Biologics Explorer 3.1 Software Release Notes



Introduction

Thank you for using the Biologics Explorer software.

Read this document carefully for information about changes, new features, and resolved and known issues. The information in this document makes installation and use of the Biologics Explorer software easier.

The Biologics Explorer software supports the characterization of therapeutic protein candidates from these analysis approaches:

- Protein mapping that uses intact molecule measurements (TOF MS)
- Peptide mapping that uses data-dependent acquisition (DDA) measurements of enzymatically digested proteins (TOF MS/MS)
- Top-down/Middle-down protein sequencing by tandem mass spectrometric analysis of intact proteins that are fragmented in the mass spectrometer (TOF MS/MS)

The software can interpret data that is collected with both the Analyst TF and the SCIEX OS software.

The Biologics Explorer software can annotate data from the ZenoTOF 7600 system, from MS/MS measurements of both collisionally-activated dissociation (CAD) and electron-activated dissociation (EAD) fragmentation.

The Biologics Explorer software is also compatible with data from TripleTOF 6600 and X500B QTOF systems.

Related Documentation

Workflow guides are available in the software. These *Quick Guides* give suggestions and best practices for the workflows for a variety of supported applications.

In addition, contextual help is available throughout the software. To open contextual help topics in a web browser, click the ? icon.

Note: An internet connection is required to get access to these topics.

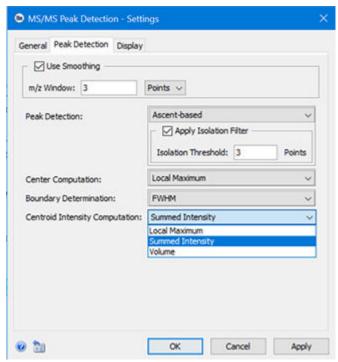
New Features in Version 3.1

• Intact Protein and Peptide Mapping: Sequential One-at-a-Time Processing: To give a result for each data file, the software can process a batch of data files in a sequential one-at-a-time queue. All data files can use the same FASTA format sequence file, or each data file

can use a different FASTA format sequence file. New template workflows are supplied for intact protein and peptide mapping analysis. For intact protein analysis, we recommend a batch size of up to 100 data files. For peptide mapping analysis, we recommend a batch size of up to 12 data files.

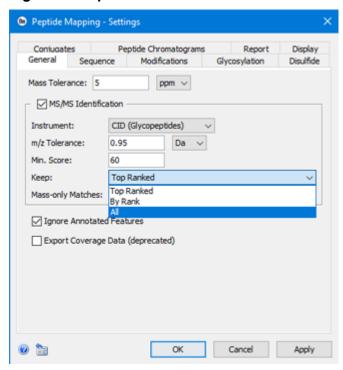
 Peptide Mapping: Peak Detection: In the peptide mapping workflow, a new option is available for the Centroid Intensity Computation field in the MS/MS Peak Detection -Settings dialog. The new option supplies another method to calculate the centroid mass intensity value.





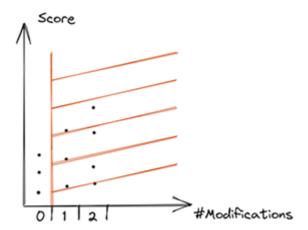
• Peptide Mapping: All Option for the Keep Filter for MS/MS Identification: When the Keep All filter is applied to peptide mapping MS/MS identifications, complex annotations are not ignored.

Figure 2 Keep Filter



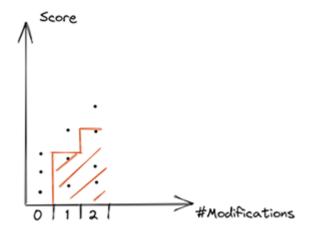
In earlier versions of the software, the filter showed only the annotations with the lowest complexity, even if a more complex annotation would have been identified with a better score. The following figure shows this behavior. Only annotations to the left of the line are kept. Annotations in the region with hash marks are ignored.

Figure 3 Before Version 3.1



This issue is now corrected, and the algorithm keeps more complex annotations with a higher score. The following figure shows the new behavior. Annotations above and to the left of the stepped line are kept. Annotations in the region with hash marks are ignored.

