SYNAPT G2

ACHIEVEMENTS ARE LIMITED ONLY BY ASPIRATIONS.

Waters

THE SCIENCE OF WHAT'S POSSIBLE.™

BE FIRST

TO DISCOVER, TO PUBLISH, TO DEVELOP,

TO SUCCEED.

the new dime

ENTER A NEW DIMENSION OF PERFORMANCE.

Your success depends on your ability to optimize laboratory productivity, understanding, and adapt to changing needs and environments.

Enter SYNAPT™ G2 from Waters – a new dimension of scientific discovery goals. We combined breakthrough Quantitative Tof and enhanced High Defin with intuitive operation, application flexibility, and a totally new level of pe

With SYNAPT G2, you'll have the capability to meet and exceed the deman your greatest ambitions.

nsion

ENTER SYNAPT G2.

generate results that advance scientific

to accelerate you towards your research
ition MS™ technologies to provide you
rformance for all your applications.

ds of your laboratory – and work toward


Waters
ESI
SYNAPT G2

WE LEAD THE TECHNOLOGY. YOU LEAD THE DISCOVERY.

We understand science drives your business, and the scientific world has never been so competitive. Whether your success depends on being first to develop products, make groundbreaking discoveries, or to publish, you'll need a mass spectrometry (MS) solution that can boost your productivity, help answer scientific questions that simply can't be solved any other way, and provide a platform for your future success.

We evolve our technology so you can move forward with your scientific goals. With our original SYNAPT, we defined an entirely new category of mass spectrometry. Now we've created a new level of performance.

game-cha

The time scales of ion mobility separation fit seamlessly between those of UPLC (or APGC) separations and oa-Tof acquisitions, introducing an additional dimension of separation to your analysis.

SYNAPT G2, our second-generation platform, is the product of our very latest innovations. With a unique upgrade pathway to meet your needs today and in the future, it's designed to drive your research and business forward like no other MS system can, with:

- **QuanTof™ capability** – for the next level in qualitative AND quantitative MS and MS/MS performance that is fully compatible with UPLC.®
- **Enhanced High Definition MS performance** – enables a new dimension of discovery, powered by high-efficiency ion mobility separations (IMS) with second-generation Triwave™ Technology and DriftScope™ Mobility Environment Software.
- **Unrivaled flexibility** – allows you to customize the world's most powerful MS system to your needs: with multiple ionization options, application-specific system solutions, and future upgrade pathways.
- **Decisions made easy** – thanks to Engineered Simplicity,™ which delivers the very highest performance and simplicity throughout your analytical workflow. So experienced and novice users alike can generate high-quality results. Consistently.

