



# SCiLS™ – Turn data into knowledge

Software for MALDI Imaging Data Analysis

Innovation with Integrity

# SCiLS Lab – Analysis and visualization in one software

SCiLS™ Lab is the industry's preferred tool for deriving insights from MALDI Imaging data.

Designed to streamline complex computational tasks, this all-encompassing software toolkit enables the transformation of MALDI Imaging data into actionable insights and enhances research productivity.



Pharma workflows



Biomarker discovery



Targeted analysis



CCS-enabled imaging



iprm-PASEF



Spatial Multiomics

Powerful analysis and visualization tools to get more insight per pixel



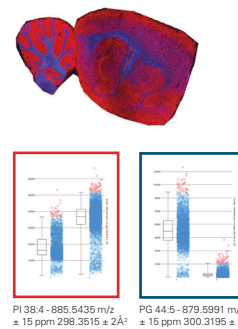
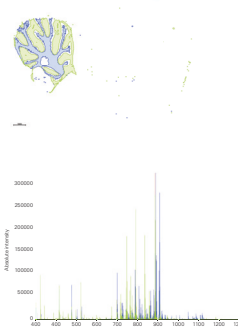
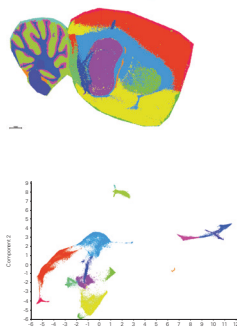
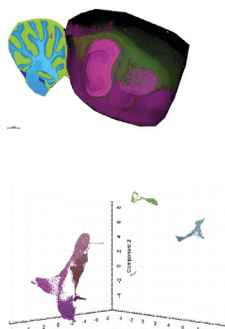
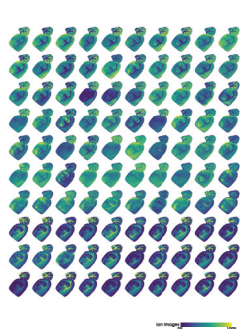
Feature List

UMAP Dimensionality Reduction

Spatial Segmentation

Create Regions of Interest

Find Discriminating Features



In biomarker discovery studies, use the combination of SCiLS Lab's on-board statistics module and powerful visualization tools to analyze and inspect your data to generate results that provide unparalleled and actionable molecular insight.

## Easy to use

User-friendly software designed for the analysis, visualization, and reporting of mass spectrometry imaging data, requiring no advanced mass spectrometry expertise or programming experience.

## Integrated

Offers native compatibility for data produced by Bruker's FLEX series and MRMS instruments. Includes optional support for native data from other mass spectrometry brands, in addition to the community imzML format. Facilitates the fusion and analysis of spatial multiomics data, and integrates with MetaboScape® for direct and confident molecular annotations

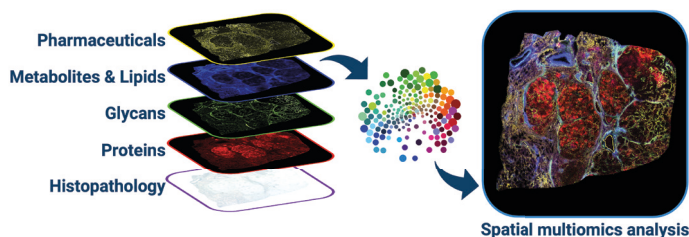
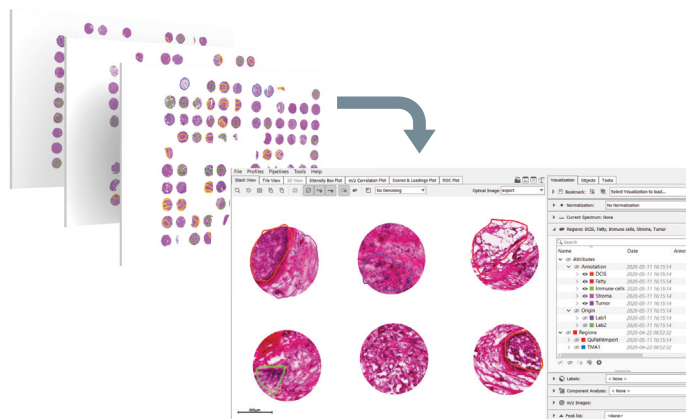
## Powerful visualization and reporting

