Waters™

Xevo MRT P10 Mass Spectrometer

Backed by science, trusted by experts, powered by MRT.

MRT technology is evolving

The Xevo™ MRT P10 Mass Spectrometer builds on the revolutionary multi-reflecting time-of-flight (MRT) technology, delivering a system capable of exceptional sensitivity, at unprecedented acquisition speeds, and expands the analytical flexibility for even the most demanding MS applications.

Whether you're in an academic lab or in industry, performing qualitative or quantitative experiments, the cutting-edge Xevo MRT P10 MS sets a new benchmark in sensitivity and speed.

Unmatched sensitivity for deeper discovery

The Xevo MRT P10 MS delivers up to 20x improvement in MS/MS sensitivity*, significantly boosting analyte detection and increasing coverage in complex samples.

The fastest benchtop HRMS available

Designed for high-throughput laboratories, the Xevo MRT P10 MS is the fastest benchtop high-resolution mass spectrometer (HRMS), supporting ultrafast acquisition rates of 200 Hz for MS/MS, data-independent (DIA), and data-dependent acquisitions (DDA).

Expanded analytical depth and workflow flexibility

The Xevo MRT P10 MS broadens analytical capabilities with advanced acquisition modes, including state-of-the-art DDA and SONAR™ Pulse Acquisition Modes. These capabilities provide greater analytical flexibility and deeper biological insights from every sample.

Sensitivity Revolution

- 20x MS/MS sensitivity boost (*m/z* 50–1200)
- Improved MS sensitivity for better detection
- Wideband enhanced duty cycle (WB EDC) for unmatched performance

Enhanced Speed

- 100 Hz MS data acquisition
- 200 Hz MS/MS data acquisition (MS/MS and DDA)

Acquisition Modes

- **Advanced DDA algorithm**
  New, intelligently, optimized DDA acquisition
- **SONAR Pulse Acquisition Mode**
  For enhanced depth of coverage
- **Hybrid acquisition mode**
  Integrating Tof MRM and MS^E for flexible quantitative workflows

