SYNAPT® G2-Si

RESOLUTION IN THREE DIMENSIONS

Waters

THE SCIENCE OF WHAT'S POSSIBLE.®

THE BENEFITS ARE CLEAR

Chromatography. Mobility. Mass. When mass resolution and chromatography are not enough, high-efficiency T-Wave™ ion mobility gives you an additional dimension of separation, based on molecular size and shape.

PROTEOMICS BIOMARKER DISCOVERY PHARMACEUTICALS LIPIDOMICS
STRUCTURAL ELUCIDATION METABONOMICS BIOPHARMACEUTICALS
STRUCTURAL BIOLOGY POLYMERS PETROLEUM CHARACTERIZATION
IMAGING METABOLITE IDENTIFICATION NANOPARTICLES FOOD RESEARCH

SYNAPT® delivers a third dimension of resolution to your analysis, proven to transform your levels of insight and confidence whatever the application.

T-WAVE™ ION MOBILITY POWERED

www.waters.com/proof


Waters
T-WAVE
ION MOBILITY

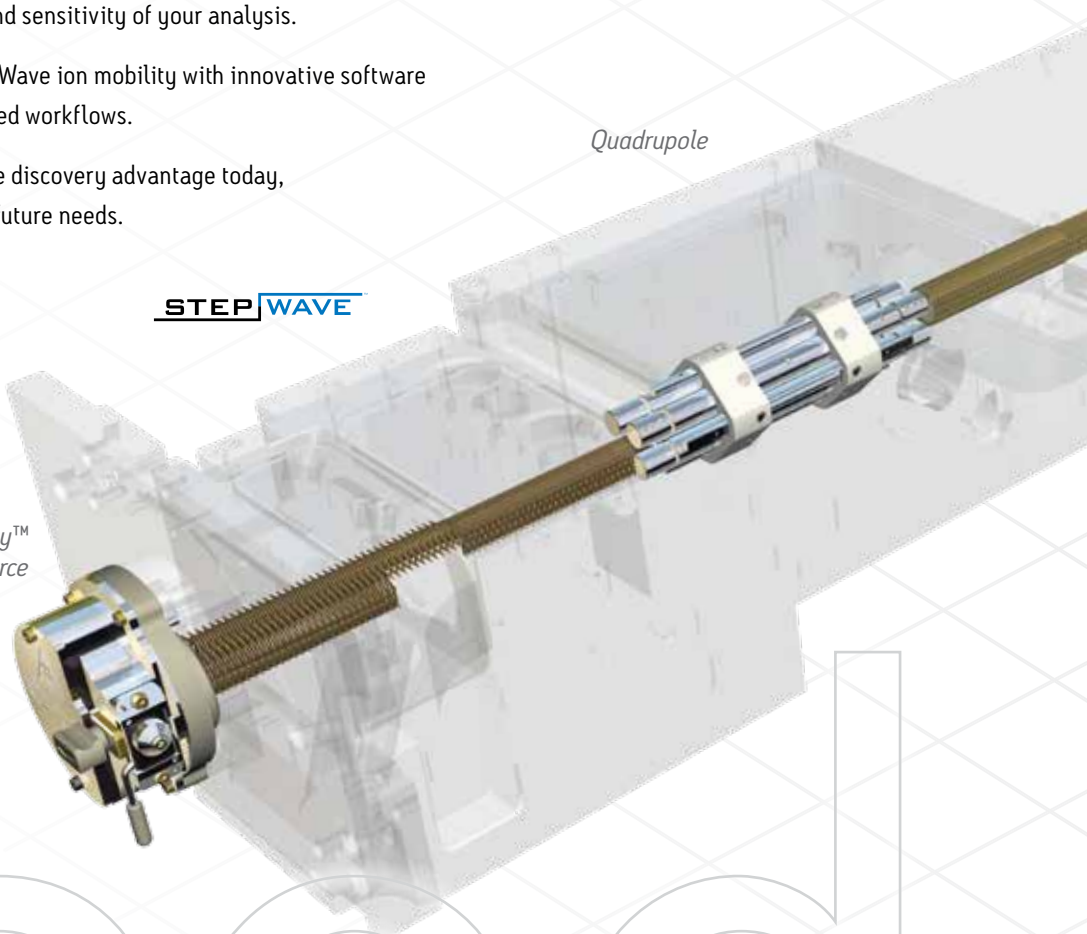
YOU LEAD THE DISCOVERY – WITH OUR LEADING TECHNOLOGY

If you need to be first to discover or first to publish, look no further than SYNAPT High Definition Mass Spectrometry.® The unique ability to use the collision cross section (CCS) property of an ion, through the use of T-Wave ion mobility, delivers unique analytical benefits to a wide range of applications.

Information. SYNAPT G2-S*i* uses high efficiency T-Wave ion mobility to significantly enhance the peak capacity, specificity and sensitivity of your analysis.

Informatics. SYNAPT G2-S*i* combines T-Wave ion mobility with innovative software to transform your targeted and untargeted workflows.

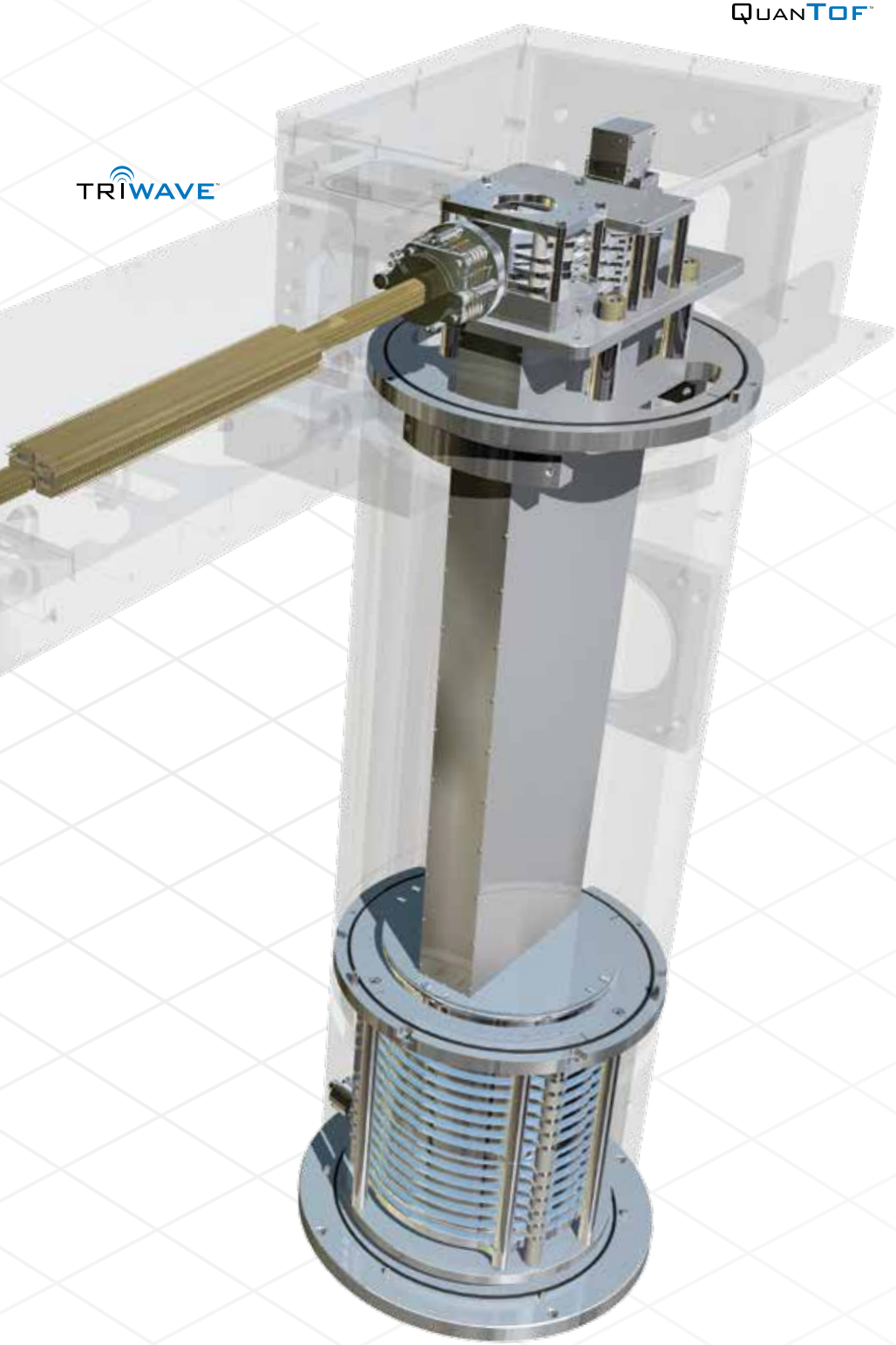
Impact. SYNAPT G2-S*i* provides a unique discovery advantage today, and the greatest potential to meet your future needs.



lead

QUANTOF™

TRIWAVE™



The ultimate in qualitative and quantitative performance

StepWave,™ QuanTof,™ and MS^E 'data independent' acquisition combine to provide the most comprehensive and confident untargeted identification and quantification of compounds with UPLC-MS/MS, at the lowest concentration levels in complex matrices.

