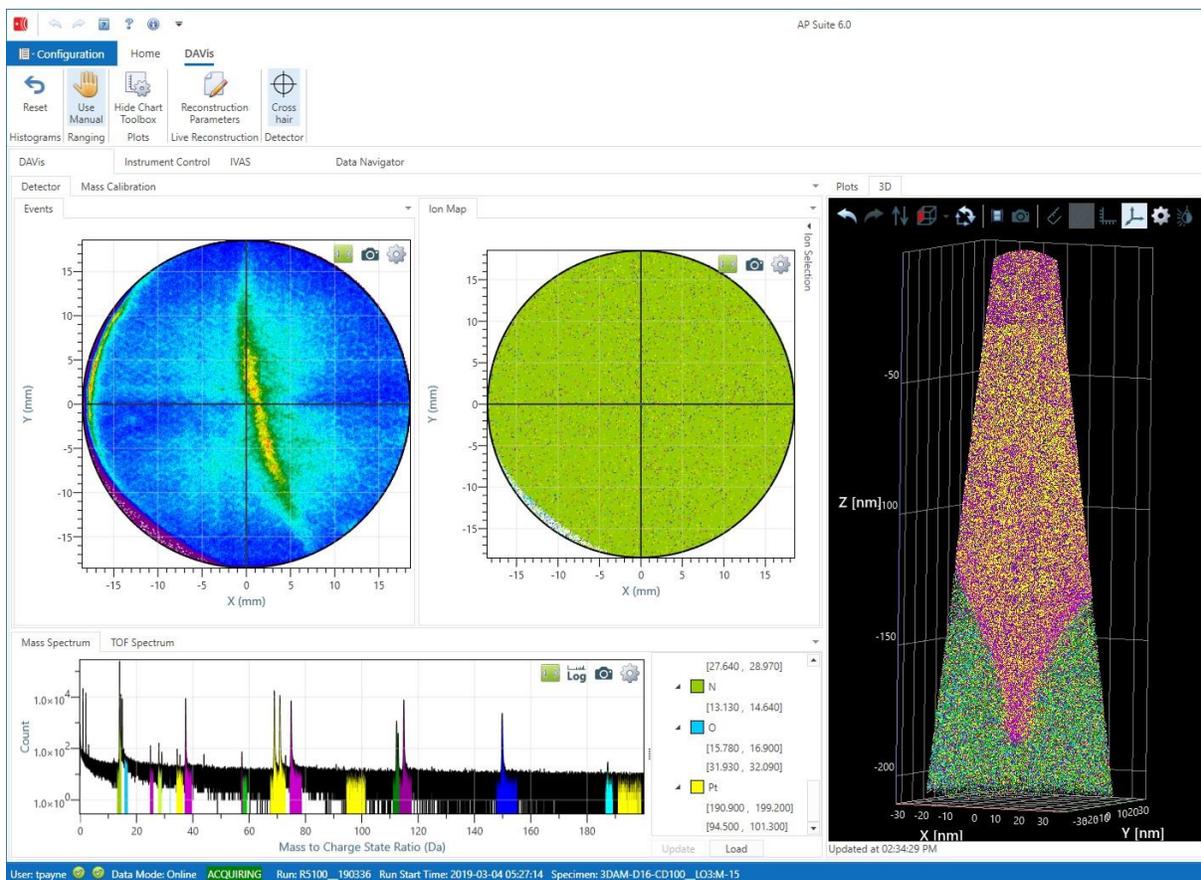




# AP Suite Software 6.1

## Release Notes

January 2021



**Live Calibrations and Reconstruction for calibrating, reconstructing, and 3D viewing of experimental data during an in-progress data acquisition**



**Attribution for data displayed in cover image of this document:**

These data were obtained under a project which received funding from the Electronic Component Systems for European Leadership Joint Undertaking under agreement No 692527. It receives support from the European Union's Horizon 2020 research and innovation programme and Netherlands, Belgium, France, Hungary, Ireland, Denmark, Israel.

CAMECA gratefully acknowledges these organizations for funding the research.