**Compared to the Xevo MRT MS*

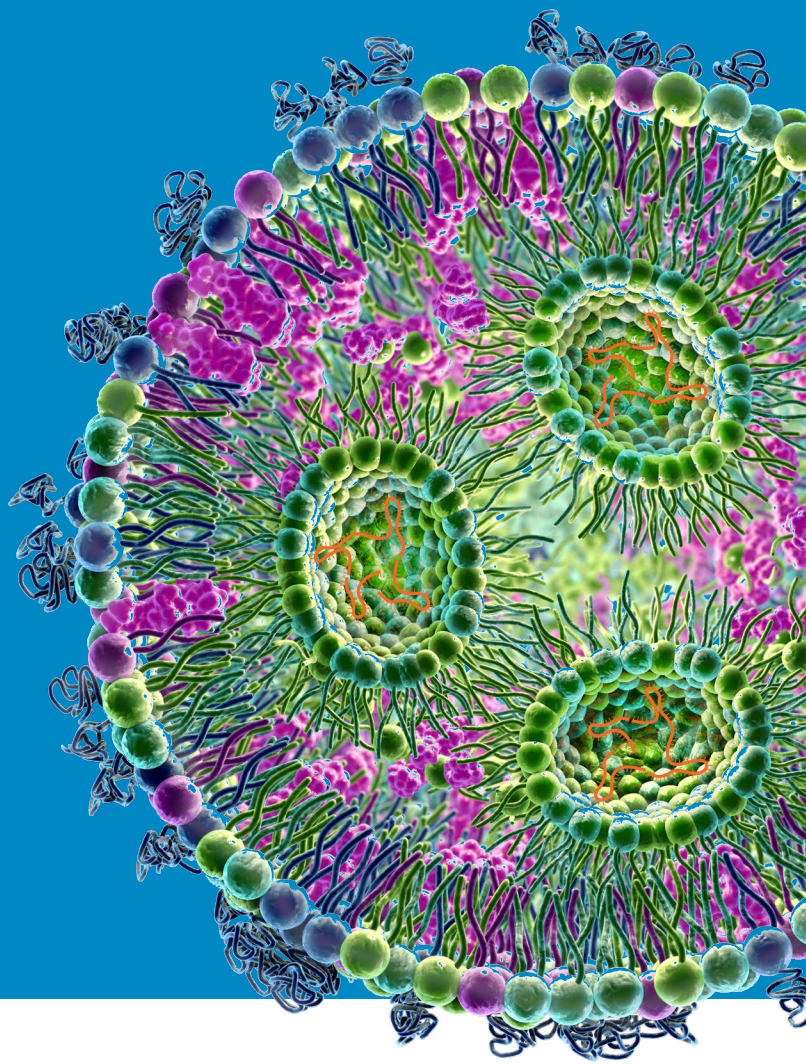
Accelerating research and discovery

Exceptional sensitivity, unrivalled speed, and deeper insight

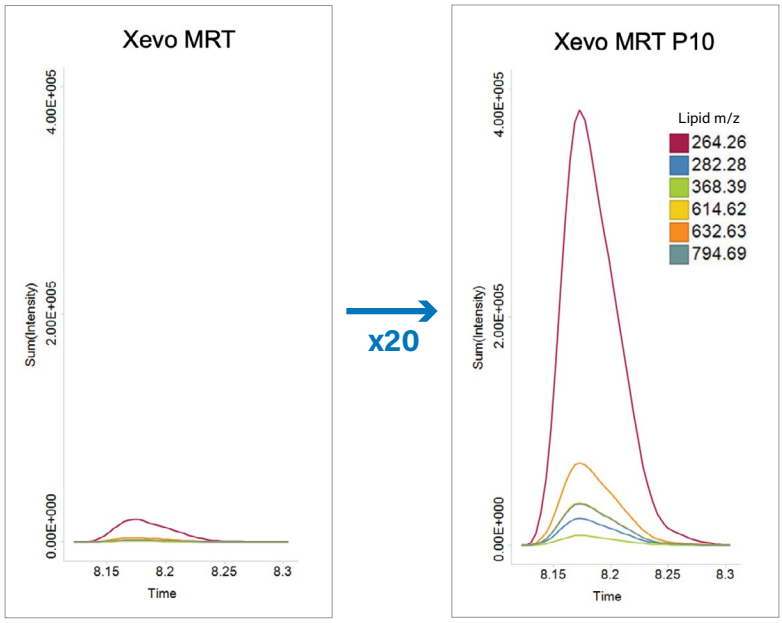
The enhanced sensitivity of the Xevo MRT P10 MS delivers high-quality MS data that gives you more confidence in identification and quantification, even for low-abundance components and single-cell analysis. The system identifies up to 40% more lipids than the next-best benchtop HRMS.

In combination with the exceptional speed, the system ensures comprehensive data capture, even in fast chromatographic separations, without compromising data quality, so researchers don't need to choose between data quality and speed.

For ultimate flexibility and integration into existing data pipeline and workflow strategies, the waters_connect™ Software Platform converts datasets into a universal file format, mzML, either at the point of acquisition or as a post-processing step.



a. Technology Improvements — Increased MS/MS Sensitivity



b. Competitive Positioning

Lipidomics analysis vs. another leading benchtop QTOF system

+30% lipids detected

+40% confidently identified

	Xevo MRT P10	Competitive Offering
Lipid IDs	1,150	880
Curated Lipids	640	460

** SRM1950 (NIST reference material — human plasma standard, MS-DIAL processing, same stringency used for Waters and the competitive offering)*

Figure 1. The Xevo MRT P10 Mass Spectrometer shows a 20x improvement in response as compared to the Xevo MRT Mass Spectrometer and up to 40% increase in lipids detected vs. another leading benchtop QTOF.