Breakthrough SYNAPT High Definition MS

Every scientist can extract unparalleled information content and make new discoveries not possible by any other method, by combining high efficiency T-wave ion mobility separations with high resolution exact mass tandem MS.

Maximum versatility

Serve the broadest range of applications with the most extensive range of targeted data acquisition methods, chromatographic inlet, and ionization source capabilities.

Instant efficiency

Realize maximum system usability and workflow efficiency across your organization through Waters design philosophy of Engineered Simplicity.™

Accelerated success

Maximize your success with complete system solutions backed by a superior applications and technical support network.

QuanTof Technology delivers an outstanding combination of performance attributes:

- Over 50,000 FWHM mass resolving power
- Exact mass (<1 ppm RMS)
- Accurate isotope abundances
- In-spectrum dynamic range and linearity in detector response of up to 10^6
- Up to 30 spectra/sec
- Maximum ToF duty cycle for HD-MRM and HD-DDA methods

QuanTof™

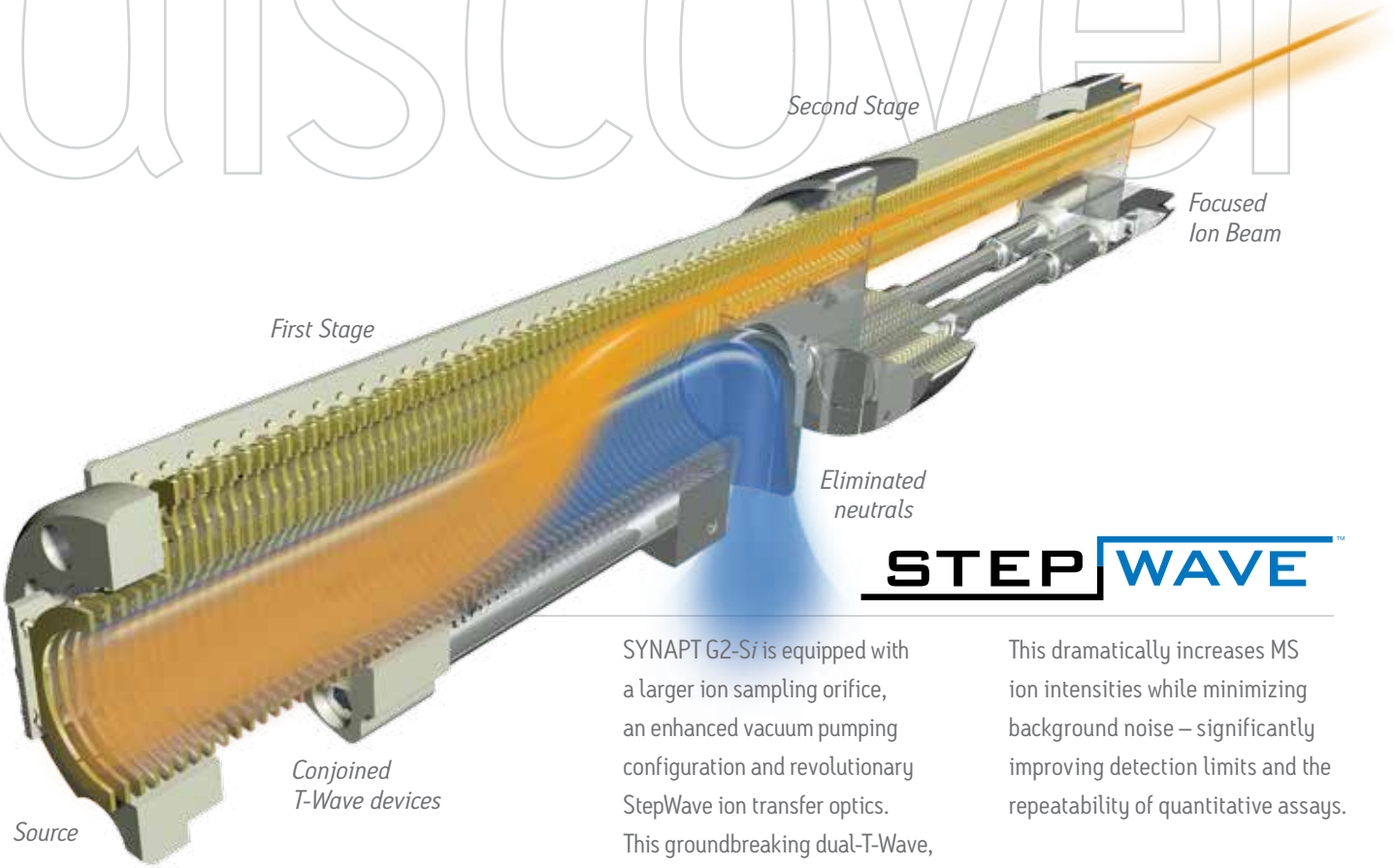
QuanTof's high-field pusher and dual-stage reflectron, incorporating high-transmission parallel wire grids, reduce ion turnaround times due to pre-push kinetic energy spread and improve focusing of high energy ions respectively.

These innovative technologies combine to provide the highest levels of Tof performance. The unique ion detection system combines an ultra-fast electron multiplier and 'hybrid ADC' detector electronics to provide outstanding sensitivity and quantitative performance.

EXPERIENCE THE ULTIMATE IN QUALITATIVE AND QUANTITATIVE PERFORMANCE

When your progress is limited by missing information or the risk of false positive results in your analysis, the combination of StepWave ion optics, the QuanTof analyzer and MS^E 'data-independent' acquisitions will maximize your chances of success. By providing the best qualitative and quantitative performance attributes, these innovative technologies significantly increase compound coverage and confidence in identification, characterization, and quantitation for your most demanding applications.

discover

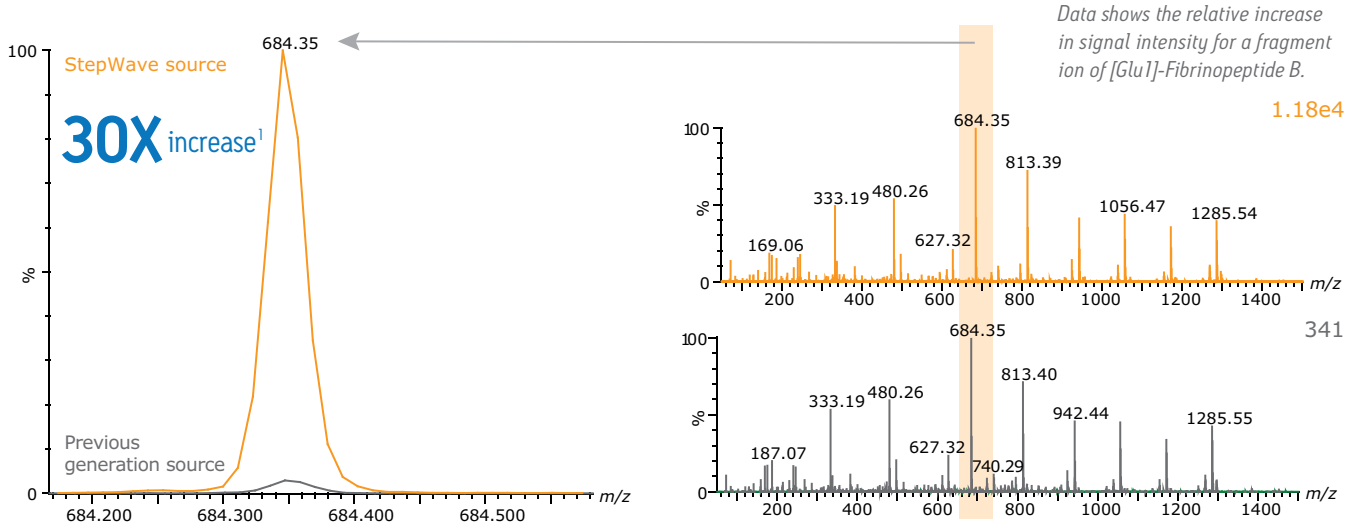


STEP WAVE™

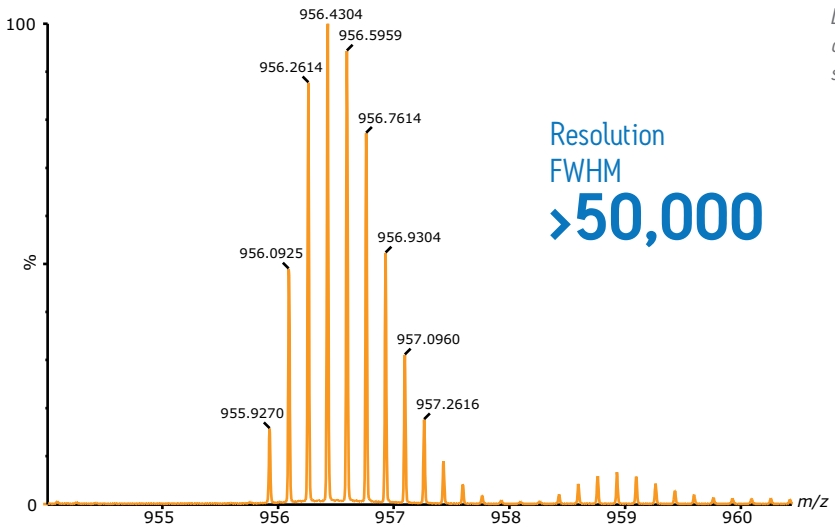
SYNAPT G2-S*i* is equipped with a larger ion sampling orifice, an enhanced vacuum pumping configuration and revolutionary StepWave ion transfer optics. This groundbreaking dual-T-Wave, off-axis design transfers ions from the ion source to the quadrupole MS analyzer with the highest possible efficiency, at the same time as ensuring undesirable neutral contaminants are actively filtered out.

