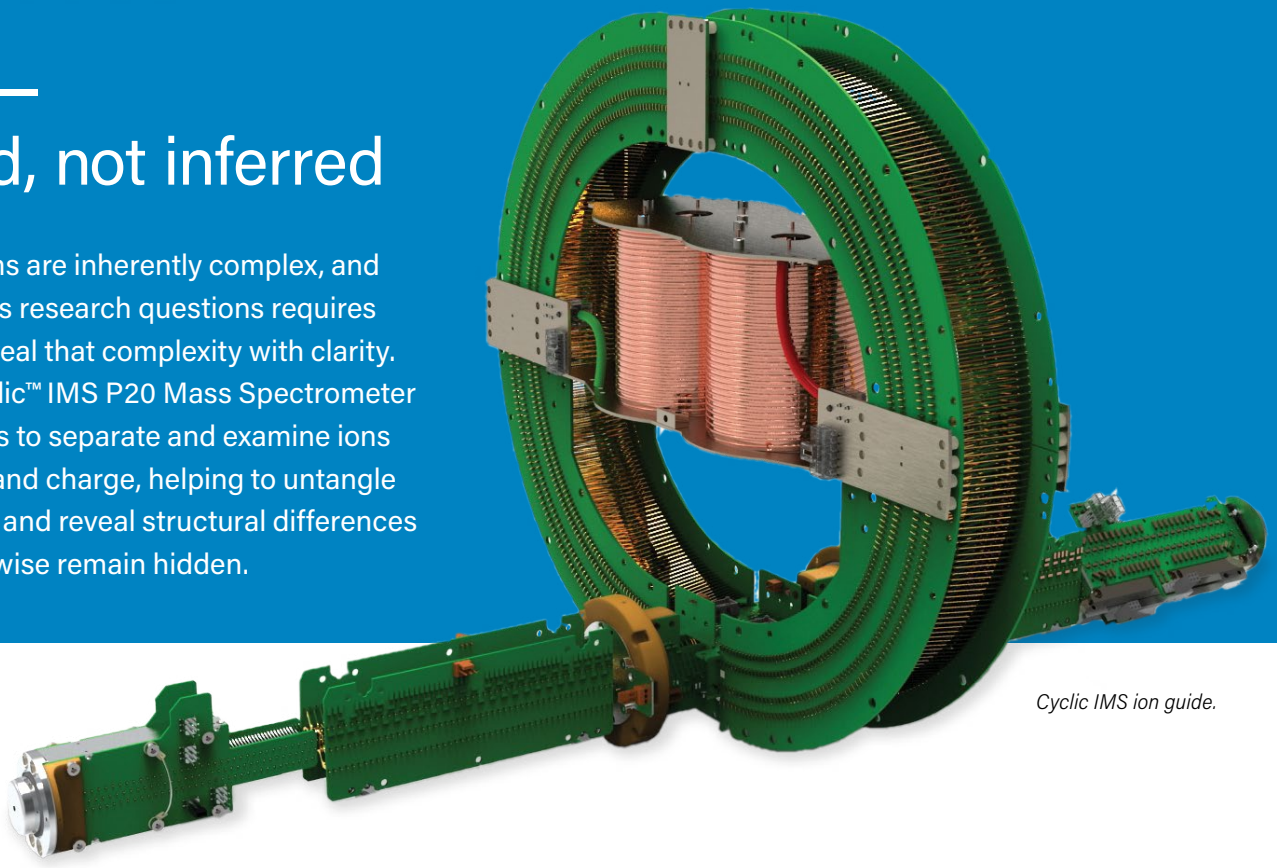
Waters™

Waters Cyclic IMS P20 Mass Spectrometer

Insight—revealed, not inferred.

Insight—
revealed, not inferred

Biological systems are inherently complex, and answering today's research questions requires tools that can reveal that complexity with clarity. The Waters™ Cyclic™ IMS P20 Mass Spectrometer enables scientists to separate and examine ions by shape, mass, and charge, helping to untangle crowded spectra and reveal structural differences that would otherwise remain hidden.



Cyclic IMS ion guide.

By combining scalable ion mobility with advanced fragmentation and, where required, spatial analysis, the Cyclic IMS P20 Mass Spectrometer supports more detailed investigation of molecular structure and interactions, whether in solution, in the gas phase, or directly from surfaces. This provides you with greater confidence in data interpretation, more freedom in experimental design, and results that better reflect the true complexity of biological systems.

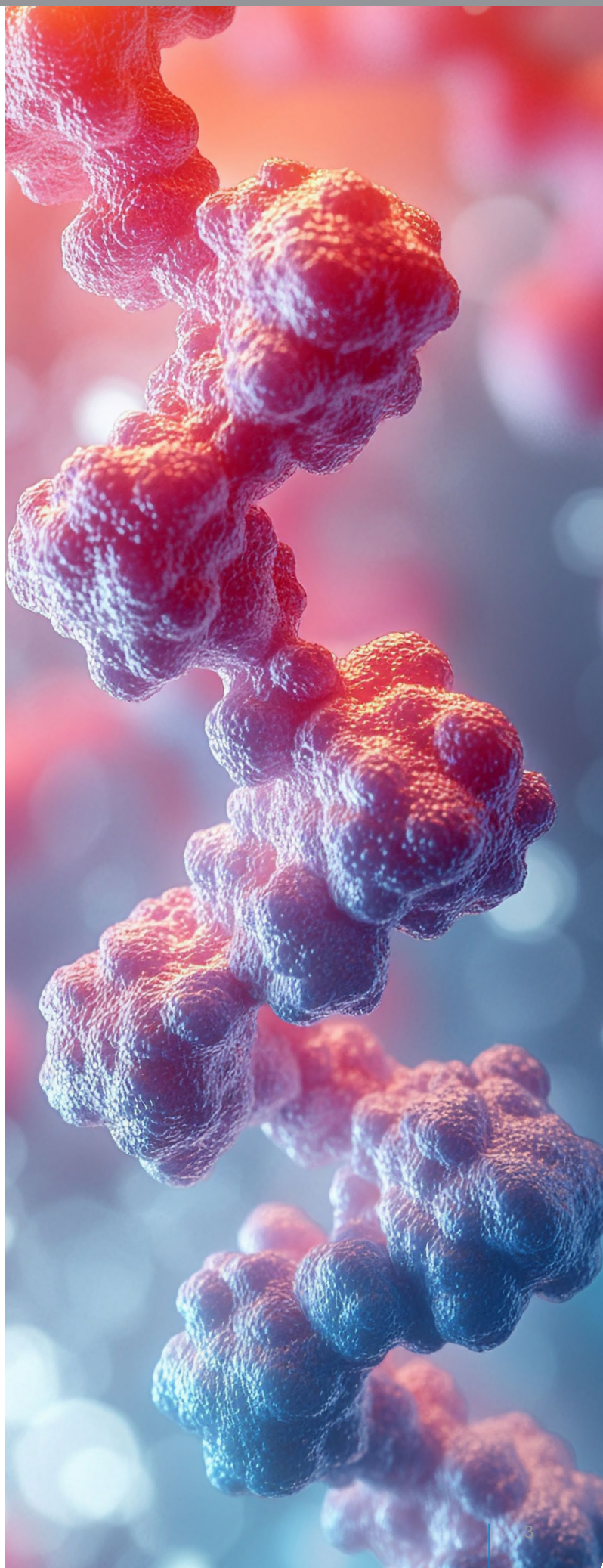
- **Design experiments around the science, not your instrument**
  Precise control over ion selection, separation, and interrogation across mass and mobility dimensions enables both routine, reproducible workflows and advanced, high-resolution studies as complexity increases.
- **See more with improved signal quality**
  Optimized ion transmission, multi-pass separations, and high-performance oaTOF detection enhance sensitivity and reduce spectral congestion, revealing low-abundance and co-eluting species.
- **Access deeper structural INSIGHT**
  Integrated techniques, including ECD, SID, CIU, DFD, and high-mass quadrupole selection, support detailed analysis of higher-order structure and molecular interactions.
- **Extend molecular visualization**
  MALDI XS and DESI XS enable complementary spatial and surface analyses, with ion mobility reducing spectral overlap to improve specificity in complex samples.
- **Adapt as research evolves**
  Streamlined workflows, intuitive software, and modular design support efficient operation today and flexibility for future applications.