- Instant and intuitive visualization of ion images and mass spectra
- Co-registration and display of high-resolution histology images
- Interactive display of statistical results and customizable reports
- Volumetric visualization of 3D MALDI Imaging studies (optional)
- Multiomics data fusion and analysis
- Available in light and dark display themes

# World-leading software for analysis of MALDI Imaging data

## Efficient processing and analysis of large sample cohorts

- Combine and process multiple measurements into a single data set
- Generate robust and deisotoped feature lists using T-ReX<sup>®</sup> Feature Finding
- Intuitive annotation of regions of interest
- Use region attributes to automatically group samples according to experimental meta-data
- Use machine learning methods for classification and prediction



Use SCiLS Lab to fuse and analyze MALDI Imaging spatial multiomics datasets obtained from a single tissue section.

## Analyze multimodal and multiomics data with ease

- Fuse spatial multiomics data sets and multimodal imaging data for unprecedented chemical insight
- Combine label-free and targeted MALDI Imaging data for ultimate specificity
- Quantify target compounds

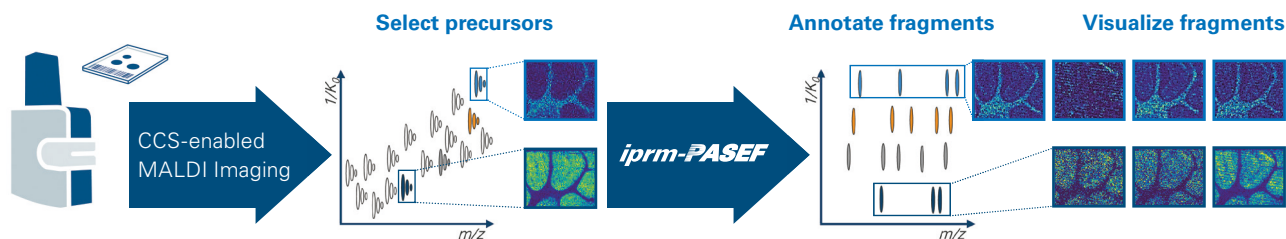
## Advanced processing and analysis

- Advanced machine learning algorithms for data sets of virtually unlimited size
- Comparative analysis for uncovering discriminative and correlated spectral features
- Unsupervised analysis tools for untargeted clustering and data mining
- Meta-data annotations for characterizing regions in clinical and pre-clinical studies
- Classification models for categorization of unlabeled samples
- Analyte quantitation based on dilution series or tissue mimetic model

## Workflow and extensibility

- Identify ions with confidence using MetaboScape<sup>®</sup>-powered molecular annotation
- Comprehensive tools for targeted and untargeted SpatialOMx<sup>®</sup> workflows
- Import digital pathology results and histological annotations from QuPath
- Extensive API for automated reporting and advanced workflow integration
- Export MALDI Imaging data to the open industry standard imzML or OME-TIFF formats
- Import from imzML or various third-party vendors' MS imaging data formats (optional)

# iprm-PASEF<sup>®</sup> for confident MS/MS-based identification of target molecules



Use the unique combination of MALDI Imaging and targeted prM-PASEF to acquire, analyze and annotate up to 25 precursors in a single MALDI MS/MS Imaging acquisition. Rely on MetaboScape<sup>®</sup>-powered molecular annotation to identify your images with confidence.

## SCiLS add-ons extend beyond the capabilities of SCiLS Lab

### Cellular morphology analysis with SCiLS Lab and QuPath

- Annotate regions in QuPath
- Import and use QuPath annotations in SCiLS Lab

### Scripted external workflows

- Access SCiLS Lab data in R and Python using the SCiLS API
- Bring your own code and design custom analysis workflows or reporting pipelines

### SCiLS Scope

- Light-weight image viewer for easy sharing of MALDI Imaging results in OME-TIFF format
- Available as a free-download from the SCiLS webpage



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