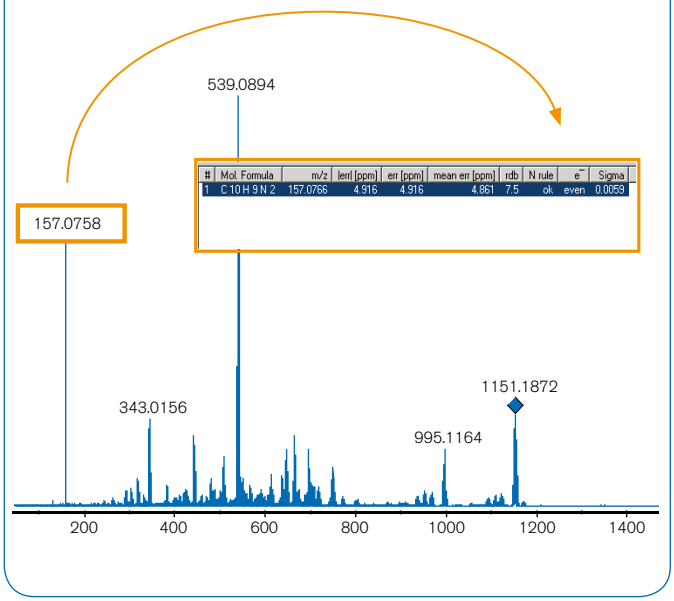
Mass accuracy is not enough: Using isotopic patterns for enhanced identification

After generation of a list of possible formulae, the measured isotopic pattern is compared with the theoretical isotopic pattern – resulting in a statistical match factor, the Sigma factor used for Smart-Formula.

micrOTOF-Q II's capability to deliver correct isotopic patterns discriminates over typically 50 possible formulae from 2-5 ppm mass accuracy alone to one single formula by SmartFormula scoring.

ISCID-MS^3 analysis of Pd-Complex in synthetic chemistry. A fragment m/z 157.0758 reveals a mass error of < 5 ppm (external calibration) for reading out a formula by SmartFormula scoring. Parent ion was m/z 1307, see above. The ion was fragmented insource followed by a CID experiment of the fragment m/z 1151. micrOTOF-Q II covers the whole mass range with high mass accuracy.

Formula generation from MS/MS fragment



SmartFormula 3D: Combining accurate mass with True Isotopic Pattern (TIP) capabilities of the micrOTOF-Q II. 15 possible sum formulae candidates from MS analysis are condensed down to one, Minocycline. (see Technical Note TN-26).

SmartFormula 3D delivers the correct formula

#	Mol. Formula	m/z	|err| [ppm]	Sigma Rank
1	C 23 H 28 N 3 O 7	458.1922	1.2	1
2	C 20 H 20 N 13 O	458.1908	1.8	2
3	C 24 H 24 N 7 O 3	458.1935	4.1	
4	C 21 H 33 N O 8 P	458.1938	4.8	
5	C 19 H 24 N 9 O 5	458.1895	4.7	
6	C 19 H 34 N 5 O 2 P 2 S	458.1903	2.9	6
7	C 27 H 30 N 3 P 2	458.1909	1.5	7
8	C 18 H 25 N 11 O 2 P	458.1925	1.8	8
9	C 25 H 33 N O 3 P S	458.1913	0.7	9
10	C 27 H 28 N 3 O 2 S	458.1897	4.3	10
11	C 18 H 33 N 7 O P S 2	458.1920	0.8	11
12	C 20 H 28 N 9 S 2	458.1904	2.8	12
13	C 24 H 32 N 3 O 2 S	458.1930	3.1	13
14	C 32 H 28 N S			
15	C 35 H 24 N			

