

[XEVO G2 TOF]



*YOUR QUANTITATIVE AND QUALITATIVE
QUESTIONS ANSWERED. **EXACTLY.***

Waters

THE SCIENCE OF WHAT'S POSSIBLE.™

Xevo G2 ToF

Quantitative and qualitative answers from a single analysis.

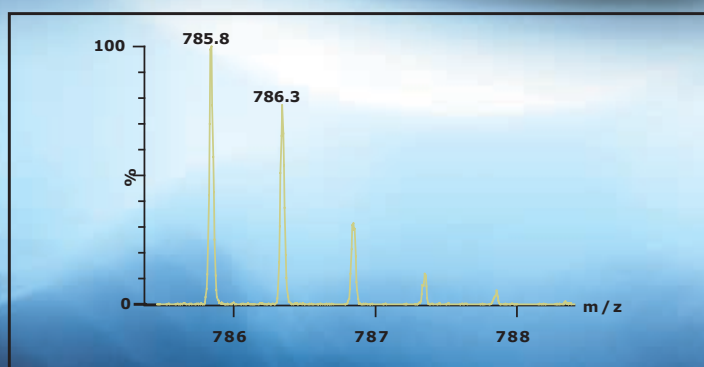
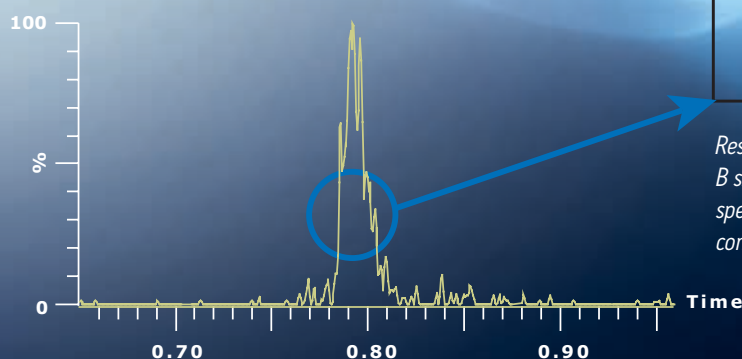
For scientists who need to confidently identify and quantify unknown compounds in complex samples, the Xevo® G2 ToF mass spectrometer – with UPLC®/MS^E and QuanTof technology – offers exceptional levels of selectivity, in-spectrum dynamic range, speed of analysis, quantitative accuracy and exact mass performance simultaneously at unparalleled levels of sensitivity.

Whether your focus is on peptide mapping experiments, protein intact mass analysis, metabolite identification, discovery DMPK quantification, food safety screening, or environmental monitoring, Xevo G2 ToF provides the highest quality information, so you can make decisions better, faster, and easier than ever before.



Detect your compounds with high resolution

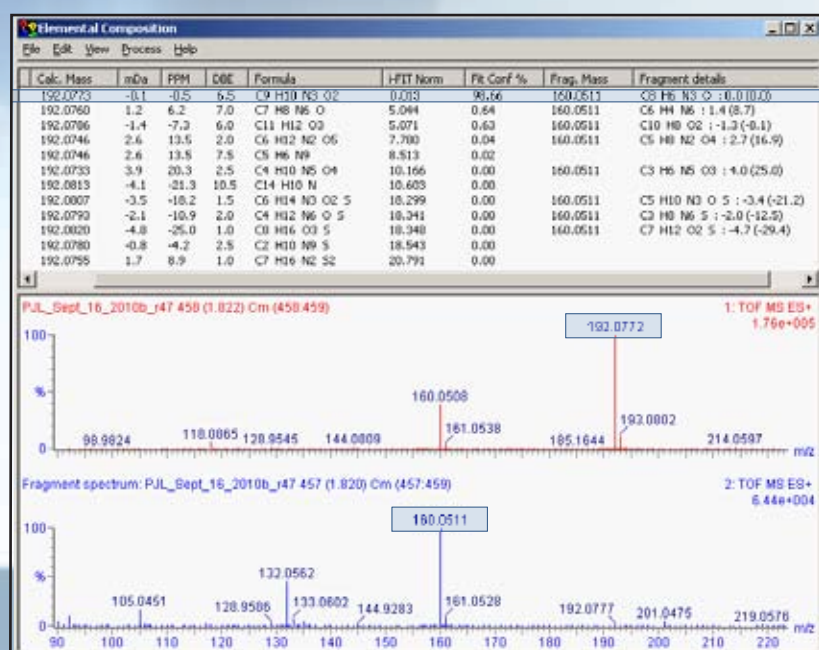
With resolution in excess of 22,500 FWHM at speeds of up to 30 spectra per second, Xevo G2 ToF coupled to UltraPerformance LC® delivers the selectivity to see low level peaks of interest in complex samples.