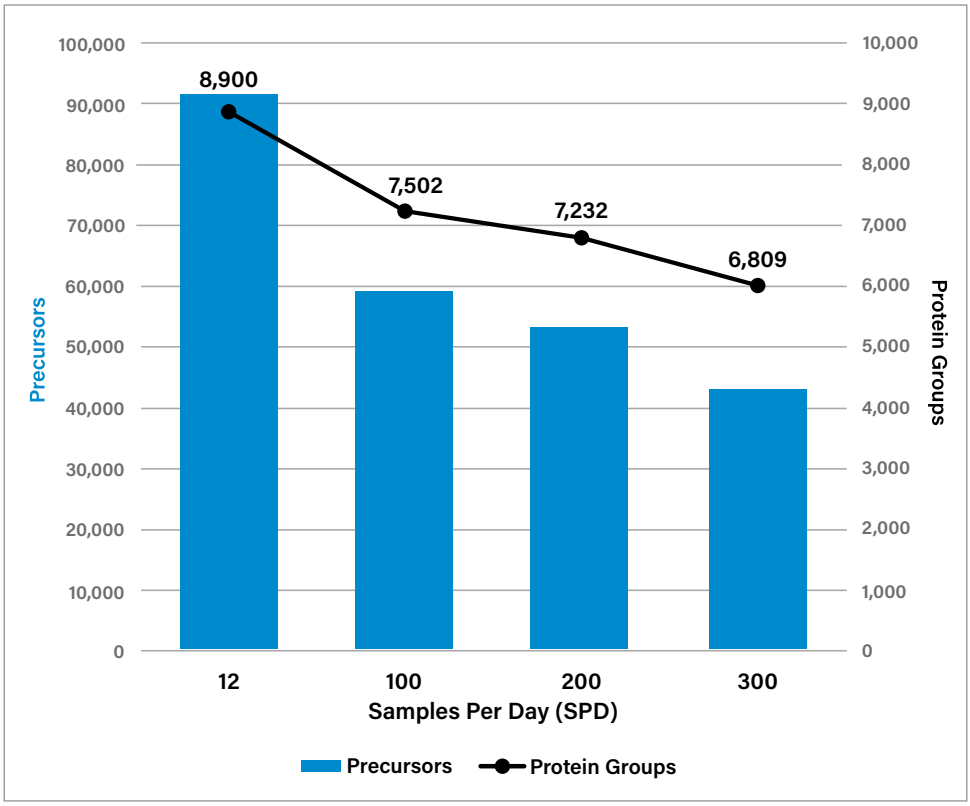
Enabling multiomics insight

Modern biological research increasingly depends on integrated multiomic MS strategies, with proteomics playing a central role in understanding biological function, regulation, and disease mechanisms. The Xevo MRT P10 MS is designed to meet the needs of core facilities to confidently support multiomics research across discovery, quantitative, and translational applications.

The exceptional MS/MS sensitivity and ultrafast acquisition speed of the Xevo MRT P10 MS enables deep proteome coverage from complex samples. High-quality fragmentation spectra and accurate mass measurement improves confidence in peptide identification, supporting comprehensive bottom-up proteomics using the advanced SONAR Pulse Acquisition Mode or DDA workflows.

a. Total Workflow

b. K562 human cell line digest | 500 ng | Protein Group and Precursor IDs per SPD



8,900
Protein Groups

91,374
Precursors

Figure 2. Bottom-up proteomics workflow.

Flexible methods for extending analytical depth

Advanced acquisition modes built for real-world complexity

Achieve deeper analytical insight through acquisition strategies optimized for complex, real-world samples. The Xevo MRT P10 Mass Spectrometer broadens your capabilities with flexible, advanced DDA and DIA modes tailored for every application.

