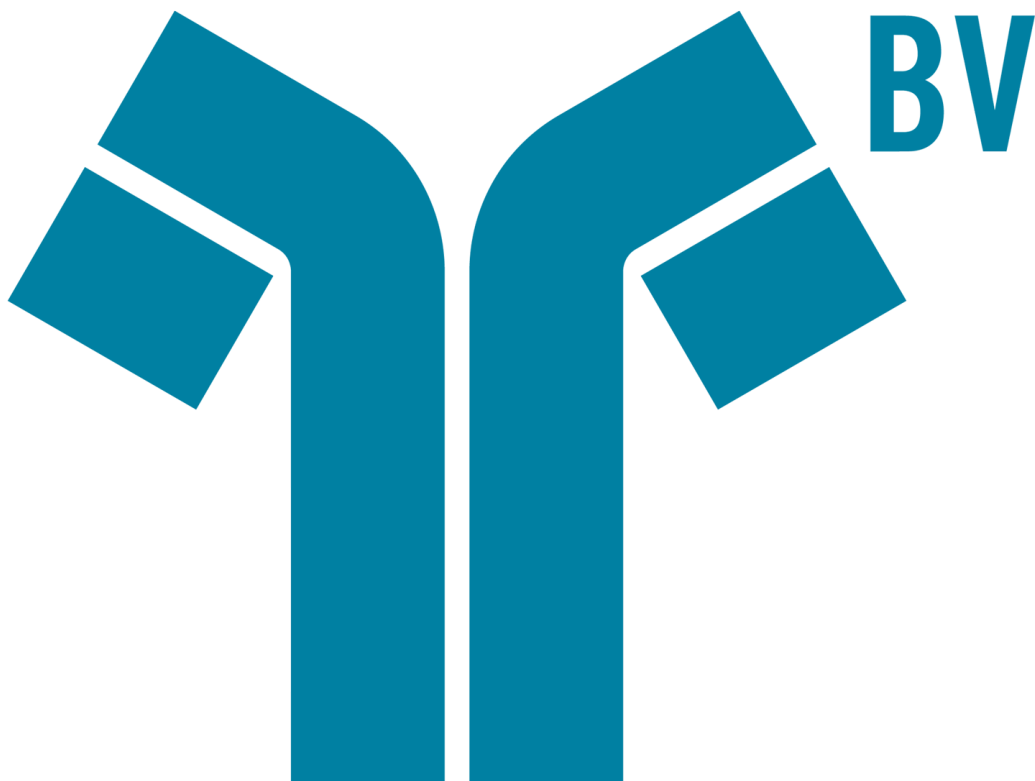




BioPharmaView™ 3.0 Software

Release Notes



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The BioPharmaView™ software is a post-acquisition processing software used for performing characterization and analysis of biologics. Use the software to complete the following tasks:

- Enter and update assay information
- Characterize standards
- Batch process files
- Review batch results
- Create reports

The BioPharmaView™ software processes data files generated by SCIEX TripleTOF® systems and the SCIEX X500 QTOF systems to support protein and peptide analysis during therapeutic drug development.

The BioPharmaView™ software supports the following workflows:

- **Intact Protein Analysis:** Determines the molecular weight of intact proteins, based on the reconstruction of a charge series envelope resulting from LC-MS.
- **Peptide Mapping Analysis:** Determines the peptide sequences resulting from the enzymatic digestion of a protein from the mass-to-charge (m/z) ratio of TOF MS data.

Each workflow enables the user to characterize samples and store the results, perform automated batch analysis, and generate reports.

All of the BioPharmaView™ software report templates, processing settings, and modifications can be customized.

Related Documentation

To access the documentation on computers configured with Microsoft Windows 7:

- *BioPharmaView™ Software User Guide:* Click **Start > All Programs > AB SCIEX > BioPharmaView > BioPharmaView User Guide.**
- *BioPharmaView™ Software Help:* Click the **Help** icon in the bottom left corner of the BioPharmaView™ software window, press **F1** from any location in the software, or click **Start > All Programs > AB SCIEX > BioPharmaView > BioPharmaView Help.**

To access the documentation on computers configured with Microsoft Windows 10:

- *BioPharmaView™ Software User Guide:* Click **Start > AB SCIEX > BioPharmaView User Guide**

- *BioPharmaView™ Software Help*: Click the **Help** icon in the bottom left corner of the BioPharmaView™ software window, press **F1** from any location in the software, or click **Start > AB SCIEX > BioPharmaView Help**.