# Welcome to AP Suite Software 6.1

AP Suite Software Release 6.1 completes the integration of the the DAVis module into AP Suite and provides a number of new features and usability enhancements in the continued maturation of the AP Suite platform.

This release also introduces several new optional upgrades to the acquisition software to improve the ease-of-use, throughput, yield, and consistency of the experiments. These include:

- Auto microtip navigation
- Auto alignment optimization
- Auto LE flat test
- Chain acquisition
- Scripted acquisition
- Tool to tool matching

Additional information about key upgrades in AP Suite Software Release 6.1 are summarized below. To learn more about how these features can be applied in your laboratory or production facility to enhance the atom probe data quality and sample throughput, contact your CAMECA Sales representative.

*Note: Please uninstall any previous AP Suite installations prior to installing AP Suite 6.1*

## AP Suite

- Multiple database configurations can be saved making switching between them fast and easy.
- In the event the connection to a networked database is interrupted, AP Suite will now attempt to reestablish the connection multiple times.
- Added “Reconstruction Paths” option. If a reconstruction path is not found in the Project Data Path folder, it will search all of the additional reconstruction paths (at root path level and under a/customer/project) path. This is an optional setting that does not need a value set.
- The AP Suite installer will allow the choice to install for all users or just the current user.

## Asset Manager

- An LE history shows the results of flat tests and the stopping voltage of experiments on the selected local electrode.
- Cloning a microtip specimen will now clone children tips from the children of the original microtip.
- The condition of multiple specimens can be edited at once by using Ctrl+click to select multiple specimens and then choosing Edit Condition from the right click menu.
- When viewing a puck in the Destination > Puck Locations screen, one can automatically navigate to the contents of the puck by choosing Select Contents from the right click menu.
- Specimen blocks can now be imported and exported.
- Bugs
  - Asset Manager destination views did not update or refresh when components added

## Data Navigator Module

- Added right-click context menu in “Files” tab in the project folder with a more fully-featured file explorer that allows for creating additional folders, renaming, and more.
- Ability to set default images per specimen instead of all being linked to the same coupon.
- If the Fib Images folder doesn’t exist, images can now be added directly from the Project or Specimen tabs and the folder will be created on demand.
- Ribbon is shown in “small” view by default. Use arrow on right side to go back to full view.
- Addition of an Ion File Inspector feature accessible from the Reconstructions Table to allow viewing of the APT file information for the currently-selected dataset.
- The FileConvert utility now includes an APT to EPOS option. If the APT file does not contain all of the required fields for an EPOS files, those columns will be empty in the resulting EPOS file. To create an EPOS file with all of the expected columns, the APT file must be created with the following sections (selected in step 7 of the reconstruction wizard):
  - Vap
  - Delta Pulse
  - Detector Coordinates
  - Mass
  - Multiplicity
  - Position
  - V
  - Epos ToF
- The chart preview panel can now be expanded.
- Most of the integer fields in Info panes have thousand separators for easier reading of the numbers.
- The reconstruction recipe (part of the optional Project Plan feature) has a new property option called ‘Set Low ZV Edge to Start of Laser Tracking’. This will set the ZV-cut at the point where auto-laser tracking is enabled.
- Bugs
  - The Import wizard now allows override when the experiment file is not found.
  - Improved Data Navigator synchronization behavior.

## DAVis Module

- The DAVis module now supports eFIM acquisition and playback.
- Added “Convert FlexTap to rhit converter” under “Run Utility” in the toolbar.
- Can now use the automatically ranged peaks identified by the live calibration to populate the charge state ratio plot.

- Bugs
  - Fixed DAVis “No Data” bug.
  - Fixed DAVis stage control view with small ribbon.
  - Laser indicator restored to the detector event histogram, enable/disable the laser indicator in Configuration > Options > DAVis.
  - Fixed DAVis plot snapshots.

