AB SCIEX

BioPharmaView™ Software

Release Notes

Contents

Introduction 1

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 or 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 deconvolution of a charge series envelope resulting from LC-MS/MS.
- **Peptide Mapping Analysis**: Determines the sequence of peptides resulting from the enzymatic digestion of a protein from the mass-to-charge (*m/z*) ratio of TOF MS/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*: Available on the installation DVD or 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 1.0 to Version 1.5

- A new column, Score, has been added to the Peptide Results table in version 1.5 of the software. This column provides an estimate of the probability that a candidate match is correct. During the review of results, users can differentiate between true-positive and false-positive identifications based on an assigned score value.

- A new tab, Modifications Summary, has been added to the Intact Protein Characterize Standard Results table. This tab summarizes Modification to Protein Ratios, including the average count of modifications attached to a single protein molecule. The Drug-Antibody Ratio (DAR) is an example of this. A DAR value of three indicates that, on average, the protein is modified with three drug attachments. Other examples include the average level of oxidation, glycosylation, or any other modification. In addition, the BioPharmaView™ software reports the fraction of the total intact protein signal that comes from versions containing "n" number of each modification.

- A new column, Modification Percent, has been added to the Peptide Results table in version 1.5 of the software. The column captures post-translational modifications which are considered to be critical quality attributes for biological therapeutics. Using this information, users can assess the level to which individual amino acids are modified over the range of all observed modifications for the same charge state.

- A new column, Validated Match, containing a check box for each entry, has been added to both the Intact Protein workflow Results table and the Peptide Mapping workflow Peptide Results table in version 1.5 of the software. All check boxes are selected by default for matched results in Intact Protein and for matched results with a Score value above the user-defined threshold in Peptide Mapping. By clearing a check box, users can exclude individual results that they consider problematic from the results list. Users also have the option to update the Assay Information with only those results identified as a Validated Match by selecting the Use Only Validated Matches to Update Assay Information option, or all results can be used to update the Assay Information by clearing that selection. It is the responsibility of the user to confirm the correct results are being reported.

- Filtering dialogs have been incorporated into many of the workflows in version 1.5 of the software. Filtering enables users to minimize the number of entries shown. Filtering preferences can be exported and saved as a .FilterSet file. This file can then be imported into subsequent results tables to filter. When filters are applied, users have the option to create reports containing all of the generated batch results or only the results that match the filter criteria applied. Refer to Appendix A in the BioPharmaView™ Software User Guide.

- Improvements have been made to the MS1 feature detection for LC chromatograms in the Peptide Mapping workflow. In version 1.5 of the BioPharmaView™ software, the generation of theoretical fragment ions is followed by MS/MS matching for any MS1 identified peptides that have MS/MS spectra available. During matching, all theoretical peptide forms within the *m/z* tolerance are evaluated and scored if an MS2 spectrum is available. The set of matches for each MS1 signal is inspected and if the top scoring match meets or exceeds the minimum score, then the result is identified as valid.

- Disulfide bond information can be imported into the Disulfide Bonds table from a .txt file or from another BioPharmaView™ software project. All information is validated during import. In addition, disulfide bond information can be exported from the Disulfide Bond table to a .txt file.

Introduction

- When drug-linker modifications are attached to an antibody through a partial reduction, this results in the breaking of some disulfide bonds, followed by modification of the free cysteines that were produced. A new check box has been added to the Modifications table. When this check box is selected, the application considers disulfide bonds as eligible for replacement with any defined cysteine modifications during the generation of theoretical Intact protein and peptide forms. For this option to function correctly, the modification Type must be Internal and the Position undefined. In addition, non-reduced disulfide bonds are required.

- The option to view a Base Peak Chromatogram (BPC) has been added for both intact proteins and peptides in the same graph pane used to show Total Ion Chromatogram (TIC) traces in version 1.5 of the software. A BPC is a more useful single-trace depiction of an LC/MS data set than the TIC is. The BPC shows the momentary intensity of the most intense ion at any given time, over time. However, the response time of the BioPharmaView™ software when opening a project might be increased when the Show BPC option is selected. As a workaround, select the Show TIC option before closing the project.

- A new column, Workflow Usage, has been added to the Modifications table in version 1.5 of the software. This column enables the user to define modifications for use only in the Intact Protein workflow, modifications for use only in the Peptide Mapping workflow, and modifications for use in both workflows. The default value for this column is Both. Workflow usage information can be assigned in the Add Modifications dialog or in the Modifications table.