Changes from Version 2.1 to Version 3.0

Note: Refer to the *Release Notes* for versions 2.01 and 2.1 for a list of changes that have been made from version 2.0 and fixes that have been implemented. The *Release Notes* are available in the BioPharmaView™ software section of the SCIEX website at sciex.com/software-support/software-downloads.

Note: Refer to [Issues Fixed in Version 3.0 of the BioPharmaView™ Software](#) for a list of all of the previous issues that have been fixed with this release of the BioPharmaView™ software.

Multi-Attribute Method (MAM)

- This version of the BioPharmaView™ software includes multi-attribute method (MAM) functionality. This feature allows users to define critical quality attributes that they consider to be important and then to monitor these attributes in the peptide mapping workflow.
- Two additional tabs have been added to the Assay Information workspace, the Quality Attributes tab and the Batch Parameters tab. The Quality Attributes tab enables the user to define the attributes to monitor during a multiple attribute methodology (MAM) workflow, create custom calculations using the XIC areas from matched peptides, and to create custom calculations using theoretical forms. The Batch Parameters tab is used to apply pass and fail criteria to the attributes that will be monitored during the batch processing.

Impurities

A new section has been added to the Sequence Features tab in the Assay Information workspace, the Impurities section. Impurity sequences that will be used in the Peptide Mapping workflow can be added to the Impurities table to enable the monitoring of impurities in the peptide samples. When the Digest check box is selected on the Assay Information—Peptide Mapping tab, the software generates a list of theoretical peptides for the protein, as well as additional peptides generated by the user-added impurity sequences. Any matched impurities are reported on the Impurities tab in Peptide Mapping Peptide Results table.

New Peak Detection

A new feature has been implemented in the Peptide Mapping workflow. New Peak Detection enables the BioPharmaView™ software to perform a binary comparison between a control and a sample. Any new LC-MS features that are detected in the sample that are not present in the control and that are above a user-defined threshold are flagged. During processing, the BioPharmaView™ software compares a control and sample that are user-designated when a batch is created. The control could or could not be the same as the characterized gold

standard. These new peaks are identified in the Newly Detected column, a column that has been added to the Peptide Results table, in the Review Results workflow.

Potential Matches

In the Intact Protein—Characterize Standard and in the Intact Protein—Review Results workflow, all potential matches are now shown. The BioPharmaView™ software identifies the closest match as the Validated Match, that is, the match with the smallest delta error between the observed and theoretical forms. However, the user can assign the validated match identification to a different match, if appropriate.

Combined List of Results

- In the Intact Protein—Characterize Standard and in the Intact Protein—Review Results workflows, a new viewing option has been added to the Table Options icon, *Display Results in Combined List*. When this option is selected, all of the information contained in the Matched and Unmatched tabs is combined into one tab labeled Combined. The Matched results are shown first in the list, followed by the Unmatched results. The result type, Matched or Unmatched is indicated in the Type column. This view enables the user to overlay results regardless of the type and easily compare all of the results in one session.
- In the Peptide Mapping—Characterize Standard and in the Peptide Mapping—Review Results workflows, a new viewing option has been added to the Table Options icon, *Display Results in Combined List*. When this option is selected, all of the information contained in the Matched, Unmatched, and Impurities tabs is combined into one tab labeled Combined. The Matched results are shown first in the list, followed by the Impurities, and then the Unmatched results. The result type, Matched, Impurity, or Unmatched is indicated in the Type column. This view enables the user to overlay results regardless of the type and easily compare all of the results in one session.

Assign Positions to Positionless Modifications

In the Peptide Mapping—Characterize Standard workflow, a new option has been added to the Filter button on the Matched, Impurities, and Combined tabs, *by Variable Modification@*". This option enables users to see modifications that have not been assigned an amino acid position due to multiple target amino acids in the sequence. When this option is selected, peptides with positionless modifications are shown in the Modifications column. When the hyperlink text is clicked, an option to Assign to position is shown. A score is provided to help the user assign the position. Higher scored peptides are likely to have more MS/MS evidence supporting that position. Users can manually assign positions to the modifications, based on MS/MS evidence or prior knowledge. For example, when the option is selected, Modification@* for a positionless modification changes to Modification@x(xxx)*, where x is the position information.

Contact Us

SCIEX Support

- sciex.com/contact-us
- sciex.com/request-support

Customer Training

- In North America: NA.CustomerTraining@sciex.com
- In Europe: Europe.CustomerTraining@sciex.com
- Outside the EU and North America, visit sciex.com/education for contact information.