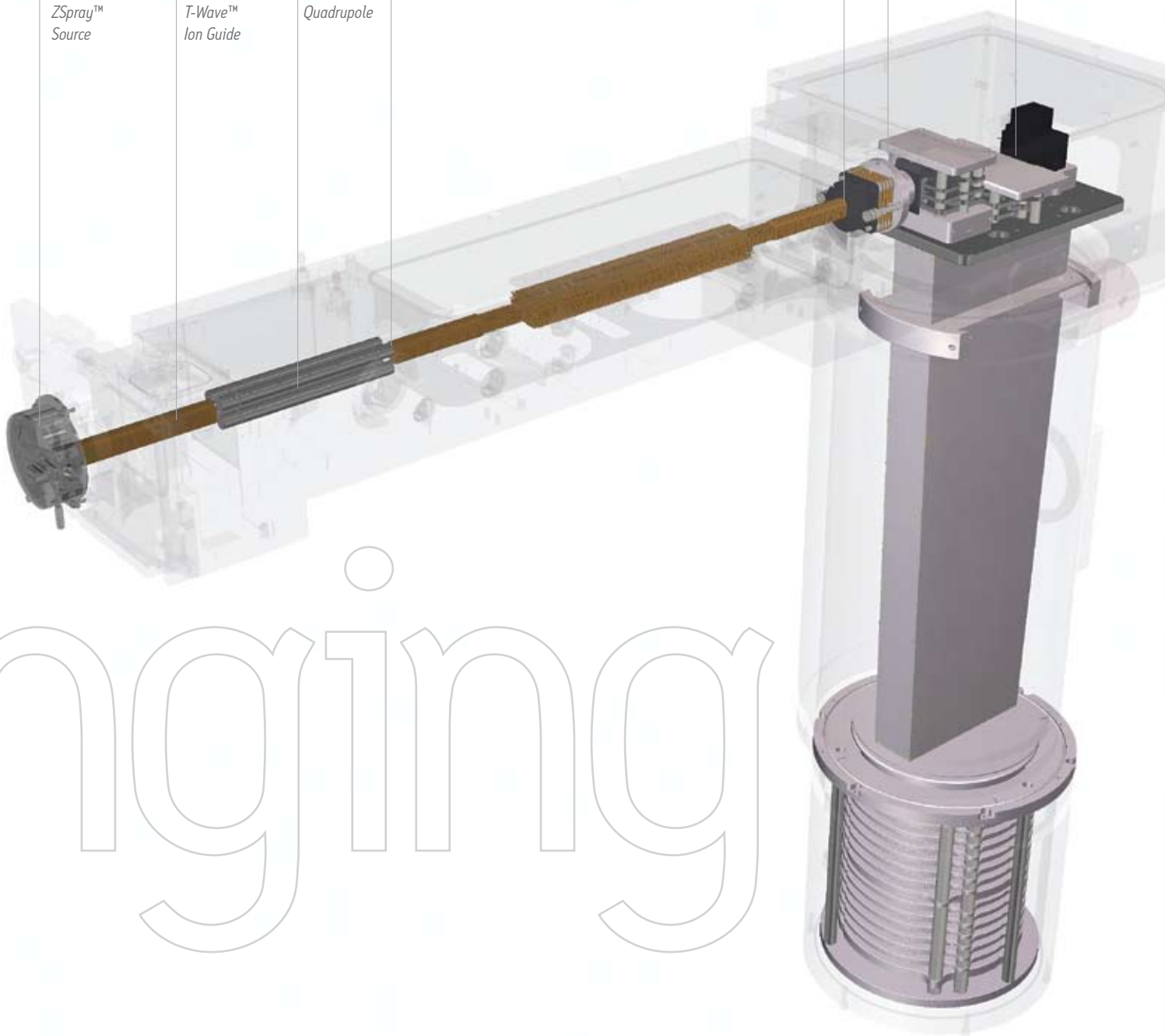
TRIWAVE

QUANTOF

ZSpray™ Source

T-Wave™ Ion Guide

Quadrupole



nging

"Incremental improvements in instrument performance are important drivers for advancing MS-based studies, but it's the combination of SYNAPT G2's high-resolution oa-Tof MS technology, wider quantitative dynamic range, and enhanced ion mobility separation power that is truly **game-changing.**"

JIM SCRIVENS, Ph.D.
Professor, Dept. of Biological MS and Proteomics
University of Warwick, UK

QUANTOF REDEFINES THE CATEGORY.

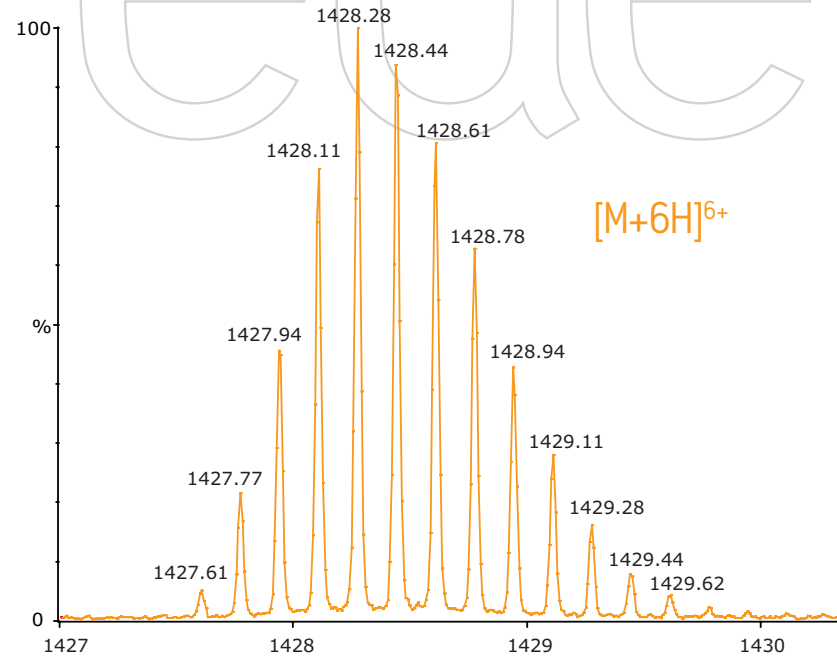
To equip you with an entirely new level of quantitative and qualitative capability for the most analytically challenging samples, Waters SYNAPT G2 incorporates a new level of performance with QuanTof Technology.

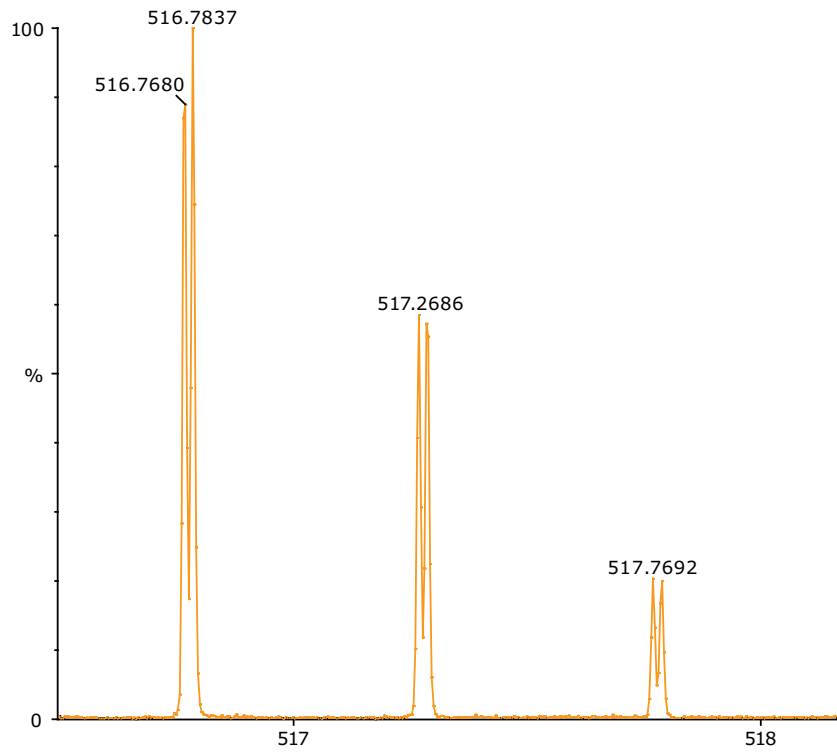
QuanTof combines innovative high field pusher and dual-stage reflectron designs with a novel ion detection system in an optimized, folded, Tof geometry. This provides a new dimension of high resolution, exact mass, quantitative performance, which – crucially – is available at acquisition rates compatible with UPLC separations.

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 novel ion detection system combines an ultra-fast electron multiplier and hybrid ADC detector electronics to provide outstanding sensitivity and quantitative performance for both MS and the elevated data acquisition rates of SYNAPT G2 HDMS™ analysis.

