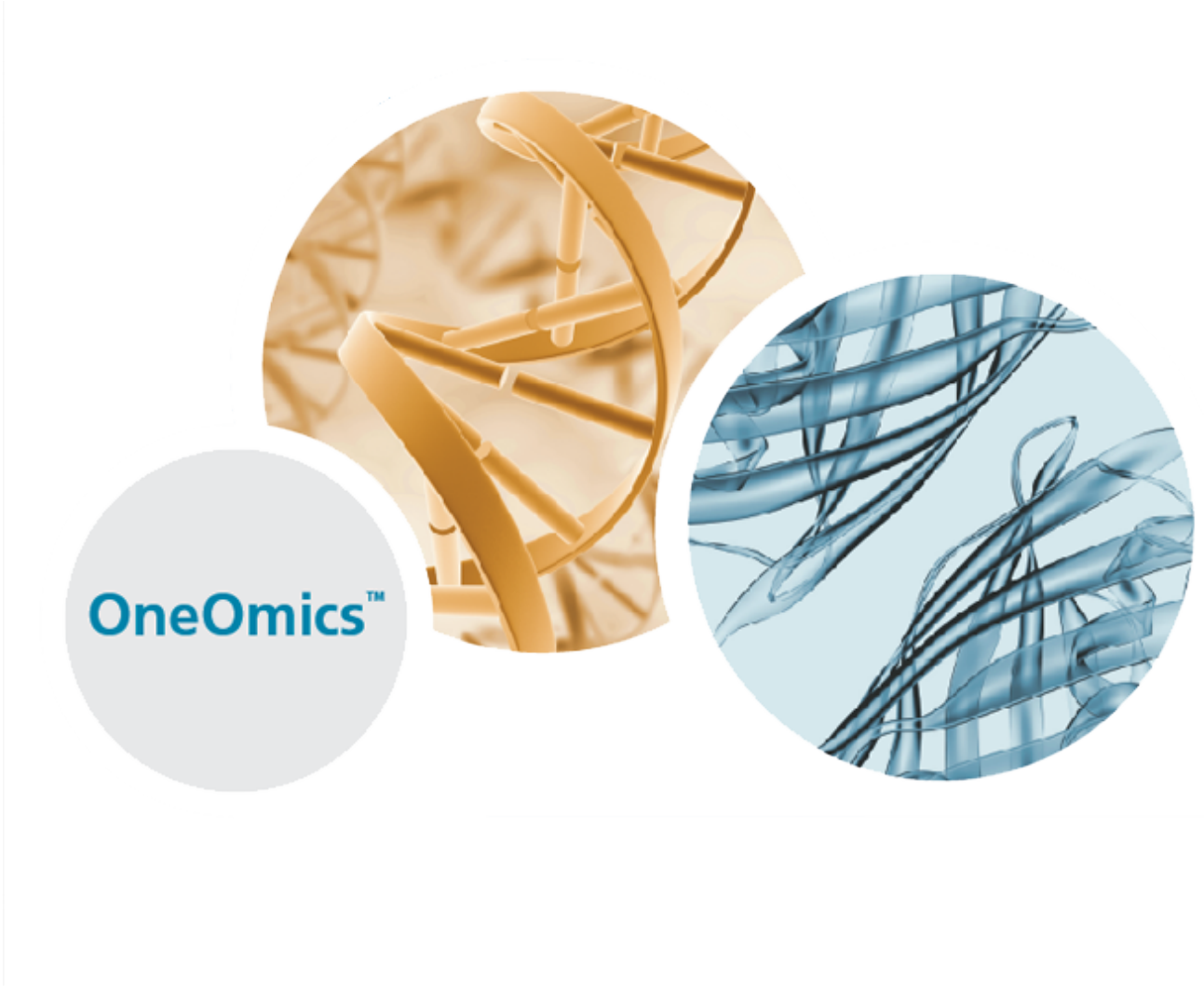
SCIEX

The Power of Precision

CloudConnect

User Guide



RUO-IDV-05-2054-D

December 2020

AB Sciex Pte. Ltd.
Blk33, #04-06 Marsiling Industrial Estate Road 3
Woodlands Central Industrial Estate, Singapore 739256