Resolution at high acquisition rates. UPLC/MS acquisition of [Glu-1] Fibrinopeptide B shows mass resolution of 25,000 FWHM at a data acquisition rate of 30 spectra per second. The chromatographic peak is 1.3 seconds wide at base and contains 40 spectra.

Identify unknowns with elemental composition

Determining the correct elemental composition of ions is critical when identifying unknown compounds. Exact mass measurement, together with accurate isotope pattern information, allows elemental compositions to be determined with maximum confidence, for both precursor and fragment ions.



A tomato extract spiked with a mixture of pesticides was analyzed by UPLC/MS^E. The precursor ion exact-mass at m/z 192.0772 matches to within 0.1 mDa of the calculated value for the elemental composition C₉H₁₀N₃O₂. The observed isotope pattern matches closely to this elemental composition, as indicated by the low i-FIT™ value displayed. The MS^E fragment ion at m/z 160.0511 has an elemental composition of C₈H₈N₃O and matches exactly to loss of CH₃OH, simultaneously confirming the elemental composition and giving structural information on the molecule, which can be identified confidently as the pesticide Carbenazim.

Capability without compromise

Our design philosophy of Engineered Simplicity™ is the combination of highest performance with system versatility and simplicity of operation

high performance

■ QuanTof technology

For the most sensitive, exact mass, quantitative and qualitative benchtop MS system

■ UPLC/MS^E

A simple, patented method of data acquisition that comprehensively catalogs complex samples in a single analysis

versatility

■ Universal Ion Source Architecture

The most extensive range of interface capabilities to service the broadest range of applications

simplicity of operation

■ Engineered Simplicity

Guarantees maximum system performance and usability

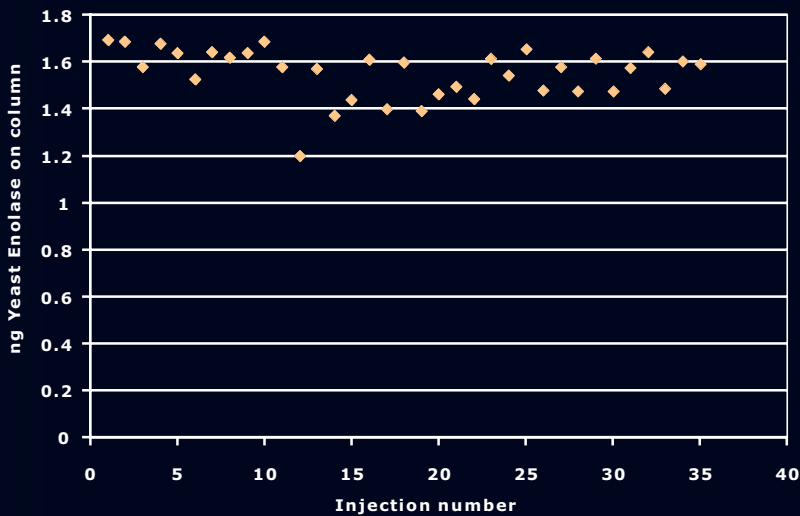
■ System solutions

The most complete system solutions backed by superior support to ensure your success

Upgrade path to QToF functionality

Future proof your laboratory investment with a simple upgrade path to exact mass MS/MS capability

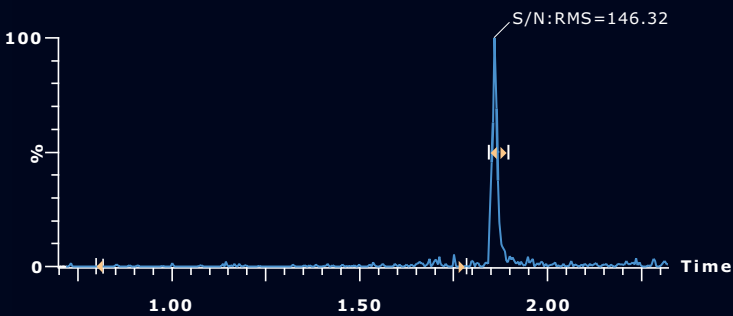




Quantitation

Precision and accuracy of quantitative measurements.