In addition to traditional DIA and an advanced DDA algorithm, which includes improved decision-making criteria, the Xevo MRT P10 MS offers:

- A hybrid workflow that combines targeted and untargeted strategies within one injection. The fast-scanning speed and exceptional sensitivity of the Xevo MRT P10 MS enables the collection of multiple Tof MRM transitions without compromising the performance of concurrent DIA analysis, making it ideal for in-depth quantification and discovery experiments.
- SONAR Pulse Acquisition Mode - a DIA mode that identifies and quantifies analytes with a high degree of precision, combining both sensitivity and selectivity within a single mode of acquisition. SONAR Pulse Acquisition Mode reduces the risk of missing critical lower-level analytes that might have otherwise been missed from typical DDA experiments, while retaining highly specific MS/MS fragmentation ion information.

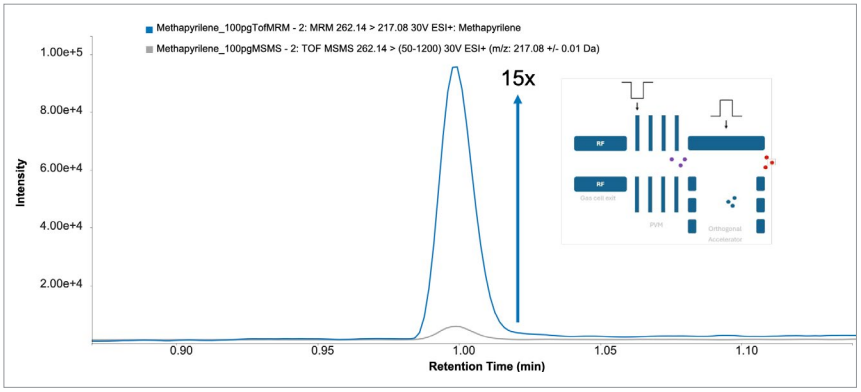


Figure 3a. A 15x improvement in response for methapyriline was observed for Tof MRM with EDC vs. a standard MS/MS analysis.

