



BioPharmaView™ 2.0.1 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 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

- *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.**

Changes from Version 2.0 to Version 2.0.1

The tables containing the atomic masses and isotopic abundances have been updated. Customers might see minor changes in average molecular mass calculations as well as in other mass calculations.

Changes from Version 1.5 to Version 2.0

Note: Refer to [Issues Fixed in Version 2.0 of the BioPharmaView Software on page 23](#) for a list of all of the previous issues that have been resolved with this release of the BioPharmaView™ software.

SWATH Acquisition and the BioPharmaView Software

This version of the BioPharmaView™ software supports data files generated through SWATH® Acquisition. SWATH® Acquisition provides a robust and consistent method of acquisition that can be used for the Peptide Mapping workflow. SWATH® Acquisition enables the MS/MS analysis of all precursor ions across a wide mass range on an LC timescale, without having to set fragmentation criteria as is required with Information Dependent Acquisition (IDA) acquisition. The Q1 quadrupole is set to a wider selection window width (typically 10 Da to 50 Da) than that used for IDA. By stepping through multiple, sequential selection windows, a wide mass range is covered rapidly. The resulting mass spectra are a composite of the fragments of all of the precursor ions that passed through the respective Q1 selection window. This technique allows for the non-targeted MS/MS analysis of all species in a sample

Performance Improvements

This version of the BioPharmaView™ software contains significant improvements to the overall performance of the BioPharmaView™ software.

m/z Recalibration

This version of the BioPharmaView™ software enables the user to recalibrate the MS1 data, if required, during processing using the Automatic m/z Recalibration option. Manual m/z Recalibration can be applied through the Optimize Matching Parameters dialog. The m/z Recalibration functionality does not impact the raw data and can be performed in both the characterize standard and batch processing workflows.

MS/MS Scoring

This version of the BioPharmaView™ software includes improvements to the scoring functionality used to rate the quality of MS/MS matches. This scoring function reduces the number of false positives received and reduces the effects of changing the MS/MS m/z matching tolerance on scores, making the comparison of results easier.

Modification Percent

Post-translational modifications are important attributes to monitor in biological therapeutics development and manufacturing. In this version of the BioPharmaView™ software, the Modification Percent functionality provides the user with the ability to detect the level of modification of a positioned amino acid on a peptide-level and provides a new dialog where the user can assess which observations were used to generate the modification percentage. Using the manual curation feature, the user can include and exclude these observations.

Optimized Matching Parameters

This version of the BioPharmaView™ software includes an Optimize Matching Parameters function. This feature provides the user with information on the False Discovery Rate, at a set auto-validation threshold. The Optimize Matching Parameters functionality provides guidance for the determination of an appropriate auto-validation score and an *m/z* matching tolerance, based on the current assay.

Export MRM Transitions

This version of the BioPharmaView™ software enables users to export MRM transitions. The Export MRM Transitions feature enables the user to export MRM transitions from TripleTOF® instrument data so that acquisition methods can be created quickly for SCIEX Triple Quad™ and QTRAP® instruments. The feature supports the export of both MRM and *Scheduled MRM*™ transitions, in .txt or .csv format.

Manual Curation and Auto-Curation

The auto-validation feature in the Peptide Mapping workflow permits the user to see which results have scores above the auto-validation threshold. As part of this feature, manual curation columns have been added to the Peptide Results table. These columns enable the user to make changes to the results generated by the BioPharmaView™ software in terms of inclusion for quantitation of modification percentage or sequence coverage calculation. An additional column has been added to the Peptide Results table, where the user can add text to annotate their observations, if appropriate.

Report Templates

This version of the BioPharmaView™ software includes additional report templates that the user can use to simplify customization of their reports. The report templates provide various options, such as more concise reports, as well as additional details (for example, the modification percentage details).

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

- training.sciex.com

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 Web site at sciex.com.

Workstation Requirements

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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 Microsoft Windows 7 (32-bit or 64-bit) operating system with SP1
- Microsoft .NET Framework 4.5.1
- Adobe Reader

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

- Microsoft Office 2010 or 2013.

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.