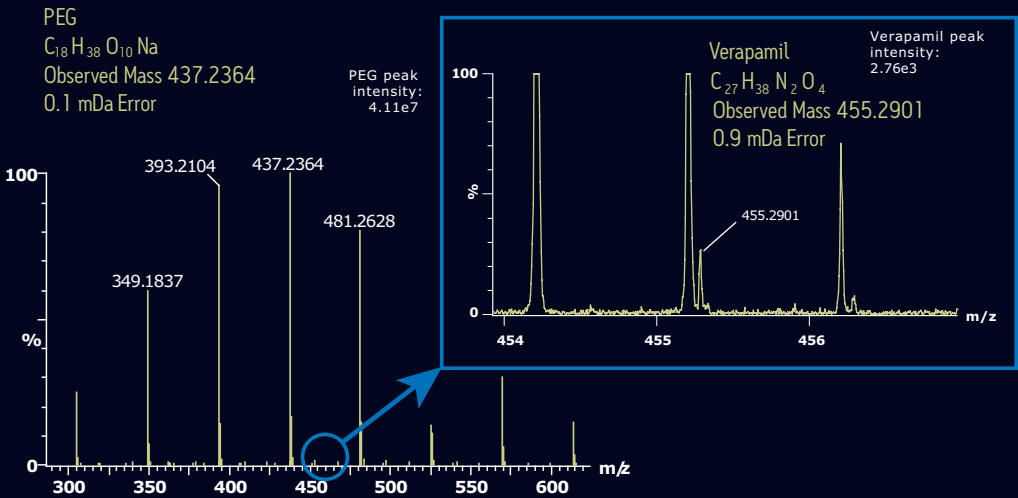
Yeast enolase was spiked into a tryptic digest of E. coli cell lysate and analyzed by a nanoscale UPLC separation with MS^E. The data was processed using Waters Expression^E Software. The average observed amount on column (1.55 ng protein) agreed within 10% of the theoretical amount on column (1.70 ng protein) with a relative standard deviation of 7% over 35 replicate injections.



Sensitivity

Reserpine, 1 pg on column.

Extracted exact mass chromatogram (609.2812±0.02 Da) showing S/N obtained for 1 pg reserpine on column.



Dynamic Range

This dynamic range is obtained even in the most complex spectra.

Verapamil was spiked at a low level into a solution of polyethylene glycol (PEG). Xevo G2 Tof shows excellent mass accuracy over greater than 4 orders of magnitude in-spectrum dynamic range without compromising mass resolution.

QuanTof

performance without compromise.

Powered by QuanTof technology, Xevo G2 ToF delivers the most sensitive, exact mass, quantitative and qualitative performance of any benchtop MS system.



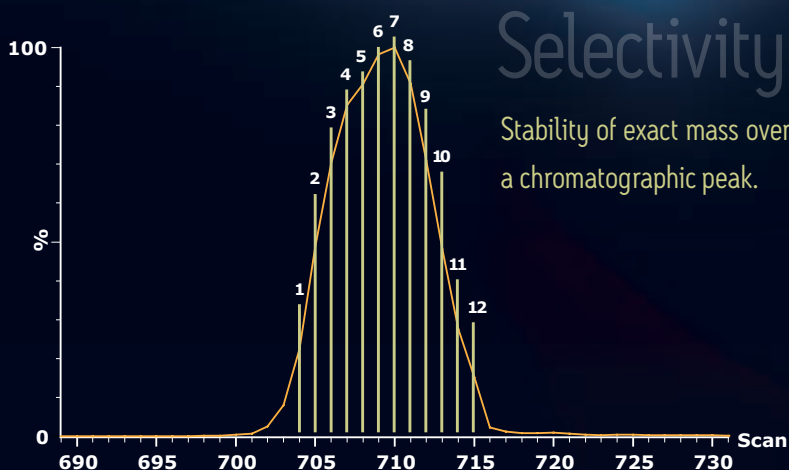
QuanTof's high-field pusher and dual-stage reflectron, incorporating high-transmission parallel wire grids, reduce ion turnaround times due to pre-push kinetic energy spread and improve focusing of high energy ions respectively. These innovative technologies combine to provide the highest levels of ToF performance. The novel ion detection system combines an ultra-fast electron multiplier and hybrid ADC detector to provide outstanding sensitivity and quantitative performance.