- In previous versions of the BioPharmaView™ software, only the first sample in the selected .wiff file could be analyzed. Any additional samples were ignored. In version 1.5 of the software, the .wiff file is automatically opened to Sample # 1 and Experiment # 1. However, if the .wiff file contains additional samples and experiments, then users can select a different TOF MS sample or experiment from the list provided.

- In previous versions of the BioPharmaView™ software, multiple peptide entries that were identical except for the protein chain of origin were generated. In version 1.5 of the software, chemically unique peptides with multiple protein chains are amalgamated into one entry, resulting in a final set of peptides that contains one entry for each unique peptide.

- In previous versions of the BioPharmaView™ software, users could identify only one chain per modification row. In version 1.5 of the software, users can identify multiple chains in sequential order (1-3) or non-sequential order (1,4) in a single row for each modification being added to the protein sequences. Chain information can be assigned in the Add Modifications dialog or in the Modifications table.

- Improvements have been made to the response time of the BioPharmaView™ software when the user is reviewing the results of characterization or results generated through the batch processing workflows.

- A new setting, Minimum Peptide Length, has been added to the Peptide Mapping Settings dialog in version 1.5 of the software. This setting enables the user to define the minimum number of amino acids on all peptide chains. This can be useful for filtering smaller peptides that contain less relevant information about the sample out of the results.

- A new column, Abundance Ratio, has been added to both the Results table in the Intact Protein—Review Results workflow and the Peptides Results table in the Peptide Mapping—Review Results workflow in version 1.5 of the software. The Abundance Ratio, which measures the relative abundance levels of quality attributes between experimental and reference standards, is calculated by comparing the protein or peptide to the values obtained through the Characterize Standard workflow. Quality attributes can be any user-defined property, such as proteins or peptides with specific modifications, disulfide bonds, sequences, and so on. The relative Abundance Ratio is reported for any batch results that were matched to characterized proteins or peptides.

Contact Us

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 SCIEX Web site at http://sciex.com.

SCIEX Support

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

Customer Training

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

Online Learning Center

- http://training.sciex.com
- http://elearning.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 Microsoft Windows 7 (32-bit or 64-bit) operating system with SP1

- Microsoft .NET Framework 4.0

- 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

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.

Installation 3

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 20*.

- The BioPharmaView™ software is not backward compatible with previous releases. Before upgrading an existing version of the BioPharmaView™ software (version 1.0) installed on a system configured with the Microsoft Windows 7 32-bit operating system, the user must remove the installed version of the TemplateContentControlManager software through the Control Panel (BPV-335).

- If using a .zip file that contains the BioPharmaView™ software installer, extract All 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 4.0 is not installed. If this occurs, then the system needs to be connected to the Internet to download additional components for the Microsoft .NET Framework 4.0 installation process. If the system fails to install the Microsoft .NET Framework 4.0, 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 4.0, 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. To begin, 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 20*.

3. Make sure that all of the applications are closed.

4. Insert the BioPharmaView™ software installation DVD into the DVD drive.

> **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.

Figure 3-1 Windows Installer Error Dialog
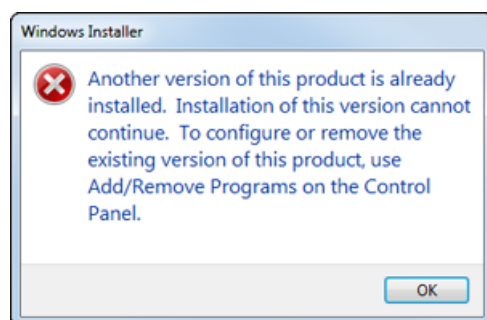
> **Note:** Click **OK** and then remove the software.

The BioPharmaView™ Software Setup dialog opens.

> **Tip!** If the BioPharmaView™ Software Setup dialog does not open, then navigate to the DVD drive and then double-click **setup.exe**.