SmartFormula hit list

SumFormula	m/z calc	err[ppm]	mSigma
☑ C 23 H 28 N 3 O 7	458.1922	1.2	4.3

SmartFormula 3D: One single formula

Accurate Mass, SmartFormula and MS/MS

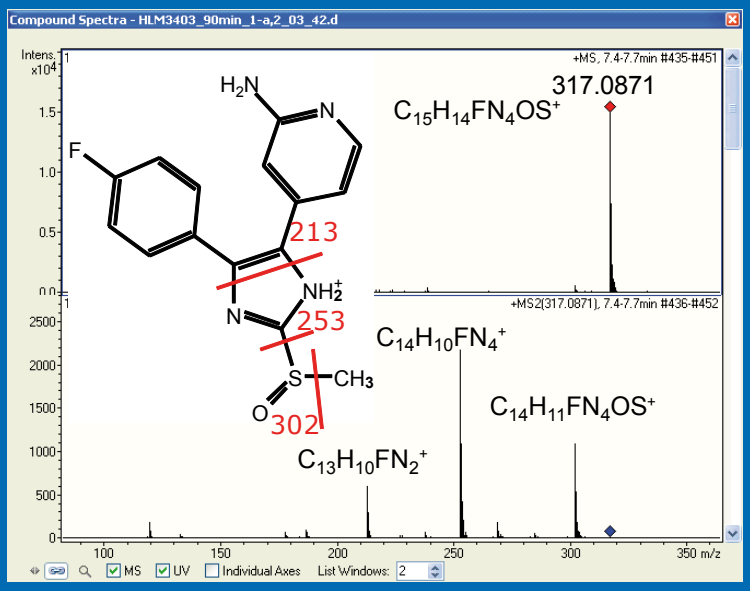
Advancing metabolomics research

Metabolic profiling promotes biomarker discovery to the metabolome level to address profiles that are powerful sensors reflecting situations at physiological endpoints.

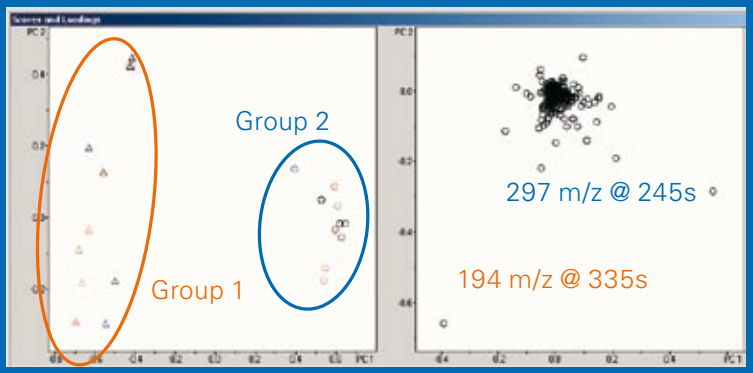
Identify small molecule biomarkers with the power of accurate mass, TIP and fragments analysis for evaluation of disease state, following drug treatment or to monitor toxic response.

Tailored tools for pattern recognition, metabolite MS and MS/MS identification complete the solution package for metabolome research.

Metabolic fragment ID and statistical analysis



Assignment of fragments in metabolite identification is made easy based on the Smart Formula results. AutoMS^2 of metabolite with m/z 317 exhibits e.g. the following losses: methyl radical and the entire sulfenyl group.



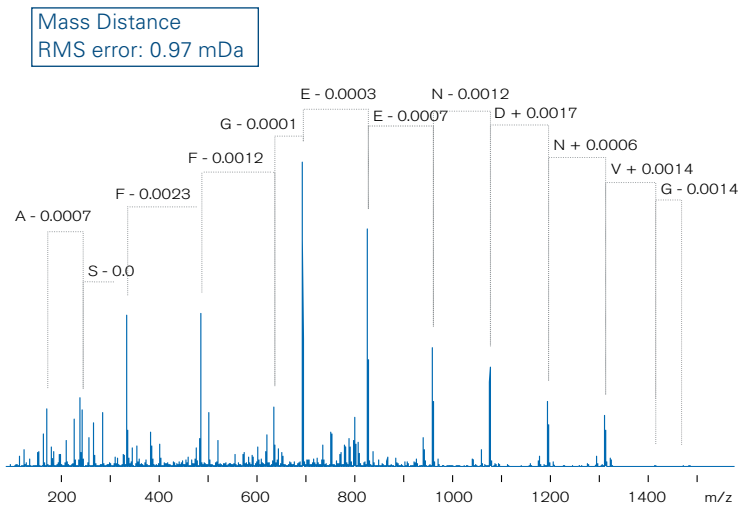
A clear separation of groups in the PCA analysis: Scores and Loadings Plot of rat urine samples from groups receiving different levels of food (reproduced with kind permission from Organon).

Super-sensitive ion funnel source

The new state-of-the-art Apollo II™ ion funnel ESI electrospray source provides 10x more ions – significantly improving sensitivity by an order of magnitude. This leads to substantial progress for applications such as detailed structural studies of low-abundance protein modifications, PTMs or natural products! All ions are collected by a radial RF field and smoothly directed towards the funnel exit. Between the first and the second funnel, ISCD energy can be freely selected for optimal performance of the experiment.

Information-Rich in Depth Analysis

De novo sequencing



MS/MS spectrum of GluFib m/z = 785.8. Exceptional mass accuracy leads to outstanding *de novo* sequencing results.