- Over 40,000 FWHM resolution
- Linear dynamic range of up to 10^5
- Exact mass (1 ppm RMS)
- Class-leading sensitivity
- 20 spectra/sec



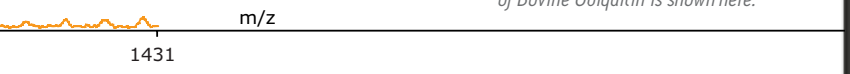


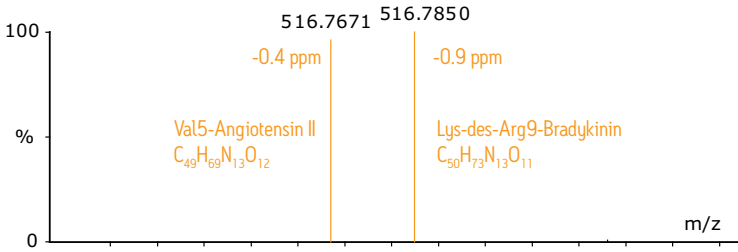
QuanTof™

fine

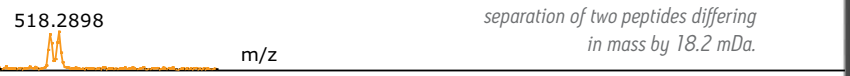
Resolution > 40,000 FWHM

QuanTof Technology is capable of providing over 40,000 FWHM resolution over a wide mass range, and in excellent agreement with the theoretical spectrum. Data for the isotope distribution of $[M+6H]^{6+}$ ion of Bovine Ubiquitin is shown here.





QuanTof provides high resolution for the enhanced detection of components in mixtures at the highest acquisition rates (up to 20 spectra/sec). Data illustrates a resolution of over 40,000 FWHM enabling separation of two peptides differing in mass by 18.2 mDa.



PREPARE

With SYNAPT G2, your system is automatically calibrated and operating at optimal performance levels.

ANALYZE

SYNAPT G2 ensures the generation of high quality, information-rich, reproducible data.

INTERPRET

Redefine your analytical workflow with an unprecedented ability to automatically visualize and interpret the most complex data.

DECIDE

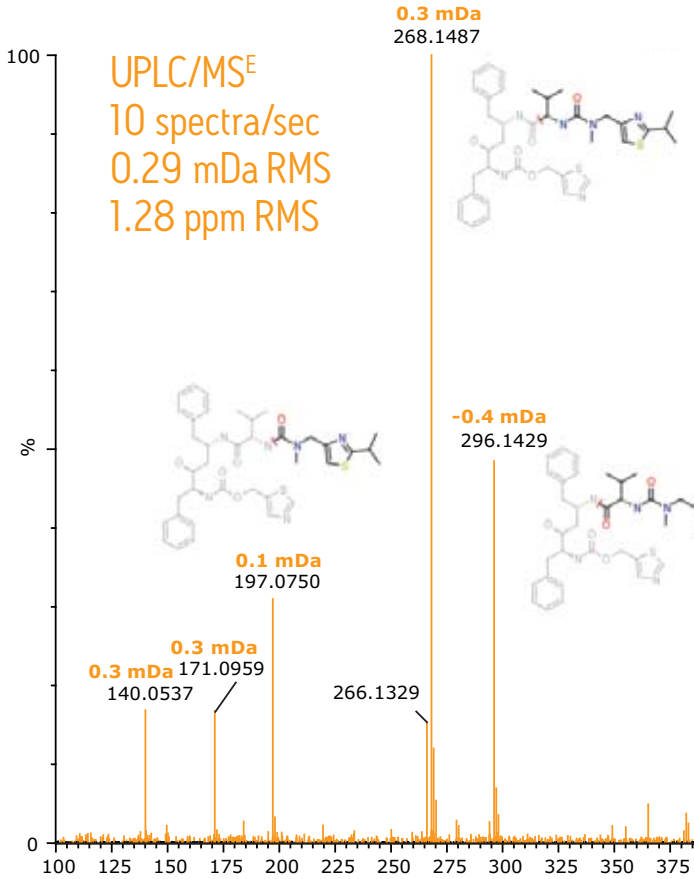
MassLynx Informatics allow you to compile clear and accessible reports to share throughout your organization.

ENGINEERED SIMPLICITY MEANS ULTIMATE PRODUCTIVITY.

Central to the design of SYNAPT G2 is Engineered Simplicity. This means that while SYNAPT G2 is engineered to handle your most complex applications, it's also engineered to add simplicity throughout your entire analytical workflow.

Waters system solutions featuring SYNAPT G2 are designed to get you to the right result, faster – no matter how challenging your application – whether you specialize in metabolite profiling, proteomics, biomarker discovery, biopharmaceuticals, or screening applications. Your solution will benefit from:

- **IntelliStart™ Technology –** for simplified system setup and automated system control.
- **ACQUITY UPLC® Technology –** for the highest chromatographic resolution, speed, and sensitivity.
- **QuanTof Technology –** ensures you'll capture the most complete and informative exact mass data in UPLC time frames, complemented by UPLC/MS^E capability to capture all of the data all of the time.
- **MassLynx™ Informatics –** dedicated Application Managers that combine the power of exact mass data and a built-in understanding of chemistry to deliver simple and rapid data interpretation and compound identification.