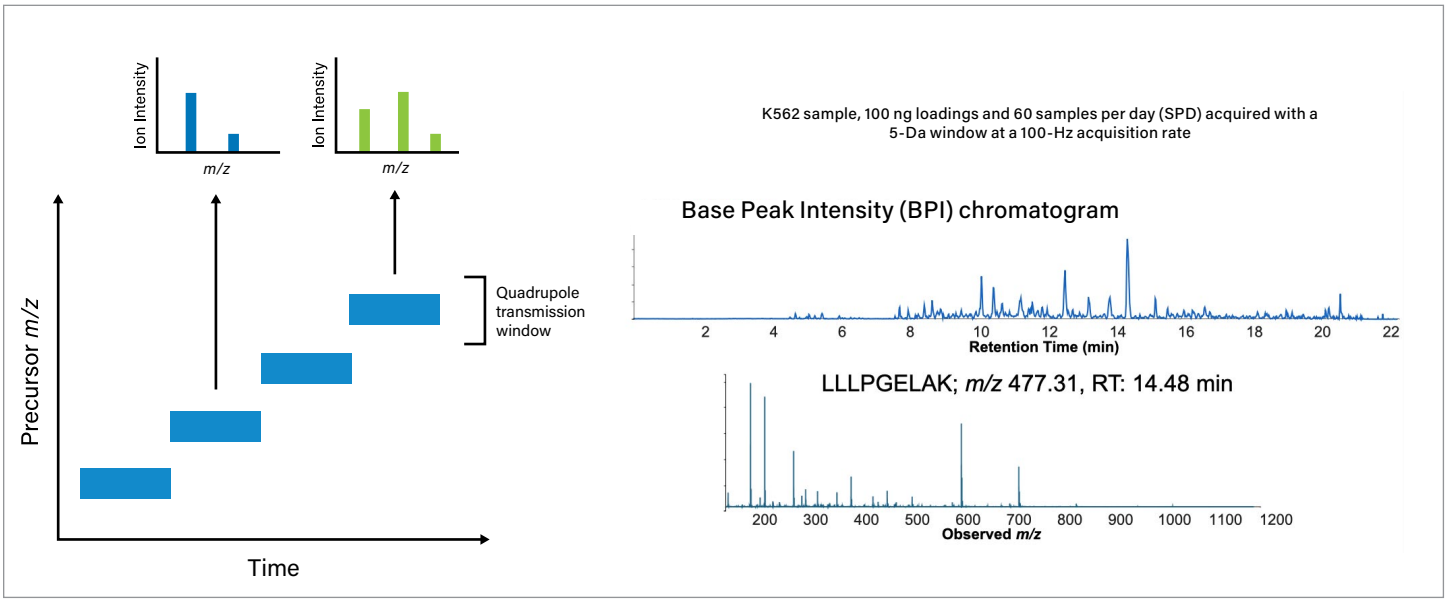
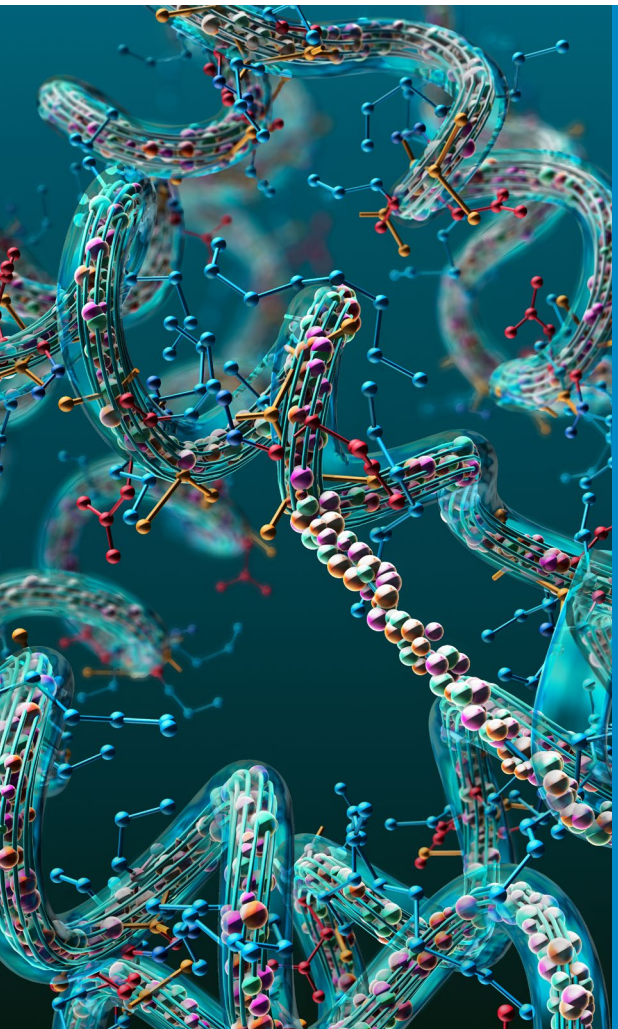


*Figure 3b. SONAR Pulse Acquisition Mode with WB EDC - a DIA combining both sensitivity and selectivity within a single mode of acquisition. Scalable and flexible - **m/z** range: MS1 and MS2 50 -1200, quadrupole windows: 2, 5, 10, and 25 Da, and speed: 20, 50, 100, 150, and 200 Hz.*