The *de novo* sequencing machine

The micrOTOF-Q II is the ideal instrument to achieve outstanding mass accuracy over a broad mass range, a prerequisite for successful de novo sequencing – from low-mass immonium ions to high-mass fragment ions.

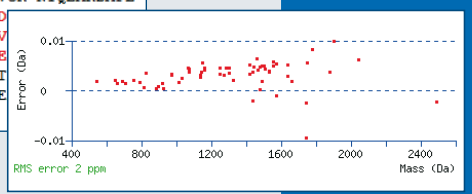
Powerful identifications over a wide dynamic range

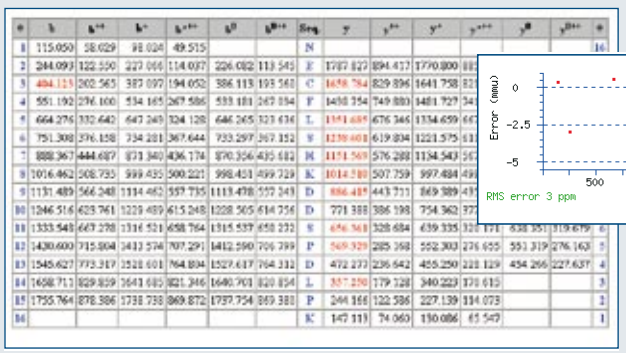
High mass accuracy is available on both the peptides and fragments levels. Impressive mass accuracy on all peptides [1] meets unrivalled mass accuracy on fragments [2] a feature delivering the highest reliability for proteomics research.

Mass accuracy

Matched peptides shown in **Bold Red**

```
    1 MKWVTFISLL LLFSSAYSRG VFRRDTHKSE IAHRFKDLGE EHFKGLVLIA
   51 FSQYLQQCPF DEHVKLVNEL TEFAKTCVAD ESHAGCEKSL HTLFGDELCK
  101 VASLRETYGD MADCCEKQEP ERNECFLSHK DDSPDLPKLK PDPNTLCDEF
  151 KADEKKFWGK YLYEIARRHP YFYAPELLYY ANKYNGVFQE CCQAEDKGAC
  201 LLPKIETMRE KVLASSARQR LRCASIQKFG ERALKAWSVA RLSQKFPKAE
  251 FVEVTKLVTD LTKVHKECCH GDLLECADDR ADLAKYICDN QDTISSKLKE
  301 CCDKPLLEKS HCIAEVEKDA IPENLPPLTA DFAEDKDVCK NYQEAKDAFL
  351 GSFLYEYSRR HPEYAVSVLL RLAKEYEATL EECCAKDD
  401 KHLVDEPQNL IKQNCDQFEK LGEYGFQNAL IVRYTRKV
  451 RSLGKVGTRC CTKPESERMP CTEDYLSLIL NRLCVLHE
  501 TESLVNRRPC FSALTPDETY VPKAFDEKLF TFHADICT
  551 ALVELLKHKP KATEEQLKTV MENFVAFVDK CCAADDKE
  601 STQTALA
```



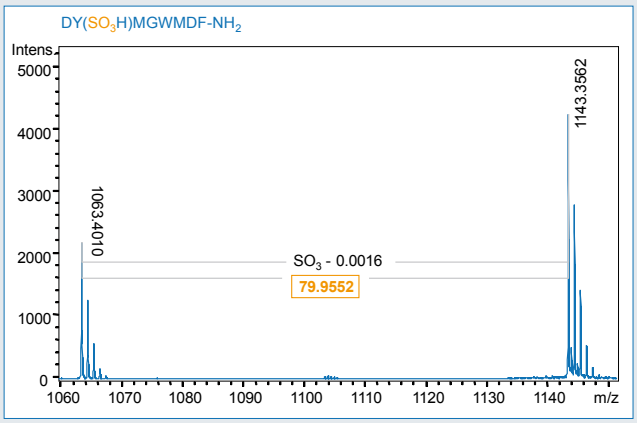


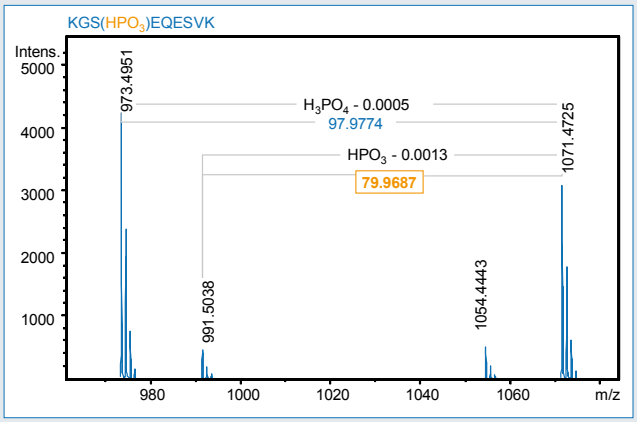
Reproducible mass accuracy: 50 fmol BSA separated by Waters UPLC™ is measured with an RMS error of only 2ppm (1).