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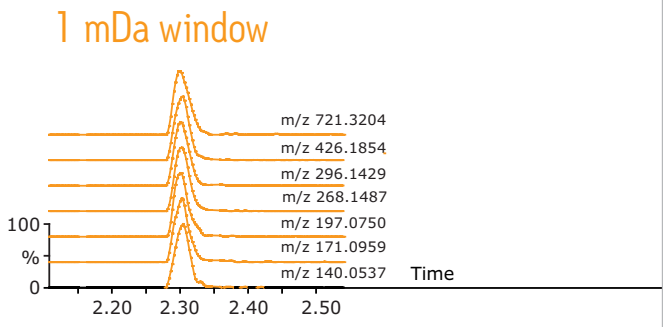
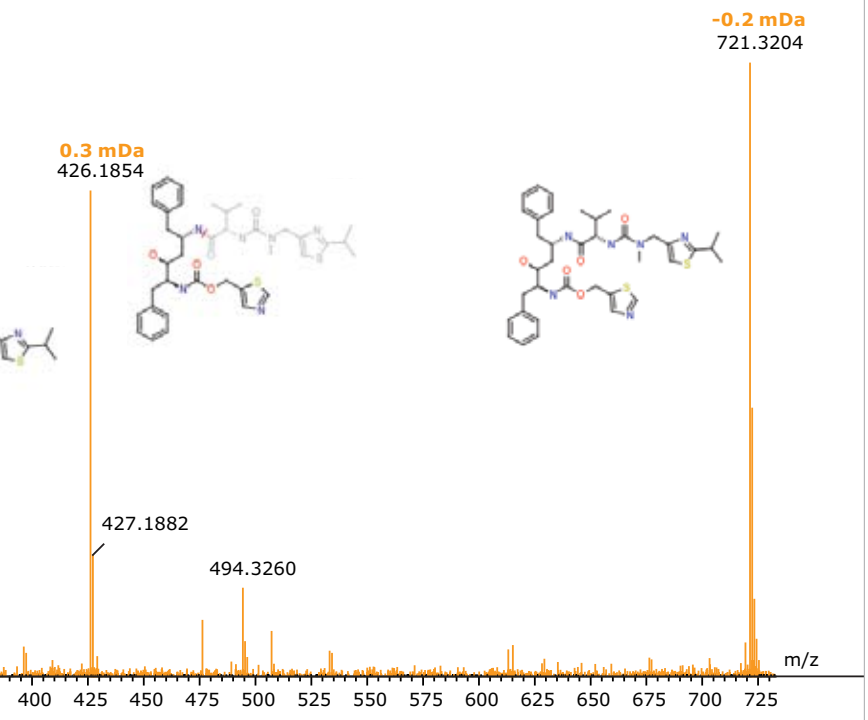




UPLC/MS^E fragment ion spectrum of Ritonavir ($C_{37}H_{49}N_6O_5S_2$) from a very complex rat bile sample. Data was acquired from a UPLC peak width of 1.5 seconds at half height. A 1 mDa window was used to generate extracted ion chromatograms (inset) and automatically determine structures (MassFragment™ Software) for each individual fragment ion. QuanTof maintains high resolution and mass accuracy for qualitative analysis (elevated energy MS^E data – fragment ion data), while simultaneously providing high selectivity and accuracy for quantitative profiling (low energy MS data – molecular ion data).

MS^E is all the data. And no compromise.

For researchers who need to exhaustively characterize complex samples, Waters UPLC/MS^E represents a groundbreaking advancement in data acquisition.

By rapidly alternating between two functions – the first acquiring exclusively low energy exact mass precursor ion spectra; the second acquiring elevated energy exact mass product ion spectra – MS^E provides a generic method to comprehensively catalog complex samples that is fully compatible with the resolution, sensitivity, and speed of UPLC separations.

Unlike conventional methods of acquisition, UPLC/MS^E provides a comprehensive exact mass record of chromatographically time-aligned precursor and product ions. You won't have to re-interrogate samples. You can keep your experiments moving forward.

"The label-free 2D UPLC/MS^E approach has enabled us to obtain more complete, reproducible quantitative protein profiles that are at least as accurate as alternative labelling or gel-based approaches, with significantly less sample and time. Crucially, the unique software of Identity^E delivers significantly increased sequence coverage and therefore confidence in protein identification."

JIM SCRIVENS, Ph.D.
Professor, Dept. of Biological MS and Proteomics
University of Warwick, UK

"In terms of efficiency for metabolite identification studies, the accurate mass LC/MS^E approach has provided significant gains...

...typical savings using the approach outlined in this paper have been in the range of 13 hours per molecule. As a result the capacity for conducting preliminary metabolite identification experiments has increased by almost an order of magnitude."

P. R. TILLER, *et al.*
Rapid Commun. Mass Spectrom.
2008; 22: 1053–1061

WHY LEADING RESEARCHERS ARE LEADING.

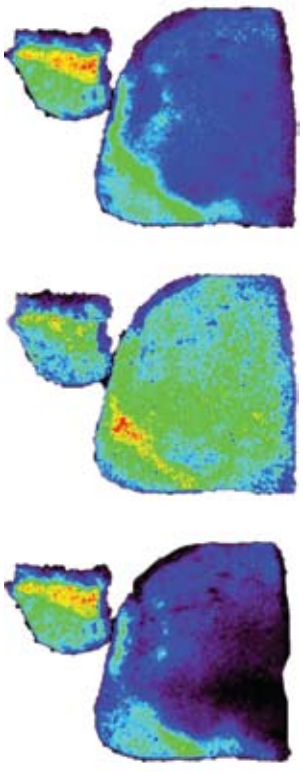
When you want to reach beyond the boundaries of conventional mass spectrometry, you can access the extra dimension of high-efficiency ion mobility separation offered by SYNAPT G2 HDMS. By enabling you to differentiate samples by size, shape, and charge – as well as mass – this unique capability allows you to make discoveries simply not possible with conventional MS systems.

SYNAPT G2 HDMS combines high-efficiency ion mobility separations with high-performance tandem mass spectrometry to enable you to more effectively and efficiently:

- Separate isomers, conformers, and compound classes
- Increase peak capacity and detection limits
- Extract more information from fragmentation studies

lead

Images acquired by conventional MS can be a composite of the distribution of multiple ions (top).



Imaging with ion mobility allows the determination of the true distribution of the ion of interest (bottom) free of interfering isobaric components (middle).

High Definition Imaging (HDI) MALDI: Achieve the spatial dimension.

