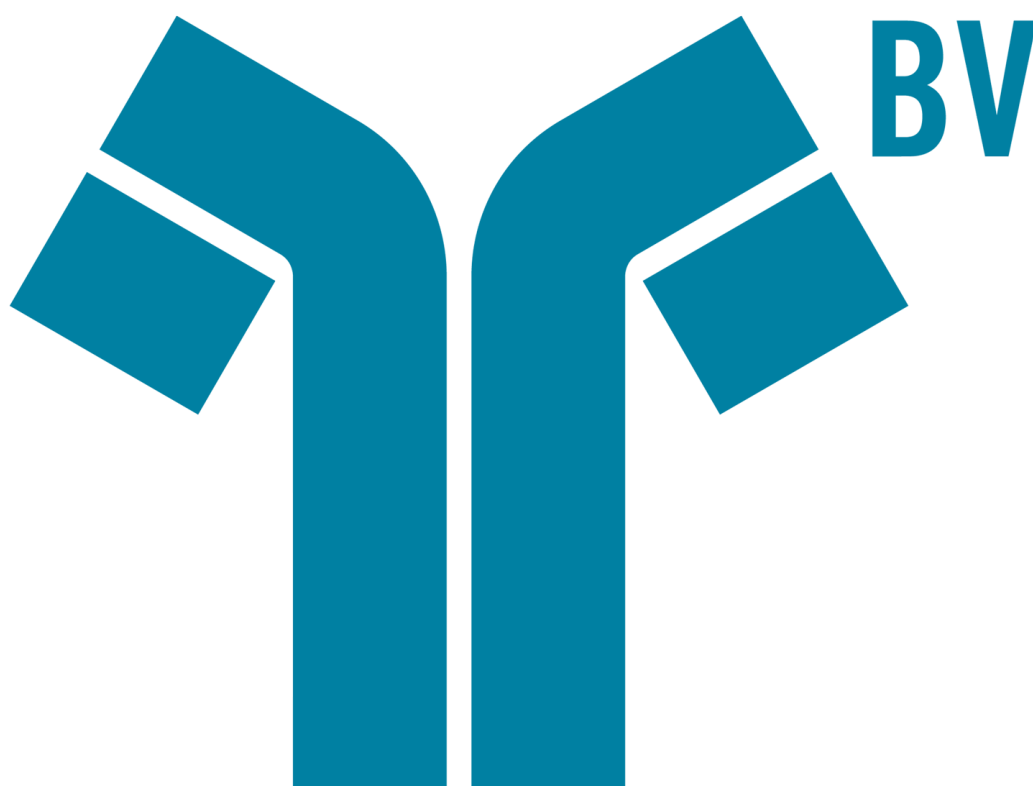




BioPharmaView™ 3.0.2 Software

Release Notes



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Key Features of BioPharmaView™ Software Version 3.0.2

The MAM BPV to Analytics converter can be used to transfer Quality Attributes information from the BioPharmaView™ Software to SCIEX OS for further analysis.

Note: For information about known issues and limitations, refer to the release notes from previous versions of the software. Previous versions of release notes can be downloaded from sciex.com/software-support/software-downloads.

Use the MAM-BPV to Analytics Converter

Use the MAM-BPV to Analytics Converter to transfer sequence and modification information from a **Quality Attribute** created in the BioPharmaView™ Software to the Analytics workspace in SCIEX OS. For more information on how to create a **Quality Attribute** on the Quality Attribute tab, refer to the *Software User Guide* for the BioPharmaView™ Software. The following steps describe how to set up the sequence and modification information in the BioPharmaView™ Software to minimize data manipulation in the **Analytics** workspace.

Known Limitations

- The Converter uses the sequence and modification information in the Query field in the Set1 tab of a given Quality Attribute.
- The Converter does not support most operators. Only the OR symbol ("|") is supported in the sequence field.
- Only modifications separated by a comma can be successfully converted, for example Oxidation@4(32), Deamidated@*. If modifications are separated by OR or "|", for example Oxidation@4(32)|Deamidated@*, then only peptides containing the first modification listed in the **Peptide Set Query** field are transferred.
- Three charges are automatically selected for each of the peptide forms. If more than 3 charge states are required then these must be manually entered in the Components table in the **Analytics** workspace.
- The Converter does not support non-reduced peptides.
- The **Use** check box in the query is not considered. If modification information is not needed, then make sure that the **Modification** field is empty.