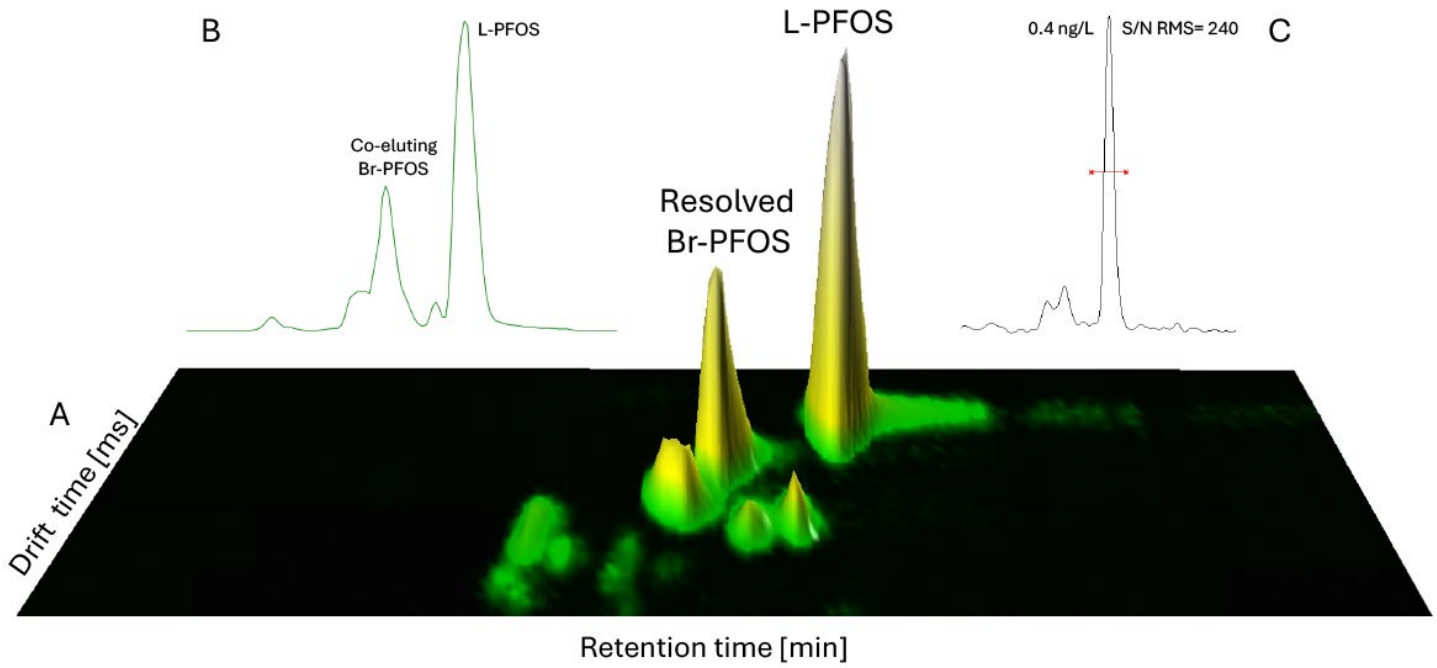
Resolving molecular complexity—on your terms

The Waters Cyclic IMS P20 Mass Spectrometer introduces the next evolution of Cyclic ion mobility, giving scientists new flexibility in how molecular complexity is resolved and explored.

This system delivers scalable, high resolution separation that can be applied selectively, which supports fast, routine measurements as well as deeper, structure focused investigations. Separation by shape, mass, and charge reduces spectral congestion and exposes subtle differences that are often masked in conventional MS workflows.

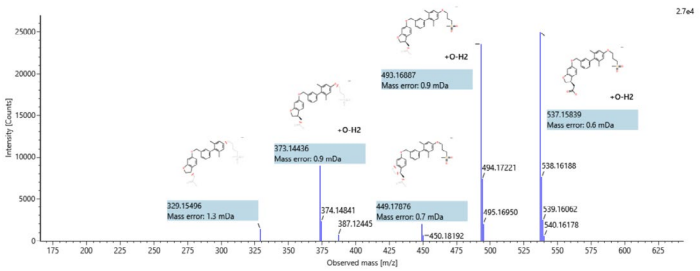
Designed for practical use in real laboratories, the Cyclic IMS P20 Mass Spectrometer combines advanced separation power with an improved user experience. Automated multipass collision cross section (CCS) calibration and built in methods support reproducible CCS measurements out of the box, while retaining control for advanced method development. Enhanced sensitivity and optimized ion transmission further enable confident analysis of low abundance species in complex matrices.

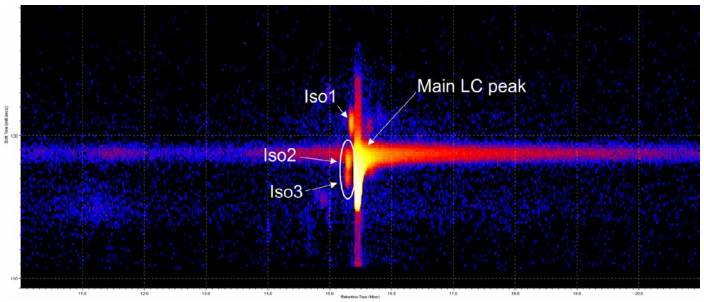




Improved selectivity for confident contaminant identification

Improved separation across both mass and mobility dimensions enhances discrimination of isomeric and isobaric contaminants, reducing interferences and supporting more confident identification in complex environmental and biological samples.