Contents

Contents

Introduction 1

CloudConnect for PeakView® Software 2.2 is a companion application installed within the PeakView® Software. It is used to migrate data to and results from a cloud storage solution supported by OneOmics™ Suite Powered by SCIEX Cloud. Supported cloud storage solutions include the Data Store, a SCIEX Cloud storage solution, and the Illumina BaseSpace Sequence Hub.

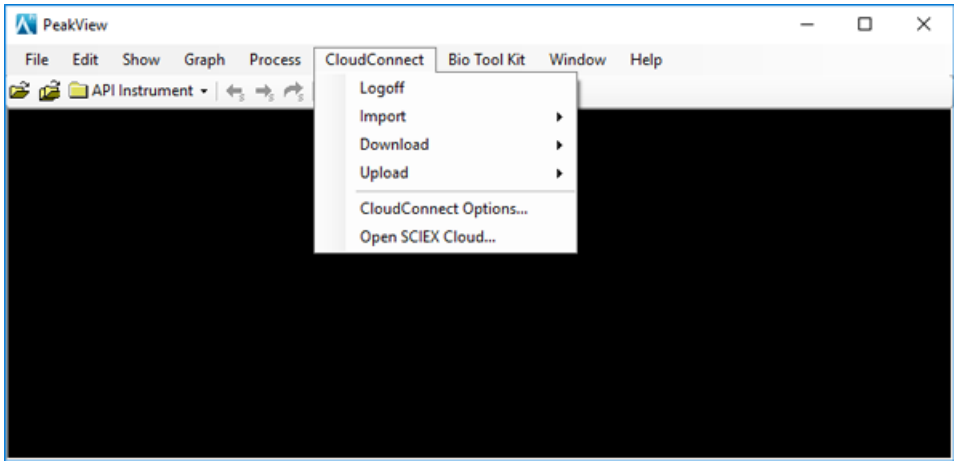
In addition, CloudConnect allows the user to perform the following tasks:

- Inspection of peak groups within SWATH® Acquisition data files processed by the Proteomics and Metabolomics apps in the OneOmics™ Suite
- Definition of retention time calibration peptides within an ion library for use in the Proteomics app in the OneOmics™ Suite

About the User Interface 2

After CloudConnect is installed, the application menu is available from the PeakView® Software menu bar. The **CloudConnect** menu manages all of the functionality of the application.

Figure 2-1 CloudConnect Main Menu

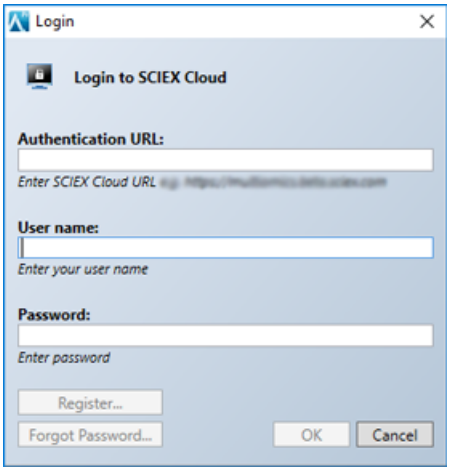


Log In to OneOmics™ Suite

Use this procedure to log in to user account in the OneOmics™ Suite Powered by SCIEX Cloud.

1. Click **CloudConnect > Login**.

Figure 2-2 Login Dialog



2. In the **Authentication URL** field, type **https://oneomics.sciexcloud.com**.

Note: This authentication URL is automatically filled in the next time that the user logs in.