Figure 4 Version 3.1



- **Standardization of Terminology:** Terms in the software have been changed to terms that are used in the industry:
 - The y-axis of UV chromatograms has been changed to **Absorbance**.
 - The **Intensity** for UV peaks has been changed to **Total Absorbance**.
 - The Max. Intensity for UV peaks has been changed to Max. Absorbance.
 - The Intensity for MS peaks has been changed to Total Intensity.
 - The **Volume** for MS and UV peaks has been changed to **AUC** (area-under-curve).
 - The UV chromatogram panes and tabs have been changed as shown in the following figure.

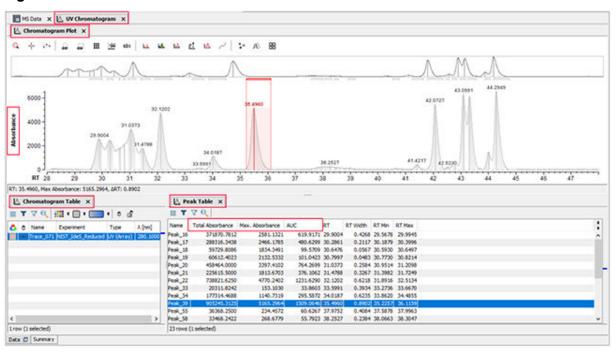


Figure 5 Pane Names

• **Peak Shading:** To more easily identify overlaid features in visualizations, such as chromatograms and mass spectra, users can click to apply shading to the peaks.

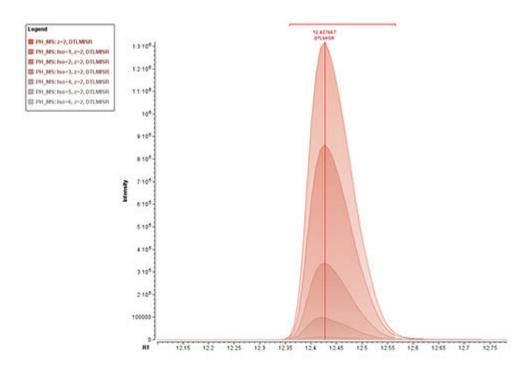


Figure 6 Peak Shading

Known Issues

• Peptide mapping batch processing is resource-intensive and makes temporary files on the C:\ drive. To free up disk space, close the software and then open it again between batches.

Installation

Requirements

Workstation Requirements

- SCIEX Workstation Plus computer with:
 - Xeon 8 core processor
 - 32 GB RAM
 - 2 × 2 TB SSD storage disks, C:\ for Biologics Explorer software installation path, and D:\ for disk cache

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 decreased performance.

Operating System Requirements

Windows 10, 64-bit, operating system

Internet Requirements

- Internet access
- Google Chrome browser

Install the Biologics Explorer Software

Prerequisites

- A Biologics Explorer license key is available. The license key, also known as an activation ID (AID), might be distributed on a printed activation certificate, or in an e-mail from SCIEX Now. If the license key is missing, then contact a SCIEX sales representative.
- 1. Log on to the computer as a Microsoft Windows user with Administrator privileges.
- 2. Download the required zip file from sciex.com/software-support/software-downloads.

Tip! To prevent possible installation issues, save the file to a location other than the computer desktop and then disconnect any external USB storage devices before the start of the installation.

- 3. After the download is complete, right-click the downloaded file and then click **Extract All**. By default, the files are extracted to the location where the zip file was saved.
- 4. Double-click biologics_explorer-3.1.1.exe. The SCIEX Biologics Explorer Setup window opens.
- 5. Follow the on-screen instructions to complete the installation. The installation wizard installs the Biologics Explorer software.

Note: When a prompt for the installation path is shown, use the default value, C:\.

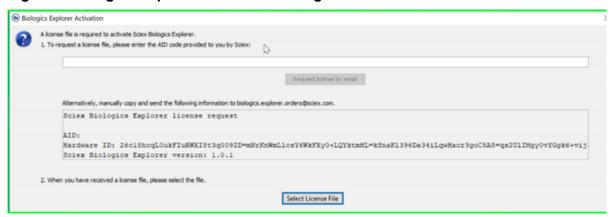
6. After the installation is completed, click **Finish**.

The installation wizard opens the Biologics Explorer software. The Biologics Explorer Activation dialog opens. Continue with the section: Activate the Software.