Even fragments are reliably analyzed (2) with only 3 ppm RMS error (20 fmol BSA) from a single external calibration.

Proteomics Applications without Compromise

Accurate mass measurements of PTMs





Sulfation? Phosphorylation? Explore the difference!

Understanding proteomes requires knowledge about posttranslational modifications. Detailed insight into the molecule's structure is achieved with the excellent mass accuracy of the micrOTOF-Q II – even with minor mass differences.

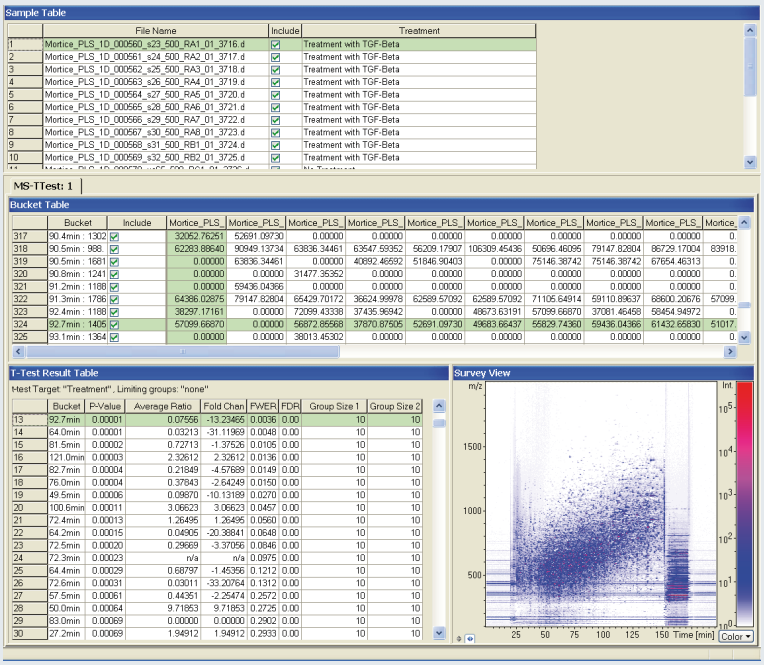
Count on the ability to quantitate

Stable isotopic labeling using iTRAQ™ or the newly invented technology ICPL™ allow fast and convenient, yet easy-to-use, quantitative proteomics research. Excellent sensitivity is achieved due to the technically advanced ion funnel ESI source design.

With its high sensitivity, high mass accuracy and high resolution over the whole mass range , the micrOTOF-Q II forms a cornerstone with Bruker Daltonic's ProteinScape 2 to build an integrated solution for Quantitation. This comprehensive system provides automatic workflows from chromatography to quantitation.

Distinction of sulfation and phosphorylation with micrOTOF-Q II's accurate mass measurement capabilities.

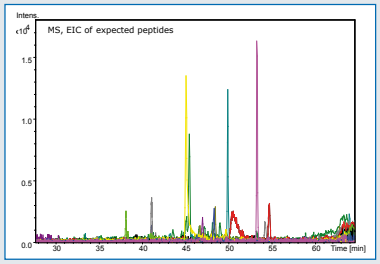
Label-free Quantitation with ProteomeQuant

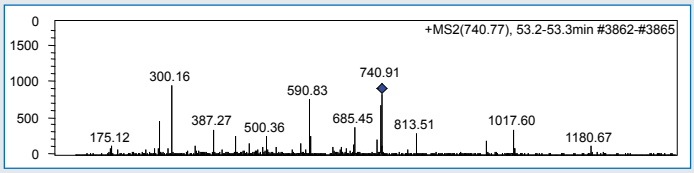


With ProteomeQuant, the label-free quantitative solution for discovery, identification, and targeting of regulated proteins, differential proteome analysis of putative biomarkers is easily feasible in a comprehensive system.

