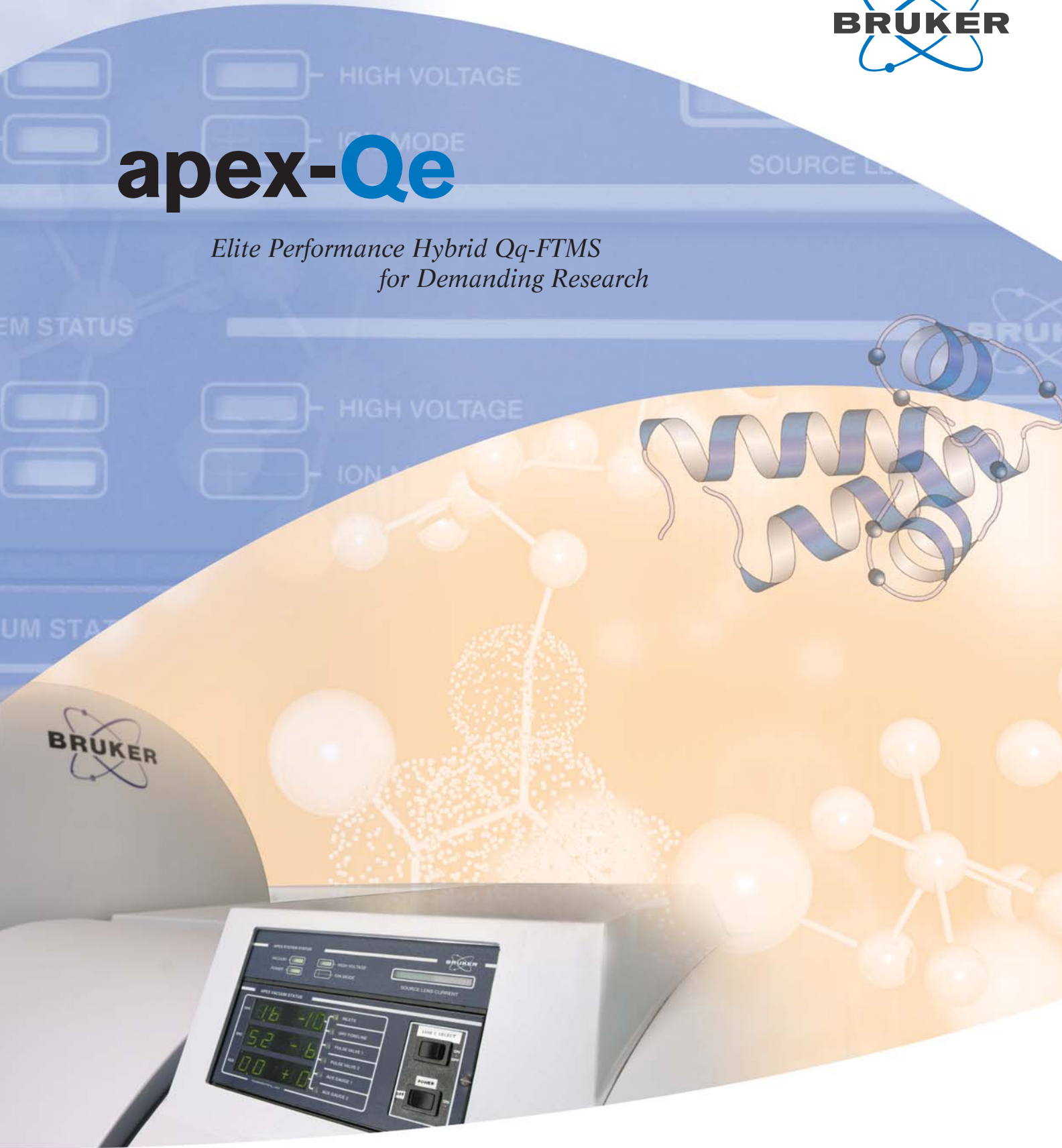




apex-Qe

*Elite Performance Hybrid Qq-FTMS
for Demanding Research*



BRUKER
DALTONICS[®]