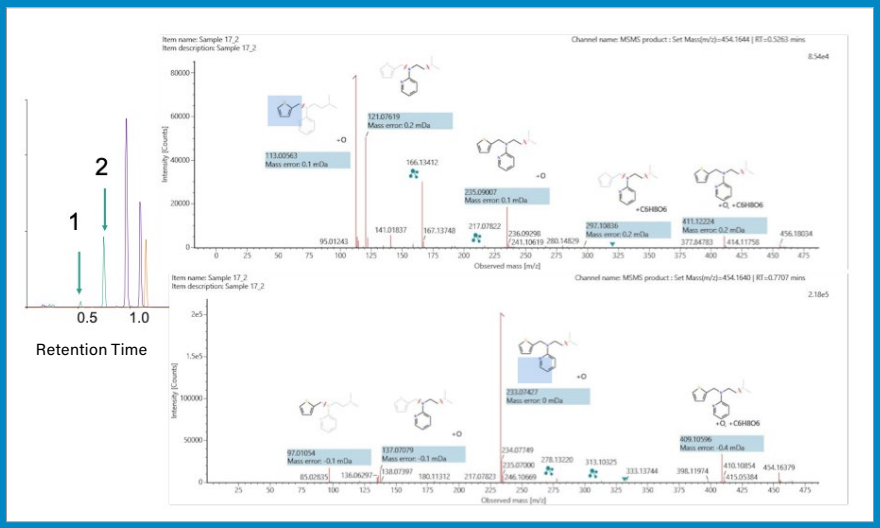


Figure 3c. Excellent mass accuracy and rich MS/MS fragmentation for characterizing the 0-glucuronide metabolites on the thiophene ring (1) and the pyridine ring (2), using DDA.

Setting a new benchmark in performance

The Xevo MRT P10 Mass Spectrometer: built on exceptional foundations

By combining industry-leading sensitivity, unmatched acquisition speed, and advanced acquisition modes in a compact benchtop platform, the Xevo MRT P10 MS gives you the tools to push the boundaries of what is possible in biological research and drug discovery and development.

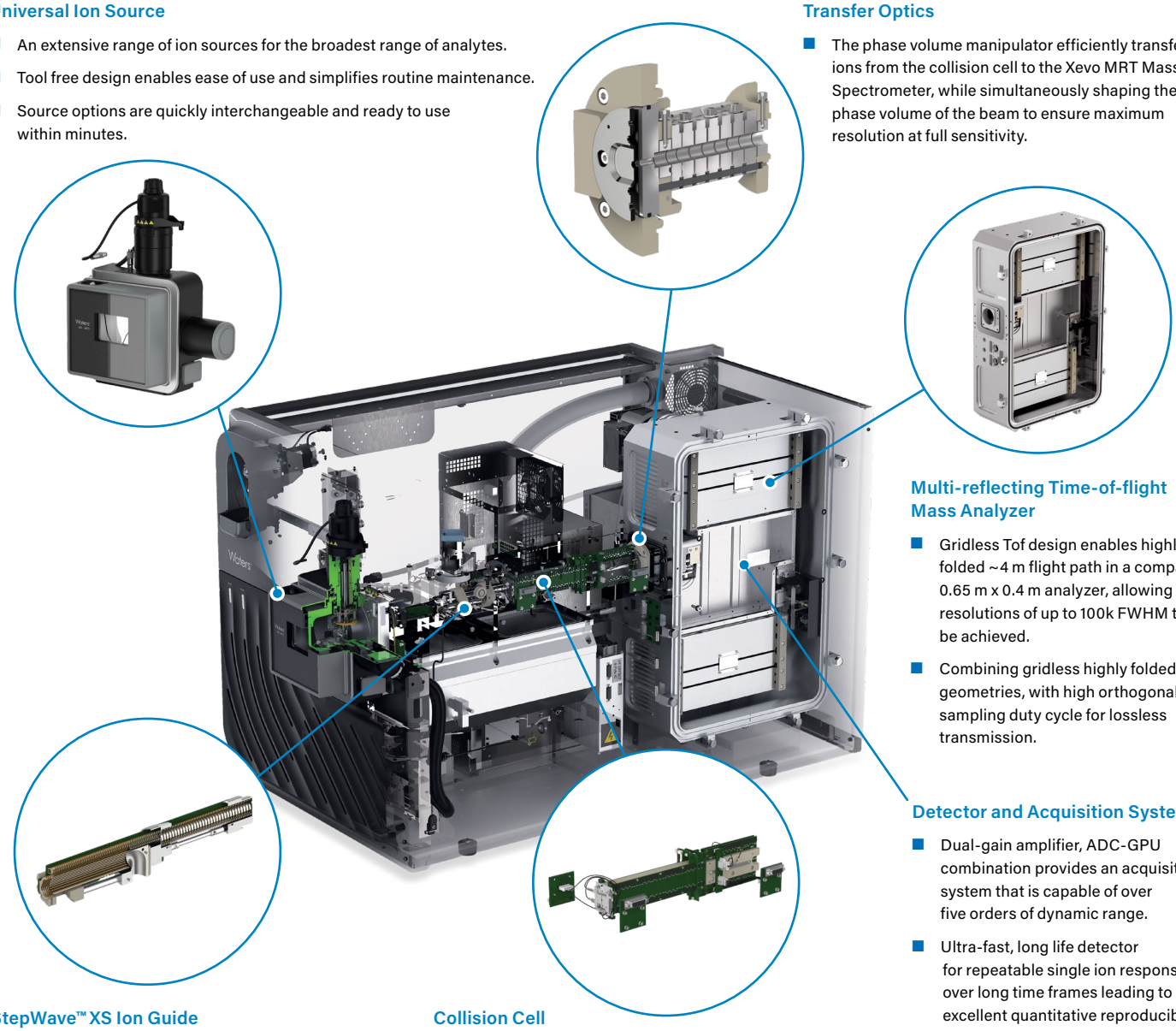
The exceptional spectral data quality of the Xevo MRT P10 MS encompasses mass accuracy, resolution, and isotopic fidelity, in both MS and MS/MS, which enables higher specificity with tighter mass tolerances for identification and fewer candidate identifications, helping researchers reach results with greater confidence and speed.