Online Learning Center

- [SCIEXUniversity](#)

CyberSecurity

For the latest guidance on cybersecurity for SCIEX products, visit sciex.com/Documents/brochures/win7-SecurityGuidance.pdf.

Technical Support

SCIEX and its representatives maintain a staff of fully-trained service and technical specialists located throughout the world. They can answer questions about the system or any technical issues that might arise. For more information, visit the website at sciex.com.

Workstation Requirements

2

CAUTION: Potential Data Loss. The BioPharmaView™ software should not be installed on the acquisition computer. Software errors and data integrity issues can result if the BioPharmaView™ software and acquisition software are used concurrently.

The workstation must be configured with the following applications:

- English version of the Microsoft Windows 7 (64-bit) operating system, with SP1 or an English version of the Microsoft Windows 10 (64-bit) operating system

Note: Cybersecurity support is included for the Windows 10 (64-bit) operating systems.

- Microsoft .NET Framework 4.6.2
- Adobe Reader

Note: Visit www.adobe.com and follow the instructions to install the latest version of Adobe Reader.

- Microsoft Office 2010, 2013, or 2016.

Note: If a trial version of Microsoft Office is installed on the computer as a temporary measure, then the full version of the Microsoft Office software must be activated before the trial period expires. The license can be purchased from your regional division of Microsoft or from an authorized distributor in your region.

Workstation Requirements

- Dell OptiPlex XE2 computer with:
 - An Intel Core i5-4570S processor (Quad core, 2.90 GHz, 6 MB with HD Graphics 4600)
 - 32 GB DDR3 1600Mhz SDRAM
 - 2*2Tb HDD (RAID1)
 - DVD+-RW

Note: Newer systems might become available. For more information, contact the local sales representative. Older computer models might be compatible. However, they have not been tested and might result in degraded performance.

Notes on Installation

- The user must be logged on to the computer as a user with Administrator privileges.
- Any existing version of the BioPharmaView™ software that is installed on the computer must be removed before this version of the software can be installed. Refer to [Remove the BioPharmaView™ Software](#).
- **For BioPharmaView™ 1.0 software users only:** Before installing this version of the BioPharmaView™ software on a system configured with the Microsoft Windows 7 (64-bit) operating system that previously had version 1.0 of the BioPharmaView™ software installed, the user must remove the installed version of the AB SCIEX Reporter Template Suite 3.2 through the **Control Panel > Programs > Uninstall a program** option.
- If using a zip file that contains the BioPharmaView™ software installer, then extract all of the files from the zip file before running the installer from the location containing the extracted files. Errors will occur if the installer is run from within the zip file.
- During installation of the BioPharmaView™ software, the system might determine that Microsoft .NET Framework 4.6.2 is not installed. If this occurs, then the system must be connected to the Internet to download additional components for the Microsoft .NET Framework 4.6.2 installation process. If the system fails to install the Microsoft .NET Framework 4.6.2, then the BioPharmaView™ software installation also fails. Resolve the situation by connecting the workstation to the Internet or contacting your local IT department to install the Microsoft .NET Framework 4.6.2, and then install the BioPharmaView™ software again.
- On computers configured with the Microsoft Windows 10 (64-bit) operating system, Microsoft .NET Framework 3.5 with SP1 must be installed. To confirm that Microsoft .NET Framework 3.5 is installed, click **Control Panel Programs and Features > Turn Windows features on or off**, make sure that the **.NET Framework 3.5 (includes .NET 2.0 and 3.0)** check box is selected, and then click **OK**.

Install the BioPharmaView™ Software

CAUTION: Potential Data Loss. The BioPharmaView™ software should not be installed on a computer used for acquisition. Software errors and data integrity issues can result if the BioPharmaView™ software and acquisition software are used concurrently.

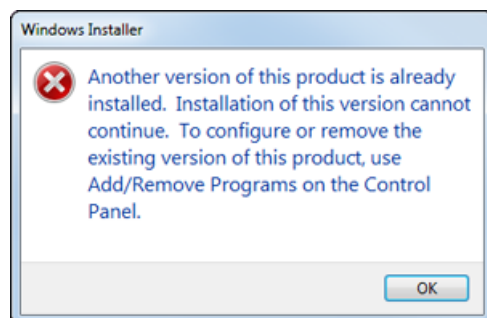
1. Log on to the computer as a Microsoft Windows user with administrator privileges.