Activate the Software

1. If required, then open Biologics Explorer.

Figure 7 Biologics Explorer Activation Dialog



- 2. Type the license key in the appropriate field.
- 3. Click Request license by email.

Note: As an alternative, copy the contents of the text box into an e-mail, type Biologics Explorer License Request in the subject line, and then send the e-mail to biologics.explorer.orders@sciex.com.

The license file will be sent by e-mail in approximately one day.

- 4. Copy the license file to the computer.
- 5. Open Biologics Explorer and then click **Select License File**.
- Browse to and select the license file and then click Load license.
 The software is activated.

Install the Workflow Package

Note: Workflow templates are updated regularly. We recommend the use of the latest available version of a template, which is available through the Package Manager.

- 1. Open the Biologics Explorer software.
- 2. Click **Tools > Package Manager**.
 The list of available workflow packages is shown.

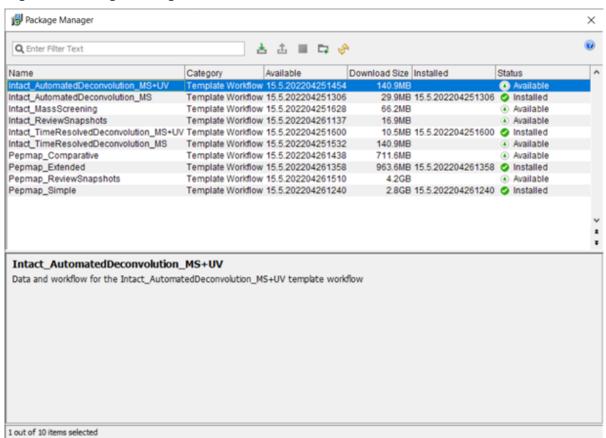
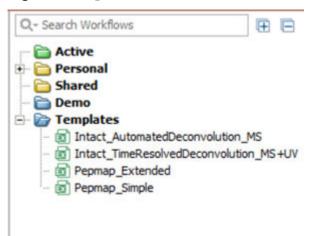


Figure 8 Package Manager Window

3. Click install package).

The downloaded workflow is now available in the Templates folder.

Figure 9 Templates Folder



Tip! To make and run customized workflows, refer to the Quick Start Guide.

Remove the Biologics Explorer Software

Prerequisites

- Remove any HotFixes.
- 1. Log on to the computer as a 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 SCIEX Biologics Explorer, and then click Uninstall.

The software is removed. User intervention is not required.

Note: The license file is not removed and can be used if the Biologics Explorer software is installed again.

Note: As an alternative, use the biologics_explorer Administration application (remove the software.



Frequently Asked Questions

The C:\ and D:\ drives contain folders for Biologics Explorer. What are these folders used for?

By default, the software is installed on the $C:\$ drive, and processed data is stored in the $C:\$ home folder. During processing, data is stored in the $D:\$ cache folder. To monitor resource consumption during processing, click **Tools > Resource Status**.

Can I install the software on a laptop that only has a C:\ drive?

For optimal performance in routine use, we recommend the use of the SCIEX Workstation Plus. Refer to the section: Workstation Requirements.

However, for the purposes of demonstration, training, and nonroutine usage, the software can be installed on a laptop with a single hard drive. The installation program automatically detects that the computer has a single hard drive and accommodates this configuration.

Can I install the software on a processing computer that does not meet the recommended requirements?

Yes. However, the software processing speed is best when the computer meets the specified requirements.

Do multiple users of the software require separate license files?

No. The license file is specific to the computer on which the software is installed.

My installation is now complete. How can I start my processing?

Select the workflow template that is applicable to the application, copy the template into a Personal folder, open the template, add data files and customize the parameters, and then save the workflow with a different name.

As an alternative, open the template in the Templates folder, add data files and customize the parameters, and then save the workflow with a different name.

How long does the installation usually take?

The installation and download of all workflow templates usually takes less than 30 minutes on the recommended computer.

We use the $D: \$ drive to store raw data files. Is there a minimum free disk space that we should keep on the $D: \$ drive?

We highly recommend that at least 250 GB of free disk space be available on the D: \ drive, to allow for efficient data post-processing in the Biologics Explorer software.

Can the software be installed on a drive other than the C:\ or D:\ drive?

No. We recommend that the software only be installed on these drives.

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Documentation

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

To see 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.

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