Universal Ion Source

- An extensive range of ion sources for the broadest range of analytes.
- Tool free design enables ease of use and simplifies routine maintenance.
- Source options are quickly interchangeable and ready to use within minutes.

Transfer Optics

- The phase volume manipulator efficiently transfers ions from the collision cell to the Xevo MRT Mass Spectrometer, while simultaneously shaping the phase volume of the beam to ensure maximum resolution at full sensitivity.



Multi-reflecting Time-of-flight Mass Analyzer

- Gridless Tof design enables highly folded ~4 m flight path in a compact 0.65 m x 0.4 m analyzer, allowing resolutions of up to 100k FWHM to be achieved.
- Combining gridless highly folded geometries, with high orthogonal sampling duty cycle for lossless transmission.

Detector and Acquisition System

- Dual-gain amplifier, ADC-GPU combination provides an acquisition system that is capable of over five orders of dynamic range.
- Ultra-fast, long life detector for repeatable single ion responses over long time frames leading to excellent quantitative reproducibility, even at high ion currents.

StepWave™ XS Ion Guide

- Co-joined ion guide, efficiently transmits thermally labile species, increasing compound coverage.
- Provides enhanced sensitivity for challenging compounds but also improves levels of analytical robustness.

Collision Cell

- Efficiently captures, optionally fragments, and transfers ions from the quadrupole to the time-of-flight mass analyzer.
- Minimizes transit times through the cell and, coupled with reduced interscan delays, enables fast MS1 switching (*e.g.*, MS/MS) at high duty cycles, leading to high sensitivity even at very fast acquisition rates.

Visualization redefined

When combined with DESI XS, the outstanding sensitivity and speed of the Xevo MRT P10 MS makes high spatial resolution mass spectrometry imaging a reality, with up to 100 K mass resolution and class leading speeds of up to 200 Hz. With this combination you have molecular visualization without compromise, expanding analytical possibilities for spatial biology at the cellular level.