This dramatically increases MS ion intensities while minimizing background noise – significantly improving detection limits and the repeatability of quantitative assays.

Ultra-high sensitivity

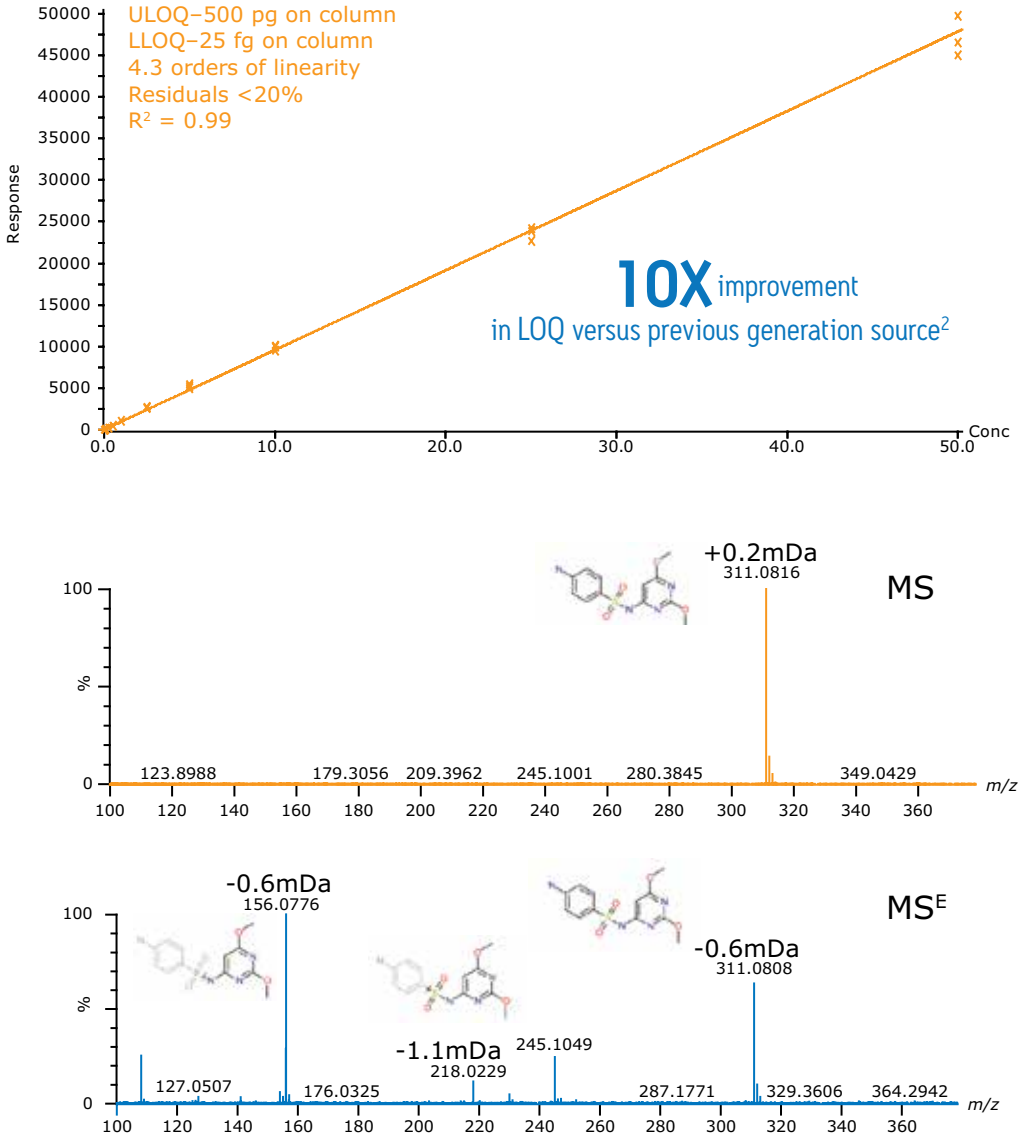


High mass resolution



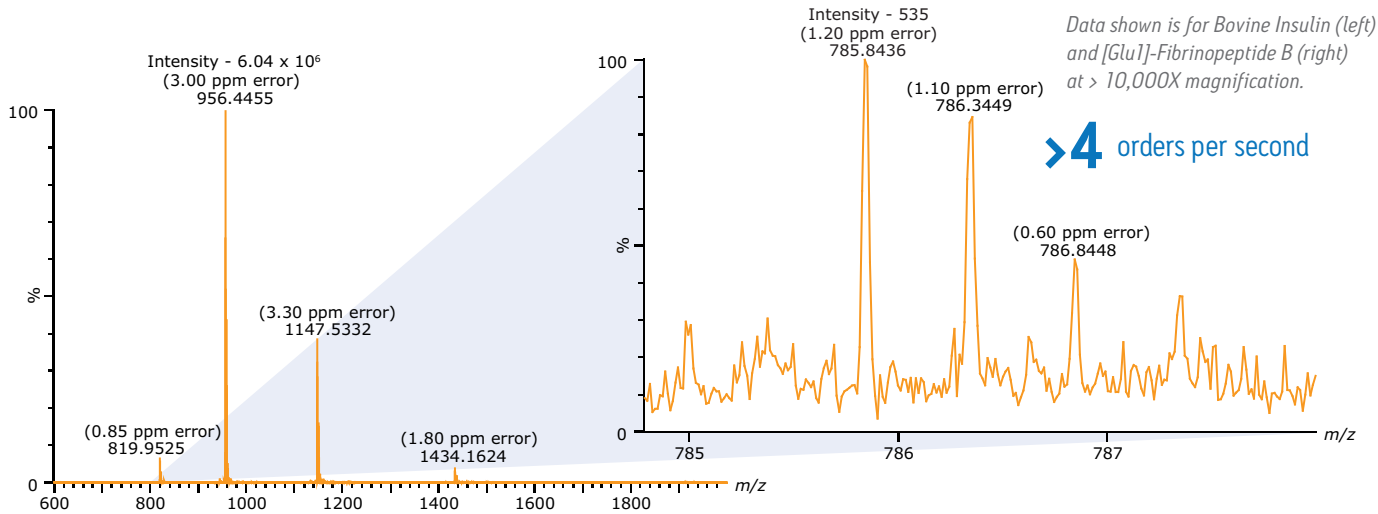
- **Selectivity and accuracy**
  QuanTof delivers high resolution, exact mass, accurate isotope abundance, a wide dynamic range and speed of acquisition, without compromise, for UPLC® separation of very complex samples.
- **Sensitivity and linearity**
  StepWave and QuanTof provide LOD, LOQs at significantly lower concentrations than ever thought possible with high resolution MS, with exceptional linearity and reproducibility, even in the most complex matrices.
- **Maximum coverage**
  Eliminate the risk of incomplete analysis with UPLC-MS^E, a simple patented method of data acquisition that comprehensively catalogs samples in a single analysis.
- **Simple, complete assays**
  Quantify with all the benefits of oa-Tof, MS^E, Tof-MRM, and HD-MRM:
  - Quantify and confirm unlimited numbers of components in one analysis
  - Eliminate or reduce time-consuming method development
  - Interrogate archived datasets to detect, identify, and quantity new compounds

Accurate quantitation > 4 orders of linearity, with UPLC-MS^E



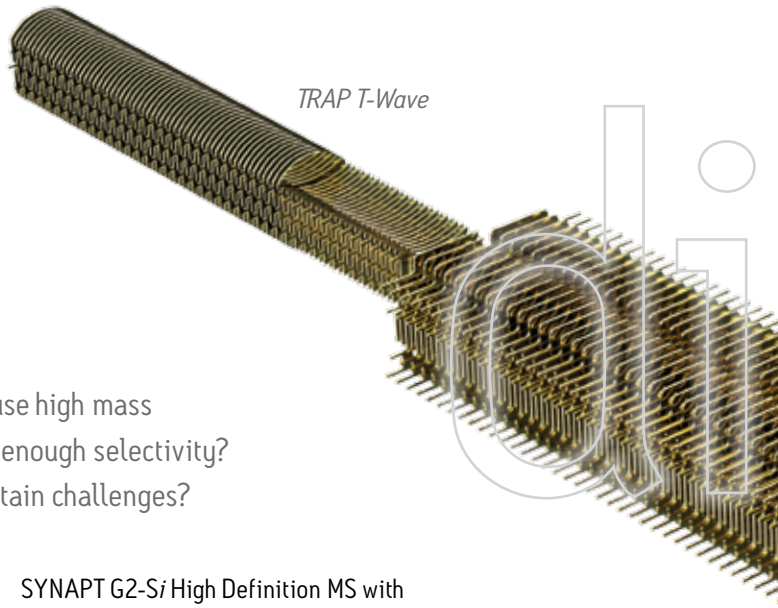
Simultaneous quantitation and identification with UPLC-MS^E. Every component is recorded with molecular (MS) and fragment (MS^E) ion spectra to aid compound identification. The mass spectral data shown is from 2.5 pg of Sulfadimethoxine on column.