QuanTof delivers exact mass with high precision across LC peaks, which in turn provides high selectivity and confidence for the detection and identification of components in complex mixtures.



Scan #	Measured Mass	Error (mDa)	Error (ppm)
1	228.1284	0.1	0.4
2	228.1288	0.5	2.2
3	228.1285	0.2	0.9
4	228.1284	0.1	0.4
5	228.1283	0.0	0.0
6	228.1286	0.3	1.3
7	228.1283	0.0	0.0
8	228.1283	0.0	0.0
9	228.1283	0.0	0.0
10	228.1287	0.4	1.8
11	228.1283	0.0	0.0
12	228.1283	0.0	0.0

Summing scans across this peak gives
 m/z 228.1284 = 0.1 mDa or 0.4 ppm

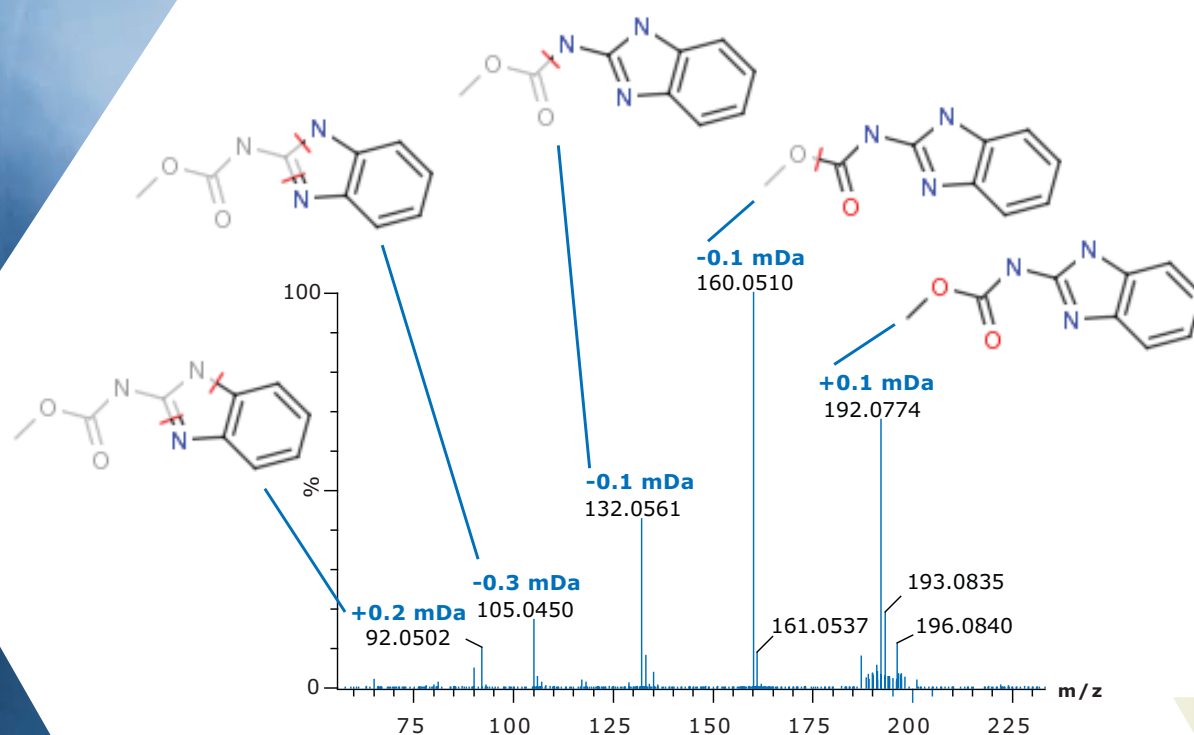


The pesticide ametryn (m/z 228.1283) spiked into tomato at 12.5 ppb. The peak is 2.4 seconds wide and each individual scan shows better than 1 mDa mass accuracy, allowing narrow mass windows for extracted mass chromatograms, increasing the selectivity of exact mass quantitative experiments.