Enabling Life Science Tools Based on Mass Spectrometry™

apex-Qe

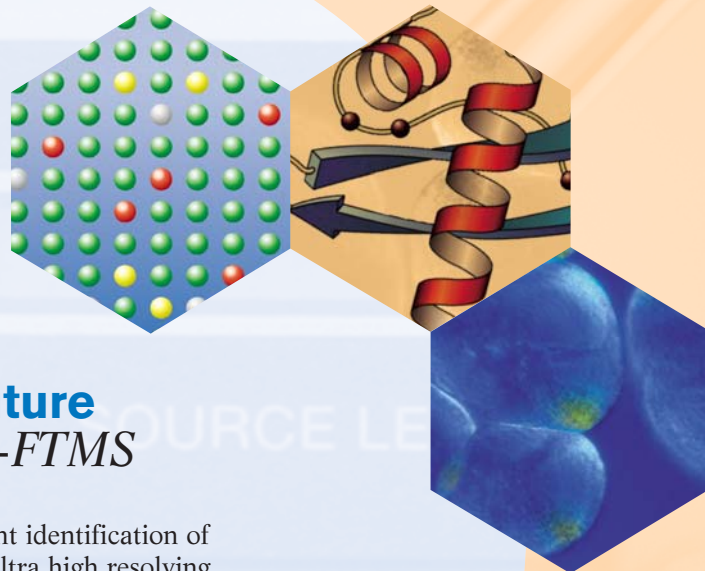
An easy to use system
*for the most demanding
life science research questions...*

The apex-Qe Hybrid Qq-FTMS combines cutting edge FTMS technology with familiar “triple quad” MS offering the latest ion trapping capability.

The resulting hybrid MS/MS system delivers the most accurate, highest resolution and highest dynamic range information available for pharmaceutical discovery, drug metabolism and proteome research.

Finally, these capabilities exist in a package that is truly straightforward to use and with pricing that's affordable — without compromising performance. The apex-Qe is seamlessly integrated with the entire Bruker Daltonics instrument family, all using Compass™, the most powerful and flexible MS software environment available today.





Technology of the future *Hybrid Qq-FTMS*

FTMS is synonymous with confident identification of chemical composition due to its ultra high resolving power and exact mass capability. Now, high duty cycle data dependent LC/MS/MS with hybrid quadrupole technology brings detailed structural and functional information for important agents in drug discovery, metabolism and proteomics. It's easy to operate, sensitive and robust.

apex-Qe leverages the complimentary nature of traditional Collisional Induced Dissociation (CID) and Electron Capture Dissociation (ECD) to provide unique new ways for probing post translational modifications and structural interrogation of intact proteins.

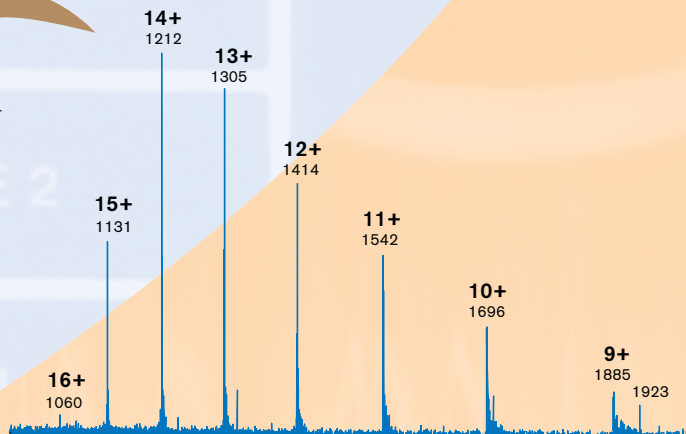
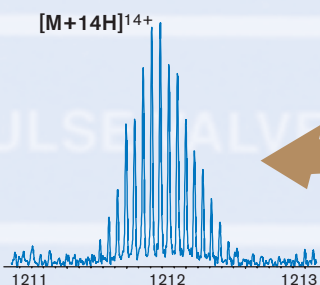
Precise answers to key questions are often facilitated by exact mass to the sub ppm level. FTMS with its ultra high resolution succeeds in analyzing complex matrices where other techniques simply fail.