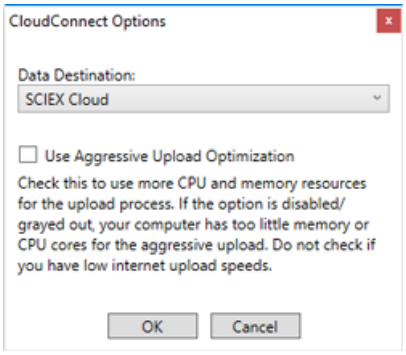
3. Type the **User name** and **Password** for the OneOmics™ Suite account.
4. Click **OK**.

Configure the Data Destination 3

Follow this procedure to configure the data storage option. Select whether to store data in the SCIEX Cloud Data Store or in the Illumina BaseSpace Sequence Hub.

1. Click **CloudConnect > CloudConnect Options**.

Figure 3-1 CloudConnect Options Dialog



2. For **Data Destination**, select one of the following options:
   - **SCIEX Cloud**: To use SCIEX Cloud, that is, the Data Store in OneOmics™ Suite, for data storage. Refer to SCIEX Cloud.
   - **BaseSpace**: To use the Illumina BaseSpace Sequence Hub for data storage. Refer to Illumina BaseSpace Sequence Hub.
3. (Optional) Select the **Use Aggressive Upload Optimization** check box.

   This option provides faster upload speeds, but uses more computer resources.

   Note: If the computer has only one logical core or a total memory of less than or equal to three GB, then the check box cannot be selected.

   Note: This option is not user-specific. The selection persists until the **User Aggressive Upload Optimization** check box is cleared. When the check box is cleared, the upload size reverts to 5 MB, but the maximum number of threads used for uploading remains at 20 until the CloudConnect Uploader service is restarted **(Start > Run > Services.msc)**.
4. Click **OK**.

SCIEX Cloud 4

Data Files

Users can upload data files. Files can be uploaded from a network drive or from any type of removable media, such as a USB drive. Files can also be uploaded from the active session in the PeakView® Software.

Note: When uploading from removable media, make sure that the media is accessible until the upload is complete.

Users can upload files to a shared folder if they have the required read and write access to the target folder.

Note: Before uploading data files, configure the data storage option. Refer to Configure the Data Destination.

Upload Data Files to the SCIEX Cloud Data Store

Use this procedure to upload data files, such as wiff, fasta, ion library, and RNA-Seq files, to the Data Store.

This feature is not available if the CloudConnect Uploader Service, which is installed with CloudConnect, is not responding. Refer to Troubleshooting.

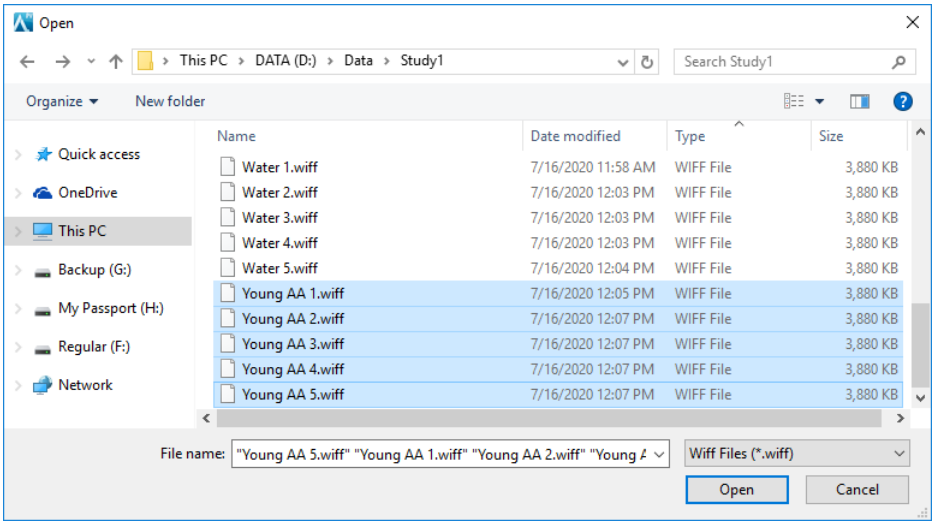
Tip! To organize files and folders, follow these guidelines:

- Before uploading files, plan how they will be organized. Files and folders cannot be moved or renamed after they are uploaded.
- Make sure that the file names of the files being uploaded are valid. File names can contain alphanumeric characters, plus the following special characters: @ ^ . ( ) - _
- Limit the number of files in a folder to less than 1,000, to avoid long load and search times.
- If the group contains more than one user, then create a separate folder for each user.
- In the folder for each user, create a folder to store uploads and results.