UPLC/MS^E all of the data, all of the time

Xevo G2 ToF offers UPLC/MS^E, so you can see all of the data all of the time. When you need to confirm the identity and structure of known or unknown compounds – you can get high-quality, unambiguous, exact mass precursor and fragment ion data quickly and easily

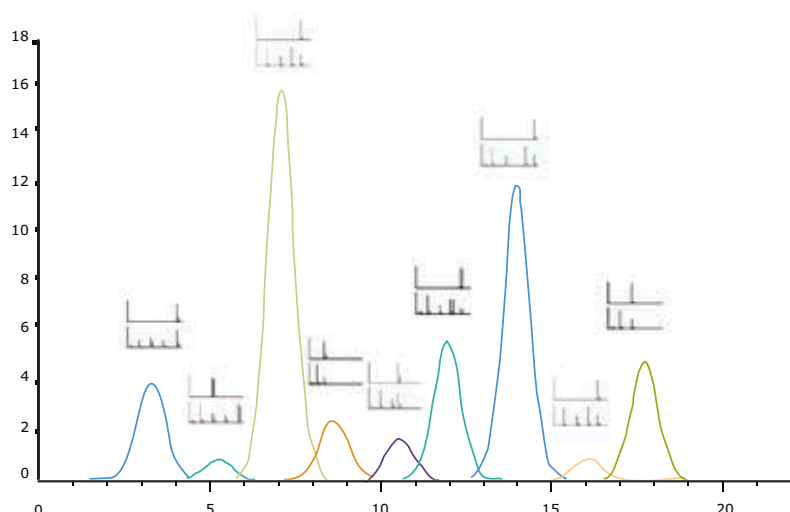
- Identify and quantify from a single dataset^{1,2}
- Maximize the UltraPerformance Liquid Chromatography advantage
- Use simple, generic methods
- Get exact mass precursor and fragment ion spectra from every detectable component in your sample



UPLC/MS^E spectrum of Carbendazim spiked into tomato at a concentration of 12.5 ppb. Excellent exact-mass performance and MassFragment Software allow fragment ions to be assigned structures automatically and compounds to be characterized with high confidence.



UPLC/MS^E: Simply thorough, thoroughly simple



UPLC/MS^E is a simple, patented method of data acquisition that comprehensively catalogs complex samples in a single analysis.



UPLC/MS^E is a method of data acquisition that records exact mass precursor and fragment ion information, while simultaneously obtaining accurate quantitative profiles from every detectable component in a sample. UPLC/MS^E rapidly alternates between two functions: the first acquiring low-energy exact mass precursor ion spectra; the second acquiring elevated-energy exact mass fragment ion; every mass is measured, and spectra for each component aligned in retention time. UPLC/MS^E records data without discrimination or pre-selection, so your samples are completely cataloged in a single analysis.

“Prior to the implementation of the accurate mass LC/MS^E approach, this level of productivity would have been extremely difficult to achieve. The capacity for conducting preliminary metabolite identification experiments has increased by almost an order of magnitude, and the turnaround time for metabolism data has been shortened to the point where the information has a much greater impact on decision making.”

TILLER PR ET AL, RAPID COMMUN. MASS SPECTROM. 2008 APR; 22(7): 1053-61.

Problem Solving has never been so efficient

The Universal Ion Source Architecture of Xevo G2 ToF allows you to use the widest range of ionization techniques as well as the very latest innovations in ionization technologies.