## IVAS Module

- Peak Identification feature.
  - Updated user interface.
  - Additive Search added and improvements in automatic searching for ion candidates.
- Added camera controls to the properties list for the Top Level ROI so the 3D view orientation can be set by the user.
- Analysis nodes (1D concentration profiles, mass spectra, etc.) can now be cloned via the right-click menu in the analysis tree.
- The error estimate calculation for 1D concentration profiles, proximity histogram profiles, and bulk compositions now incorporates the background estimate when selected. Note, the error estimate for the bulk composition is only visible in the CSV export.
- Improvements to isosurfaces:
  - Analysis nodes can be added directly to isosurfaces in the analysis tree, no need to create a subgroup if all surfaces are to be included (subgroups must be created to create analyses on specific groups of surfaces).
  - Subgroups can be broken out via the “Detached ROI” right-click menu option which can be used for spatial ranging.
  - The analysis panel has additional filtering options and can also incorporate custom calculations by creating a custom expression column in the table and defining a formula in the Expression Editor. For example,  $[\text{Radius X}]/[\text{Radius Z}]$  for a measure of “oblateness”.
  - When an isosurface definition changes, IVAS will attempt to update any defined subgroups by matching the center values of the new surfaces.
- A new method for viewing 3D data without AP Suite is available. A “Web Export – 3D Model” option is available from the IVAS analysis tree which allows several generic export options. These files can be used to open up a 3D data file in the Windows 3D viewer app, a web browser (some organizations may restrict this with their security settings), or in a powerpoint presentation.
- Text annotations can be added to the mass spectrum chart.
- The IVAS workspace right-click menu now includes options to jump to the selected data in the Data Navigator module in either the Experiments or Reconstructions table.
- A laser direction indicator is now available for the 3D display, enable/disable the laser indicator in Configuration > Options > IVAS.

- 1D concentration profiles and proximity histogram profiles can now have their background corrections truncated. This will treat any negative corrected values as 0.
- Improved the readability and consistency of .CSV files exported from 1D concentration profiles and proximity histogram profiles.
- The 3D display can be adjusted via the keyboard.
  - The up and down arrow keys will rotate the dataset about the 3D display's X (horizontal) axis.
  - The left and right arrow keys will rotate the dataset about the 3D display's Y (vertical) axis.
  - Shift + the left and right arrow keys will rotate the dataset about the 3D display's Z (into the screen) axis.
  - Shift + the up and down arrow keys will zoom the dataset.
- The plugin support has been improved, allowing:
  - The ability to read and write custom APT sections using the IonData class.
  - The ability to create in memory only IonData sections for temporary storage of results.
  - Access to all CAMECA-generated APT sections beyond the standard X, Y, Z, and m/q.
  - Easier use of the correlation histogram plugin created by GPM.
- Addition of an Ion File Inspector feature accessible from the Analysis Tree to allow viewing of the APT file information for the currently-active dataset.
- The reconstruction wizard can now resample the scatter plots and histograms for the selected volume.
- The reconstruction wizard can now create a reconstruction based on a GPM Dynamic Reconstruction if the appropriate parameters plot has been calculated with the plugin module.
- Step 2 of the reconstruction wizard now has a merged plot option which allows an overlay of multiple history plots in a single chart.
- Bugs:
  - Fixed SDM issue: now uses coordinate system of parent ROI.
  - Reconstruction Explorer: Generate SDM with Element selected and zero ions crashed AP Suite.
  - Click on an element in the Expected Ions periodic table dialog crashed AP Suite.
  - Fixed handling/crashing of 1D concentration (and other analyses) on inverted ROIs.
  - Fixed a rounding/float<->double conversion error with ranging that was causing test results to not match the actual application.
  - Improvements to Save Analysis Tree such that the 3D view appears the same after reloading.
  - Improved dropped database connection behavior so that a retry dialog will appear instead of crashing AP Suite.
- Known Issues:
  - There is an issue creating an analysis (mass spectrum, bulk composition, etc.) from an interface defined only with closed surface(s) that are defined such that the higher concentration/density is outside the enclosed volume(s); for example when defining precipitates with something enriched in the matrix rather than something enriched in the precipitates. In this some fraction of the ions inside the enclosed volume will be excluded and some fraction of the ions outside of the enclosed volume will be included and the

analysis will return incorrect results. Proxigrams are not affected by this bug. The workaround is to create the isosurface from the inverse of the initial surface by selecting all the ions in the numerator except the ion(s) of interest and then selecting the opposite gradient when defining the interface as appropriate.