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."

J. A. M^{C}LEAN, *et al.*
J Mass Spectrom. 2007 Aug; 42(8):1099-105

Structural Biology: Fulfill your aspirations. Go beyond conventional mass spectrometry.

Providing a totally new dimension, SYNAPT G2 HDMS is the instrument of choice for the rapid structural analysis of large heterogeneous protein complexes. In fact, dozens of papers have been published based on the unique abilities of SYNAPT High Definition MS.[1]

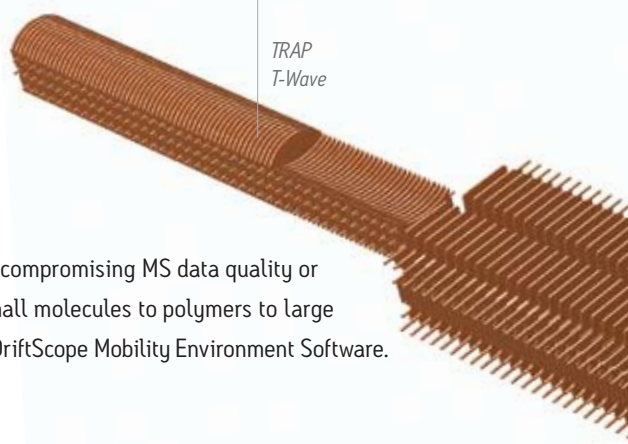
the pack

"Ion mobility mass spectrometry has become an essential tool for our Structural Biology research, providing an extra dimension of information that helps us better understand the role of protein complexes in biological systems. SYNAPT G2 HDMS, with its enhanced separation power and software tools, is enabling us to characterize the composition and dynamics of protein complexes at **a level of detail that simply wasn't possible before.**"

BRANDON RUOTOLO, Ph.D.
Post Doctoral Research Associate
Dept. of Chemistry, University of Cambridge, UK


SYNAPT G2
High Definition Mass Spectrometry

TRIWAVE AND QUANTOF. THE POWER OF TWO.



Triwave and QuanTof combine to provide high-efficiency ion mobility separations without compromising MS data quality or sensitivity. So you can separate, detect, and confidently characterize compounds from small molecules to polymers to large protein complexes. What's more, you'll be able to fully exploit the unique information with DriftScope Mobility Environment Software.

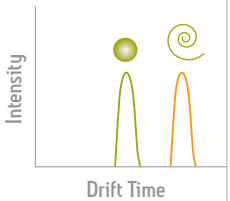
SYNAPT G2 HDMS offers:

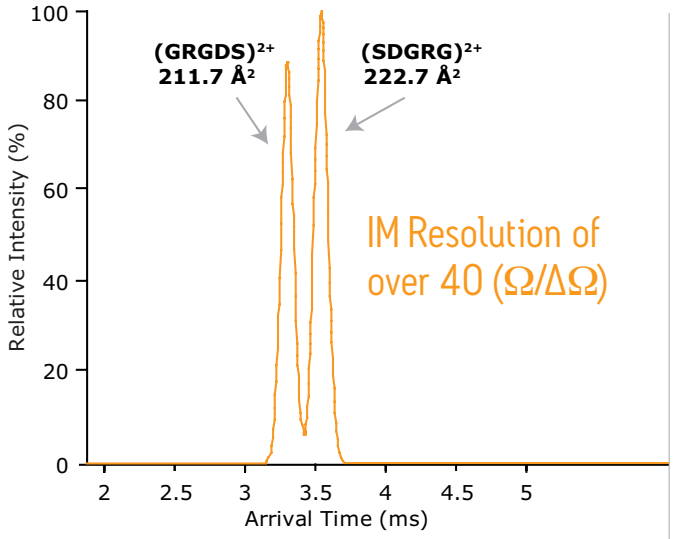
- Enhanced ion mobility resolving power [over 40 (Ω/ΔΩ)]
- Facile exact mass measurement
- Simple, rapid Collisional Cross-Section determination (CCS, Ω)
- Time Aligned Parallel Fragmentation provides first- and second-generation product ions for extensive structural characterization
- Automated, comprehensive component detection
- New visualization tools ensure easier interpretation of SYNAPT G2 HDMS data and identification of molecular trends or partially resolved components
- Peak list export enables downstream processing, including direct links to MassLynx for automated structural assignment of known compounds with MassFragment,™ or elemental composition determination of unknowns

power

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.