Figure 3-2 BioPharmaView Software Setup Dialog
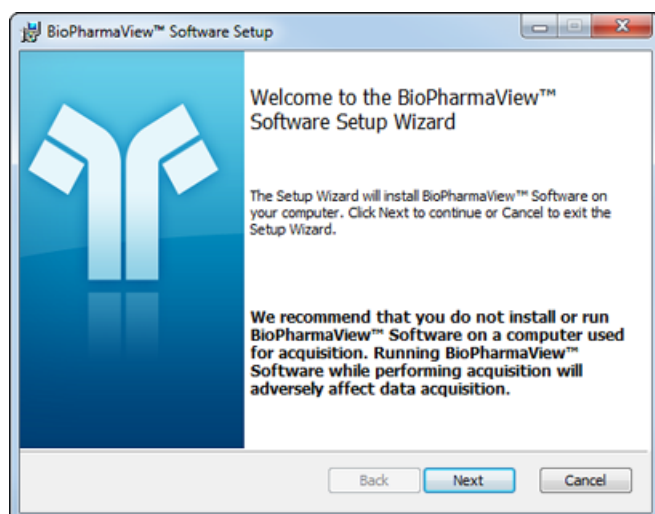
5. Click **Next**.

6. On the End-User License Agreement dialog, click the **I accept the terms in the License Agreement** check box and then click **Next**.

7. On the Destination Folder dialog, click **Next**.

> **Tip!** The user can change the software installation locations and the data folders before clicking Next.

8. Click **Install**.

9. After installation is complete, click **Finish**.

10. If this is a new installation of the BioPharmaView™ software, then continue with *License the BioPharmaView Software*. If this is an upgrade to an existing version of the software, then the previous license file activates this version.

License the BioPharmaView™ Software

The BioPharmaView™ software is a licensed product. If a current license is not installed, then 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.
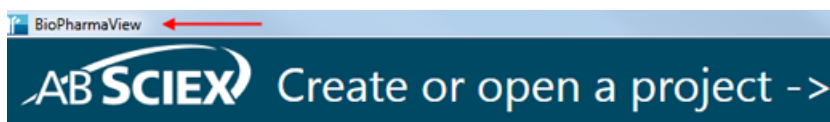
   - If a valid license file does not exist, then the title bar contains the software name and a message indicating that there is an issue with the license.
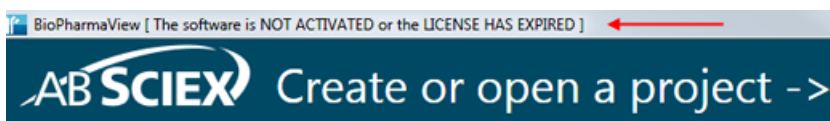
3. If there is a licensing issue, then click **About** in the lower left corner of the software.

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

Figure 3-3 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 current license is not installed.

- The computer network connection is not available. The licensing components used by SCIEX 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 3-4 BioPharmaView™ Software Activation Dialog

5. Type the license key, exactly as shown, in the appropriate field.

   If a license key is not available, then contact the SCIEX Sales Representative.

6. Click **Generate Computer ID**.

   This creates a unique identifier for the workstation.

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

8. Click the SCIEX licensing link and then paste the copied computer ID in the **Computer ID** field.

9. Follow the instructions to obtain the license.

Note: Internet access is required to obtain the license. If the computer does not have Internet access, then make a copy of the generated computer ID. On a computer with Internet access, go to the licensing page of the SCIEX Web site and then follow the instructions to obtain a license.

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

10. Close the browser window.

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.

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 1.5.

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

Performance Issues

- The improvements made to increase the number of detected peptides in version 1.5 of the BioPharmaView™ software might result in an increase in the response time in the Peptide Mapping workflow when compared with version 1.0 of the software.

- When a large number of peptides (>20 000) is included in the Peptides list, the BioPharmaView™ software might become slow to respond or indicate that it is not responding when Process or Update Assay Information is clicked in the Peptide Mapping—Characterize Standard workflow. No user action is required. The requested task will be completed. (BPV-67)

- As the number of entries in the Peptides table increases in the Peptide Mapping workflow, the response time of the BioPharmaView™ software increases each time the number of Maximum Missed Cleavages is increased and Digest is clicked. Occasionally, the software will indicate that digestion has completed but the Peptides list is empty. Other actions, for example, save the project, open the project, and so on, continue to function as expected. (BPV-110)

- When a large number of peptides (>20 000) is included in the Peptides list, the BioPharmaView™ software might become slow to respond or indicate that it is not responding when the user is editing information on the Sequence Features tab. No user action is required. The requested task will be completed. (BPV-670)

- In the Intact Protein—Review Results workflow, when the Copy All Data in Table option is selected from the right-click menu, 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. (BPV-806)

- If large data files or batches are processed multiple times under certain conditions, then all of the available RAM might be consumed and the software stops responding. If this occurs, close and then open the BioPharmaView™ software.