Sensitivity, Dynamic Range & Resolution

MS/MS ID from 100 amol BSA





Analysis of 100 amol BSA digest on column. BSA was unequivocally identified by five peptides. Left: Extracted Ion Chromatograms of identified peptides.

Sensitivity

Ultimate sensitivity is demonstrated with a 100 amol digested BSA sample. Even for this small sample amount, solid peptide identification is possible.

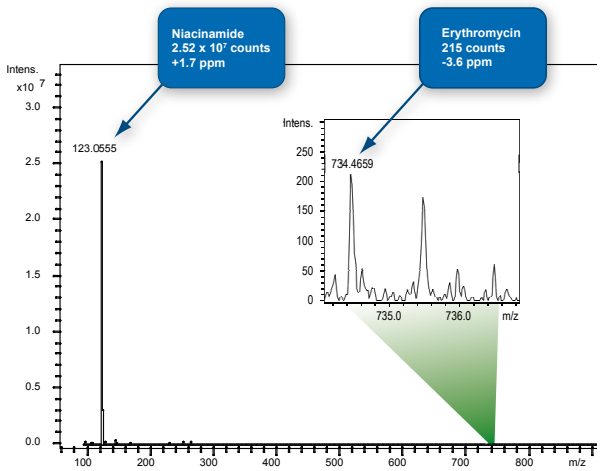
Dynamic range

More than 5 orders dynamic range - excellent stability of mass measurement without tedious recalibration routines is key for screening and LC-MS applications and enables the simultaneous detection of high and low abundance compounds.

Mass resolution

Both small molecules and intact proteins are analyzed with excellent resolution. Isotopic resolution is even achieved for deconvoluted spectra. The simulated pattern fits perfectly to the measured mass spectrum.

More than 5 orders dynamic range

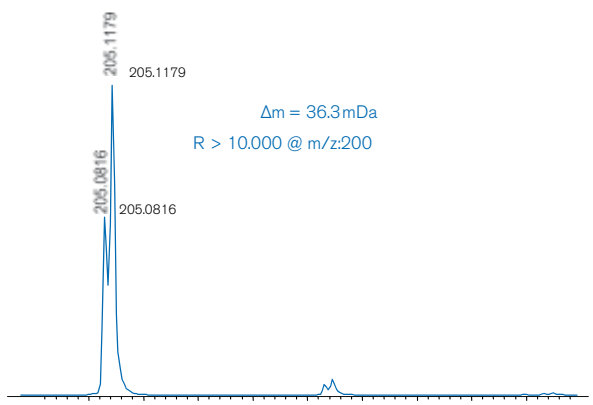


Real measured intraspectrum dynamic range of 5.1 demonstrate the exceptional capabilities of the micrOTOF-Q II.

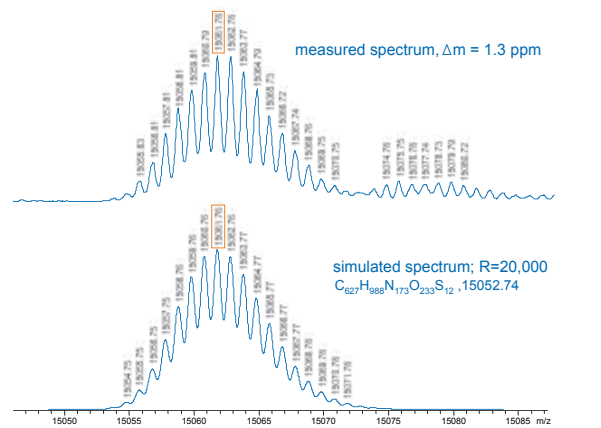
Differentiation of isobaric dipeptides. $C_7H_{13}N_2O_5$ (AD) MW physical = 205.0819, $C_8H_{17}N_2O_4$ (SV) MW physical = 205.1183 delta MW = 0.0364 Da. For separation of the dipeptides at m/z 200, a resolution > 10,000 is achieved.

Ribonuclease B. A spectrum of the intact protein acquired with the micrOTOF-Q II. The mass difference to the calculated mass is only 1.3 ppm. A resolution of > 20,000 FWHM is achieved.