Faster clarity for complex metabolic pathways

In drug metabolism and identification studies, orthogonal ion mobility separation helps distinguish closely related metabolites and biotransformation products, reducing chimeric spectra and improving structural clarity. This supports faster interpretation, localization of sites of metabolism and more confident decision making across drug discovery and development workflows.

View isomerism in unprecedented detail

For biotherapeutics and next generation peptides, including glucagon-like peptide-1 (GLP 1)–based modalities, the Cyclic IMS P20 Mass Spectrometer enables detailed interrogation of higher order structure, conformational heterogeneity, and modification states—scaling from routine characterization to more in depth structural studies.

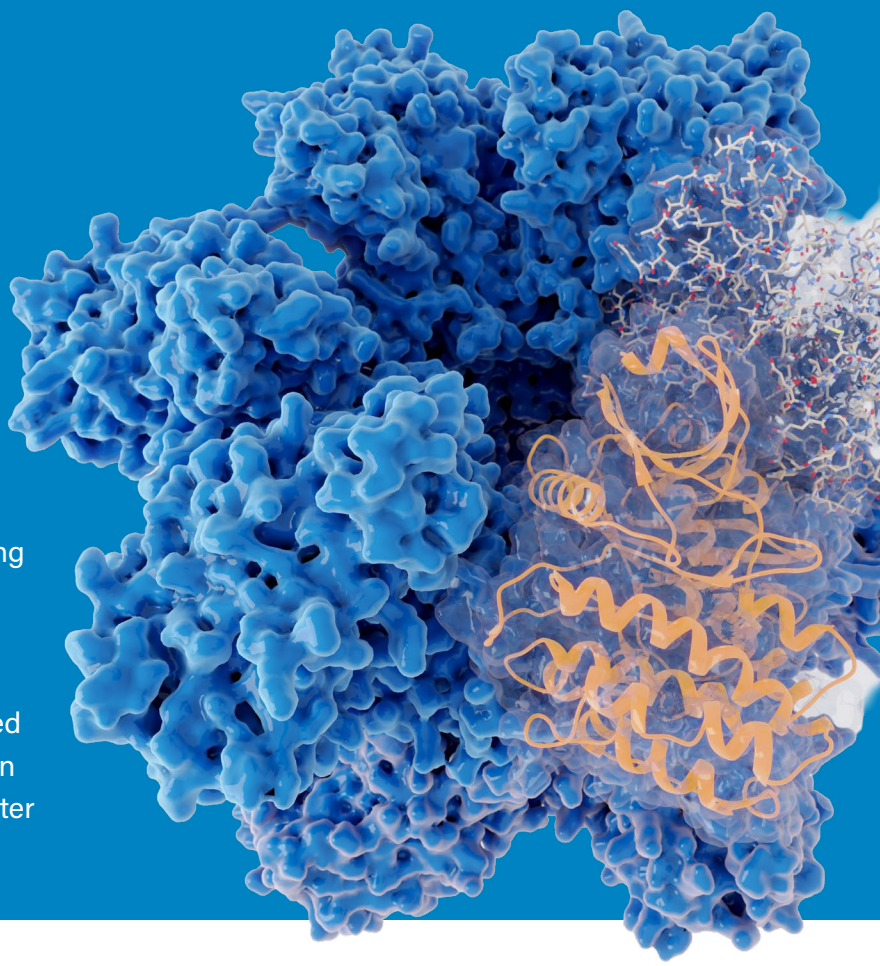
More confident identifications in complex omics data

Across metabolomics, and lipidomics, Cyclic IMS P20 Mass Spectrometer improves separation of isomeric and isobaric species, increasing molecular specificity and confidence in identification. Robust, automated CCS measurements support reproducibility while maintaining flexibility for complex biological analyses.

Structure—revealed not inferred

Addressing the demands of native MS

Revealing conformational heterogeneity within intact protein assemblies is critical for understanding structure, stability, and molecular interactions. The Waters Cyclic IMS P20 Mass Spectrometer supports confident structural interpretation by enabling high resolution separation of mass selected native ions, allowing multiple structural states within a single protein assembly to be examined with greater clarity and reduced ambiguity.



As biological research advances toward increasingly complex systems, native mass spectrometry is being called on to move beyond compositional analysis toward deeper insight into protein structure and dynamics. Cyclic ion mobility separation is an established approach for resolving gas phase conformational diversity, supporting interrogation of higher order protein structure within intact proteins and non covalent assemblies. By isolating defined *m/z* populations prior to ion mobility separation, the Cyclic IMS P20 Mass Spectrometer enables targeted analysis of conformational heterogeneity within native protein complexes.

> "The increase in sensitivity delivered by wideband enhancement will significantly accelerate our analyses, potentially by an order of magnitude, and enables us to probe critical low abundance species in far greater detail".

Kostas Thalassinos
Professor of Mass Spectrometry, UCL

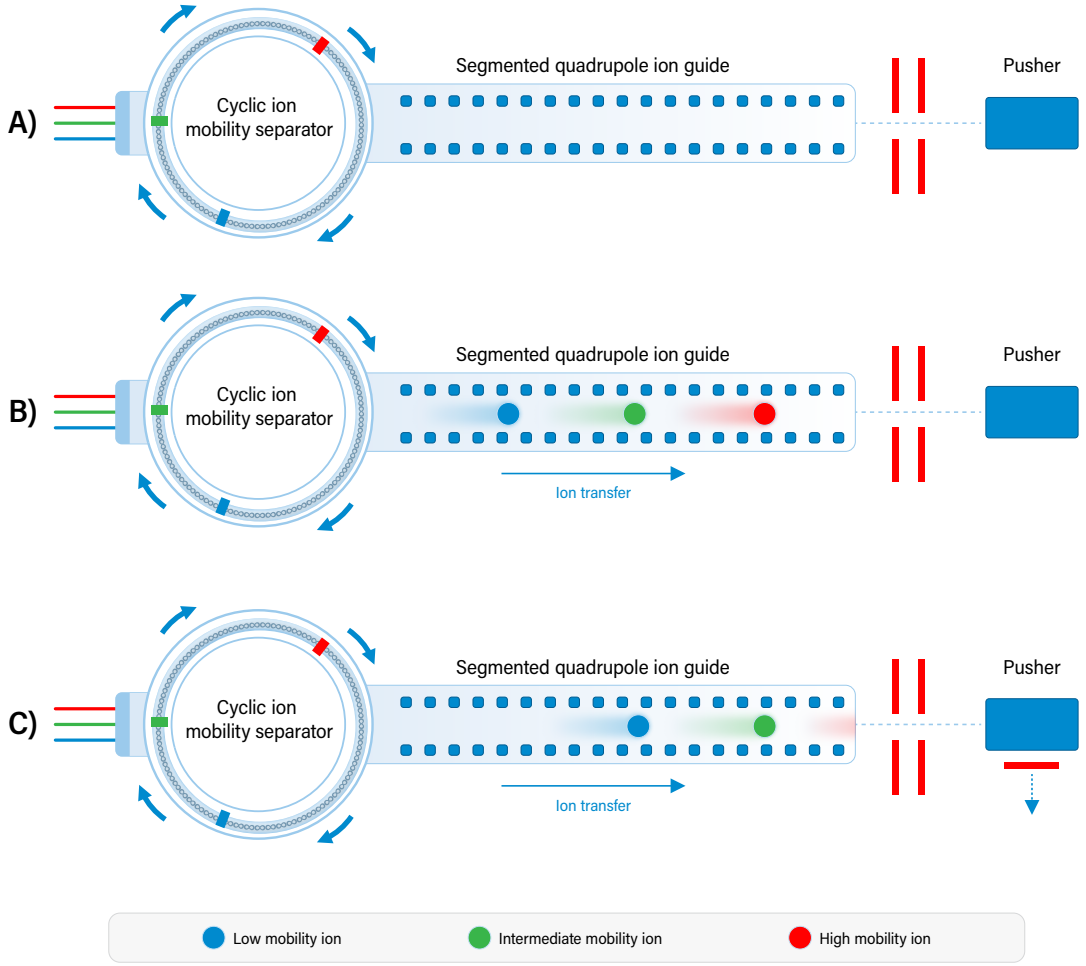
The platform supports flexible configuration to address a broad range of native MS and structural workflows, including:

- Dynamic Field Declustering (DFD) implemented within the StepWave™ Ion Guide region to support removal of residual solvent and non specific adducts prior to mass analysis
- Quadrupole mass selection extending to 32,000 *m/z* for targeted isolation of high mass native species
- Extended upper mass capability beyond 100,000 *m/z* to accommodate large protein assemblies and complexes
- ECD and SID for complementary fragmentation of native ions
- Advanced CIU workflows integrated with Cyclic ion mobility for conformational stability assessment

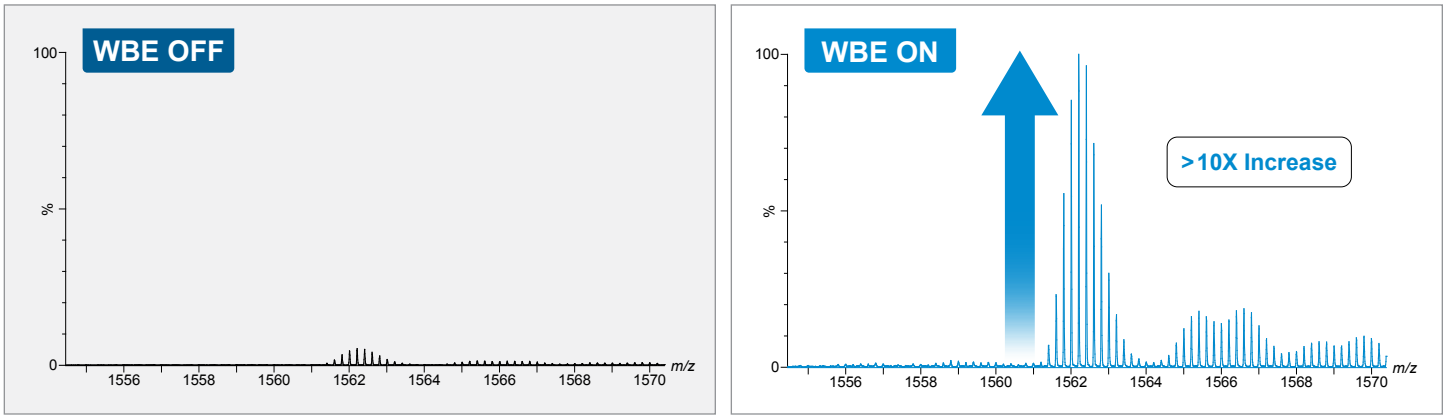
Together with Wideband Enhancement (WBE), which provides a 10x improvement in MS/MS sensitivity, these capabilities support detailed interrogation of protein architecture, stability, and intermolecular interactions across a broad mass range.

Detect more across a broad *m/z* range

Wideband Enhancement (WBE) boosts MS/MS sensitivity across a wide *m/z* range, supporting confident detection of low-abundance species.