1. Click **CloudConnect > Upload > Upload files**.

Tip! If the user is not logged in to OneOmics™ Suite, then this menu command is not available. Complete steps 2 to 4 of Log In to OneOmics™ Suite and then return to this procedure.

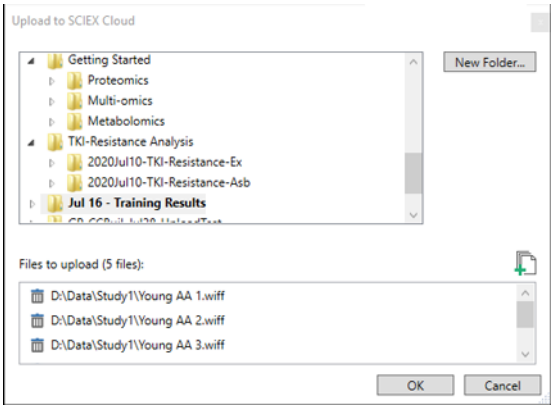
Figure 4-1 Open Dialog



Note: By default, files of type **Wiff Files (*.wiff)** are shown. To upload other file types, select **All files (*.*)**.

2. Browse to and select the files to be uploaded, and then click **Open**.

Figure 4-2 Upload to SCIEX Cloud Dialog



3. Select the destination folder, and then click **OK**.

> **Tip!** To create a new folder, click **New Folder**. Folder names can contain alphanumeric characters and the following special characters: @ ^ ( ) - _ = [ ] ` ~ $ % ; ' , !

The Upload Queue And Status dialog opens, showing the progress of the upload. Refer to Show the Upload Queue.

4. Click **OK**.

The Upload Queue And Status dialog closes. The uploads continue in the background.

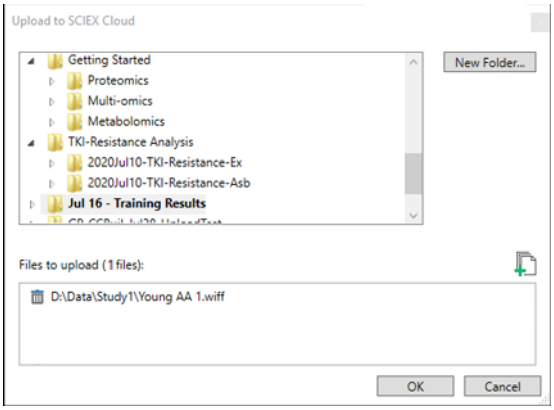
Upload the Active Data Files to the SCIEX Cloud Data Store

Prerequisites
• Open samples in the PeakView® Software. Refer to the *PeakView® Reference Guide*.

1. Click **CloudConnect > Upload > Upload Active Wiff files**.

> **Tip!** If the user is not logged in to OneOmics™ Suite, then this menu command is not available. Complete steps 2 to 4 of Log In to OneOmics™ Suite and then return to this procedure.

Figure 4-3 Upload to SCIEX Cloud Dialog



2. Select the destination folder and the **File to upload**, and then click **OK**.

> **Tip!** To create a new folder, click **New Folder**. Folder names can contain alphanumeric characters and the following special characters: @ ^ ( ) - _ = [ ] ` ~ $ % ; ' , !

3. (Optional) Click the **Remove from the list** icon to the left of the file name in the **Files to upload** list to remove a file from the upload job.
4. (Optional) Click the **Add files to upload** icon to the right of the **Files to upload** list to add extra files, such as ion library files, to the upload job.
5. Click **OK**.