Supported Equipment

- Dell OptiPlex 9010
- 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 on page 21](#).
- **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. (BPV-335)
- If using a .zip file that contains the BioPharmaView™ software installer, 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 4.5.1 is not installed. If this occurs, then the system must be connected to the Internet to download additional components for the Microsoft .NET Framework 4.5.1 installation process. If the system fails to install the Microsoft .NET Framework 4.5.1, 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 4.5.1, and then install the BioPharmaView™ software again.

Install the BioPharmaView™ Software

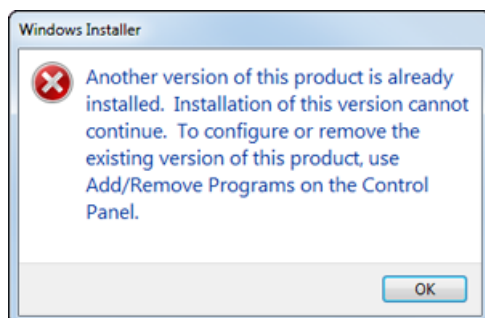
CAUTION: Potential Data Loss. The BioPharmaView™ software should not be installed on a computer used for acquisition. Software errors and data integrity issues can result if the BioPharmaView™ software and acquisition software are used concurrently.

1. Log on to the computer as a Microsoft Windows user with administrator privileges.
2. Remove any existing version of the BioPharmaView™ software. Refer to [Remove the BioPharmaView Software on page 21](#).

Installation

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

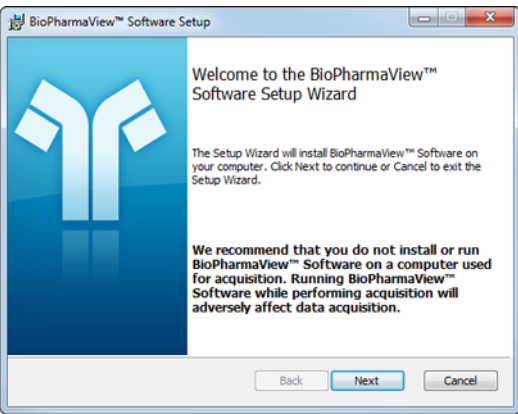
To install from a file downloaded from the SCIEX Web site ...	To install from the BioPharmaView™ software installation DVD ...
<p>Download the .zip file from the SCIEX Web site (sciex.com/software-downloads-x2110 or sciex.com/products/software/biopharmaview-software).</p> <p>Tip! To prevent potential 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_2.0.1.zip.</p>	<p>Navigate to the DVD and then double-click setup.exe.</p> <p>Tip! If the Reporter Software 3.2 is not installed on the system, then click Accept on the Reporter Software v3.2 End User License Agreement dialog.</p> <p>The BioPharmaView™ Software Setup dialog opens.</p> 
<p>Click Extract All.</p> <p>Note: By default, the files are extracted to the BioPharmaView_2.0.1 folder in the same location where the BioPharmaView_2.0.1.zip was saved.</p>	<p>Click Next.</p>

Table 3-1 Installation Instructions (continued)

To install from a file downloaded from the SCIEX Web site ...	To install from the BioPharmaView™ software installation DVD ...
<p>After the extraction is complete, browse to the extraction folder and then double-click BioPharmaView_2.0.1.exe.</p> <p>Note: The BioPharmaView 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>
<p>Click Install.</p> <p>Tip! If the Reporter Software 3.2 is not installed on the system, then 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 Destination Folder dialog, click Next.</p> <p>Tip! The user can change the software installation locations and the data folders before clicking Next.</p>
<p>Click Next.</p>	<p>Click Install.</p>

Table 3-1 Installation Instructions (continued)

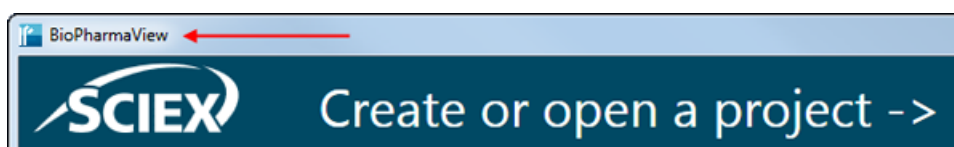
To install from a file downloaded from the SCIEX Web site ...	To install from the BioPharmaView™ software installation DVD ...
On the End-User License Agreement dialog, click the I accept the terms in the License Agreement check box and then click Next .	—
On the Destination Folder dialog, click Next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

- After the installation is complete, click **Finish**.
- Continue with [License the BioPharmaView Software on page 13](#).