*Drug
Discovery*

*Structural
Elucidation*

Metabolomics

Proteomics



Highest Resolution for Large Molecules

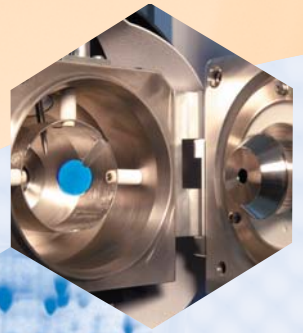
FTMS allows detailed analysis of molecules such as large proteins and provides unrivaled structural information. This protein ESI-FTMS example easily resolves the isotopes of a 17 kDa protein (Myoglobin) expansion showing the high resolution detection for the 14+ charge state.

A power merger

Our quantum leap in capability results from merging the latest quadrupole technology (complete with linear ion trapping modes), a superb multipole collision cell, and the highest performing FTMS available.

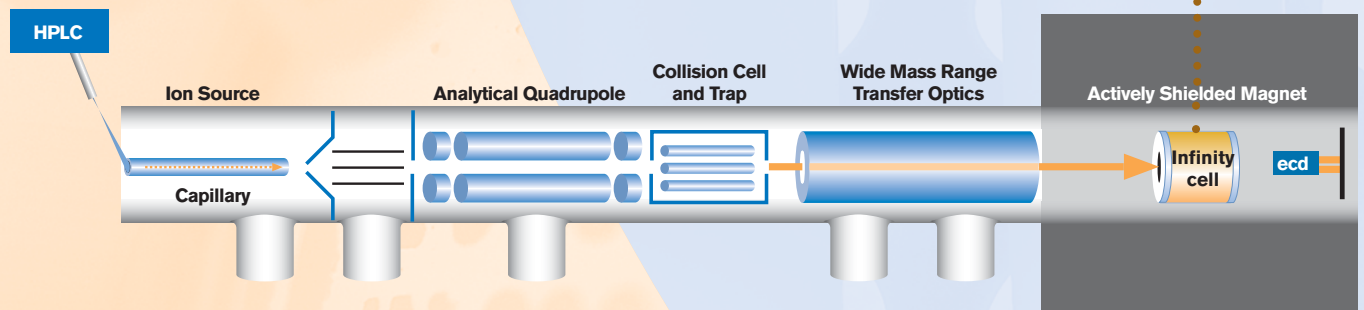
The combined power of the new hybrid configuration features:

- LC/MS/MS with data dependent acquisition using Bruker's simple, unified Compass software package
- Exact mass MS analysis to sub-ppm levels for unambiguous determination of elemental chemical composition. Automated software to confirm composition with m/z and isotopic pattern information
- Exact mass MS⁽ⁿ⁾ capability for detailed structural analysis and peptide sequencing
- Qq-hybrid along with CID and ECD for "top-down" proteomics (Top!Pro™) facilitates selected gas phase ion enrichment
- Extreme resolution capability for direct analysis of complex mixtures (> 600,000 FWHM)
- Wide m/z range simultaneous detection of ions (e.g. 100 - 7,000 m/z)
- Sub fmol sensitivity



Infinity Cell®

The heart of the FTMS detection system is Bruker's Infinity Cell. Through shimming of the RF excitation field, the Infinity Cell provides ultimate FTMS performance.

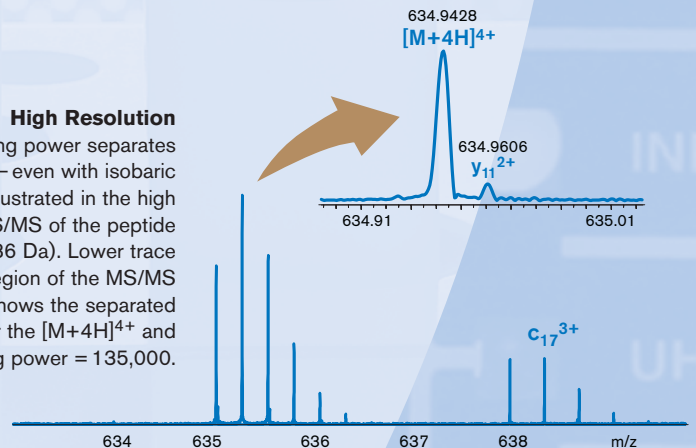
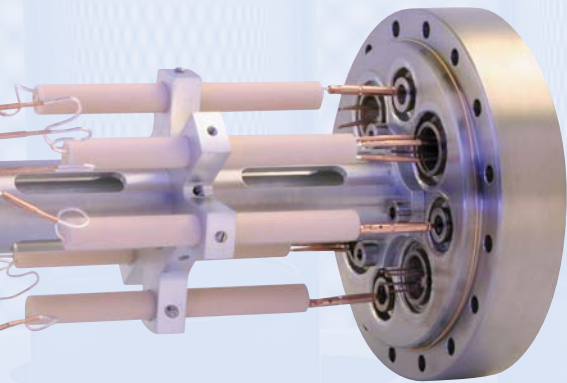


Elite performance *results with confidence*

Mass accuracy with absolute confidence — first time, every time.