Filtering Issues

- When invalid criteria is added to a Filtering dialog, an error icon is shown in the field containing the invalid information. If the invalid information is not corrected and the project is closed without saving the changes, then when the project and the Filtering dialog are opened, the invalid criteria is retained, but the error icon is not. When filtering is turned on, a red funnel is shown in the header of the filtered column but the invalid filter is not applied to the contents of the column. To determine which filter criteria is invalid, clear and then select each check box. An error icon is shown in the field containing the incorrect Filtering Criteria. (BPV-727)

Known Issues and Limitations

- When an imported .FilterSet file is used to populate a Filtering dialog, the project must be saved to persist the filter criteria. If the project is closed without saving, the filter criteria is discarded and must be imported again. (BPV-808)

- 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)

- If filtering is applied to the Modification Percent column in the Peptide Mapping—Review Results workflow, but no filtering criteria is specified, then the BioPharmaView™ software filters the Peptide Results table resulting in the information in the filtered table being removed. Clear the Modification Percent check box on the Filtering dialog to remove the filter and populate the Peptide Results table again. (BPV-856)

Reporting Issues

- When a Peptide Mapping report is generated, the user might find that there are labels included in the LC-MS TIC section of the report that are not visible in the BioPharmaView™ software interface. To view the additional labels in the software, zoom in on the specific timeframe containing the extra labels. (BPV-74)

- When a Microsoft Word (.docx) version of a report is generated, the Created by BioPharmaView {timestamp} information in the report header contains 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 is generated, the Created by BioPharmaView {timestamp} information in the report header is correct. (BPV-314)

- When the batch contains Drug-Antibody Ratio (DAR) 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)

- In Microsoft Windows 7, when saving a report to either the C:\ or 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 (x86)\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 (x86)\AB SCIEX\ReporterOfficeAddins\TemplateContentControlManager folder, double-click the **TemplateContentControlManager.vsto** file, and then install the component.

- 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: http://www.microsoft.com/en-us/download/details.aspx?id=44074, and then double-click the vstor_redist.exe file and follow the installation prompts.

- After the processing of a large batch (for example, 50 data files), generation of the Peptide Mapping Batch Report might fail. If this occurs, close and then open the BioPharmaView™ software and then create the batch report.

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)

- In the Peptide Mapping—Characterize Standard workflow, the labels in the BPC/TIC/XIC pane applied to peptides with disulfide bonds are formatted incorrectly. Refer to *Table 4-1*. (BPV-721)

Table 4-1 BPC/TIC/XIC Labels

Label formatted as ...	Label should be formatted as ...
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 is inconsistent between files. For example, if two files are submitted in a batch and both files are selected, then, when the user is navigating through the results of the first file, the BioPharmaView™ software zooms the x-axis to an area that is ± 2 minutes of the RT and a blue, vertical line identifies the protein. However, when the user is navigating through the results of the second file in the batch, the x-axis returns to the default view (non-zoomed) and there is no blue, vertical line identifying the peak. If the batch contains two files but only one file is selected, then when the user is navigating through the results of the selected file, the x-axis is not zoomed and the blue, vertical line identifying the protein is missing. If the batch contains three files and all three files are selected, then when the user is navigating through the results of the first file, the x-axis is zoomed correctly and the blue, vertical line identifying the protein is shown in the correct location. However, when the user is navigating through the results of the second file in the batch, the x-axis is zoomed correctly but the blue, vertical line identifying the protein is shown at an incorrect retention time. (BPV-807)

Known Issues and Limitations

Error Messages

- **"The project could not be opened. Sequence contains no matching element."**

  - The BioPharmaView™ software incorrectly allows the user to import a peptide list containing a modification that has 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 attempts to open the project, the message "The project could not be opened. Sequence contains no matching element." opens. To resolve this issue, the user must create a project and import a valid peptide list. (BPV-858)

- **"The image format is unsupported."**

  - If the message "The image format is unsupported." is shown, then click **Control Panel > Display Settings > Color Quality > Highest (32 bit).** The BioPharmaView™ software cannot be opened on a system that is unable to display 32-bit graphics.

- **"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)

- **"The assay information has been modified and no longer matches the characterization result. You must reprocess and update the assay information before saving the result."**

  - If the message "The assay information has been modified and no longer matches the characterization result. You must reprocess and update the assay information before saving the result." 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.