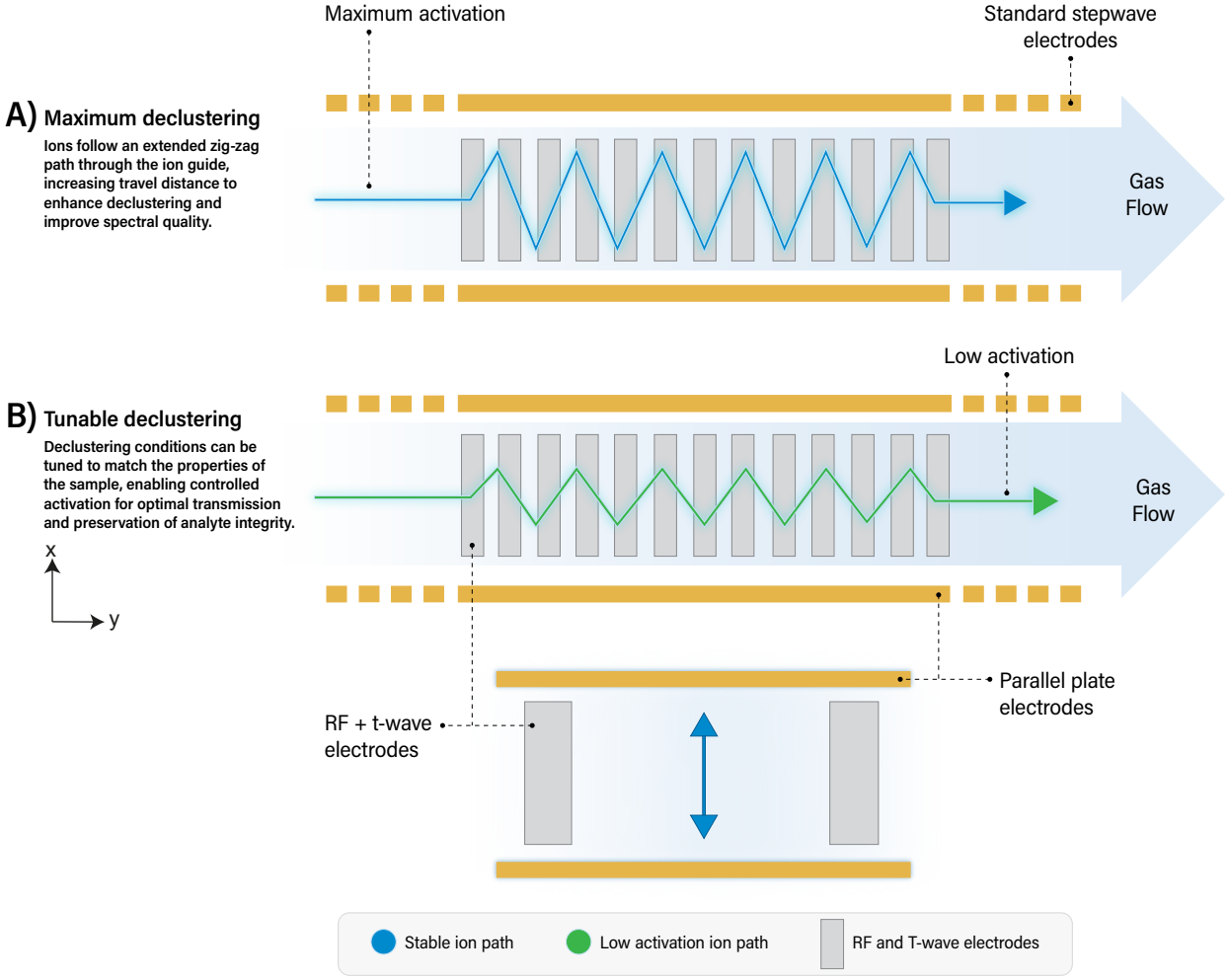


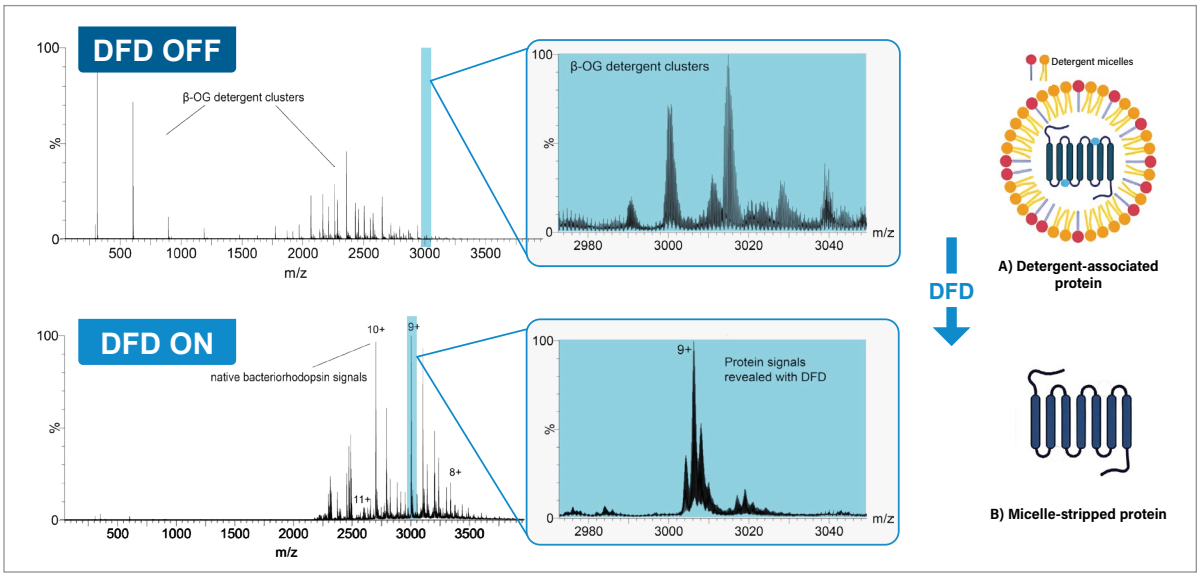
In normal Time of Flight operation, not all ions from a continuous ion beam are pushed to the detector. Wideband Enhancement (WBE) can be employed to maximize the duty cycle for a broad m/z range, increasing the proportion of ions reaching the detector. Shown in (a), ions enter the IMS region and are separated based upon mobility. In (b) ions then exit the IMS region as distinct packets which arrive at the pusher region in ascending m/z (descending mobility). The synchronization of this arrival with a duty cycle-enhancement pulse results in drastically-increased response over the m/z range being studied.



Sensitivity for low abundance species is drastically increased.

Dynamic Field Declustering - DFD is an optional novel device in the StepWave region of the Cyclic IMS P20 Mass Spectrometer. The device employs two parallel plates with an applied radio-frequency (RF) oscillating voltage to drive ions off-axis, increasing controlled collisions with the background gas. The collisions promote effective desolvation and adduct removal, producing cleaner spectra and enabling more confident interpretation of native protein data.

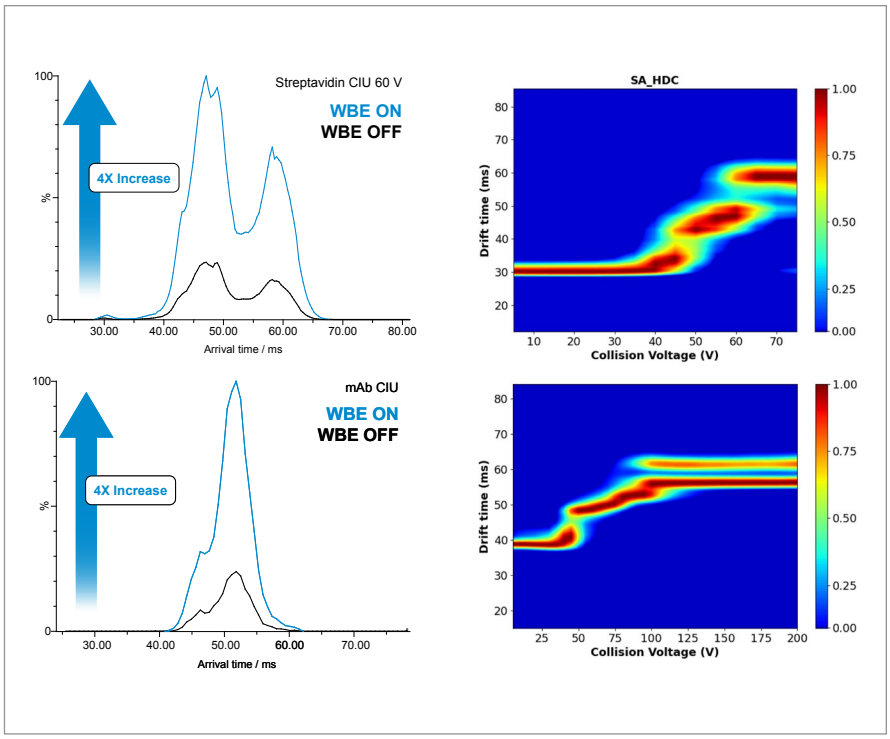




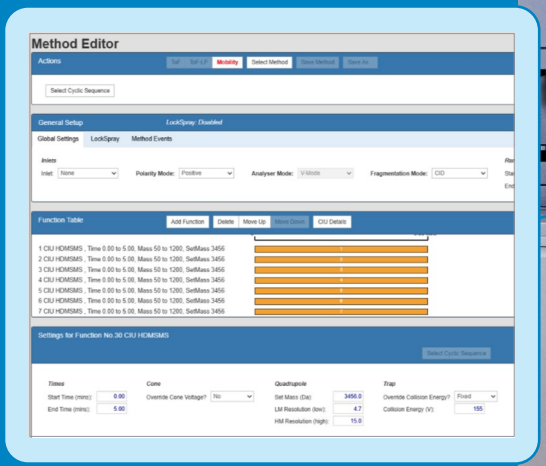
Utilizing DFD to study native bRreleases the protein from the micelle to reveal protein signals on the native mass spectra. The blue inset highlights the 9+ charge state of monomeric native bR, demonstrating how DFD effectively declustersthe protein signals from detergent to reveal the isotopically resolved monomer.