In-spectrum dynamic range



Data shown is for Bovine Insulin (left) and [Glu1]-Fibrinopeptide B (right) at > 10,000X magnification.

BREAK THROUGH WITH SYNAPT HIGH DEFINITION MS



Ever wondered what components you might be missing because high mass resolution or your current tandem MS methods don't provide enough selectivity? Frustrated that your existing MS techniques can't address certain challenges?

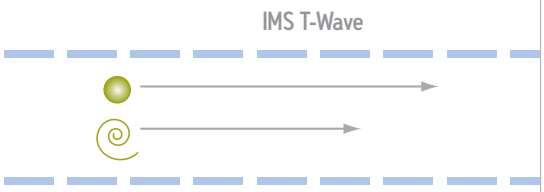
The SYNAPT G2-S*i* System provides a unique platform to further your discovery efforts by providing capabilities that go beyond conventional MS instrumentation.

SYNAPT High Definition Mass Spectrometry is the combination of high-efficiency T-Wave ion mobility measurements and separations with high-performance tandem MS, enabling the differentiation of samples by size, shape and charge, as well as mass.

By introducing the orthogonal dimension of gas-phase ion mobility separation, you can take advantage of a molecule's Collision Cross Section to significantly enhance separation, specificity, sensitivity and structural insight in your analysis.

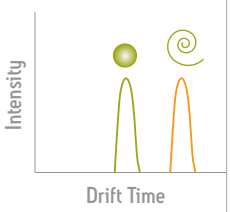
SYNAPT G2-S*i* High Definition MS with Triwave Technology offers:

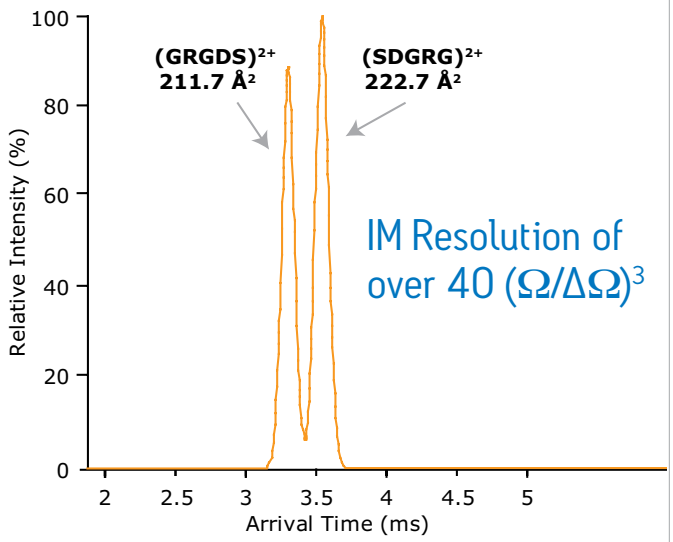
- Rapid, high-efficiency, T-Wave ion mobility separations
- Removal of interferences, purification of spectra
- Significant increases in analytical peak capacity
- Separation of isomers, conformers, and isobaric compounds
- Enhanced compound ID and structural characterization
- Simple, reproducible CCS measurements
- Comprehensive informatics tools to accelerate visualization, processing, and interpretation of multidimensional SYNAPT G2-S*i* HDMS data



Why ion mobility?

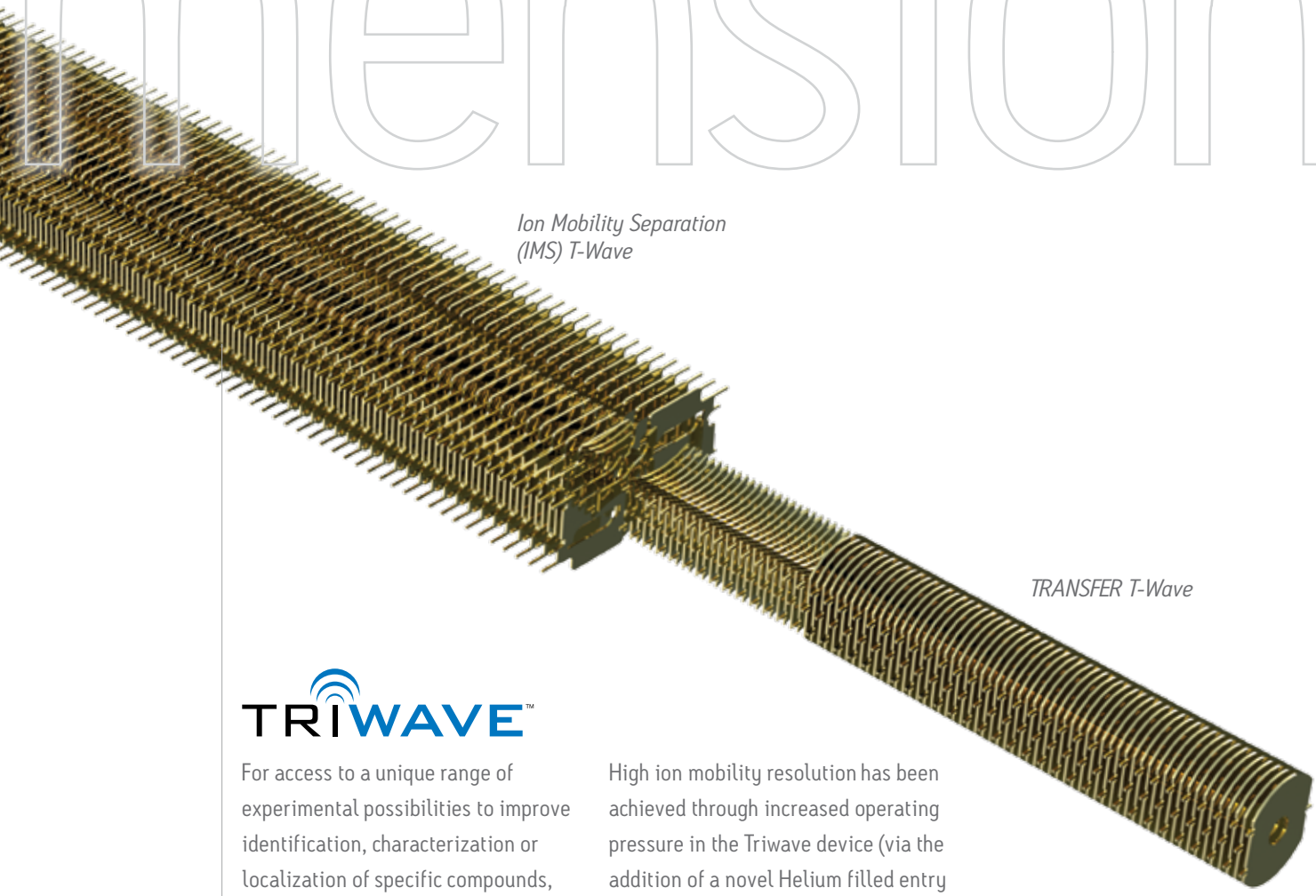
Measuring the mobility, or drift time, of an ion can yield information about its structure, as compact ions with small collision cross-sections drift quicker than extended ions with large collision cross-sections. Mixtures of compact and extended ions can be separated in the gas phase.





Enhanced IM separation power – the high ion mobility resolving power of SYNAPT G2-Si enables a mixture of two reverse sequence peptides (GRGDS and SDGRG) differing in CCS (Ω) by only 5%[3] to be easily separated. A mobility resolution in excess of 40 (Ω/ΔΩ) is indicated.

mension



Ion Mobility Separation (IMS) T-Wave

TRANSFER T-Wave

TRIWAVE™

For access to a unique range of experimental possibilities to improve identification, characterization or localization of specific compounds, Triwave is the key. Triwave employs three T-Wave ion guides, allowing ions to be trapped and accumulated, separated based on their mobility, and then transferred to the QuanTof analyzer for high-resolution analysis. Triwave's innovative configuration also ensures that the introduction of IM is not made at the expense of sensitivity.