Sorting Issue

- When sorting the information in the Peptide column of the Peptide Results table, the information is sorted first alphabetically and then numerically, one digit at a time. For example, if the column contains four entries, T2, T3, T19, and T25, then after the column is sorted, the entries are listed in the following order: T19, T2, T3, and T29. (BPV-646)

Miscellaneous Issues

- The columns of information being imported into the Peptides table or the Characterized Proteins table must be in the same order as the default column order in these tables the BioPharmaView™ software. In addition, all columns must be present. If the user has modified the column order in the .txt file and then attempts to import peptides or characterized proteins, the import fails.

- 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)

- If all of the Peptide Results are selected in the Peptide Mapping—Characterize Standard and the Peptide Mapping—Review Results workflows, then the BioPharmaView™ software shows a maximum of 10 traces in the XIC, TOFMS, and MS/MS graphs. In the Characterize Standard workflow, the visible traces are based on the last results selected and are updated when the information is sorted and different results are selected. However, in the Review Results workflow, the visible traces are always the same, regardless of how the information is sorted and the results that are selected. (BPV-94)

- When assay information includes both matched and unmatched theoretical peptides, the BioPharmaView™ software occasionally matches two different peptides to the same observed *m/z* ion. (BPV-113)

- When characterizing standards, only the last processing result for each workflow can be saved and opened. Previously saved results are overwritten by more recent results and cannot be saved or opened.

- When importing peptides or proteins, the software searches the list of modifications, attempting to find the imported modification by name or by symbol. If the imported modification name matches the symbol of an existing modification, then the imported modification is replaced by the existing modification.

- 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 versions of the same peptide have the same Batch Usage setting. (BPV-874)

- When a peptide list containing a modification that has not been defined in the Assay Information is imported into the Peptides table in the Assay Information—Peptide Mapping workflow, the software incorrectly enables the user to complete the characterization, update the Assay Information, and save the project. However, when the user creates and submits a batch using this updated file, the software does not add the invalid batch to the queue. No information is provided to the user, indicating why the batch cannot be submitted. (BPV-875)

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, click **Start** > **Control Panel** > **Programs** > **Programs and Features** > **Uninstall a program.**

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3. Select BioPharmaView™ Software and then click **Uninstall**.

The software 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 software project data.

- If the product is licensed, the C:\Program Files (x86)\AB SCIEX\BioPharmaView folder, which contains the license file.

- The AB SCIEX Reporter Template suite.

- Microsoft .NET Framework 4.

Download the Software from the SCIEX Web Site

A

1. Download the BioPharmaView™ software from the SCIEX Web site.

   Note: To prevent potential installation issues, it is recommended that the file is saved to a location other than the computer desktop.

2. After the download is complete, double-click the **BioPharmaView_1.5.exe** file.

   The BioPharmaView Setup dialog opens.

3. Click **Install**.
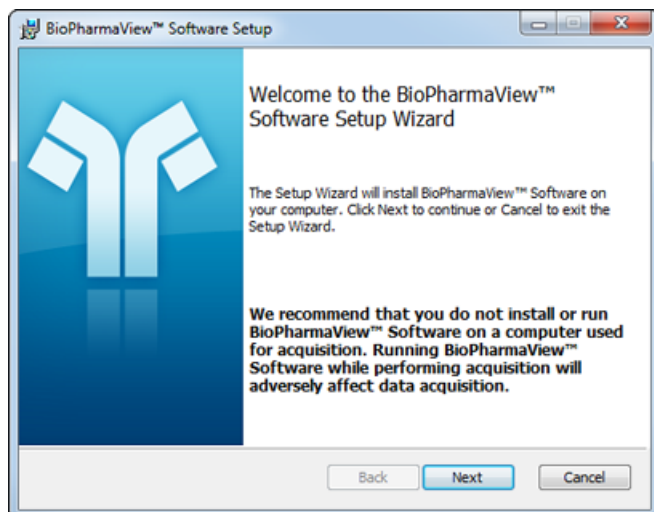
   Tip! By default, the files are extracted to the C:\AB SCIEX\BioPharmaView\BioPharmaView Installer v1.5 folder. However, the user can choose the location.

   After the extraction is complete, the BioPharmaView™ Software Setup dialog opens.

   Figure A-1 BioPharmaView Software Setup Dialog

4. Continue with step 5 of *Install the BioPharmaView ™ Software on page 9*.

Revision History

Revision	Reason for Change	Date
A	First release.	July 2015