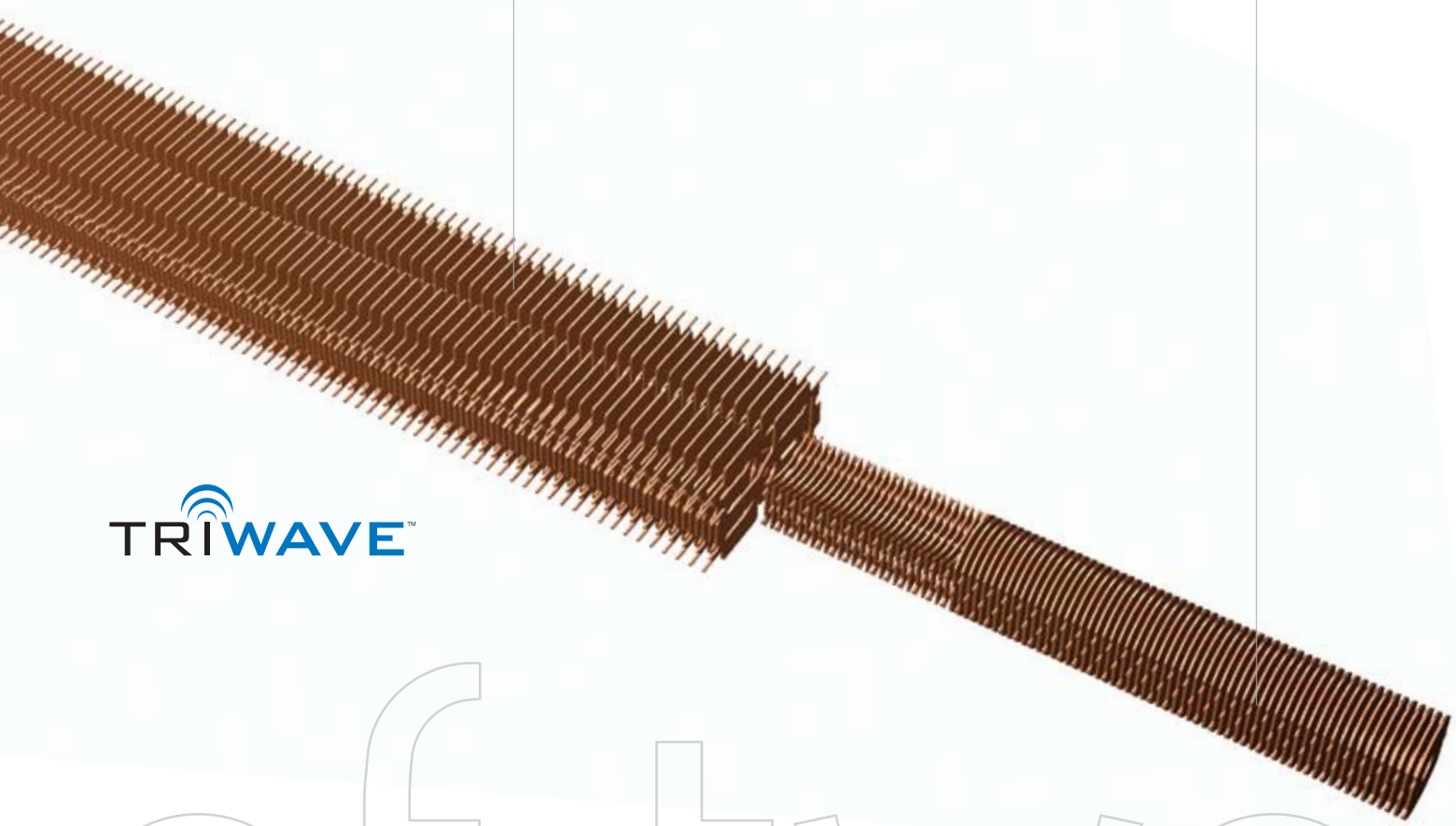




Enhanced IM Separation Power *– The increase in ion mobility resolution of SYNAPT G2 enables a mixture of two reverse sequence peptides (GRGDS and SDGRG) differing in CCS (Ω) by only 5%[2] to be easily separated. A mobility resolution in excess of 40 (Ω/ΔΩ) is indicated.*

Ion Mobility Separation (IMS) T-Wave

TRANSFER T-Wave



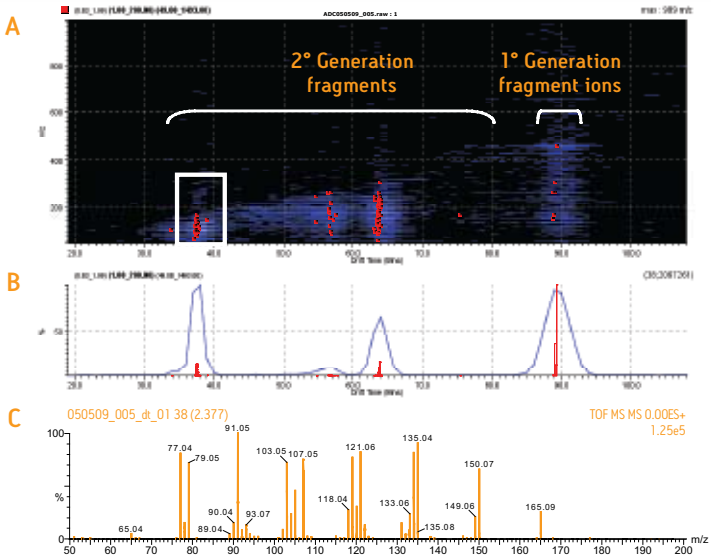
TRIWAVE™

of two

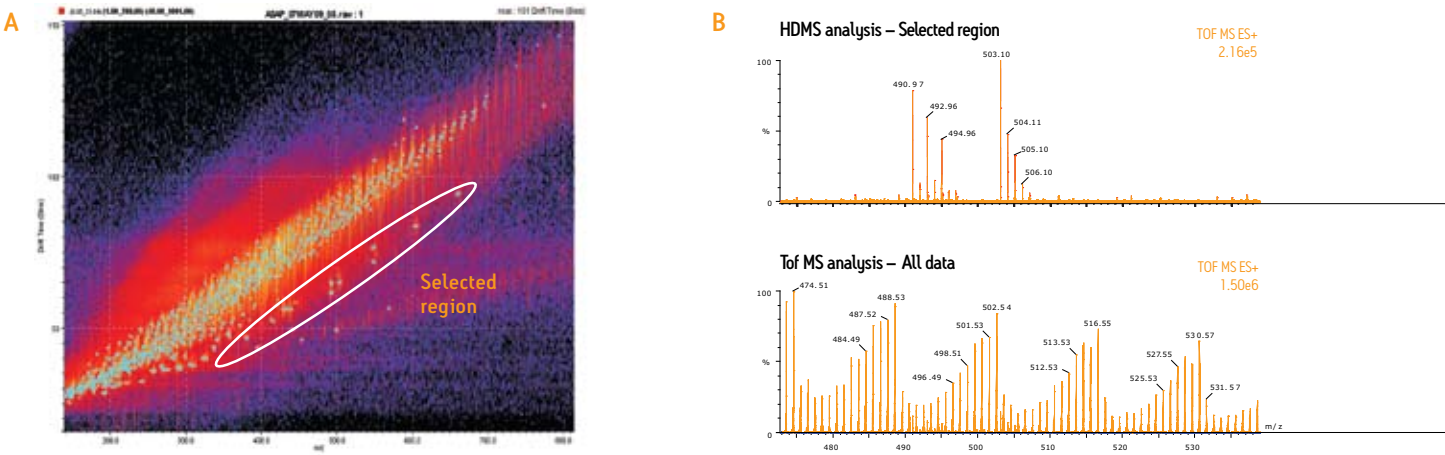
Triwave: Unconventional performance.