High ion mobility resolution has been achieved through increased operating pressure in the Triwave device (via the addition of a novel Helium filled entry cell in the IMS T-Wave).[3] The TRAP and TRANSFER T-Wave regions can be used independently or together as collision cells, with (HDMS mode) or without (TOF mode) ion mobility separations, providing a unique and diverse range of experimental possibilities for improved and more complete structural characterization.

TRANSFORM YOUR CAPACITY TO DISCOVER

Uncovering unknown compounds fuels discovery and progress in scientific understanding. If you want to be able to see what others never have, the unique geometry of SYNAPT systems provide an unrivalled discovery advantage.[6,9]

PEAK CAPACITY

By combining high-efficiency ion mobility separations with a high resolution time-of-flight analyzer, SYNAPT G2-S*i* provides a large increase in analytical peak capacity, and delivers more information than is available with the highest chromatographic or mass resolution alone.

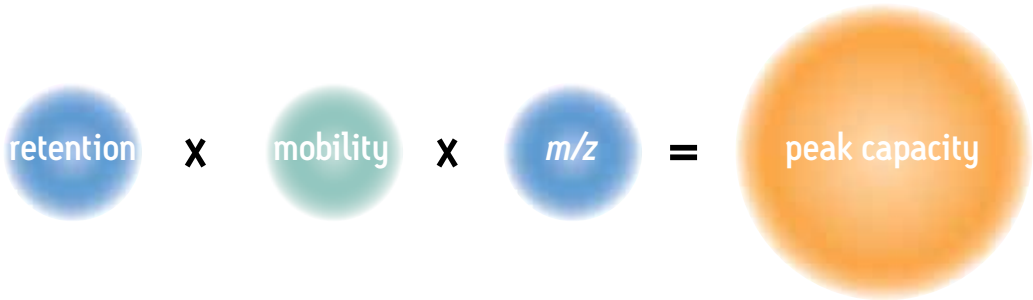
ION MOBILITY SEPARATION

The orthogonal separation afforded by high-efficiency IM separation dramatically increases the number of detectable and identifiable components in complex mixtures by rapidly separating molecules of the same mass-to-charge ratio, while also providing measurements related to their gas-phase conformation.

HDMS^E AND CCS WORKFLOWS

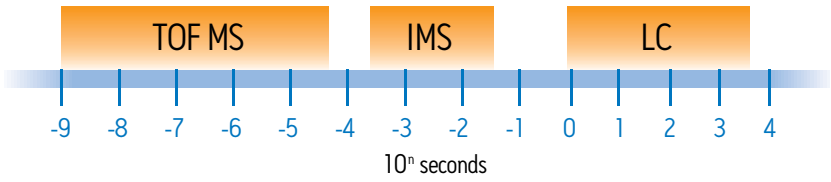
To provide unambiguous confirmation of compound identity, the combination of ion mobility and MS^E 'data independent' acquisition (HDMS^E) means fragment ion information is attainable for every detectable component and with TransOmics,™ BiopharmaLynx,™ High Definition Imaging, DynamX™ (HDX), and UNIFI® CCS Research Edition (for small molecules) you can now access all these benefits quickly and easily across a wide range of applications.

singly charged up to 5x total MS peak capacity
multiply charged up to 10x total MS peak capacity



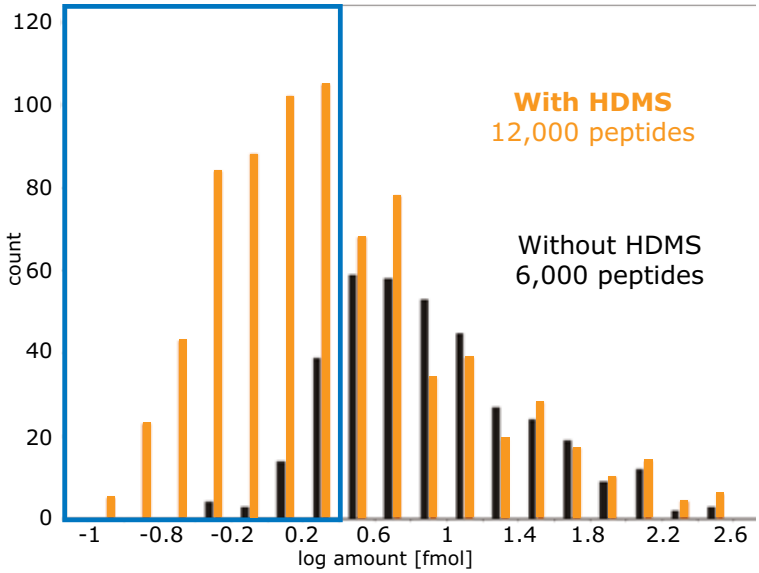
UPLC T-Wave IMS QuanTof LC/HDMS

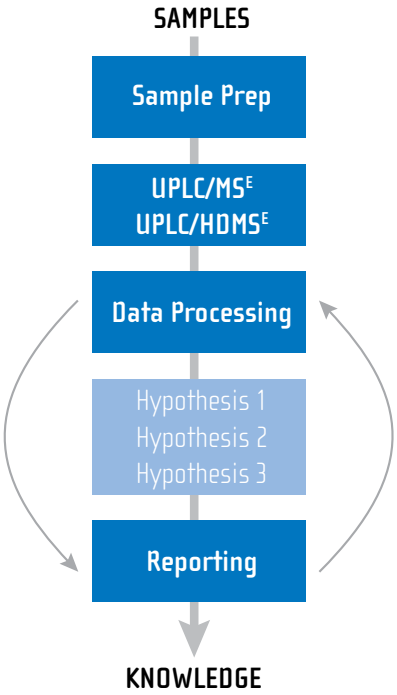
A fully nested, parallel acquisition methodology is the key to harnessing the full power of UPLC (secs), high-efficiency IM separation (msecs), and high resolution TOF MS (µsecs). The three separation techniques provide seamless capability for separating the most complex mixtures.

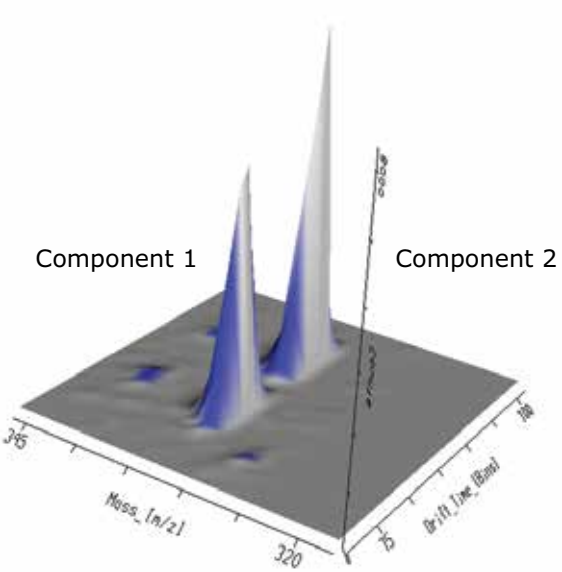


Ion Mobility Separation gives an increase in analytical peak capacity with UPLC-IMS/MS

Increased numbers of peptide identifications at the lower concentrations (indicated by the blue box) are achieved with the introduction of T-Wave ion mobility separations. Data is from a proteomics study using UPLC-HDMS^{E}[4]





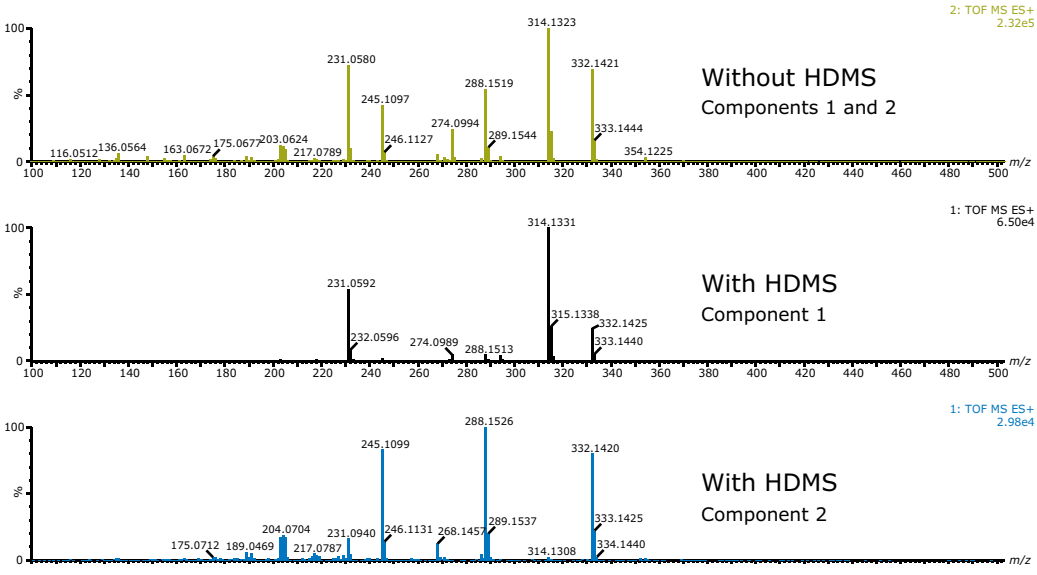


Providing isomer separation, and purified higher quality spectra[5]

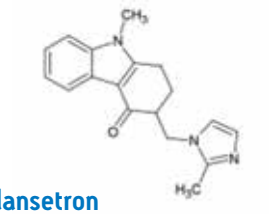
MS^{E} and HDMS^{E} provide a simple, generic method to enable comprehensive profiling of the most complex datasets so you don't have to redesign experiments for different sample sets. High quality molecular and fragment ion spectra are generated for every detectable component using retention time and/or (ion mobility) drift time alignment.