Installation

2. Remove any existing version of the BioPharmaView™ software. Refer to [Remove the BioPharmaView™ Software](#).

Note: If any version of the BioPharmaView™ software is already installed on the computer, then a Windows Installer error dialog opens before the installation starts. Click **OK** and then remove the software.

Figure 3-1 Windows Installer Error Dialog



3. Make sure that all of the applications are closed.
4. Install the BioPharmaView™ software as described in [Table 3-1](#).

Table 3-1 Installation Instructions

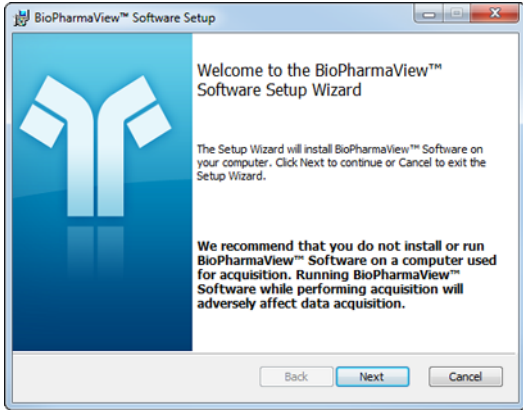
To install from a file downloaded from the SCIEX website ...	To install from the BioPharmaView™ software installation DVD ...
<p>Download the zip file from https://sciex.com/software-support/software-downloads.</p> <hr/> <p>Tip! To prevent potential installation issues, we recommend that the file is saved to a location other than the computer desktop.</p>	<p>Load the BioPharmaView™ software installation DVD in the DVD drive.</p>
<p>After the download is complete, right-click the BioPharmaView-3.0.zip.</p>	<p>Navigate to the DVD and then double-click setup.exe.</p> <hr/> <p>Note: If the Reporter Software 3.2 is not installed on the system, the Reporter software installation begins automatically.</p> <hr/> <p>Click Accept on the Reporter Software v3.2 End User License Agreement dialog.</p> <p>The BioPharmaView™ Software Setup dialog opens.</p> 

Table 3-1 Installation Instructions (continued)

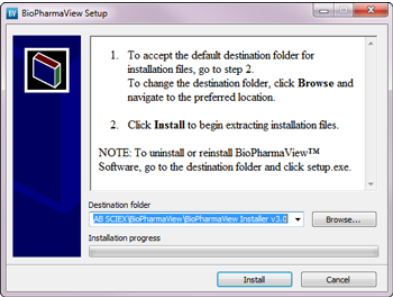
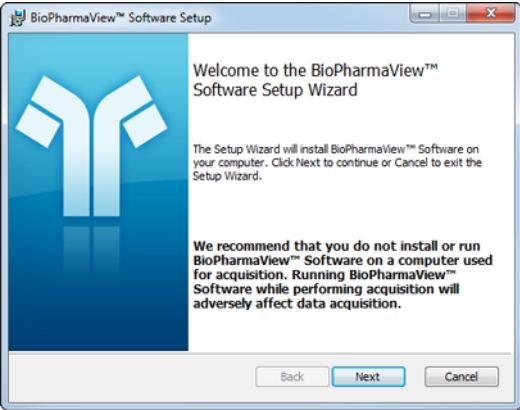
To install from a file downloaded from the SCIEX website ...	To install from the BioPharmaView™ software installation DVD ...
<p>Click Extract All.</p> <p>Note: By default, the files are extracted to the BioPharmaView-3.0 folder in the same location where the BioPharmaView-3.0.zip was saved.</p> <p>Note: After the extraction is complete, the BioPharmaView Setup dialog opens.</p> 	<p>Click Next.</p>
<p>Click Install.</p> <p>Tip! If the Reporter Software 3.2 is not installed on the system, the Reporter software installation begins automatically.</p> <p>Click Accept on the Reporter Software v3.2 End User License Agreement dialog.</p> <p>The BioPharmaView™ Software Setup dialog opens.</p> 	<p>On the End-User License Agreement dialog, click the I accept the terms in the License Agreement check box and then click Next.</p>

Table 3-1 Installation Instructions (continued)