Triwave is the enabling technology within the SYNAPT G2 HDMS System. Three T-Wave[3] ion guides are employed, allowing ions to be trapped, separated based on their mobility, and transferred to the QuanTof analyzer for high-resolution mass analysis. The innovative configuration of the Triwave ensures the introduction of IMS is not made at the expense of sensitivity.

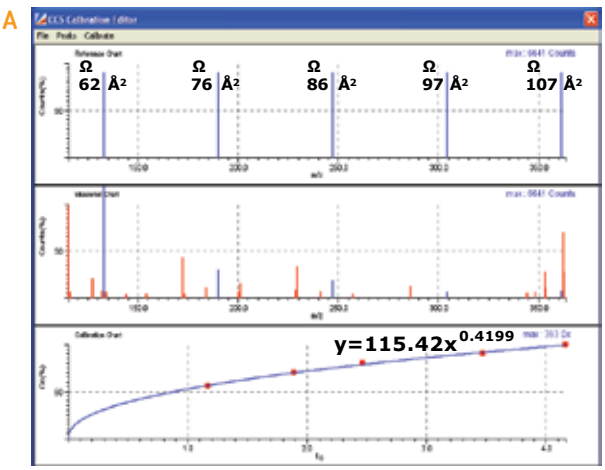
Enhanced ion mobility resolution has been achieved through increased pressure (with the use of a novel Helium filled entry cell in the IMS T-Wave) and length of the IMS T-Wave. The TRAP and TRANSFER T-Wave regions can also be used as collision cells, and in combination with ion mobility separations, can provide a unique route to more comprehensive structural characterization.

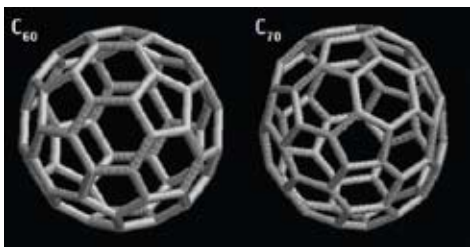


Enhanced Structural Characterization *– SYNAPT G2 HDMS provides novel methods to retrieve fragmentation information (IMS/CID, CID/IMS or CID/IMS/CID) with facile Exact Mass measurement for use in elemental composition determination, or structural assignment with MassFragment Software. These data show the Time Aligned Parallel (TAP) fragmentation (CID/IMS/CID) of Verapamil. The red spots and sticks show detected peaks overlaid on the raw data (A) drift time vs. m/z (B) drift time vs. intensity. Selected low mass second-generation ions (from A, in white box) are displayed in the mass spectrum (C), which are particularly informative and are often absent in MS[3] spectra from ion trap instrumentation.*



Separating Mixtures and Increasing Detection Limits *– ASAP/IMS/MS analysis of lubricating oil demonstrates how the orthogonal gas-phase IM separation provides increased separation and peak capacity. (A) Raw data (increasing intensity shown as blue to yellow) and detected peaks (cyan spots) are displayed together in DriftScope. (B) Mass spectra for all data (lower spectrum) and a selected region (upper spectrum) shows how HDMS enables detection of low level components not visible with Tof MS analysis alone.*





C

	T-Wave (Å²)	Waters CCS (Å2)	MOBCAL Trajectory Method (Å2)
C_{60}	121.4 (+/- 0.73)	122.1 (+/- 0.1)	123.2 (+/- 5.5)
C_{70}	133.3 (+/- 0.8)	132.4 (+/- 0.1)	135.0 (+/- 5.7)

Measuring Shape and Conformation *– (A) DriftScope provides the ability to rapidly generate a calibration profile for T-Wave ion mobility separations based on standard samples of known collision cross-section. (B) CCS values can be derived using the IM calibration and compared with theoretical CCS values derived from .pdb structures using the Waters CCS calculator in DriftScope or other publicly available methods such as MOBCAL.[4] (C) Data shown here for the known structures of two different Buckminster Fullerene compounds (C_{60} and C_{70}), analyzed by ESI/IMS/MS.*

ESI – Electrospray Ionization
APCI – Atmospheric Pressure Chemical Ionization
ESCi® – Dual ESI and APCi

nanoFlow™ ESI

APPI – Atmospheric Pressure Photo Ionization
APCI – Atmospheric Pressure Chemical Ionization

APGC – Atmospheric Pressure Gas Chromatography

MALDI – Matrix Assisted Laser Desorption Ionization

ASAP – Atmospheric Solids Analysis Probe

TRIZAIC UPLC™ – Plug and Play nanoFlow

THE PLATFORM FOR TODAY. THE SPRINGBOARD FOR TOMORROW.

A single platform. Total flexibility.

You need to focus on your research goals, and you have your aspirations for the future. Waters SYNAPT G2 is the most versatile technology platform available today.

When you need to extract the maximum amount of information from a diverse range of compounds, you require the ultimate in ionization flexibility and performance.

SYNAPT G2 universal source technology enables the widest range of ionization techniques to be utilized. You can analyze the broadest range of compounds and have ultimate flexibility in experimental options. Providing high performance with simplified maintenance and operation, the ionization source options are easy to integrate into your analytical workflow.

the next

Transform your data into usable results.

For data acquisition and its transformation into usable results, MassLynx easy-to-use Application Managers allow you to focus on your laboratory's specific tasks.