With the apex-Qe, high quality, exact mass measurement tools are only a mouse click away. 1 ppm is routine for both intact molecular analysis by MS and structural questions via MS/MS without internal standards or recalibration.

The GenerateFormula tool lists and rates possible empirical formulas consistent with the mass measurement. In addition, comparison of the entire experimental true isotope pattern of the sample with candidate theoretical profiles further validates the elemental composition.

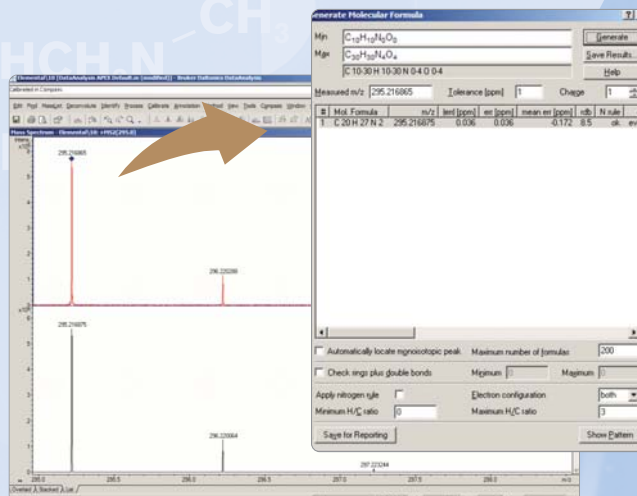


High Resolution

Ultra high resolving power separates complex mixtures — even with isobaric components as illustrated in the high resolution ESI-FTMS/MS of the peptide hecate (MW = 2,536 Da). Lower trace shows the expanded region of the MS/MS spectrum. Inset shows the separated monoisotopic peaks for the $[M+4H]^{4+}$ and y_{11}^{2+} ions. Resolving power = 135,000.

Exact Mass

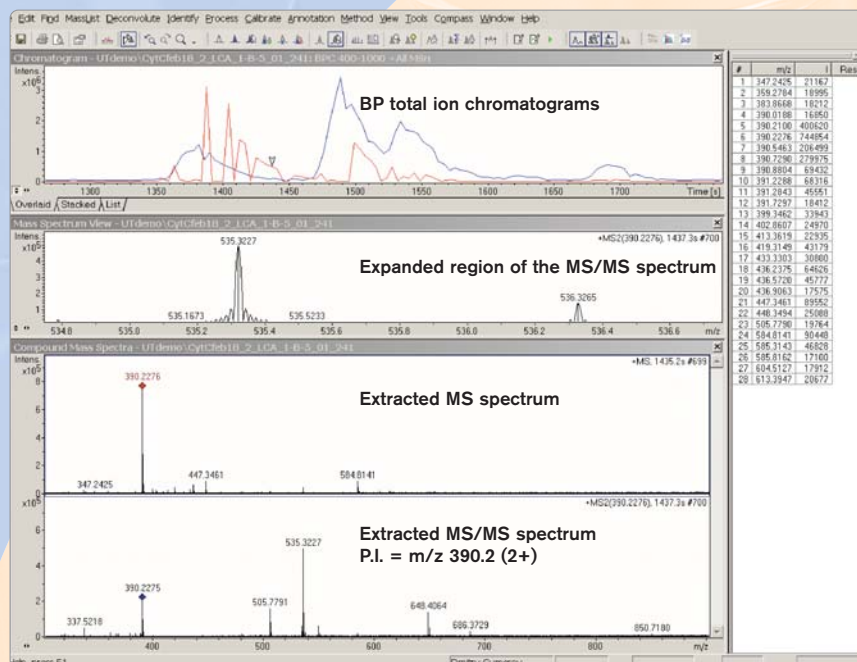
The GenerateFormula tool correctly identifies the elemental composition of an organic synthesis product. The observed m/z 295.216865 is within 0.05 ppm of the theoretical m/z of the top hit ($C_{20}H_{27}N_2$) and the isotopic envelope closely matches the theoretical profile which is displayed below in black.



