



# Epitope Release Notes

Updated May 2024

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## Epitope 1.9.2.4463

Release May 2024

- Features
- Updates
- Known Issues

## Changes Since Last Release

### Features

- **Misc**
  - Epitope 1.9.2.4463 will be the last version to support .lsadata files
- **File Opening and Saving**
  - No New Features
- **Data Tab**
  - No new features
- **Processing Tab**
  - No new features
- **Binning Tab**
  - Default heat map Sort option is now By Dendrogram which matches the order between the dendrogram and heat map
- **Report Point Tab**
  - No new features
- **Array View Tab**
  - No new features
- **Data Export**
  - No new features

### Updates

- **Misc**
  - No new updates
- **File Opening and Saving**
  - Error when opening previously processed files resolved
- **Data Tab**
  - No new features
- **Processing Tab**

- No new updates
- **Binning Tab**
  - No new updates
- **Report Point Tab**
  - No new features
- **Array View Tab**
  - No new features

### Known Issues

- In Peptide Mapping module colors of individual constituents in the stacked plot can sometimes be difficult to distinguish

## Epitope 1.9.0.4167

Release October 2023

- Features
- Updates
- Known Issues

## Changes Since Last Release

- Features
- Updates
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### Features

- Add Axis Label Size option to all plots

### Updates

- Mismatch corrected between dendrogram and network plots
- Premix Binning mode: The "Epitope Tool" modal is displayed after clicking on the "Undo All" button on the Processing > Referencing/Blank pages
- The "Measurement" feature is present on the Data > Batch Analysis page and Binning page in Premix Binning mode
- Classical / Premix Binning mode: The sensorgram panel is empty on the Binning page after Batch Analysis fitting
- Classical and Premix Binning modes: The "Id" is different in the "Reports" tab in the Binning page each time the application opens
- An unstable error appears when using the "Exclude (remove) all except selected" option
- An unstable error appears when using the "Exclude all except selected ligands/analytes" option
- Array View page: Background color for excluded items isn't displayed on the Analyte Overlay tab and doesn't save to .ebp file
- Classical / Premix Binning mode: The Binning tab has different selections than the state that was saved
- The app stopped working while checking "Is Control" checkbox
- Processing > Y-Align page: Values aren't saved in input fields
- Chords sometimes disappear when moving nodes
- Updating Windows Regional Settings causes errors when opening/saving .ebp files
- Error opening classical binning file with spaces at end of sample names
- Error opening merged premix binning file

### Known Issues

- Coloring of peptide mapping plots can fail to separate distinct peptides

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