Resolution of Isobaric peptides



Intact protein mass resolution

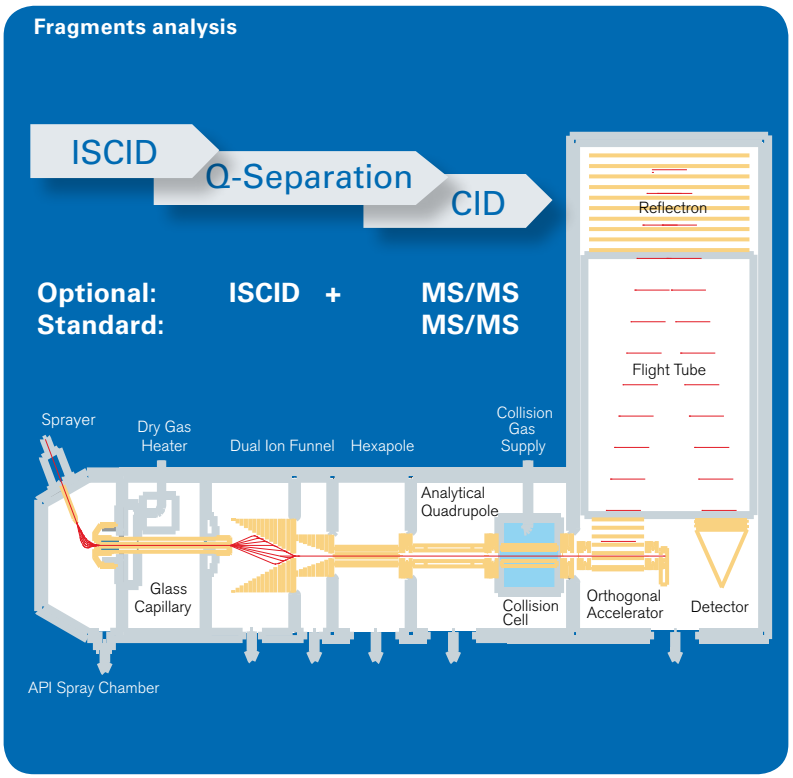


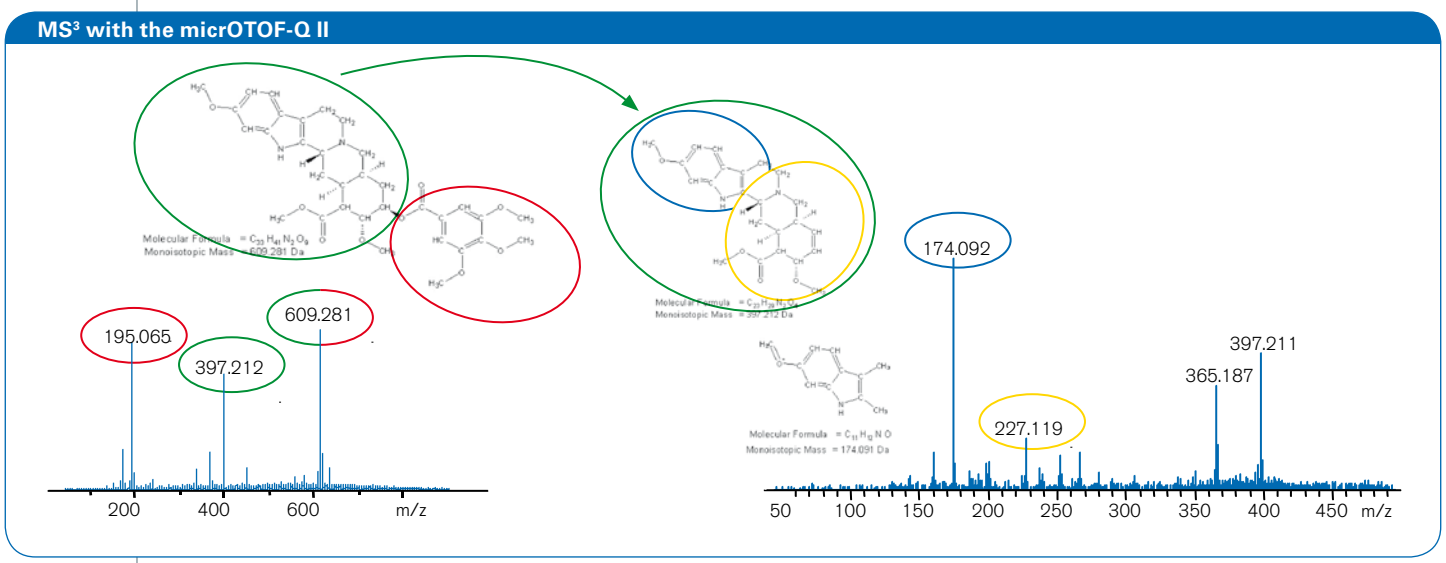
Ultimate Performance with Superior Detection Power

Fragment analysis

The micrOTOF-Q II provides exceptional mass accuracy in MS/MS for metabolite and protein identification.