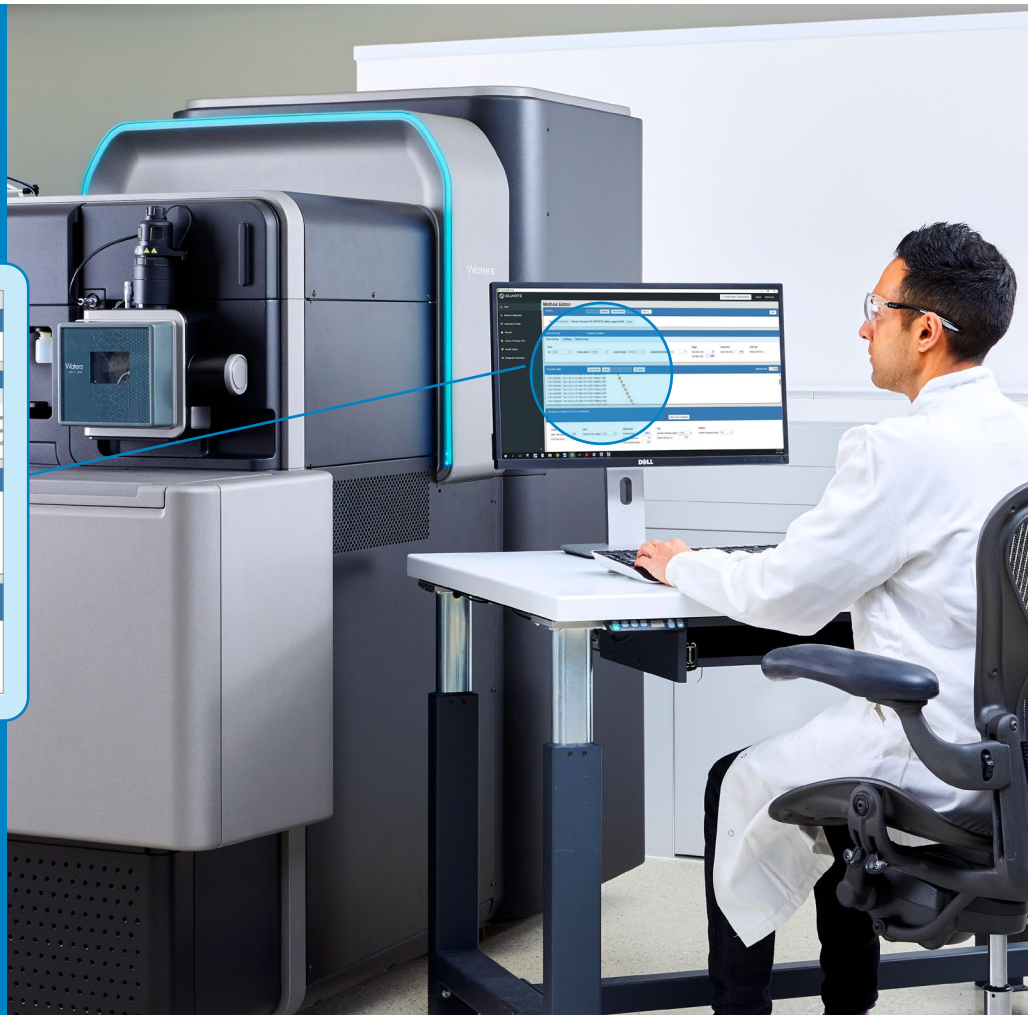
Collision-induced unfolding - Assessing conformational stability requires sensitive, repeatable unfolding measurements of mass selected native ions. The Waters Cyclic IMS P20 Mass Spectrometer streamlines CIU experiments by simplifying method setup and improving sensitivity for native protein ions.

Wideband enhancement increases signal intensity even for high mass species, enabling faster acquisition of CIU profiles and supporting higher throughput assessment of protein and complex stability. This allows conformational changes to be monitored with greater clarity and confidence, even for low abundance species.



Cyclic IMS improves CIU efficiency through simplified setup and enhanced sensitivity, supporting rapid, high throughput analysis of protein conformational stability.





Visualization—revealed not inferred

Molecular imaging enabled by Cyclic IMS

Confident molecular imaging depends on the ability to distinguish closely related species within complex biological tissues. The Waters Cyclic IMS P20 Mass Spectrometer extends the principle of revealed, not inferred into mass spectrometry imaging by enabling separation of isobaric and isomeric species prior to visualization, providing clearer spatial insight and stronger molecular confidence.