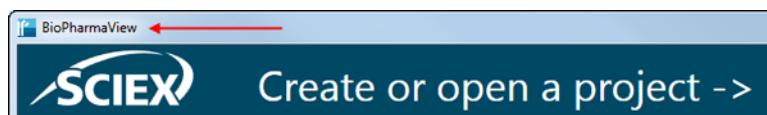
To install from a file downloaded from the SCIEX website ...	To install from the BioPharmaView™ software installation DVD ...
Click Next .	On the Destination Folder dialog, click Next . Tip! The user can change the software installation locations and the data folders before clicking Next .
On the End-User License Agreement dialog, click the I accept the terms in the License Agreement check box and then click Next .	Click Install .
On the Destination Folder dialog, click Next . Tip! The user can change the software installation locations and the data folders before clicking Next .	—
Click Install .	—

5. After the installation is complete, click **Finish**.
6. Continue with [License the BioPharmaView™ Software](#).

License the BioPharmaView™ Software

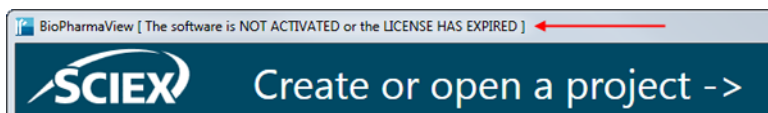
The BioPharmaView™ software is a licensed product. If a valid 3.0 license is not installed, or if the license has expired, then the processing and saving functions are not available.

1. Open the BioPharmaView™ software.
2. View the software title bar.
 - If a valid license file exists, then the title bar only contains the software name.



Installation

- If a valid license file does not exist, then the title bar contains the software name and a message indicating that there is an issue with the license.

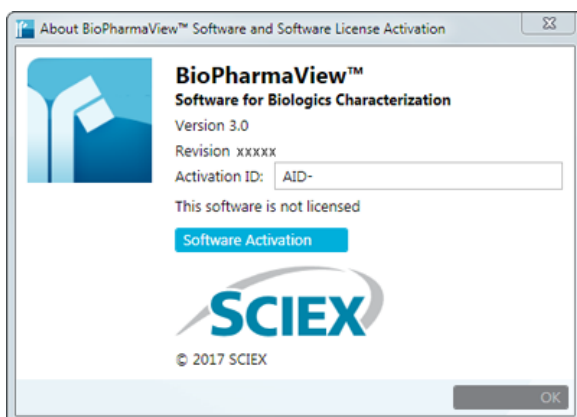


3. If there is a licensing issue, then click **About** in the lower left corner of the software.



The About BioPharmaView™ Software and Software License Activation dialog opens.

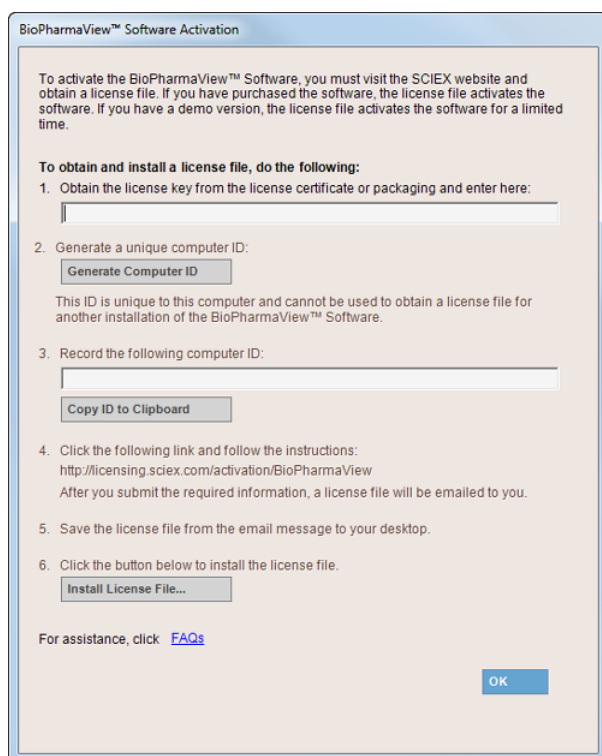
Figure 3-2 About BioPharmaView™ Software and Software License Activation Dialog



Any of the following conditions can result in the "This software is not licensed" message being shown:

- A valid 3.0 license is not installed.
 - The computer network connection is not available. The licensing components used by BioPharmaView™ software require that the computer's network adapter be enabled, although a physical connection to the network is not required.
4. Click **Software Activation**.

The BioPharmaView™ Software Activation dialog opens.

Figure 3-3 BioPharmaView™ Software Activation Dialog

5. Type the license key in the appropriate field.

If a license key is not available, then contact sciex.com/request-support.

