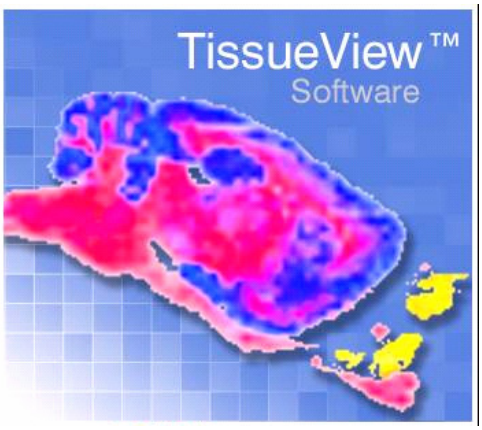
TissueView™ 1.0 Software on the QSTAR® Elite System

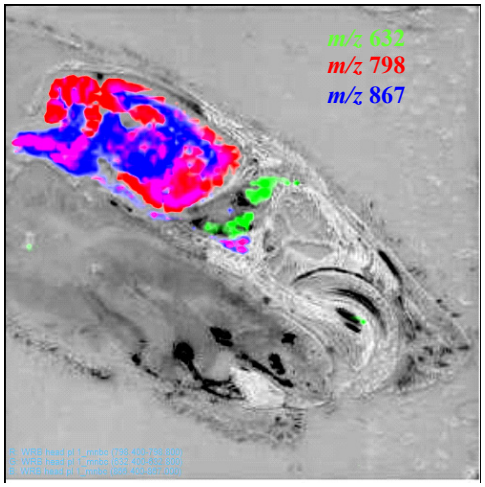


TissueView™ Software is powerful new software designed to simplify the processing of mass spectrometry imaging (MSI) data acquired on Applied Biosystems/MDS Sciex instruments.

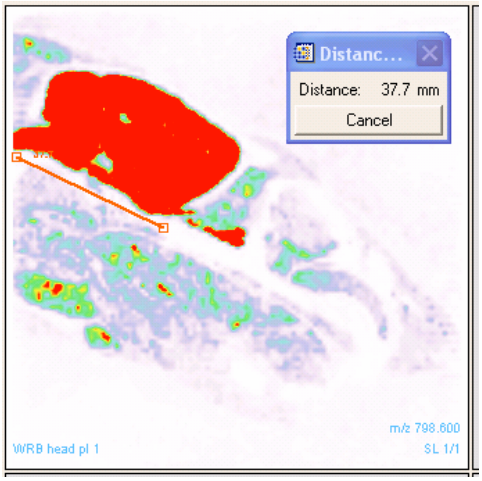
Features

TissueView™ Software has streamlined the processing of MSI data, allowing rapid review of data for novice users. For researchers who need to perform in-depth data mining, the advanced functionality within TissueView Software make it a must-have application package.

- Instantly generate ion images by clicking on or scrolling across peaks in the mass spectrum
- View mass spectra on the fly by scrolling across the image
- Select from multiple color profiles with automatic intensity optimization for ease of viewing
- Display overlaid images of up to 4 different mass ranges to clarify distribution of individual species
- Import optical images and overlay these with MSI images to gain additional biological insight
- Measure distances between two points and sizes within images using a digital ruler
- Overlay or stack mass spectra created from different regions of interest to simplify data comparison
- Define regions of interest, view averaged mass spectra, and calculate average intensity of a mass within a region of interest
- Perform mathematical operations on images such as subtracting or dividing one extracted ion image from another
- Average spectra from adjacent pixels for better data visualization
- Perform baseline corrections of noisy data
- Export images as .tiff or .jpeg images, or simply copy and paste images into other programs



Rat head slice showing images of m/z 632, 798, 867 overlaid on an optical image of the tissue slice

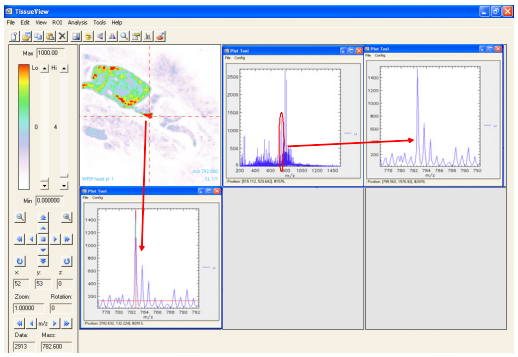


Use of ruler feature to calculate distances within mass spec images

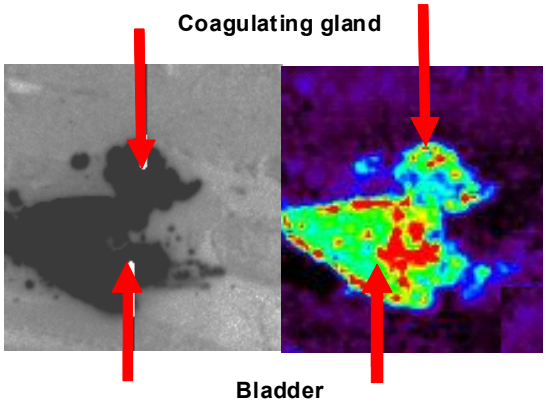
QSTAR® Elite System

The accurate mass and high resolution capabilities of the QSTAR® Elite System enable researchers to determine not only spatial localization information about drugs in tissues, but also to get conclusive compound identification.

- Orthogonal TOF design allows acquisition of accurate mass data even from irregular tissue surfaces
- MS/MS capabilities critical for eliminating matrix interference and for enabling compound identification
- Perform looped experiments to obtain MS and MS/MS on multiple ions in one experiment, greatly increasing throughput
- Fast data acquisition rates increase instrument sensitivity when combined with the high repetition laser
- High repetition Nd:YAG laser operates at rates up to 1000 Hz
- Less than 10 µm MALDI plate movements allow excellent spatial resolution, especially when combined with oversampling



Create images by selecting ions from the mass spectra, display mass spectra by selecting points on images



Comparison between ^{14}C autoradiography (left) and mass spec MS/MS (right) images in mouse prostatic region[1]. MSI of drug metabolite illustrating specificity of differentiating drugs and metabolites with this technique

Compatibility

Designed with the multi-platform user in mind, TissueView™ Software can process data acquired on a wide variety of instruments

- QSTAR® Pulsar i, QSTAR® XL and QSTAR® Elite Systems running Analyst® QS 1.1 or Analyst® QS 2.0 Software, along with oMALDI™ Server 4.0/5.0/5.1 with imaging
- 4700/4800 MALDI TOF/TOF™ Systems
- Data from any other mass spectrometry platforms in the Analyze file format

References

1. J. Bunch et al, *Proceedings of the American Society for Mass Spectrometry Annual Conference, Seattle 2006*.

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