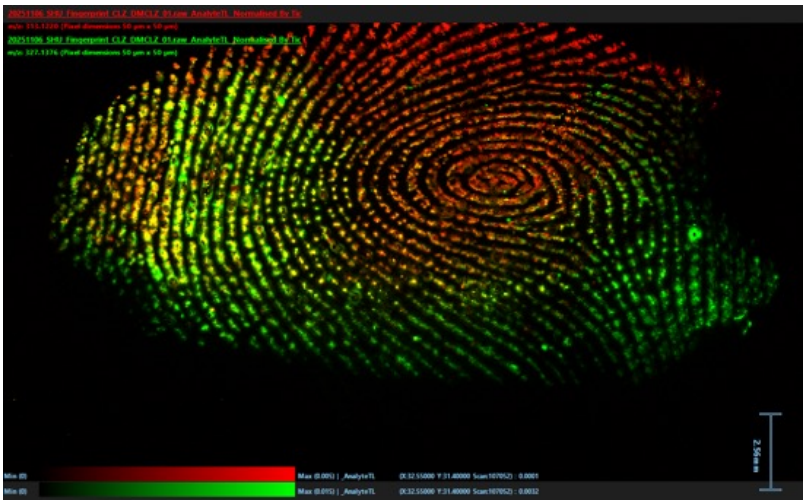


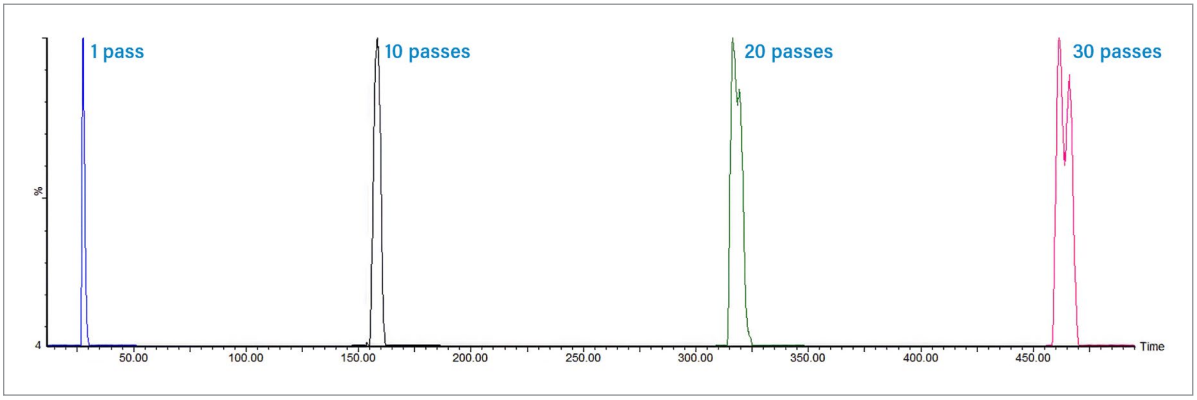
Image provided by Rohith Krishna, PhD student, Centre for Mass Spectrometry Imaging, Sheffield Hallam University. Showing MALDI imaging analysis of a human fingerprint contaminated with the prescription drug clozapine, green, and its metabolite, green (10 Hz acquisition rate and 50 µm pixel size).

By integrating complementary MALDI XS with DESI XS workflows on a single platform, the Cyclic IMS P20 Mass Spectrometer expands molecular coverage while maintaining consistency across ionization techniques. When combined with multipass Cyclic ion mobility and IMS^n capabilities, subtle compositional and conformational differences can be resolved with greater clarity, reducing ambiguity and enabling direct molecular evidence rather than assumption based interpretation.

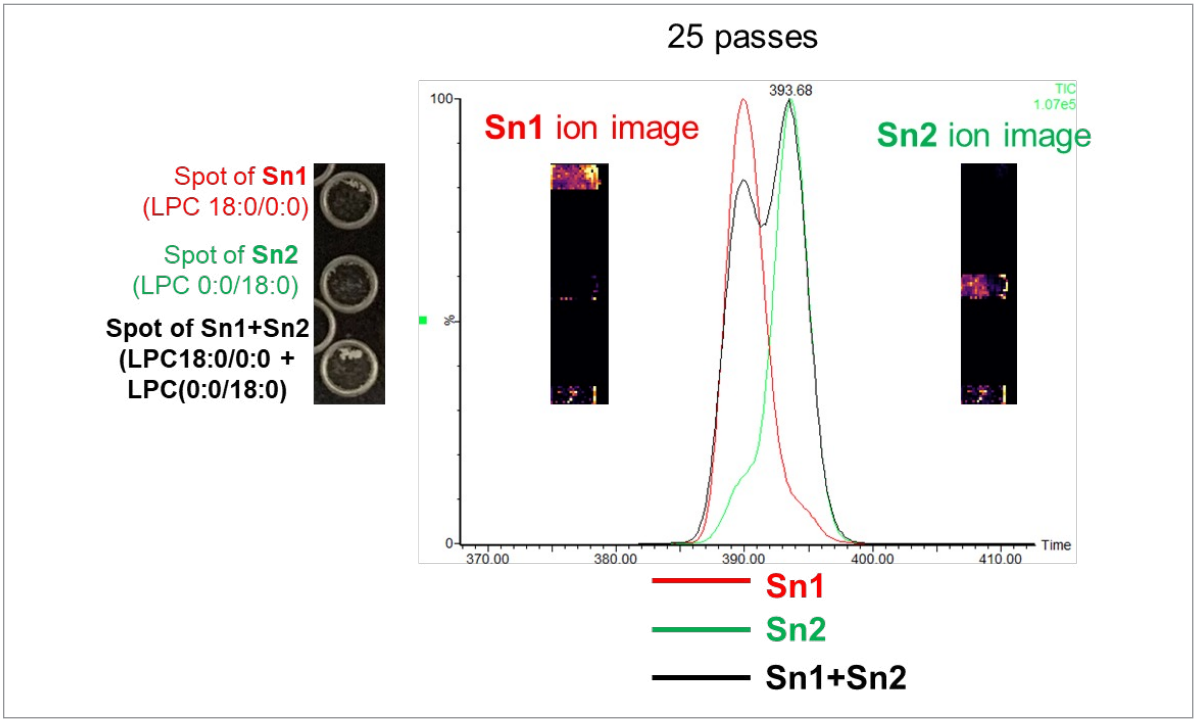
These capabilities support a more complete and reliable understanding of biological organization, from lipid heterogeneity to small molecule localization. In fingerprint imaging studies, for example, the Cyclic IMS P20 Mass Spectrometer enables differentiation of endogenous and exogenous compounds and their metabolites, supporting secure identification and contextual interpretation of molecular signatures.

Combining the Cyclic IMS P20 Mass Spectrometer with MALDI XS - further enhances molecular specificity in MALDI MSI workflows. High resolution ion mobility separation enables confident discrimination of isobaric and isomeric lipids, even in complex matrices dominated by matrix clusters.