A new benchmark high resolution and exact mass LC/MS/MS over a wide mass range

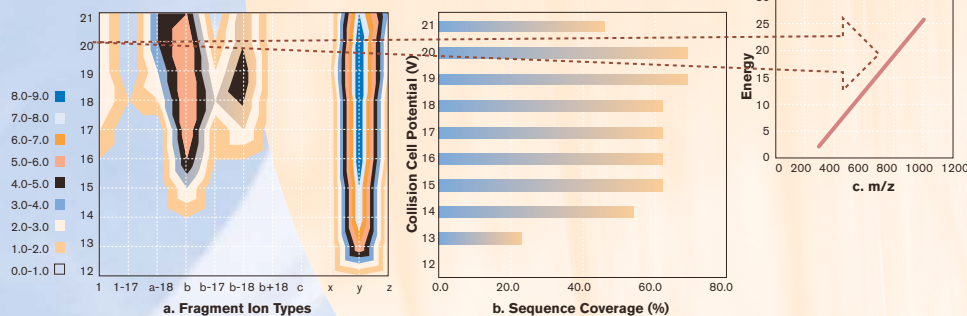
Ultra high resolution over a wide mass range gives you an order of magnitude more m/z data channels to directly handle the most complex samples.

Trace Component Caption
Data-dependent LC-FTMS/MS of cytochrome c tryptic digest. Optimal collision energies determined by SmartFrag™.



SmartFrag

For optimal data-dependent FTMS/MS operation, the apex-Qe utilizes the power of SmartFrag™. SmartFrag automatically determines the most effective collision energy settings for the MS/MS acquisitions. The collision energy correlation is dependent on the class of compounds (i.e. peptides, oligonucleotides, etc.), charge state, and m/z of the parent ion.



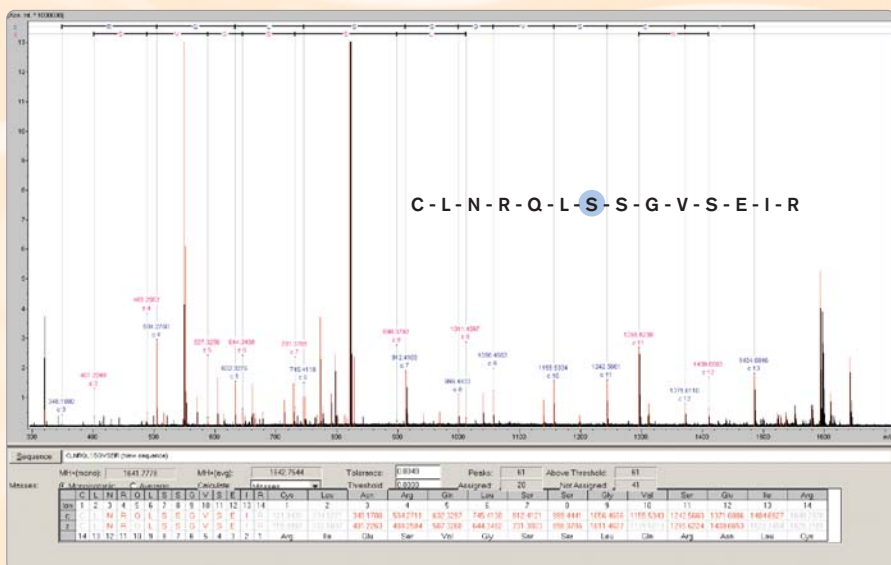
The contour plot (a) represents the appearance of various sequence specific fragment types observed for a peptide as a function of collision energy. The middle plot (b) shows overall sequence coverage for the same peptide as a function of collision energy. A series of such relationships are translated automatically by SmartFrag in auto MS/MS mode to maximize fragmentation coverage. A summary plot (c) illustrates the collision energy vs. m/z relationship for peptides.