The comprehensive nature of every dataset means that you can simply re-interrogate your data, not re-analyze your sample.

The extra selectivity afforded by ion mobility separations provides more identifications and overall coverage for the most complex mixtures.

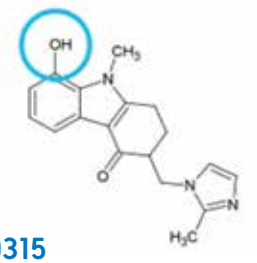


MAXIMIZE YOUR ANALYTICAL CAPABILITY



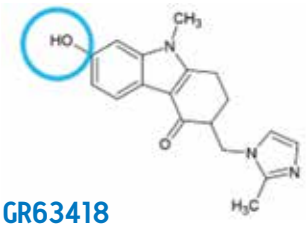
Ondansetron

Theoretical	107.7 Å²
T-Wave	**107.4** Å²



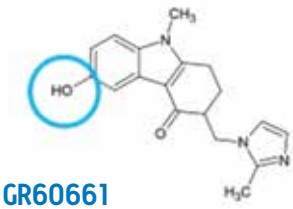
GR90315

Theoretical	109.8 Å²
T-Wave	**110.4** Å²



GR63418

Theoretical	111.2 Å²
T-Wave	**111.5** Å²



GR60661

Theoretical	111.4 Å²
T-Wave	**111.7** Å²

Investigation and differentiation of the drug Ondansetron and metabolite structures using travelling wave ion mobility mass spectrometry (both MS and MS/MS data) and molecular modelling.[7]

SYNAPT G2-S*i* provides a unique and extensive range of analytical capabilities, making it possible to target and characterize specific molecules or families of components in much greater detail and with more confidence than ever before.

Collision cross section – because shape matters

The collision cross-section (CCS)[7] is an important distinguishing characteristic of an ion that is related to its chemical structure and three-dimensional conformation in the gas-phase. A molecule's conformation can be influenced by a number of factors, such as the number and location of charges. The measured CCS of an ion can be used to help confirm its identity or investigate its structure.

CCS can be determined from T-Wave ion mobility separations simply and quickly, for a wide range of analytes from small molecules, lipids and peptides, to larger species such as polymers and protein complexes.

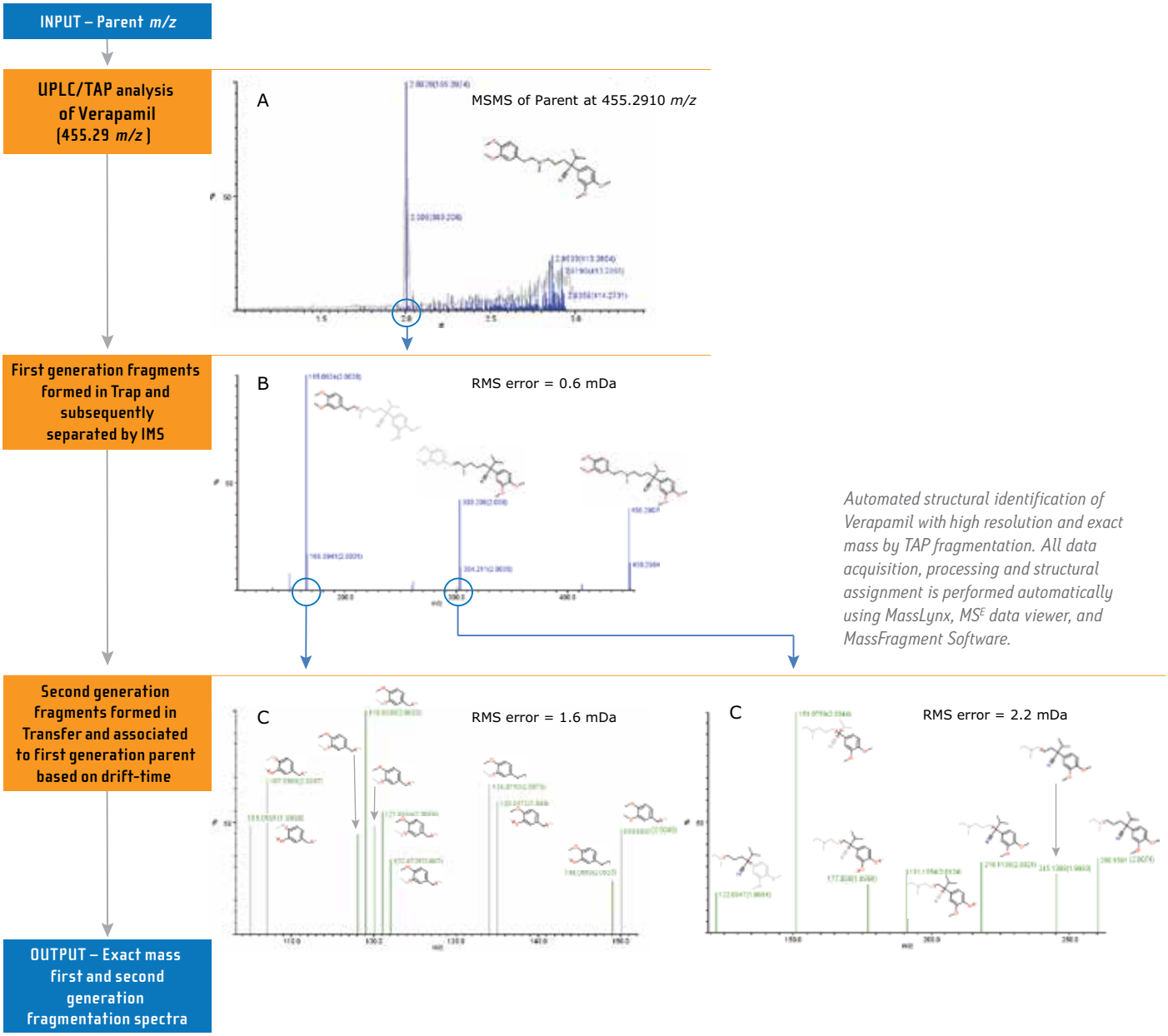
- Separation of individual isomers, conformers, and isobaric compounds
- Determine sites of biotransformation
- Study structure at physiological concentrations
- Analysis of heterogeneous samples
- Wide mass range capability
- An additional 'matrix-tolerant' identification point
- Minimize false positive and negatives in results

	No CCS	With CCS	With CCS
m/z error (+/-)	5 ppm	5 ppm	10 ppm
rt error (+/-)	2.5%	2.5%	2.5%
CCS error (+/-)	–	2%	2%
Correct IDs	7/8	7/8	8/8
False Negatives	1	1	0
False Positives	1	0	0

CCS increases confidence in screening for targets.

In the analysis of a small scale proficiency sample (containing 8 target compounds with known CCS), a CCS filter of 2% was used to eliminate a false positive (not matching the CCS of the 8 target compounds) and a false negative (with correct CCS, and mass error of 7.5 ppm) by allowing the mass error tolerance to be relaxed.

struct



Automated structural identification of Verapamil with high resolution and exact mass by TAP fragmentation. All data acquisition, processing and structural assignment is performed automatically using MassLynx, MS^E data viewer, and MassFragment Software.

Time Aligned Parallel (TAP) fragmentation – for more complete structural elucidation

Confident structural characterization of components, from small organic molecules to modified peptide species demands the best in structural coverage and data quality. TAP fragmentation provides a distinct advantage for building a complete structure, through superior fragment ion coverage, sensitivity and accuracy compared to traditional MS^n or MS/MS techniques.

Multiple components of interest can be individually selected for TAP fragmentation in a UPLC gradient and then subjected to two stages of CID which provide extensive fragmentation with high resolution and exact mass to aid unambiguous structural elucidation.

Ion mobility separation plays a key enabling role, separating first generation fragments and second generation fragments and then, through 'drift time' values, aiding the automated association of fragments within the MS^E data viewer software.