6. Click **Generate Computer ID**.

This creates a unique identifier for the workstation.

7. Click **Copy ID to Clipboard**.

8. Click the <http://licensing.sciex.com/activation/BioPharmaView> link.

9. Log in to access the software activation page.

10. Follow the instructions to obtain the license.

After the required information is submitted, a license file is sent to all of the e-mail addresses provided.

11. When the e-mail containing the license file is received, copy the license file to the workstation desktop.

12. Click **Install License File** on the BioPharmaView™ Software Activation dialog.

The Select the new license file to be installed dialog opens.

Installation

13. Browse to and select the license file and then click **Open**.

Both the Select the new license file to be installed and the BioPharmaView™ Software Activation dialogs close.

14. Click **OK** to close the About BioPharmaView™ Software and Software License Activation dialog.

Known Issues and Limitations

4

Everyone should read this section of the Release Notes.

This section applies specifically to issues that are known in the BioPharmaView™ software, version 3.0. For information related to issues from previous versions of the software, refer to the *Release Notes* that came with that version of the software.

Tip! We recommend that the BioPharmaView™ software is closed and then opened again after processing large data files to make sure that the memory cache is cleared. This will help to maintain acceptable response times for subsequent processing.

Note: The numbers in brackets are reference numbers to each issue or feature in our internal tracking system.


Reporting

- When editing a report template for the first time, the message “Are you sure you want to install this customization?” might be shown. To resolve the issue, close any open report templates and then close any open copies of Microsoft Word. Navigate to the C:\Program Files\AB SCIEX\ReporterOfficeAddins\TemplateContentControlManager folder, double-click the **TemplateContentControlManager.vsto** file, and then install the component.
- After installing the MasterView™ software on a 64-bit workstation where the BioPharmaView™ software is installed, an error might occur when editing a BioPharmaView™ software report template. To resolve the issue, close any open report templates and then close any open copies of Microsoft Word. Navigate to the C:\Program Files\AB SCIEX\ReporterOfficeAddins\TemplateContentControlManager folder, double-click the **TemplateContentControlManager.vsto** file, and then install the component.
- When saving a report to the C:\Program Files folder, an error message is shown and the report is not created. Reports must be saved to a different location, preferably to a folder on the D:\ drive.
- If the ClearType option in Microsoft Windows is turned on, then the text in the generated reports might be fuzzy. We recommend that this option is turned off. Refer to [Turn ClearType Option in Microsoft Windows Off](#).

Discrepancies in labeling in the user interface

- Occasionally, in the Peptide Mapping—Characterize Standard and the Peptide Mapping—Review Results workflows, the chromatogram label for a selected peptide in the BPC graph is slightly different than the RT value listed for the peptide in the Peptide Results table. (BPV-695)

Known Issues and Limitations

- If the Auto-Validated Matches option is selected for Chromatogram Peak Labeling in the Peptide Mapping Settings dialog, then the labels shown in the XIC graph and in the Peak List table are those of all of the auto-validated peptides with the same retention time as the selected peptide instead of the label of the selected non-auto-validated peptide. (BPV-3962)
- In the Peptide Mapping—Characterize Standard workflow, if a processed TOF MS wiff file cannot be located and the user clicks the  icon to link the data file again, then occasionally the labels shown on the peaks in the TOF MS pane do not match the values shown in the Observed Mono m/z column. This occurs most often if the results have been calibrated. To resolve this issue, close and then open the project again. (BPV-4521)

Discrepancies in values shown in the user interface

- The values shown in the XIC Area column of the Peptide Results table in the Characterize Standard for Peptide Mapping workflow are determined by the processing functionality and are used by the BioPharmaView™ software for evaluation purposes. The peptide values are also shown in the Area column of the XIC Peaks tab in the BPC/TIC/XIC pane. However, because there might be slight differences in the values, the values in the XIC Peaks tab should be used for information purposes only. (BPV-868)
- When a position is assigned to a positionless modification, the value in the Score column of the Peptide Results table is updated. However, the score value is not updated on the Optimize Matching Parameters dialog nor in the FDR Data. (BPV-3422)
- In the user interface, values that include decimals are shown rounded. For example, the Retention Time Tolerance is rounded to two decimal places. XIC Area can be rounded to four decimal places, or, in some cases, to two decimal places and shown in scientific notation format. Tooltips, where available, will show the actual non-rounded value. The actual non-rounded value is always used during processing. (BPV-3506)