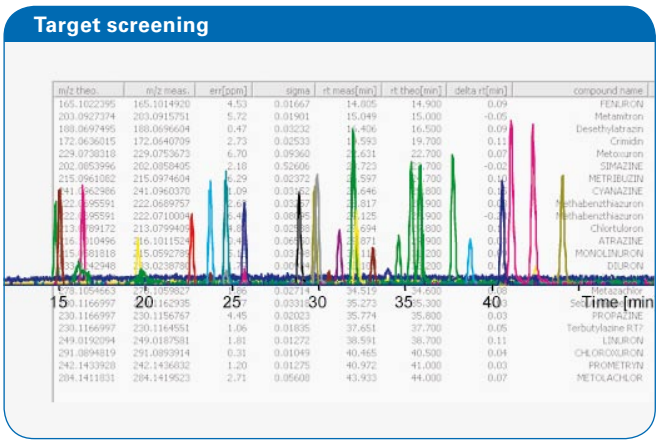
Achieve optional additional fragmentation performance with a source designed for ion fragmentation prior to the quadrupole (In-Source CID). After isolation in the analytical quadrupole, the ISCID fragments can be further fragmented in the collision cell (CID).





Reserpine: In-Source CID (left), Isolation of ISCID ions and fragmentation: MS^3 (right).

Outstanding Solutions and Software Environment



Multitarget Pesticide Screening: hr EIC of detected compounds with ± 0.002 Da mass window.

High-Resolution extracted ion chromatograms(hrEICs) are ideal for screening applications:

- Dramatically reduce chemical background
- Improve specificity
- Screen an unlimited number of targets
- Archive the whole sample-information
- ID of unknowns with MS/MS

Confident quantitative and qualitative multi-target screening – forensics, doping control and residue analysis

The TargetAnalysis™ application allows multi-target compound screening in complex matrices, providing high specificity and enhanced SmartFormula™ molecular formula determination.

Multi-target Screening

Due to a full-scan accurate mass approach, the solution is able to screen thousands of compounds from a single sample LC/ESI-TOF run and enables screening for large compound libraries with a confidence level and reproducibility unsurpassed by any other system. This workflow saves significant time when running multi-target applications like drugs/metabolites in urine, food safety analysis, forensic toxicology or environmental testing.

Create own databases

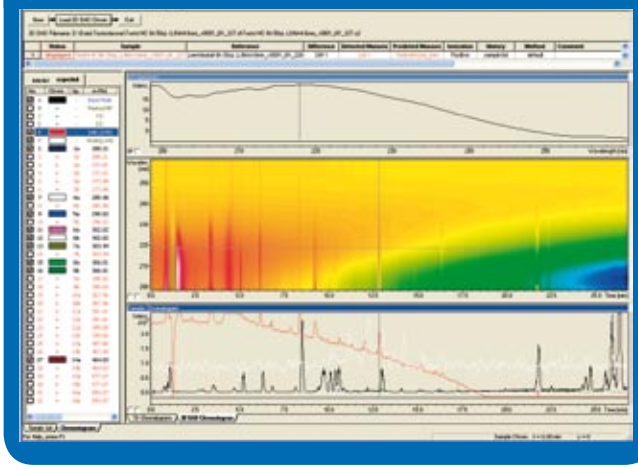
Users are given the power to generate custom, application-specific accurate mass databases. The unique hrEIC (high resolution Extracted Ion Chromatograms) technique, with a tolerance down to +/- 0.002 Da, dramatically reduces chemical background interference and greatly improves specificity.

ID of unknowns

Retrospective in silico screening for new or unexpected compounds is possible because, unlike in triple-quad based MRM methods, the full molecular information content is retained.

Empowering Accessories

Metabolite ID user interface



Chemical formula generation

Compass OpenAccess™ provides an automated walk-up LC/MS system for chemical formula generation, molecular formula confirmation and generic LC/MS measurements. This client-server based software supports LC/MS workflows especially for chemists in laboratories with various levels of instrumental analysis experience.