MS/MS flexibility with Top↓Pro™ for top-down and bottom-up proteomics

Electron Capture Dissociation (ECD) is making scientific headlines for localization of labile Post-translational Modification sites and for “top down” proteome strategies.

With ECD, classic CID, and available Infrared Laser Fragmentation (IRMPD), the apex-Qe brings three times more fragmentation options for the most possible structural information.

The apex-Qe combines the robust CID capabilities of the Qq front-end with the unique and powerful new Top↓Pro™ technology for top-down proteomics. Top↓Pro™ integrates the uniquely sensitive selective ion enrichment capabilities of our Qq front-end with ECD, and our BioTools™ software for top-down de novo protein sequencing and the discovery of Post-translational Modifications (PTM's).

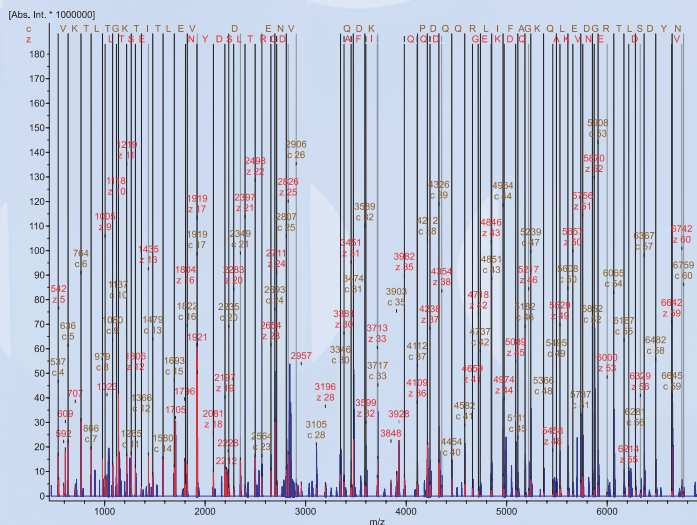


Localize Labile Post-Translational Modifications

In “Bottom-Up” proteomics ECD is utilized to probe for fragile post-translational modifications. In this example, the site of a phosphorylation is localized in addition to providing sequence information. In CID alone, the modification is too fragile to be observed.

Top-Down Proteomics

A single spectrum resulted in sequencing 90% of an 8.5 kDa protein (ubiquitin) using ECD fragmentation of the (+9) charge state of the parent ion. Deconvolution of the resulting ions allows much of the sequence to be read directly in BioTools.

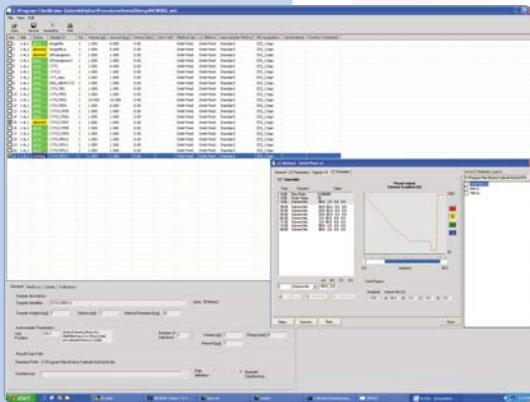


Unified software environment for all Daltonics life science instruments

The apex-Qe features Compass, Bruker Daltonics' unified software environment for all life science instruments. Compass provides full system control and data handling by an intuitive and easy-to-use graphical user interface (GUI). Compass integrates the acquisition modules of the apex software suite with a new, global method management wizard and an additional module for work in regulated environments.

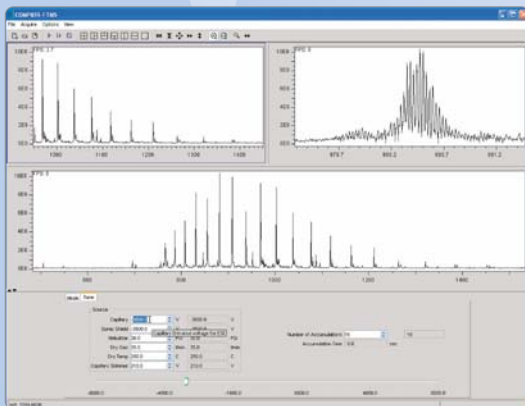
Method

The LC/MS sample table reports all information about sample and method, including the current acquisition status.