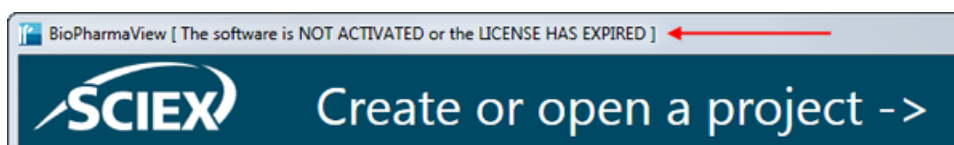
License the BioPharmaView™ Software

The BioPharmaView™ software is a licensed product. If a valid 2.0 license is not installed, or if the license has expired, then the processing and saving functions are not available.

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



- 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.



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

Installation



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 2.0 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

BioPharmaView™ Software Activation

To activate the BioPharmaView™ Software, you must visit the SCIEX website and obtain a license file. If you have purchased the software, the license file activates the software. If you have a demo version, the license file activates the software for a limited time.

To obtain and install a license file, do the following:

1. Obtain the license key from the license certificate or packaging and enter here:
2. Generate a unique computer ID:

This ID is unique to this computer and cannot be used to obtain a license file for another installation of the BioPharmaView™ Software.
3. Record the following computer ID:
4. Click the following link and follow the instructions:
<http://licensing.sciex.com/activation/BioPharmaView>
After you submit the required information, a license file will be emailed to you.
5. Save the license file from the email message to your desktop.
6. Click the button below to install the license file.

For assistance, click [FAQs](#)

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. 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.
10. When the e-mail containing the license file is received, copy the license file to the workstation desktop.
11. Click **Install License File** on the BioPharmaView™ Software Activation dialog.
The Select the new license file to be installed dialog opens.
12. 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.

Installation

13. 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 were known in the BioPharmaView™ software, version 2.0. No additional issues have been introduced with this release.

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

Performance Issues

- 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-67, BPV-110, BPV-670)

Filtering Issues

- Occasionally, the BioPharmaView™ software does not apply the active filters when alternating between the different tabs in the Intact Protein—Review Results workflow. To resolve this issue, close and then open the project again. (BPV-850)

Reporting Issues

- 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-846)
- 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.
- 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 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 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.

Known Issues and Limitations

- When attempting to open a report template for the first time on a system with Microsoft Office 2010 Professional installed, a message "Exception from HRESULT: 0x8004063E", a Microsoft Office Document Customization error message might open. This occurs because the Visual Studio 2010 Tools for Office Runtime is missing from the system. To resolve this issue, download the component from the Microsoft Web site using the following URL: <https://www.microsoft.com/en-us/download/details.aspx?id=48217>, and then double-click the vstor_redist.exe file and follow the installation prompts. (BPV-137)
- 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 on page 22](#).

Labeling Issues

- 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)
- In the MS/MS Graph pane of the Peptide Mapping—Characterize Standard workflow, the Experiment numbers included in the labels of the graph are the Information Dependent Acquisition (IDA) experiment numbers and not the experiment number selected in the Characterize Standard for Peptide Mapping pane. (BPV-701)