With the Atmospheric Pressure GC (APGC) source you have the capability to perform GC and LC separations on a single MS platform. You'll benefit from the ability to analyze volatile and semi-volatile compounds of low and intermediate polarity – traditionally analyzed only by dedicated vacuum GC/MS instruments.³

The Atmospheric Solids Analysis Probe (ASAP) allows spectra to be rapidly generated from virtually any sample with minimum sample preparation.⁴





Total flexibility

Change your ion sources >

< Not your instrument

When you need options and time is critical, the ion sources are quickly interchangeable and ready to use within minutes.



ESI – Electrospray Ionization
APCI – Atmospheric Pressure
Chemical Ionization
ESCI® – Dual ESI and APCI



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



APGC – Atmospheric Pressure
Gas Chromatography



ASAP – Atmospheric Solids
Analysis Probe



Plug and Play nanoFlow



nanoFlow™ ESI

Also compatible with DESI (Prosalia),
DART (IonSense), LDTD (Phytronix),
TriVersa NanoMate (Advion) sources

INTELLIⁱSTART™

Simplicity starts with IntelliStart

Xevo G2 ToF 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.



Automated MS Resolution
& Calibration Checks



Simple setup of
diverse experiments

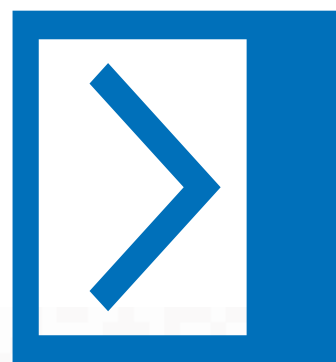


Automated LC/MS
System Check



Automated System
Monitoring

Upgrade to **Xevo G2 QTof**



System solutions for the way you work

REVOLUTIONIZE YOUR WORKFLOW WITH XEVO G2 ToF AND ENGINEERED SIMPLICITY



PREPARE

IntelliStart ensures your system is ready to run, for experts and beginners alike.



ANALYZE

Waters' Universal Ion Source Architecture, QuanTof technology, UPLC/MS^E and FastDDA 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 targeted informatics software.



DECIDE

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

Xevo G2 ToF enables you to future-proof your laboratory investment with a simple onsite upgrade path to QToF functionality. Xevo G2 QToF delivers full scan, exact mass MS/MS for targeted qualitative and quantitative analyses and

UPLC/FastDDA for rapid, automated, intelligent exact mass MS/MS for full structural characterization as well as isobaric labelling quantitative proteomics experiments.

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 21 6156 2666**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 7191**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 7000**Taiwan** 886 2 2501 9928**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. Silva, Gorenstein, Li, Vissers, Geromanos; Absolute Quantification of Proteins by LC/MS²; Mol. Cell. Proteomics; 5.1, 144-156.
2. Tiller, Yu, Castro-Perez, FillGrove, Baillie; High-Throughput, Accurate Mass Liquid Chromatography/Tandem Mass Spectrometry on a Quadrupole Time-of-Flight System as a "First-Line" Approach for Metabolite Identification Studies; *Rapid Commun. Mass Spectrom.*, 2008, 22, 1053-1061.
3. Portoles, Sancho, Hernandez, Newton, Hancock; Potential of Atmospheric Pressure Chemical Ionisation Source in GC-QToF MS for Pesticide Residue Analysis; J. Mass. Spectrom.; 2010, 45, 926-936.
4. Twohig, Shockcor, Wilson, Nicholson, Plumb; Use of An Atmospheric Solids Analysis Probe for High Throughput Screening of Biological Fluids: Preliminary Applications on Urine and Bile; J. Proteome Res., 2010, 9 (7), 3590-3597.

www.waters.com/XevoG2Tof

Waters

THE SCIENCE OF WHAT'S POSSIBLE.™

Waters, Xevo, UltraPerformance LC, ACQUITY UPLC, NuGenesis, ESCi, nd UPLC are registered trademarks of Waters Corporation. The Science of What's Possible, Engineered Simplicity, MassLynx, IntelliStart, MetaboLynx, MarkerLynx, BiopharmaLynx, iFIT, and ProteinLynx Global SERVER are trademarks of Waters Corporation. All other trademarks are the property of their respective owners.

©2010 Waters Corporation. Printed in the U.S.A.
December 2010 720003832EN-A4 AO-CP