New global method management

The Compass software allows easy access to all system and method selections for an experiment. The operator can edit if appropriate and resave a new protocol.

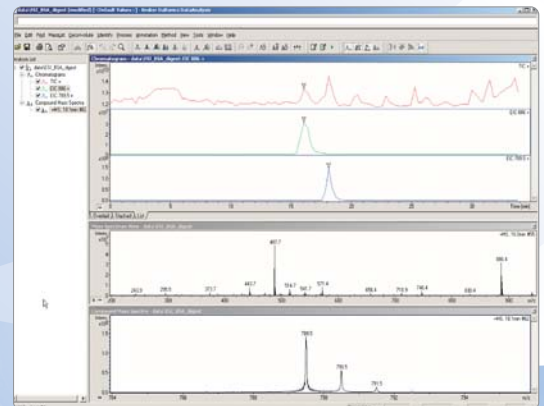


apex Control Screen

The MS system control screen organizes parameters in a simple notebook and features a flexible data display window.

Process

Export of mass spectra, chromatograms and peak reports as graphics files or via clipboard are all standard features for smooth integration into office applications.



Automation & Customization

Batch processing of LC/MS data is performed by the Automation Engine™. Recurring tasks can be automated via Visual Basic scripting; scripts for typical tasks like ICAT analysis are pre-installed.

21 CFR 11 Compliance

Sample Preparation

Data Acquisition

Data Processing

Data Interpretation

HyStar™ LC/ Control

- Global Method Management
- Autosampler control and sample tracking
- Supports popular HPLC and nanoLC systems
- Advanced multidimensional chromatography and column switching

apexControl™

- Operator and expert access levels
- Quick and easy method setup
- SmartSelect™ for automated MS/MS
- SmartCal™ auto calibration with any standard
- SmartFrag™ automatic setting of fragmentation energy for efficient and reproducible MS/MS

DataAnalysis™

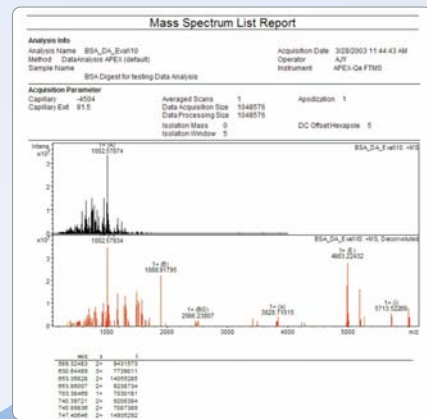
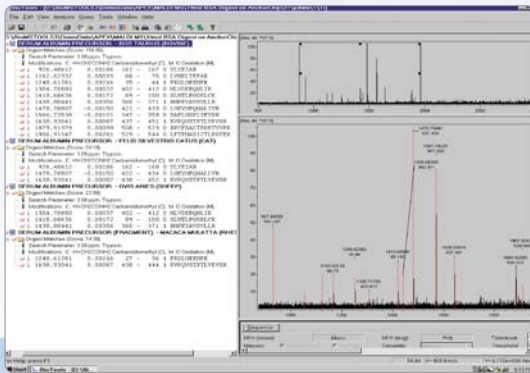
- Automated and interactive LC/MSⁿ data browsing
- MassAnalysis™ accurate mass module
- AutomationEngine™ for recurring application-specific tasks via visual basic scripting (i.e. ICAT)

Results

- BioTools/RapiDeNovo™ for protein data interpretation, database searches, and characterization (PTMs and other mutations)
- MetaboliteTools™ for identification of drug metabolites
- LibraryEditor™ and LibrarySearch™ for MS and MSⁿ Libraries
- ProteinScope™ database system for proteome project management

Compatibility & Integration

Within the Compass environment, a customized selection of modules will serve your system configuration and application requirements. A unified look and feel ensures full compatibility to other Daltonics life science instruments, including Esquire, microTOF, BioTOF, and the Flex series including MALDI TOFs and TOF/TOFs.



Analysis Report

Flexible report printing: The Report-Designer allows both predefined and customized reports to match your GLP requirements.

Interpretation

Analysis of peptide and protein data is made easy through the use of application specific tools. In this example, BioTools is embedded with specific features such as de novo sequencing, sequence annotation, modification analyses, and database searching capabilities.