Changes made to Validated Match in Intact Protein batch results are not propagated to the report

When the check box for a selected Validated Match is cleared in the Intact Protein—Review Results workflow, the information in the Details column in the Results table is removed to reflect the change and the Validated Match check box on the Candidate Protein Matches pane is cleared. However, when a report is generated, the information in the Protein Summary Details column in the report is not removed. (BPV-4560)

Save As option does not save all of the updated parameters with the new project

If changes are made to the processing parameters in the Intact Protein—Characterize Standard workflow, and then the project is saved using the **Save As** option, all of the updated parameters are saved with the project except for the following Reconstruction Processing parameters: Signal To Noise Threshold, Resolution, and Gaussian Smoothing. For these parameters, the previous values are retained. The **Save** option functions as expected. (BPV-3724)

Software is slow to respond or stops responding

- In the Peptide Mapping—Review Results workflow, if the results file contains a large amount of information, then the software might become slow to respond if the **Show BPC** option is turned on. We recommend that the user turn the **Show BPC** option off when working with large files. (BPV-3828)
- When creating a report, if the batch results file contains a large number of results, the BioPharmaView™ software might be slow to respond or might become unresponsive. To prevent this issue, we recommend that the memory on the computer is expanded from the default 32 GB to a minimum of 128 GB. Even if the memory is expanded, the response time might be slow. However, the report will generate with no user intervention required. (BPV-4116)

Removal of BioPharmaView software fails

On computers configured with SCIEX OS, if the BioPharmaView™ software was installed before SCIEX OS was installed, then the removal of the BioPharmaView™ software will fail. To resolve this issue, remove SCIEX OS first and then remove the BioPharmaView™ software. (BPV-2092)

Changes made to data processing settings during processing are not reflected in the results

If changes are made to any of the data processing settings during processing, then the changes are not reflected in the results nor is the user informed that the data should be reprocessed. However, the user is informed that changes have been made when attempting to save the project. We recommend that the settings are only changed before processing, or, if changes are made during processing, then the data should be reprocessed to use the updated settings. (BPV-4310)

Modification Percent not calculated for Impurities in Peptide Mapping

In the Peptide Mapping workflow, the Modification Percent field value is not shown for peptides that are found only as Impurities. If the Modification Percent is required, then move the sequence to the Protein Sequence portion of the Assay Information—Sequence Features tab. Or, optionally, define the required metric on the Assay Information—Quality Attributes tab. (BPV-4571)

Deleting a set does not update Peptide Set Query

If a set is removed from the Assay Information—Quality Attributes tab, then the information in the Peptide Set Query pane is not updated immediately. To update the Peptide Set Query pane when a set is removed, select a different set or tab. (BPV-4606)

Remove the BioPharmaView™ Software

5

Note: On computers configured with SCIEX OS, if the BioPharmaView™ software was installed before SCIEX OS was installed, then the removal of the BioPharmaView™ software will fail. To resolve this issue, remove SCIEX OS first and then remove the BioPharmaView™ software.

1. Log on to the computer as a Microsoft Windows user with Administrator privileges.
2. Do one of the following:

For computers equipped with Microsoft Windows 7 ...	For computers equipped with Microsoft Windows 10 ...
Click Start > Control Panel > Programs and Features .	Click Start > AB SCIEX .
Tip! If the control panel components are shown by Category , then click Start > Control Panel > Programs > Programs and Features > Uninstall a program .	
Select BioPharmaView™ Software and then click Uninstall .	Right click BioPharmaView and then click Uninstall .

The software is removed, with no user intervention required.

During the removal, the software name is removed from the Installed Programs list, the shortcut to the BioPharmaView™ software is removed from the desktop, and the shortcuts to the software and the user documentation are removed from the Start menu.

Note: The following components remain on the computer:

- The C:\AB SCIEX\BioPharmaView\Data folder, which might contain BioPharmaView™ software project data.
 - If the product is licensed, the C:\Program Files\AB SCIEX\BioPharmaView folder, which contains the license file.
 - The C:\ProgramData\AB SCIEX\BioPharmaView folder, which contains the Intact Protein and Peptide Mapping report templates.
 - The AB SCIEX Reporter Template Suite 3.2.
 - Microsoft .NET Framework.
-