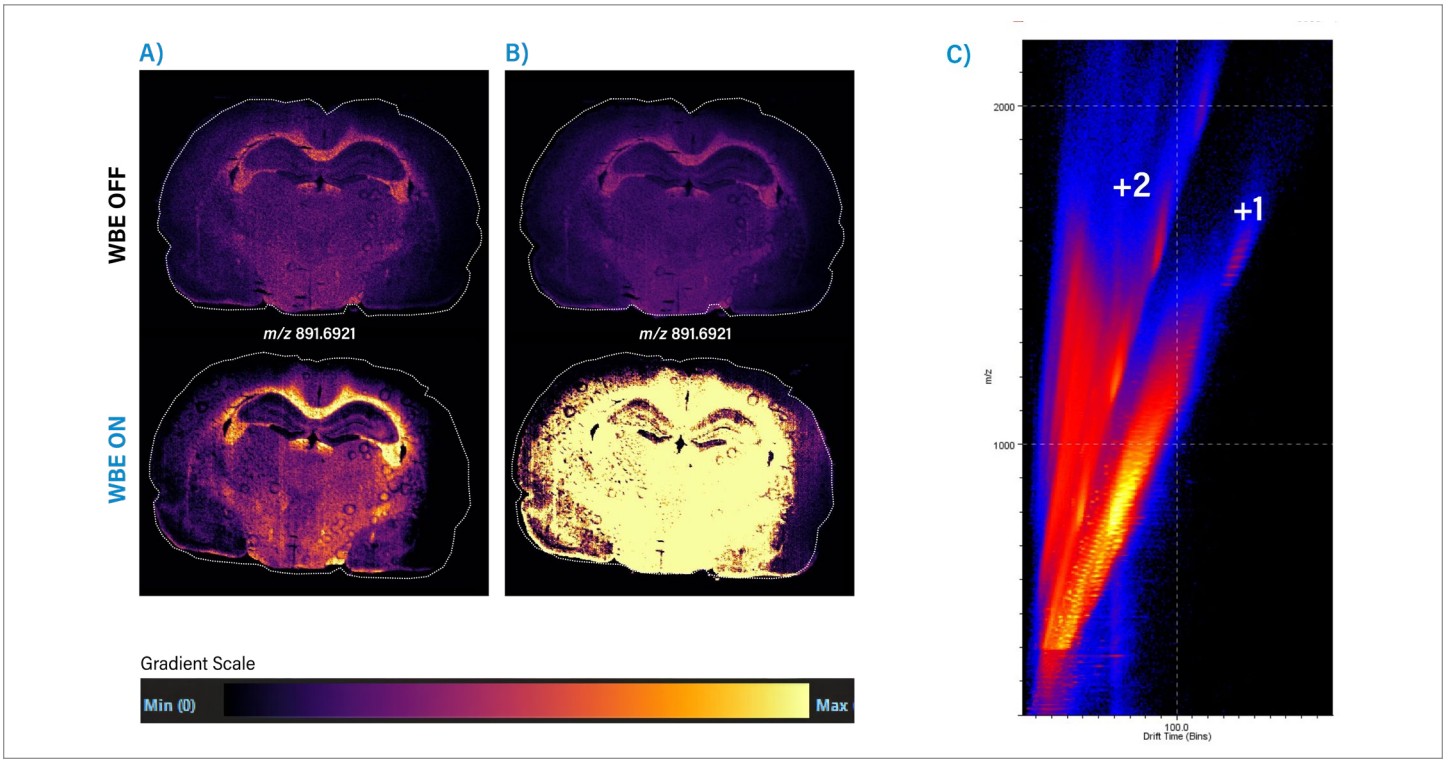
The platform also supports wideband enhancement (WBE) for MS imaging, enabling substantial sensitivity gains across a broad mass range—from small molecules to complex lipids and higher mass species. Enhanced ion transmission improves visualization of low abundance components and enables selective enhancement of ions with distinct mobility or charge state trends, such as per- and polyfluoroalkyl substances (PFAS). The result is richer, more informative molecular images that support clearer spatial interpretation and deeper biological insight.



The cIMS device gradually separating out lipid positional isomers from 1 to 30 passes of the cyclic device for subsequent visualization.



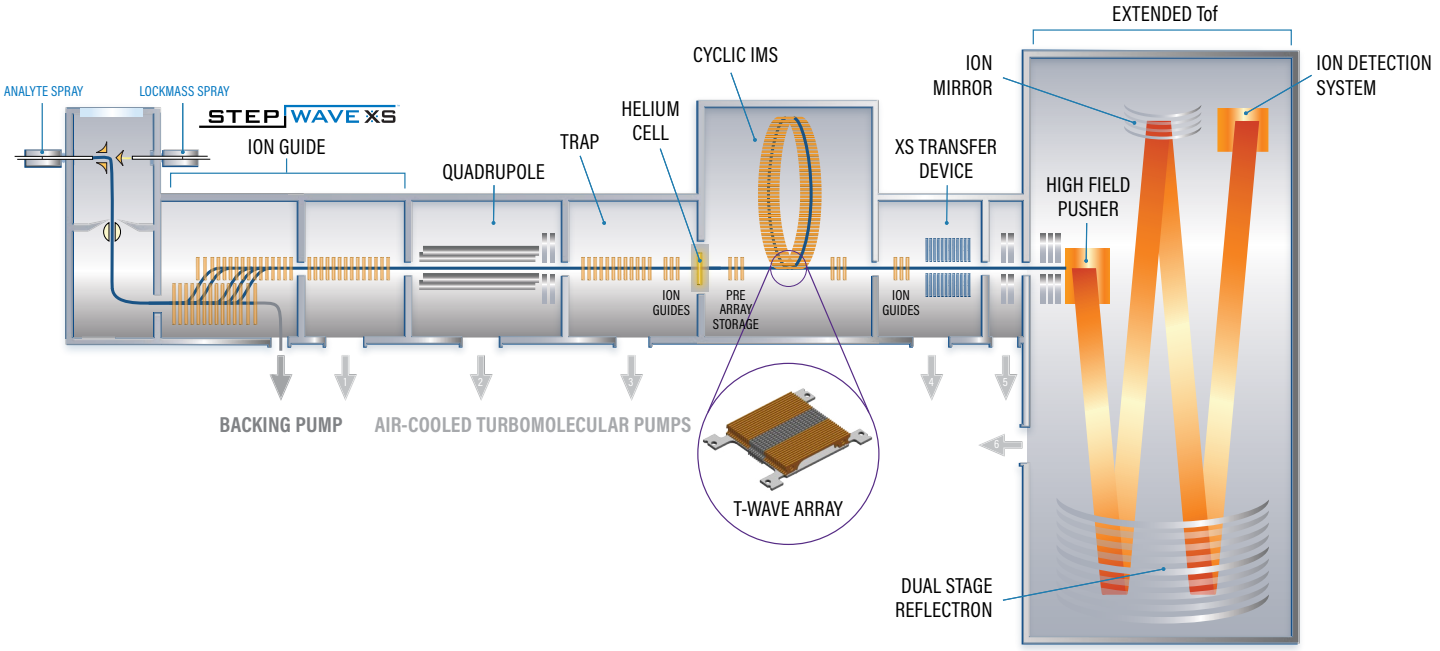
Using isomeric lysophosphatidylcholine (LPC) standards, both individual and mixed, spotted for a MALDI IMS profiling experiment, up to 30 mobility passes enabled clear differentiation of biologically important lipid species linked to inflammation, atherosclerosis, and cellular signalling (A). LPC 18:0/0:0 =Sn1, LPC 0:0/18:1 Sn2 and mixed Sn1+Sn2 lipids were spotted onto 44-well microscope slide at 0.5 mg/ml with 25 mg/mL DHB. B) Mobilograms of MALDI MSI experiments of the individual Sn spots and mixed Sn 1 and Sn2 spot acquired at 1 Hz with 20, 25, and 50 IMS passes, with a laser repetition rate of 250 Hz at 100 µm pixel size.



*DESI XS imaging of mouse brain on Cyclic IMS P20. A) 2D Driftscope plot (**m/z** vs drift time) resolving charge states of phospholipids and lipid dimers, used to define trendlines for targeted WBE. B) 1:10 scale comparison (WBE off vs on) highlighting relative signal gains for singly charged lipids along the IMS trendline. C) Same Image, shown at a fixed intensity scale, illustrating the magnitude of signal enhancement achieved with WBE.*

Flexible Configurations—Supports multiple acquisition approaches enabling different applications, whilst ensuring consistent performance, reducing set-up time and increasing experimental flexibility.

CYCLIC IMS P20



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Waters Corporation
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Milford, MA 01757 U.S.A.
T: 1 508 478 2000
F: 1 508 872 1990
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