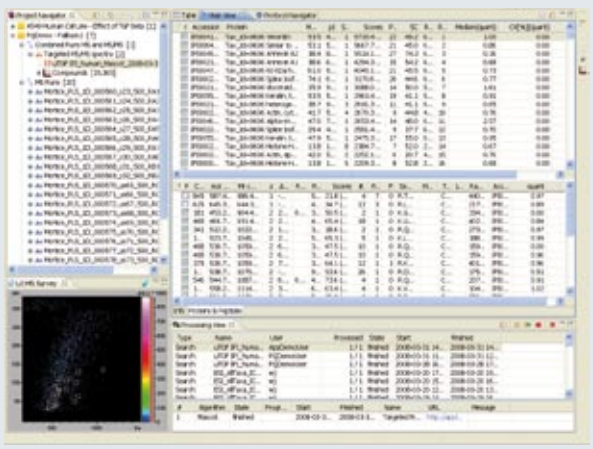
Metabolic Profiler™

Advance biomarker profiling to the metabolome level to address metabolomic profiles that are powerful sensors reflecting situations at physiological endpoints. An application feasible with the micrOTOF-Q II in nutraceutical, pharmaceutical and clinical research.

Metabolite ID

Metabolite and small molecule prediction and detection is performed by MetaboliteTools™, allowing detailed evaluation of samples and sample batches based on the sophisticated eXpose™ detection algorithm and accurate mass capabilities of micrOTOF-Q II. MetaboliteTools predicts possible metabolites from a given drug structure, and extracts relevant information on existing metabolites for LC-MS data.

ProteinScape quantitation result



Proteomics screening and in-depth analysis

Translate mass spectra into knowledge. ProteinScape 2 and BioTools™ provide unique software backbones to mass spectrometric proteome and protein analysis. Visualization tools for validation, such as the LC-SurveyViewer or quantification box-plots, are complemented with protein identification tools, *de novo* sequencing support and PTM discovery. ProteomeQuant, the label-free quantitative solution for discovery, identification, and targeting of regulated proteins allows differential proteome analysis of putative biomarkers in a comprehensive system.

The unified software environment

Our unified Compass™ software environment for all our life science instruments integrates instrument control, data acquisition, processing and interpretation – speeding research and enhancing productivity.

Regulatory compliance

Compass Security Pack™ provides all necessary functions for work in compliance with FDA and EU regulations (21CFR part 11/Annex 11):

- electronic signatures
- audit trailing
- user management
- result history
- system protection during breaks

Technical Specifications

Cutting-edge performance

- Advanced micrOTOF-Q II technology
- World-leading combination of mass accuracy, resolution and sensitivity without compromise
- SmartFormula 3D™, the novel combination of accurate mass of parent and fragment ions with True Isotopic Pattern (TIP™)
- Wide dynamic range for ultra-stable accurate mass
- High-performance Q-q-front end
- Dimensions 640 x 949 x 1320 mm, weight 160 kg

Source options

- Apollo II ion funnel ESI Electrospray source
- APCI atmospheric pressure chemical ionization source
- ESI/APCI multimode source
- APPI atmospheric pressure photo ionization source
- Online / offline NanoElectrospray source
- CE/MS coupling with grounded ESI needle

Analytical performance

- Mass range 50 – 20,000 m/z
- Mass accuracy 1 - 2 ppm RMS Error (internal), 5 ppm RMS Error (external)
- Mass resolution 17,500 (FWHM), typically 20,000 FWHM at LC-speed
- Temperature compensated
- Acquisition rate (2GHz sampling rate) 20 Hz (profile and peak detected spectra to disk)

Compass & application software suites

Integrated LC-MS/MS control and data processing

- SmartFormula and novel SmartFormula 3D
- BioTools™/RapiDeNovo™ software for protein data interpretation
- MetaboliteTools™ for metabolite identification
- ProteinScape™ database system for proteome project management
- TargetAnalysis™ – for multi-target compound screening
- Compass OpenAccess™: Walk-up LC/MS chemical formula generation

The micrOTOF-Q II seamlessly integrates into Bruker Daltonics' system solutions:

- Metabolic Profiler™: The unique NMR-MS solution for Metabolomic Studies
- PROTEINEER™: 2D Gel-MS/MS-based proteomics suite
- ProteomeQuant™: LC-MS/MS-based proteomics suite
- LC-NMR/micrOTOF-Q II coupling

Support of:
HPLC and sample inlet systems from the following vendors: Bruker EASY-nLC, Advion TriVersa NanoMate, Agilent, Dionex, VWR/Hitachi, Waters (incl. UPLC), Autosamplers from CTC

For research use only. Not for use in diagnostic procedures.

www.bdal.com

Bruker Daltonik GmbH

Bremen · Germany
Phone +49 (421) 2205-0
Fax +49 (421) 2205-103
sales@bdal.de

Bruker Daltonics Inc.

Billerica, MA · USA
Phone +1 (978) 663-3660
Fax +1 (978) 667-5993
ms-sales@bdal.com