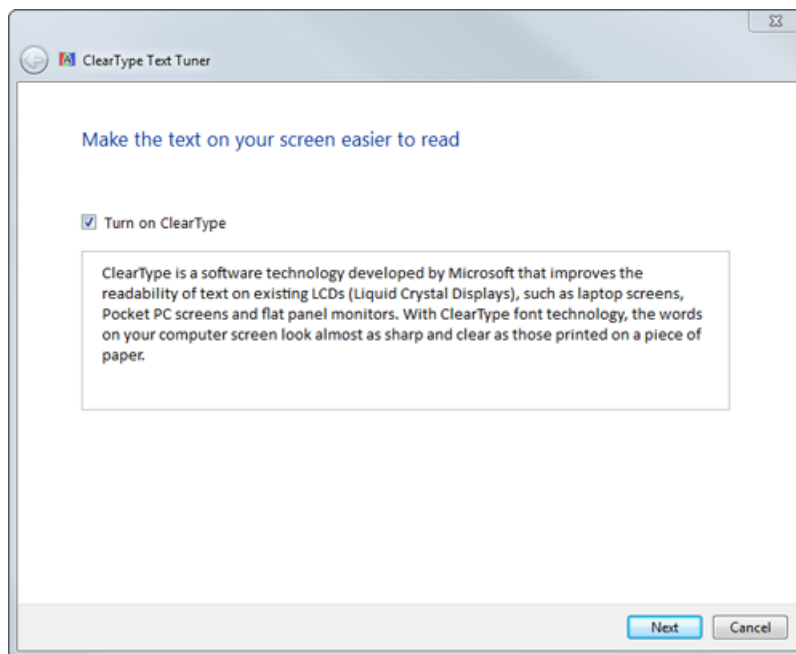
Turn ClearType Option in Microsoft Windows Off

A

1. Click **Start**.
2. In the Search field, type **ClearType**.
3. Click **Adjust ClearType text**.

The ClearType Text Tuner dialog opens.

Figure A-1 ClearType Text Tuner Dialog



4. Clear the **Turn on ClearType** check box.
5. Click **Next** and then follow the on-screen instructions.

Issues Fixed in Version 3.0 of the BioPharmaView™ Software

B

Note: This section applies specifically to issues that have been fixed with the release of version 3.0 of the BioPharmaView™ software. For information related to issues that were fixed in previous versions of the software, refer to the *Release Notes* that came with that version of the software.

Table B-1 Fixed Issues

Issue	Description
BPV 67, BPV-110, BPV-670	When the peptide list contains a large number of theoretical peptides, the BioPharmaView™ software might become slow to respond or indicate that it is not responding. No user action is required. The requested task will be completed. We recommend that the user consider the complexity of the sample being used for characterization to make sure that the BioPharmaView™ software is being used as efficiently as possible and to make sure that the best results are achieved without compromising the performance of the software.
BPV-846	When the batch contains mean ratio to protein information, and a report is requested, the Detailed Modifications section of an Intact Protein Single Sample Report or the Intact Protein Batch Results Report does not contain the multiplicity data. However, the multiplicity data is included at the beginning of the Modification Summary section.
BPV-1321, BPV-1327	Because version 2.0 is not fully compatible with previous releases of the BioPharmaView™ software, version 2.0 is unable to determine the MS/MS tolerance that was used for processing in 1.5 projects. As a result, the information in the MS/MS fragments table cannot be recalculated and populated. The Basic tab shows the theoretical fragments, without any green highlighting. The Advanced tab shows the error message "No data available for display". To resolve this issue, the information must be reprocessed. However, this can result in difference between the original (1.5) values and the new (2.0) values.
BPV-1986	If the dad.scan file or the dad.sidx file is missing when a corresponding wiff file is submitted in a batch, the processing of the batch completes but the results cannot be opened. Make sure that all required files are present when submitting a batch.
BPV-2081	A sample that is being used in the Characterize Standard workflow should have a minimal Retention Time window. For example, if a peptide is eluting at multiple times within the gradient, then the BioPharmaView™ software might use multiple potential matches for the abundance ratio calculation and users might be required to make changes to the chromatography used.

Issues Fixed in Version 3.0 of the BioPharmaView™ Software

Table B-1 Fixed Issues (continued)

Issue	Description
BPV-2164	If the wiff file or wiff.scan file is corrupted or missing, then the BioPharmaView™ software stops responding and the following error is shown: BioPharmaView has encountered an unexpected error.
BPV-2165	The software might become slow to respond when creating a batch from wiff2 files.
BPV-2356	Occasionally, the BioPharmaView™ software signal processing functionality does not detect all of the peaks that are detected by other SCIEX software products.