Error Messages

- **"The assay information has been modified and no longer matches the Intact Protein [Peptide Mapping] characterization results. You must reprocess and update the assay information before saving the project."**
 - In the Intact Protein—Characterize Standard and the Peptide Mapping—Characterize Standard workflows, if the user clicks Process and then clicks Cancel before the processing is completed, the software incorrectly instructs the user to reprocess and update the assay information before the project can be saved. To resolve this issue, click Process and then click Update Assay Information before saving. (BPV-119)
- **Chain N: The following modification has changed since the project was created. You must reprocess: DrugLinker<....>**
 - If the message "Chain N: The following modification has changed since the project was created. You must reprocess: DrugLinker<....>" is shown, then delete the modification and add it again. (BPV-1478)
- **"The parameters have changed. Before saving the project, update the assay information. If the update option is not available, then open a data file."**
 - If the message "The parameters have changed. Before saving the project, update the assay information. If the update option is not available, then open a data file." is shown, then click Update Assay Information. This might need to be done in the workflow that is not currently active. For example, when working in the Peptide Mapping workflow, the Intact Protein workflow assay information might need to be updated. (BPV-2011)

Miscellaneous Issues

- When adding Position or Maximum Mods per Chain information to the Modifications table, users must double-click inside the appropriate cell to move the focus from the previous cell. (BPV-83)

- 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)
- If the Assay Information contains multiple versions of the same peptide, but the peptide has different Batch Usage settings (for example Optional, Required, and so on), then during batch processing, the BioPharmaView™ software might match peptides with different batch settings. To resolve this issue, make sure that all peptides that share sequence and modification information are labeled with the same Batch Usage setting. (BPV-874)
- 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-1321, BPV-1327)
- The columns of information being imported into the Peptides table or the Characterized Proteins table must be arranged in the same order as the default column order in the BioPharmaView™ software. In addition, all of the columns must be present and visible. If the user has modified the column order in the .txt file, removed columns from the .txt file, or has hidden a column and then attempts to import peptides or characterized proteins, the import fails. (BPV-1468)
- If a peptide sequence is added in the Assay Information–Sequence Features tab and the user neglects to type a Protein Name, then when the user clicks Peptide Mapping an error icon is shown in the Protein Name field and an error message opens prompting the user to correct errors before navigating away from the page. When the user types a valid Protein Name and presses Enter, the error icon remains, the error message prompting the user to correct the errors is shown again, and the valid Protein Name is removed. To resolve this issue, the user must shift the focus to another field on the Sequence Features tab before attempting to navigate away from this page. (BPV-2049)
- 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. (BPV-2081)
- Occasionally, when importing peptides, the BioPharmaView™ software only validates that the XIC Area and the Retention Time columns are populated. The software does not always validate the information in the Mono. Mass column. (BPV-2094)
- For position-less modifications, occasionally the MS/MS Fragment tab shows the Basic view instead of the Advanced view. The Basic view shows b- and y-ion MS/MS evidence for the peptide assignment. For peptides with disulfide bonds, we recommend that the Advanced view be used. If internal fragmentation or neutral loss ions are of interest, then we recommend that the Advanced view be used. (BPV-2133)
- Occasionally, when the Revert Calibration option is clicked on the Optimize Matching Parameters dialog, the BioPharmaView™ software will generate an exception condition. (BPV-2134)

Known Issues and Limitations

- Occasionally, when the Copy All option is selected from the right-click menu in the Peptide Results table, the BioPharmaView™ software will generate an exception condition. (BPV-2135)
- The BioPharmaView™ software does not prevent the user from adding an invalid modification. This can result in exceptions occurring in subsequent tasks, for example, when generating peptide mapping results, when opening the Optimize Matching Parameters dialog, and so on. Users should use caution when adding or editing modifications to make sure that they are valid. (BPV-2136, BPV-2140)

Remove the BioPharmaView Software

5

1. Log on to the computer as a Microsoft Windows user with Administrator privileges.
2. Click **Start > Control Panel > Programs and Features**.

Tip! If the control panel components are shown by **Category**, then click **Start > Control Panel > Programs > Programs and Features > Uninstall a program**.