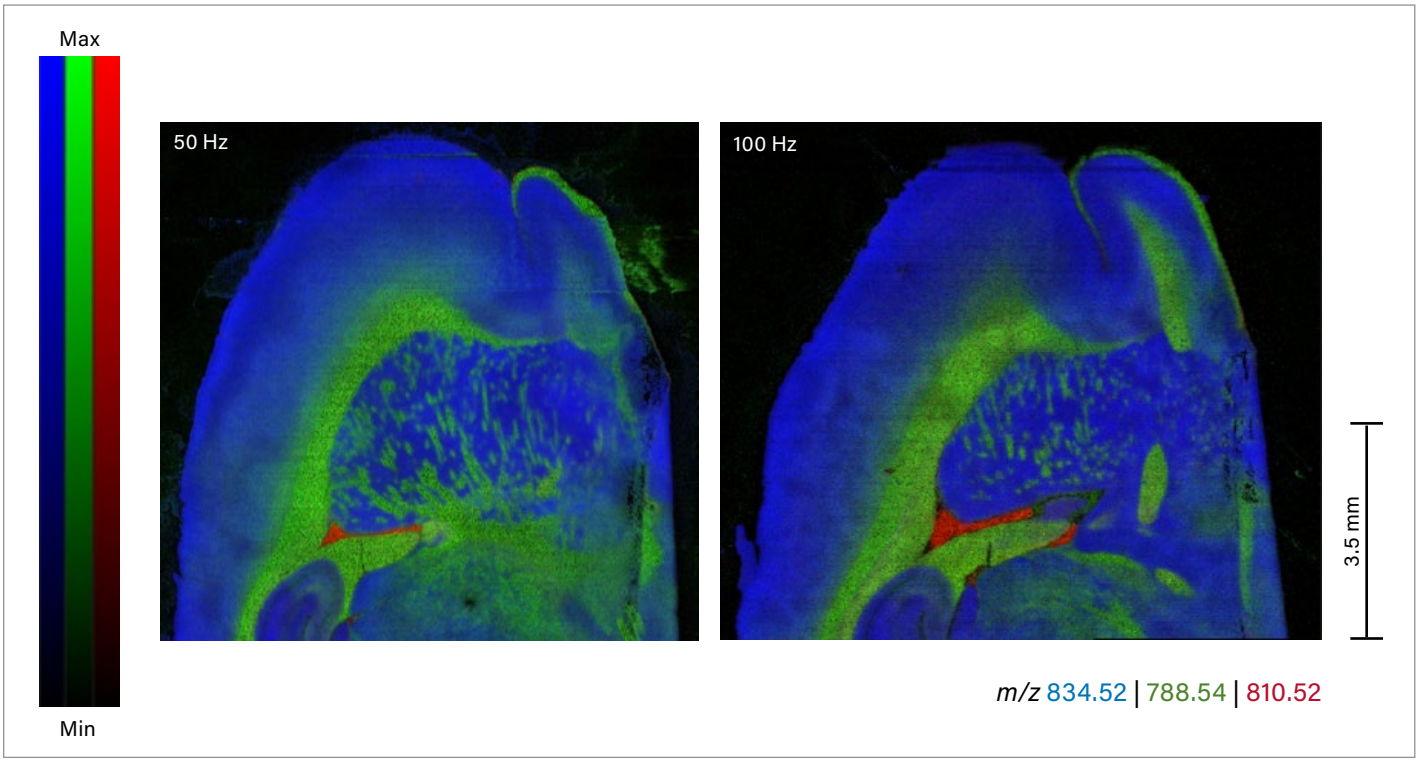


Figure 4. DESI XS rat brain lipid imaging acquired in ECD mode at 10 µm pixel sizing at 50 and 100 Hz showing single cell image resolution at speed.

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