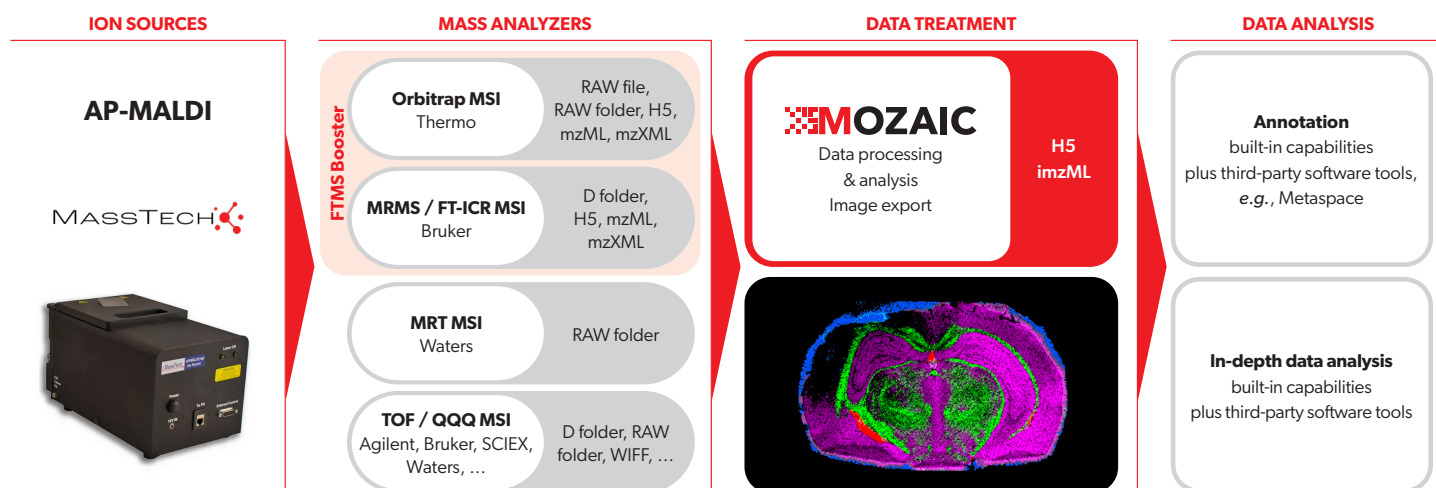


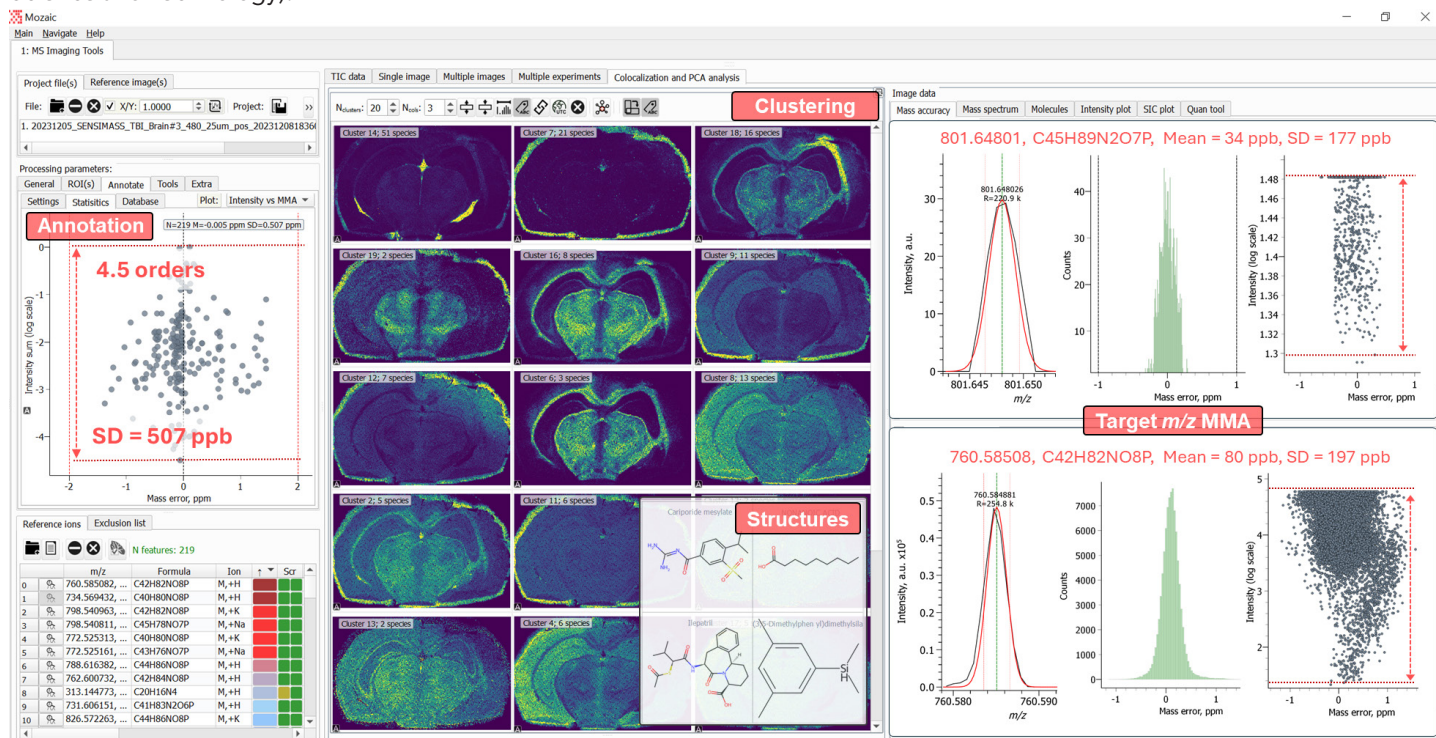
Empower Your Mass Spectrometry Imaging Research