Extended performance accessories

Magnet Choices:

Bruker Daltonics offers ultra high performance actively shielded magnet technology with 7 Tesla on the standard apex-Qe system. In addition extended performance versions of apex-Qe are available at 9.4 Tesla and now 12 Tesla — the world's highest commercially available FTMS field strength.

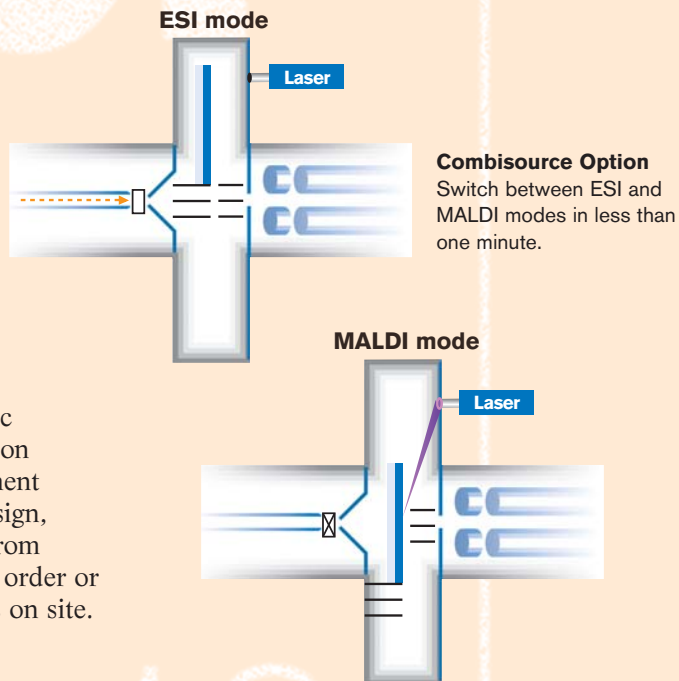
P² = Power x Performance:

Many important analytical properties increase with the square of magnetic field strength. Capabilities such as FTMS dynamic range, center of mass collision energy and ion storage capacity show quadratic enhancement with field. With the modularity of our design, obtaining higher field strength systems from Bruker Daltonics can be done on initial order or as a magnet retrofit to existing systems on site.

Ion Source Flexibility:

While FTMS is ideally suited to liquid introduction, atmospheric pressure ionization techniques such as Electrospray (standard), APCI and Nanospray, Bruker Daltonics now offers a unique integrated ESI and MALDI ion source solution — Combisource™. In just 60 seconds Combisource gives users the ability to switch to and from ESI and MALDI ionization with just the touch of a button. The intermediate pressure MALDI source offers exquisite sensitivity and preserves parent ion fidelity throughout the complete FTMS detection process.

By integrating the Flex series MALDI TOF standard microtiter plate target design, users have immediate access to our patented Anchorchip technology for 10–100x sensitivity boost over standard plate technology, 96, 384 or 1,536 sample spots/plate and full compatibility with our Proteineer suite of automated sample preparation robotics from gels to sample spotting.





Partners for progress

Managing Evolution

Bruker Daltonics recognizes that our customers' analytical needs are constantly evolving and require ever more performance and efficiency to stay ahead. We're ready to work with you to help you optimize your solution for today, while anticipating tomorrow and planning for your ongoing success.

Our modular FTMS has been designed from the ground up for forward compatibility to leverage new developments as they become available. This approach adds tremendous value and lifetime to the technology. Key innovations such as the world's first 12 Tesla FTMS magnet, the first commercially available ESI external source FTMS, and now the first Qq FTMS illustrate our upgradability. Our dedicated team of applications scientists, R & D professionals and software engineers are constantly leading the way with FTMS and stand ready to respond to evolving user needs.

Ongoing Support

Customers enjoy our ongoing comprehensive support for applications development with state-of-the-art laboratories and a staff with a wealth of mass spectrometry experience. The Daltonics CENTER (CENTralized TECHNical Response) provides instant access to the highest level of MS customer support by connecting you with the appropriate technical support/engineering staff. The CENTER also is the focal point for scheduling routine maintenance visits, access to all our CARE products (Consumables And REagents) and any general questions for parts and applications.

Work with us over the entire process, from planning to results, to get maximum performance, throughput and value. We're ready to be your partner for progress!





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