carterra®

Epitope Release Notes

Updated August 2025

Epitope 2.0

Release August 2025

The latest Carterra Kinetics and Epitope Analysis Software brings many exciting feature updates to enhance ease-of-use and improve the user experience when analyzing large data sets.

Please carefully read the following notes before downloading the software for use. Additional details about the software and platforms can be found in the User Manual, available for download: https://carterra-bio.com/resource-category/user-manuals/

Changes Since Last Release

Features

- Kinetics and Epitope now support calibration; response normalization over the full range of your data.
- Heatmap font sizes are now adjustable.

Updates

- If nodes in the Network plot are moved in the Communities tab, they will automatically be moved in the Bins tab.

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
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Changes Since Last Release

- Features
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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.

Carterra technology is protected by the following patents and other patents pending:
8,210,119, 8,211,382, 8,383,059, 8,999,726, 9,682,372, 9,682,396