Process, Analyze, & Visualize MSI Data – No Matter the File Size or the MS Platform

Since 2020, researchers worldwide have trusted **Mozaic** to power routine and advanced MSI workflows with high-performance data processing and analysis. Fully compatible with **MassTech Inc.**'s innovative (sub)atmospheric pressure **MALDI ion sources**, Mozaic integrates seamlessly with virtually any mass spectrometer. Built for flexibility and packed with unique, robust features, Mozaic is constantly evolving — and we welcome **your ideas** to shape what's next!



Application Example: Mozaic was used for the data processing and analysis of a traumatic brain injury (TBI) tissue sample dataset acquired using an Exploris™ 480 Orbitrap FTMS (Thermo Fisher Scientific) coupled with an AP MALDI ion source (MassTech Inc.) at 25 μm spatial resolution. Data courtesy of Dr. Hua Tian (University of Pittsburgh) and Dr. Gilles Frache (Luxembourg Institute of Science and Technology).

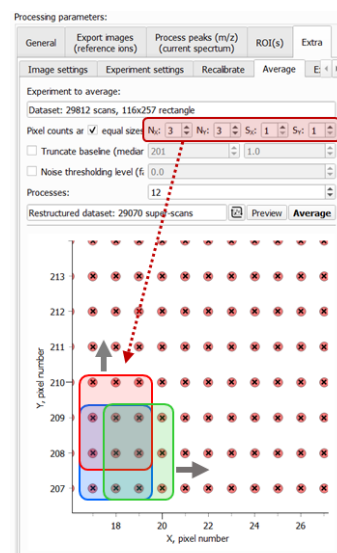


Polyamine and Lipid Metabolism in Optic Nerve: Spatial Omics with AP/MALDI MSI, by Nivedita Bhattacharya et al., WP270, 73rd ASMS, Baltimore, MD, 4 June 2025

Mapping Biochemical Markers of Post-Harvest Microbial Spoilage in Table Grapes with AP/MALDI MSI, by Caleigh O'Connor et al., WP275, 73rd ASMS, Baltimore, MD, 4 June 2025

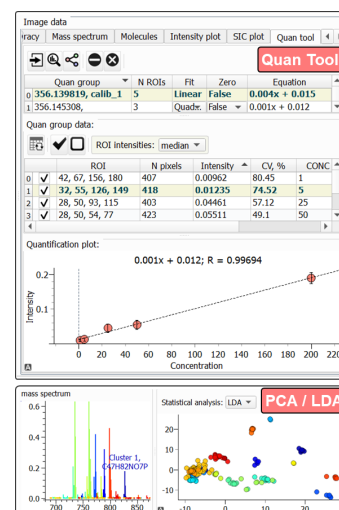
Key Features: Data Processing

- A full cycle of MSI data processing, also for the unreduced data of **any size**
- Directly compatible with all MALDI ion sources from MassTech Inc.
- Forms an integrated hardware-solution to access and process **transients** in FTMS-based MSI
- High speed of calculations: python, HDF file structure, & multi-threading
- Mass spectra **re-calibration** and data validation via mass accuracy evaluation
- No m/z scale binning: avoiding artifacts & increasing processing speed
- **Accurate** simulations of isotopic envelopes: avoiding artifacts (instrument-specific!)
- Peak **annotation & clustering**: spectral matching of experimental and simulated data
- Sensitivity & quantitation: **running average** of MSI data from adjacent pixels
- Resolution & throughput: **super-resolution** signal processing (least-squares fitting)



Key Features: Data Analysis

- Instant visualization of interactive images and mass spectra (click and see)
- Manual and automatic definition of regions of interest (ROI), analysis and geometry handling
- Comparative analysis of (averaged) mass spectra from multiple ROIs for the same or different data sets
- Multiple pixel interpolation approaches, image sharpening
- Co-localization and overlay of (multi-mode) images
- Image transparency, add color function, customizable and adjustable color maps
- Results are readily exportable in common (imzML) and advanced (H5) data formats
- High quality images are exportable in different formats: PDF, png, jpeg, tiff, svg, etc.
- Peak annotation, clustering, and further data analysis: embedded and external workflows, e.g., via imzML upload to third-party software tools. For example, Mozaic performs centroiding and re-calibration of DESI (MR)TOF MS (Waters) data and generates imzML files compatible with Metaspace.



Enhanced MSI via Unreduced Data Acquisition and Processing

Integrated hardware-software solution to access and process time-domain transients



Mozaic is a stand-alone software tool. In addition, it can form an integrated solution with the Spectroswiss **FTMS Booster** - a high-performance data acquisition system providing access to the time-domain transients from Orbitrap and Ion Cyclotron Resonance (ICR) FTMS instruments, see <https://spectroswiss.ch/hardware/>



Spectroswiss

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