UNPARALLELED VERSATILITY FOR TARGETED ANALYSIS

Electron Transfer Dissociation – for when CID isn't enough

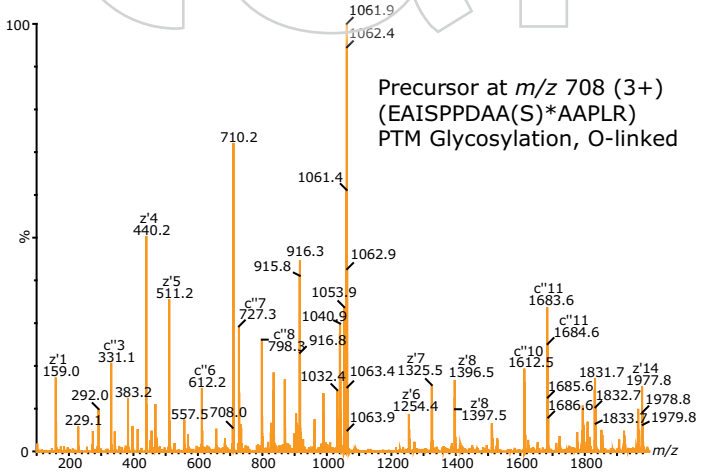
When analyzing post-translational modifications and top-down sequencing are all important, Electron Transfer Dissociation (ETD) complements collision induced dissociation (CID). Developed specifically to maximize confidence, flexibility, and ease-of-use, the optional ETD capability of SYNAPT G2-S*i* is a uniquely powerful feature for sequencing of biomolecules.

TRAP T-WAVE	IMS T-WAVE	TRANSFER T-WAVE
ETD	No IMS IMS	CID Supplemental Activation

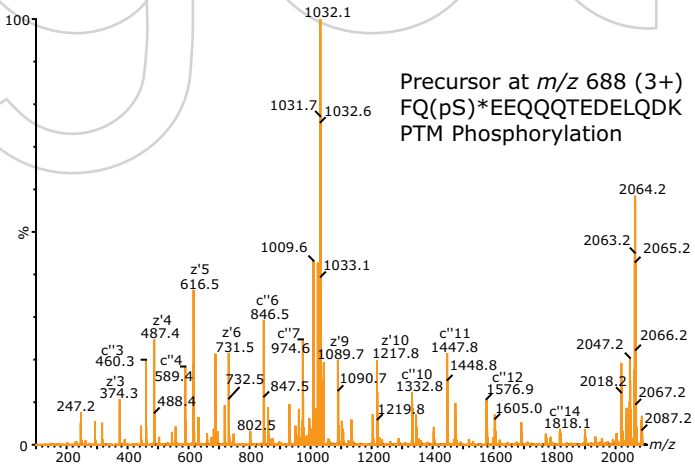
Triwave provides a very flexible analytical platform for ETD studies.

- **High performance** – high resolution, Exact Mass data, and high reaction efficiency generate the highest quality sequence data
- **Flexible** – to utilize a range of high-efficiency reagents as well as employ Ion Mobility Separations with ETD for advanced fundamental studies
- **Easy-to-use and maintain** – easy, stable introduction and quick replenishment of ETD reagent to the MS through the simplicity of the ETD glow discharge source

www.waters.com/ETD



Characterization of o-linked glycosylated peptide from Erythropoietin using LC-MS/MS with ETD. The ETD spectrum shown here exhibits fragment ions of the peptide ion enabling location of modification to be determined.



Supplemental activation is employed routinely to deliver high levels of ETD fragmentation for enhanced sequence coverage. The data shown here is for the phosphopeptide at m/z 688 from a digest of bovine ßeta-Casein. Mixed mode CID/ETD DDA analysis provides high quality sequence information on the basis of charge state.

High sensitivity MS/MS workflows

Targeted Discovery

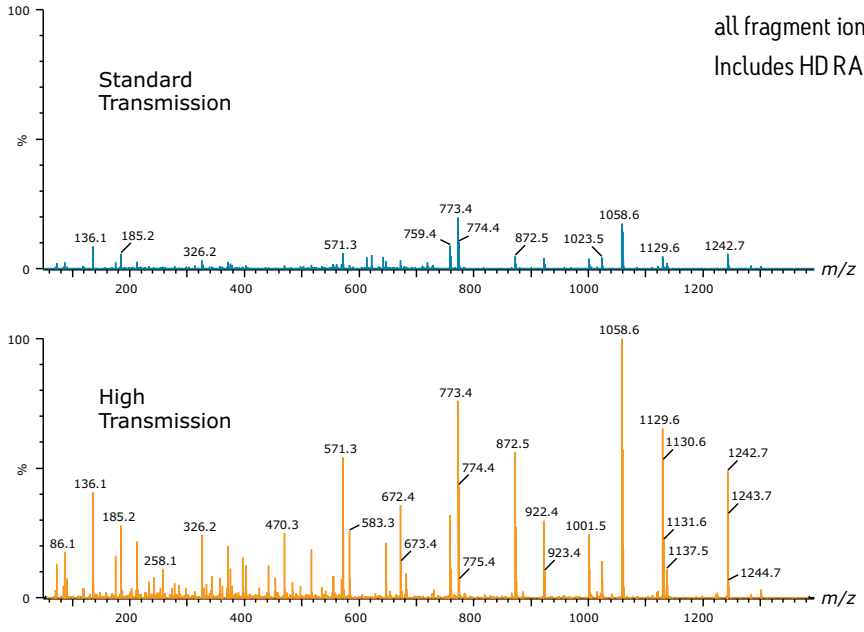
High Definition Data Directed Analysis (HD-DDA) significantly increases limits of detection, and the number of detectable compounds in mixtures with enhancements in[10,11]:

- **Sensitivity –** up to 10x increase in MS/MS signal intensity, using an ion mobility-enabled high transmission mode.
- **Speed –** faster, smarter decision making for optimized spectral acquisition time and increased number of MS/MS switches.

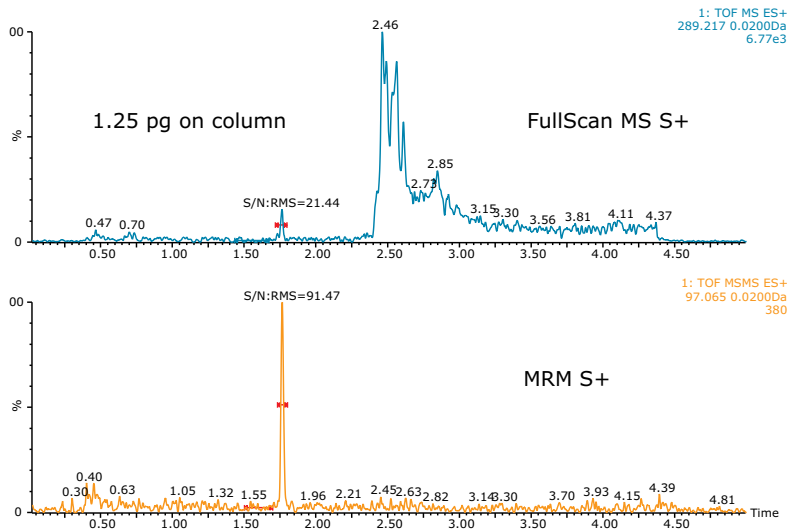
Targeted Quantitation

The SYNAPT G2-S*i* MRM methods enable more sensitive and selective targeted quantitation, with the benefits of high resolution MS/MS, and ion mobility separations[12,13]:

- **Tof-MRM mode** – High transmission mode giving up to 10x sensitivity increase for improved LLOD and LLOQ. Includes RADAR technology for full scan data to assist method development.
- **HD-MRM mode** – uses T-Wave ion mobility separations to increase selectivity on precursors or fragments, or to acquire all fragment ion data simultaneously with up to 10x sensitivity.[13] Includes HD RADAR for more selective full scan data.



Increase in spectral quality comparing standard and high transmission modes. LC-MS/MS data for peptide VILAGEVTTPVTVR from a tryptic digest of Escherichia coli acquired at the same point in the chromatographic peak.



Illustrating the enhancements in selectivity (from MS/MS) and sensitivity (high transmission mode) using high resolution MRM compared to standard full scan MS mode. The lower LOD for MRM was 250fg testosterone on-column.[12]

VERSATILITY– BECAUSE YOUR CHALLENGES DEMAND IT

SYNAPT G2-S*i* MS and MALDI SYNAPT G2-S*i* MS are next-generation quadrupole orthogonal acceleration Time-of-flight systems, which can be upgraded on site to incorporate next generation HDMS® functionality.

System upgradability – future proof your lab

Because you never know what challenges are around the corner, more inlet choices will serve you better:

- The ACQUITY UltraPerformance LC® family of products is proven to be the most powerful and flexible chromatographic inlet for mass spectrometry based analysis today, featuring 2D RP/RP, Hydrogen Deuterium Exchange (HDX), UltraPerformance Convergence Chromatography (UPC²®), Advance Polymer Chromatography (APC™) and 'plug and play' nanoTile™ Technology.
- Waters Universal Ion Source Architecture, engineered to take maximum advantage of UPLC allows the widest range of ionization techniques as well as the very latest innovations in ionization technologies.

SYNAPT G2-S*i* HDMS

MALDI SYNAPT G2-S*i* HDMS

SYNAPT G2-S*i* HDMS Systems (HDMS Mode and Tof Mode)

Access unique benefits of high-efficiency IMS and enhanced tandem MS to carry out conformational studies, reduce spectral complexity/background interferences, and retrieve more information from fragmentation studies.