3. Select BioPharmaView™ Software 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:

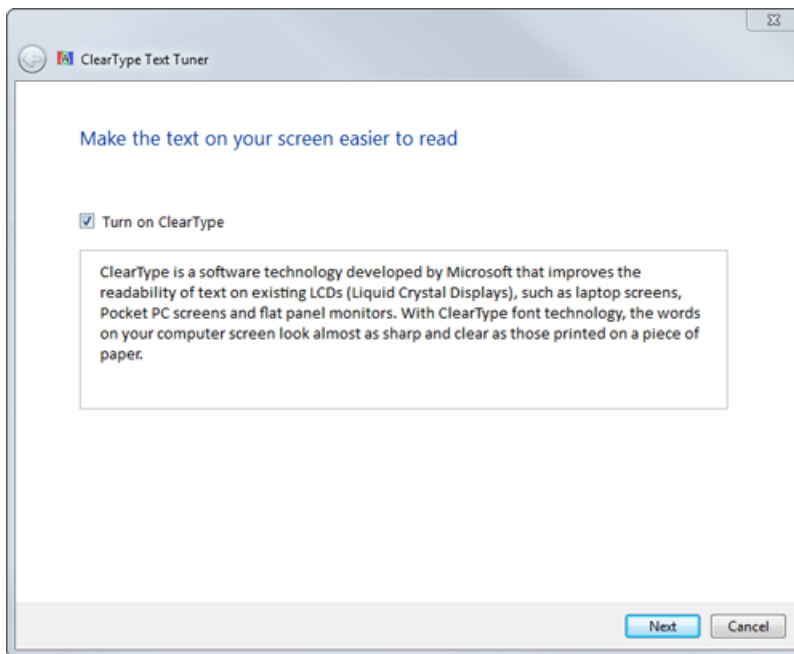
- The C:\AB SCIEX\BioPharmaView\Data folder, which might contain BioPharmaView™ software project data.
 - If the product is licensed, the C:\Program Files\AB SCIEX\BioPharmaView folder, which contains the license file.
 - The C:\ProgramData\AB SCIEX\BioPharmaView folder, which contains the Intact Protein and Peptide Mapping report templates.
 - The AB SCIEX Reporter Template Suite 3.2.
 - Microsoft .NET Framework 4.5.1.
-

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 2.0 of the BioPharmaView Software

B

Note: The following issues were fixed with the release of version 2.0 of the BioPharmaView™ software. No additional issues have been fixed with this release.

Performance Issues

- In the Intact Protein—Review Results workflow, when the Copy All Data in Table option was selected from the right-click menu, the BioPharmaView™ software might have been slow to respond or indicated that it was not responding. No user action was required. The requested task was completed. This issue has been fixed. (BPV-806)

Filtering Issues

- When invalid criteria was added to a Filtering dialog, an error icon was shown in the field containing the invalid information. If the invalid information was not corrected and the project was closed without saving the changes, then when the project and the Filtering dialog were opened, the invalid criteria was retained, but the error icon was not. When filtering was turned on, a red funnel was shown in the header of the filtered column but the invalid filter was not applied to the contents of the column. To determine which filter criteria was invalid, the user had to clear and then select each check box. An error icon was shown in the field containing the incorrect Filtering Criteria. This issue has been fixed. (BPV-727)
- When an imported .FilterSet file was used to populate a Filtering dialog, the project had to be saved to persist the filter criteria. If the project was closed without saving, the filter criteria was discarded and had to be imported again. This issue has been fixed. (BPV-808)
- If filtering was applied to the Modification Percent column in the Peptide Mapping—Review Results workflow, but no filtering criteria was specified, then the BioPharmaView™ software filtered the Peptide Results table resulting in the information in the filtered table being removed. The Modification Percent check box on the Filtering dialog had to be cleared to remove the filter and populate the Peptide Results table again. This issue has been fixed. (BPV-856)

Reporting Issues

- After the processing of a large batch (for example, 50 data files), generation of the Peptide Mapping Batch Report might have failed. If this occurred, the user had to close and then open the BioPharmaView™ software and then create the batch report. This issue has been fixed. (BPV-7)
- When a Microsoft Word (.docx) version of a report was generated, the Created by BioPharmaView {timestamp} information in the report header contained the date and time that the selected report template was last modified instead of the date and time the report was created. However, when a .PDF version of a report was generated, the Created by BioPharmaView {timestamp} information in the report header was correct. This issue has been fixed. (BPV-314)