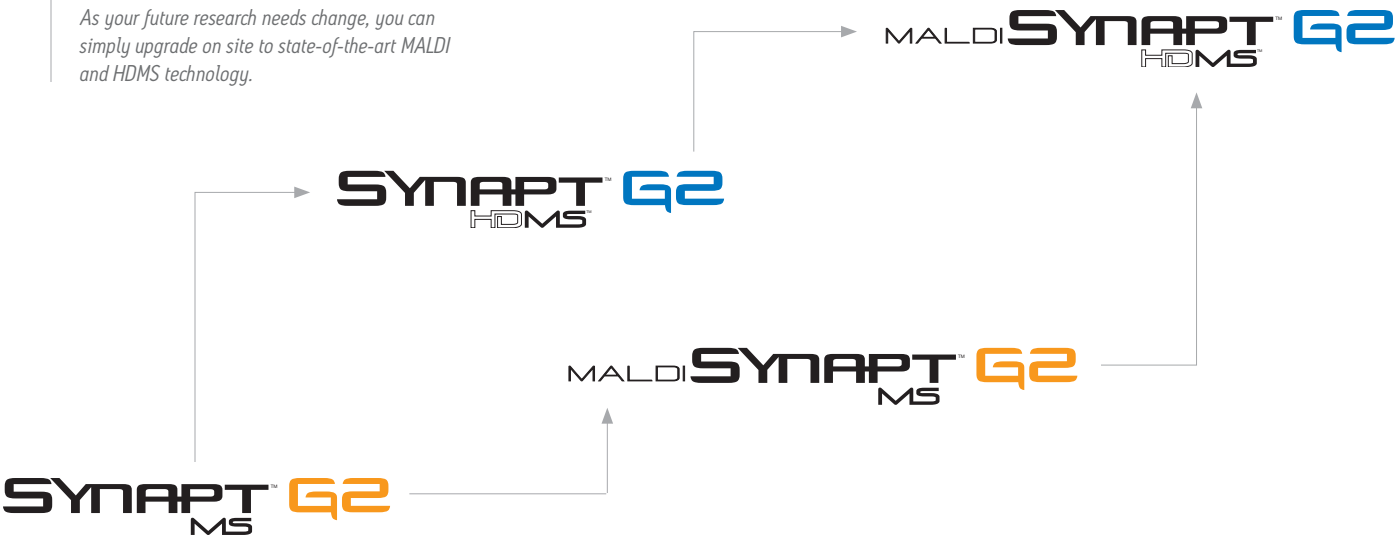
MassLynx Software features general purpose and specialized Application Managers that can perform:

- Targeted quantitative analysis
- Metabolite identification
- Deconvolution of complex chromatograms
- Screening of complex mixtures
- Metabonomics and metabolomics
- Qualitative and quantitative protein profiling
- Biomarker discovery
- Biopharmaceutical characterization
- Structural elucidation and characterization
- Open Access

Simply choose the Application Manager that's right for you.

MetaboLynx™ XS MarkerLynx™ XS BiopharmaLynx™ i-FIT™ ChromaLynx™ TargetLynx™ MassFragment™ OpenLynx™ ProteinLynx Global SERVER™

As your future research needs change, you can simply upgrade on site to state-of-the-art MALDI and HDMS technology.



generation

Future proof your lab.

SYNAPT G2 MS and MALDI SYNAPT G2 MS are second-generation quadrupole oa-Tof systems, which can be upgraded on site to incorporate second-generation HDMS functionality.

SYNAPT G2 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.

MALDI and API: Provide the ultimate flexibility in Tof mode and HDMS mode for high-efficiency IMS separations of ions from MALDI and API.

SYNAPT G2 MS Systems: Provide access to new levels of Tof performance and productivity with application specific system solutions.

We created SYNAPT G2 with your specific needs in mind. With the very best in performance and flexibility, and an upgrade pathway to unique HDMS capability, you can be confident that you're best equipped to achieve your goals today and into the future.

WHERE WILL SYNAPT G2 TAKE YOU?

SALES OFFICES:

Austria 43 1 877 18 07

Australia 61 2 9933 1777

Belgium and Luxembourg 32 2 726 1000

Brazil 55 11 4134 3788

Canada 1 800 252 4752

China 86 10 5293 6688

Czech Republic 420 2 617 11384

Denmark 45 46 59 8080

Finland 358 9 5659 6288

France 33 1 30 48 72 00

Germany 49 6196 400 600

Hong Kong 852 2964 1800

Hungary 36 1 350 5086

India 91 80 2837 1900

Ireland 353 1 448 1500

Italy 39 02 265 0983

Japan 81 3 3471 7094

Korea 82 2 6300 4800

Mexico 52 55 52 00 1860

The Netherlands 31 76 508 7200

Norway 47 6 384 6050

Poland 48 22 833 4400

Puerto Rico 1 787 747 8445

Russia/CIS 7 495 727 4490 / 290 9737

Singapore 65 6593 7100

Spain 34 93 600 9300

Sweden 46 8 555 115 00

Switzerland 41 56 676 70 00

Taiwan 886 2 2543 1898

UK 44 208 238 6100

US 1 800 252 4752

Waters Corporation
34 Maple Street
Milford, MA 01757 U.S.A.
T: 508 478 2000
F: 508 872 1990
www.waters.com

References

1. Visit **www.waters.com/hdmspapers** for a complete list of peer-reviewed publications.
2. C Wu, WF Siems, J Klasmeier, HH Hill, *Anal. Chem.*, 72 (2000) 391.
3. The travelling wave device described here is similar to that described by Kirchner in US Patent 5,206,506 (1993).
4. http://www.indiana.edu/~nano/Software.html

www.waters.com/synaptG2

Waters

THE SCIENCE OF WHAT'S POSSIBLE.™

June 2009 720003022EN LB-UM