SYNAPT G2-S*i* MS

MALDI SYNAPT G2-S*i* MS

SYNAPT G2-S*i* MS System (Tof Mode)

Access new levels of Tof performance and productivity with application specific system solutions.

Also compatible with DESI (Prosalia), DART (IonSense), LDTD (Phytronix), LAESI (Protea Biosciences), and TriVersa NanoMate (Advion) sources.

INSTANT EFFICIENCY AND ACCELERATED SUCCESS WITH ENGINEERED SIMPLICITY

High performance is key to productivity, but why should you have to work any harder to take advantage? Central to the design of SYNAPT G2-S*i* is Engineered Simplicity. This means that while SYNAPT G2-S*i* is engineered to handle your most complex applications, it's also engineered to add simplicity and automation throughout your entire workflow.

PREPARE

IntelliStart ensures your system is ready to run for experts and beginners alike, whether you utilize MS, UPLC-MS or nanoUPLC-MS.

ANALYZE

Waters' Universal Ion Source Architecture, QuanTof, StepWave, Triwave, UPLC-HDMS^E, HD-DDA, HD-MRM, and ETD technologies, will equip you with an entirely new level of quantitative and qualitative capability.

INTERPRET

Process, visualize, compare, and interpret the most complex data automatically. Then turn it into meaningful information quickly with Informatics software that support both MS and High Definition MS workflows across applications.

DECIDE

Generate reports, share results and archive information easily with Waters laboratory informatics. Make decisions faster and better than ever before.

Be Assured. Choose Waters Global Services

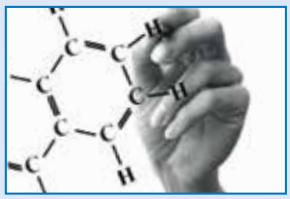
Waters Global Services helps customers optimize laboratory operations by providing superior service, support, upgrades, training, and Waters Quality Parts.®
For more information, go to **www.waters.com/services**.

Simplicity starts with IntelliStart

Get up and running quickly and the discoveries come even faster! SYNAPT G2-S*i* features IntelliStart™ Technology, an intuitive interface that automates routine tasks. This technology ensures that all levels of scientist can operate the instrument quickly and confidently, to generate reproducible UPLC-MS data of the highest quality.

INTELLISTART™

AUTOMATED MS RESOLUTION AND CALIBRATION CHECKS



SIMPLE SETUP OF DIVERSE EXPERIMENTS

AUTOMATED LC-MS SYSTEM CHECK

AUTOMATED SYSTEM MONITORING

WHY LEADING RESEARCHERS ARE LEADING WITH SYNAPT HIGH

To reach beyond the boundaries of conventional mass spectrometry, you can access the extra dimension of high-efficiency ion mobility separation offered by SYNAPT G2-S*i* HDMS, across a wide range of applications. When leading researchers are saying the benefits of the SYNAPT Mass Spectrometry Systems are this good, can you risk being out of the game?

Enhancing qualitative and quantitative proteomic analysis

"The Waters **SYNAPT G2 with ion mobility has greatly enhanced selectivity for proteomic analysis**. An orthogonal measure, ion mobility dramatically improves the label-free MS^E methodology used in our research. Relative to earlier technology, the new G2 $HDMS^E$ platform enables detailed fragment ion determination with well characterized chromatographic measures, **producing more accurate peptide sequence determination with precise, reproducible quantification**."

ANDREW K. OTTENS, Ph.D.
Assistant Professor of Anatomy & Neurobiology and Biochemistry, Virginia Commonwealth University, VA, USA

Increasing efficiency in pharmaceutical research and discovery

"**We didn't expect the results to be as good as they are.** If we had to synthesize just these three metabolites, it would probably have taken several months, whereas the ion mobility LC-MS experiment and modeling calculations is probably around a week's worth of work."

DRUG METABOLITE ID MADE EASY
Chemistry World, July 2010
www.chemistryworld.org

Improved confidence in challenging screening applications

"CCS measurements have the potential to transform the way people screen for known compounds, because unlike parameters like retention time, CCS values are unaffected by different matrices and chromatographic methods, and **give you a much higher level of confidence that you found what you're looking for**."

SEVERINE GOSCINNY
Scientist
WIV-ISP, Belgium

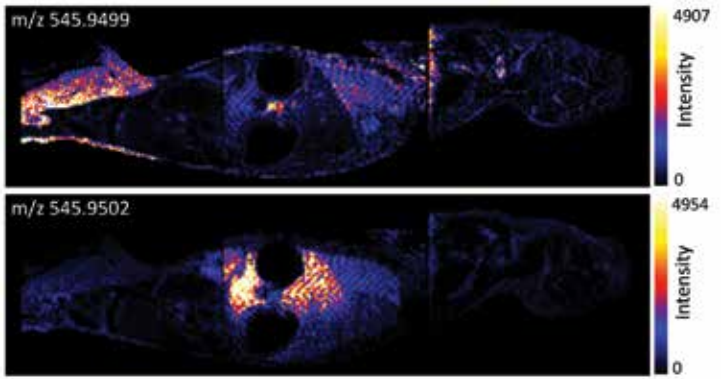
Helping understand the role of structure in biopharmaceutical characterization

"It is shown that IMMS reveals 2 to 3 gas-phase conformer populations for IgG2s. In contrast, a single gas-phase conformer is revealed using IMMS for both an IgG1 antibody and a Cys-232 Ser mutant IgG2, both of which are homogeneous with respect to disulfide bonding. This provides strong evidence that the observed IgG2 gas-phase conformers are related to disulfide bond heterogeneity. Additionally, IMMS analysis of redox enriched disulfide isoforms allows unambiguous assignment of the mobility peaks to known disulfide structures. These data clearly illustrate how **IMMS can be used to quickly provide information on the higher order structure of antibody therapeutics**."

BAGAL D., *ET AL.*
Rapid Commun. Mass Spectrom. 2008; 22: 2898–2904.

success

DEFINITION MASS SPECTROMETRY



>1.8 Million Effective Resolution

Visualization of the distributions of two ions (shown in red in the m/z versus drift time plot) which differ significantly in drift time but have a mass difference so small that it would require a m/z resolving power in excess of 1.8 million to achieve differentiation of the ions without T-Wave IMS separation.

The spatial distributions of the two ions are clearly different, when plotted using m/z and drift time to generate the images, as shown in the two panels for m/z 545.9499 and m/z 545.9502.

The MALDI SYNAPT G2-Si uses a 2.5KHz solid state laser and enables imaging to be performed down to 15 µm spatial resolution.

Expanding scientists ability to better characterize polymer microstructure

"IMS-MS is starting to attract devotees among analytical scientists who **recognize the decisive benefits that come from coupling mass analysis with shape-dependent ion separation**. As Prof. [Jim] Scrivens [from the University of Warwick, UK] put it, 'The ability to track families of ions is one extraordinarily powerful aspect of this technique.' More generally, he added, **IMS-MS offers a platform 'for separating and visualizing all of these different types of compounds in one high-information-content experiment that is superior** to other approaches.'"

DOUBLING UP ON MASS ANALYSIS
Chemical & Engineering News. March 29, 2010 Volume 88, Number 13 pp. 35–37.

Structural Biology: Unique insights into biological mechanisms

Providing a totally new dimension, SYNAPT is the MS platform of choice for the rapid structural analysis of large heterogeneous protein complexes. Dozens of papers have been published based on the unique abilities of SYNAPT High Definition MS.[1]

Enhancing structural characterization of proteins with HDX and ion mobility

"Importantly, **ion mobility separations provided an orthogonal dimension of separation in addition to the reversed-phase high-performance liquid chromatography** (RP-HPLC). The additional dimension of separation allowed for the deconvolution of overlapping isotopic patterns for co-eluting peptides and extraction of valuable deuterium incorporation data for those peptides. Taken together, these results indicate that including ion mobility separation in HX MS analyses further improves the mass spectrometry portion of such experiments."

IACOB R. E., *ET AL.*
Rapid Commun. Mass Spectrom. 2008; 22: 2898–2904.

Enhanced spatial localization in tissues: High Definition Imaging (HDI) MALDI

To determine the efficacy of a drug, it is critical to understand how it's distributed within plant or animal tissue. Imaging by MALDI MS provides this capability. Whether you want to determine the location of peptides, lipids, drugs, or drug metabolites, HDI® MALDI – the combination of high-efficiency ion mobility separations and MALDI – uniquely offers the ability to determine the distribution of your target compound without interference from simultaneously ionized background ions.

"...**imaging IM-MS provides several unique advantages** including (1) selective imaging of isobaric species (i.e. lipids versus peptides) or structural/conformational subpopulations of the same species on the basis of IM, (2) separation/rejection of undesirable endogenous chemical noise, (3) reduction of ion suppression effects in the source of the Tof-MS, by temporal IM separation of analytes, and (4) potential utility for nearly simultaneous IM-MS/MS of all analytes at a particular pixel coordinate."

McLEAN J. A., RIDENOUR W. B., CAPRIOLI R. M.
J Mass Spectrom. 2007 Aug; 42(8):1099–105.

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