BioPharmaView™ Software 3.0.1

Release Notes

To view information about a previous software release, refer to the *Release Notes* that came with that version of the software.

New Features

This software release provides an updated custom modifications list that contains a comprehensive glycan list.

Install the Software

Prerequisite
• Back up and then remove any current custom modifications lists. The lists are found in the C:\ProgramData\SCIEX\BioPharmaView\ folder.
Note: Any customer-created custom modifications lists cannot be automatically merged with the custom modifications list installed with this software update. We recommend that any customer-specific custom modifications be manually added to the list after the software is installed. For help updating the list, contact sciex.com/request-support.

1. Log on to the computer as a user with Administrator privileges.
2. Close the BioPharmaView™ software.
3. Download the **BioPharmaView-3.0.1.zip** from sciex.com/software-support/software-downloads.

   Note: To prevent potential installation issues, we recommend that the file be saved to a location other than the computer desktop.

4. After the download is complete, right-click the **BioPharmaView-3.0.1.zip** file.
5. Click **Extract All** and then select the file destination folder.
6. After the extraction is complete, navigate to the selected extraction folder and then double-click the **setup.exe** file.
7. Follow the on-screen instructions to complete the installation.

8. Restart the computer.

   The software installs the CustomModifications file in the C:\ProgramData\SCIEX\BioPharmaView\ folder.

9. Open the BioPharmaView™ software.
10. (Optional) Manually enter any additional custom modifications.

Note: If a custom modifications list was previously created and used to process projects, then any projects processed using that list cannot be processed using the new list. Projects must be reprocessed using the new list. For help reprocessing projects, contact sciex.com/request-support.

Remove the Software

1. Open **Control Panel**.
2. Select the BioPharmaView™ software version 3.0.1.
3. Click **Uninstall**.

Known Issues

The software significantly slows down or becomes unresponsive if more than 8 positioned modifications, for example, glycans, are applied in combination with a variable modification, for example, oxidation, to both intact protein and peptide mapping workflows. To avoid this issue, we recommend that the variable modifications be set to **Peptide Mapping** in the **Workflow Usage** column instead of **Both**, thus enabling the theoretical form generation for intact proteins to complete in a reasonable amount of time. (BV-5232)

When Chymotrypsin is used as the digestion enzyme with the **Cysteine modifications can replace disulfide bonds** option enabled, theoretical peptide forms are not generated if the maximum missed cleavages is set to **> 0**. To generate theoretical peptide forms that are caused by more than 0 missed cleavages:

1. Set the digest agent option to Lys C + Chymotrypsin and then click **Digest**.
2. After the theoretical forms are generated, type **K** in the row corresponding to **Sequence** in the Filter dialog to filter the sequences containing Lys residues.
3. Select the rows that contain the peptides terminating with K and then click **Delete** to obtain peptide forms that are generated only by Chymotrypsin activity. (BPV 5224)

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Documentation

This version of the document supercedes all previous versions of this document.

To view this document electronically, Adobe Acrobat Reader is required. To download the latest version, go to https://get.adobe.com/reader.

For the latest versions of the documentation, visit the SCIEX website at sciex.com.

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