1. Create a **Quality Attribute** by populating the Peptide Set Query pane with the sequences and modifications that are to be converted to components. Refer to the "Add Quality Attribute" section in the *Software User Guide*.
2. Make sure that the peptides with modifications are in the Set 1 tab.

The converter automatically creates analogous unmodified peptides using the sequence information in the query field on the Set 1 tab.

The screenshot shows the 'Quality Attributes' configuration window. On the left, a table lists attributes with their values. The 'Oxidation M32' attribute is selected, showing a value of 6.35%. The main area displays the 'Sum(Set 1)/Sum(Set 2)' formula and a table of peptide data. The 'Peptide Set Query' pane at the bottom shows the configuration for the selected attribute, including the sequence 'VGVMHWYQQKPGK' and the modification 'Oxidation@4(32)'.

Attribute Name	Value
1 Oxidation M4	100.00 %
2 Oxidation M34	0.00 %
3 Oxidation M32	6.35 %
4 Oxidation W49/WS4/WS5	0.00 %
5 Oxidation W280	0.00 %
6 Oxidation W316	0.00 %
7 Oxidation W384	0.00 %
8 Oxidation M431	-

Batch Usage	Chains	Sequence	Modifications	Mono. Mass	Matched	Mono. m/z	Charge	XIC Area	Retention Time	
1	Optional	1	VGVMHWYQQKPGK	Oxidation@4(32)	1636.7820	✓	819.3983	2	5.5171e2	12.23
2	Optional	1	VGVMHWYQQKPGK	Oxidation@4(32)	1636.7820	✓	546.6013	3	4.5542e3	12.24
3	Optional	1	VGVMHWYQQKPGK	Oxidation@4(32)	1636.7820	✓	410.2028	4	2.6131e3	12.23

Use	Column	Value
1	Sequence	"VGVMHWYQQKPGK"
2	Modifications	"Oxidation@4(32)"
3	Use for Quant	"Use" Unknown
4	Retention Time	11-13

3. Click **Export**, select the **Quality Attributes** to transfer, and then save the cqa file.
4. Drag the cqa file over the MAM-BPV to Analytics converter.bat file.

A txt file is created with the same name in the same location as the cqa files. The bat file is located in the C:\AB SCIEX\BioPharmaView\Data folder.

5. Open SCIEX OS and then click the **Analytics** tile.
6. Click **Process Method > New**.
7. On the Workspaces page, select the text file created in step 4. The default workflow is appropriate.
8. In the left panel, click **Components**.
9. Click **Import > Import components from a text file**.

The peptides associated with the **Quality Attributes** previously selected in the BioPharmaView™ Software are now available as components.

10. Create a processing method using the converted data. Refer to "Create a Processing Method" in the *System User Guide*.

Install the Software

Use the information in the following table to prepare for the upgrade to version 3.0.2. Previous versions of release notes can be downloaded from sciex.com/software-support/software-downloads. For information regarding workstation requirements, refer to the release notes for version 3.0 of the BioPharmaView™ Software.

Table 1-1 Installation Paths

Currently Installed Version	Prerequisites
BioPharmaView™ Software version 2.x	Read the release notes from version 3.0.1 and these release notes.
BioPharmaView™ Software version 3.0	Read the release notes from version 3.0.1 and these release notes.
BioPharmaView™ Software version 3.0.1	Read these release notes.

1. Log on to the computer as a user with Administrator privileges.
2. Download the **BioPharmaView-3.0.2.zip** file 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.

3. After the download is complete, right-click the **BioPharmaView-3.0.2.zip** file.
4. Click **Extract All** and then select a destination folder.
5. After the extraction is complete, navigate to the selected destination folder and then double-click the **setup.exe** file.
6. Follow the on-screen instructions to complete the installation.
7. Restart the computer.
8. Open the BioPharmaView™ Software.

For information about software licensing, refer to the release notes for version 3.0 of the BioPharmaView™ Software.

Remove the Software

1. Open **Control Panel**.
2. Select the BioPharmaView™ Software version 3.0.2.
3. Click **Uninstall**.

Contact Us

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

- [SCIEX University™](#)

SCIEX 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 SCIEX website at sciex.com or contact us in one of the following ways:

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

CyberSecurity

For the latest guidance on cybersecurity for SCIEX products, visit sciex.com/productsecurity.

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>.

The latest versions of the documentation are available on the SCIEX website, at sciex.com/customer-documents.

Release Notes

Note: To request a free, printed version of this document, contact sciex.com/contact-us.