Issues Fixed in Version 2.0 of the BioPharmaView Software

Labeling Issues

- In the Peptide Mapping—Characterize Standard workflow, the labels in the BPC/TIC/XIC pane applied to peptides with disulfide bonds were formatted incorrectly. Refer to [Table B-1](#). This issue has been fixed. (BPV-721)

Table B-1 BPC/TIC/XIC Labels

Format of Label in the BioPharmaView™ 1.5 Software	Format of Label in the BioPharmaView™ 2.0 Software
2,3= 2,3 T19-20 =T24	2,3. T19-20 = 2,3. T24
90.64	90.64

- In the Intact Protein—Review Results workflow, when the batch contains multiple files, the information shown in the BPC/TIC graph pane was inconsistent between files. For example, if two files were submitted in a batch and both files were selected, then, when the user navigated through the results of the first file, the BioPharmaView™ software zoomed the x-axis to an area that was ± 2 minutes of the RT and a blue, vertical line identified the protein. However, when the user navigated through the results of the second file in the batch, the x-axis returned to the default view (non-zoomed) and there was no blue, vertical line identifying the peak. If the batch contained two files but only one file was selected, then when the user navigated through the results of the selected file, the x-axis was not zoomed and the blue, vertical line identifying the protein was missing. If the batch contained three files and all three files were selected, then when the user navigated through the results of the first file, the x-axis was zoomed correctly and the blue, vertical line identifying the protein was shown in the correct location. However, when the user navigated through the results of the second file in the batch, the x-axis was zoomed correctly but the blue, vertical line identifying the protein was shown at an incorrect retention time. This issue has been fixed. (BPV-807)

Error Messages

- **"The project could not be opened. Sequence contains no matching element."**
 - The BioPharmaView™ software incorrectly allowed the user to import a peptide list containing a modification that had not been defined in the Assay Information into the Peptides table in the Assay Information—Peptide Mapping workflow and then save the project. However, when the user attempted to open the project, the message "The project could not be opened. Sequence contains no matching element." opened. This issue has been fixed. (BPV-858)

Sorting Issue

- When sorting the information in the Peptide column of the Peptide Results table, the information was sorted first alphabetically and then numerically, one digit at a time. For example, if the column contained four entries, T2, T3, T19, and T25, then after the column was sorted, the entries were listed in the following order: T19, T2, T3, and T29. This issue has been fixed. (BPV-646)

Miscellaneous Issues

- If all of the Peptide Results were selected in the Peptide Mapping—Characterize Standard and the Peptide Mapping—Review Results workflows, then the BioPharmaView™ software showed a maximum of 10 traces in the XIC, TOFMS, and MS/MS graphs. In the Characterize Standard workflow, the visible traces were based on the last results selected and were updated when the information was sorted and different results were selected. However, in the Review Results workflow, the visible traces were always the same, regardless of how the information was sorted and the results that were selected. This issue has been fixed. (BPV-94)
- When assay information included both matched and unmatched theoretical peptides, the BioPharmaView™ software occasionally matched two different peptides to the same observed m/z ion. This issue has been fixed. (BPV-113)
- When a peptide list containing a modification that had not been defined in the Assay Information was imported into the Peptides table in the Assay Information—Peptide Mapping workflow, the software incorrectly enabled the user to complete the characterization, update the Assay Information, and save the project. However, when the user created and submitted a batch using this updated file, the software did not add the invalid batch to the queue. No information was provided to the user, indicating why the batch could not be submitted. This issue has been fixed. (BPV-875)

Revision History

Revision	Reason for Change	Date
A	First release.	July 2015
B	Updated the list of Related Documentation. Added the list of changes from version 1.5 to version 2.0. Updated the installation and activation procedures. Updated the list of known issues and limitations. Added the procedure to turn off the ClearType Option in Microsoft Windows. Moved the Fixed Issues to an Appendix.	June 2016
C	Updated software version. Added the list of changes from version 2.0 to version 2.0.1. Updated the installation and activation procedures. Updated the download link for Visual Studio 2010 Tools for Office Runtime. Updated the title of Appendix B and added a note to clarify that the issues listed were fixed in the version 2.0 release.	October 2016