   The Upload Queue And Status dialog opens, showing the progress of the upload. Refer to Show the Upload Queue.
6. Click **OK**.

   The Upload Queue And Status dialog closes. The upload continues in the background.

Results Files

Note: Before working with results files, configure the data storage option. Refer to Configure the Data Destination.

Download a Session File

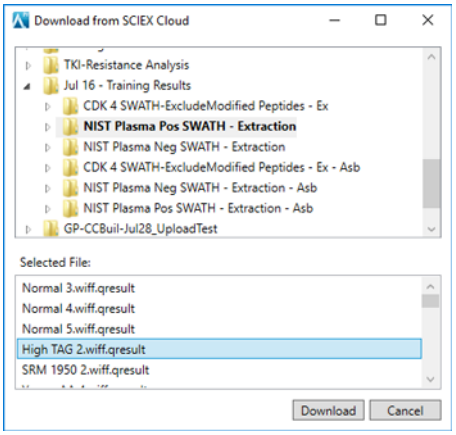
Follow this procedure to download the extraction results for a SWATH® Acquisition from the Proteomics or Metabolomics apps.

1. Click **CloudConnect > Download > Load Session**.

   Tip! If the user is not logged in to OneOmics™ Suite, then this menu command is not available. Complete steps 2 to 4 of Log In to OneOmics™ Suite and then return to this procedure.

   Note: The menu item is not available if a session is already open in the PeakView® Software.

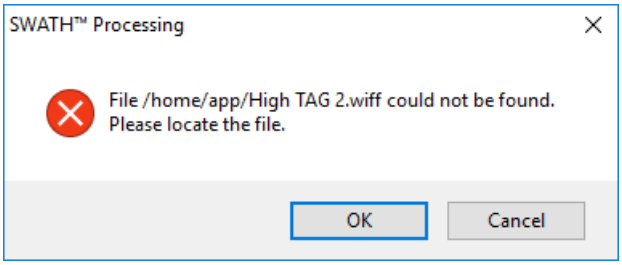
Figure 4-4 Download from SCIEX Cloud Dialog



2. Browse to and select the results file to be downloaded, and then click **Download**.

   The session file is downloaded to a temporary location on the local computer and then opened in CloudConnect. The software prompts the user to associate a data (wiff) file with the results file.

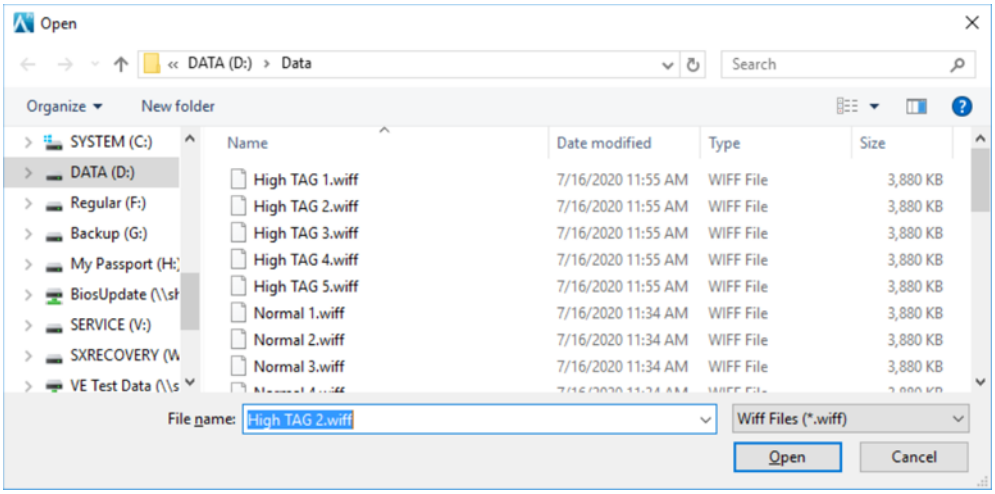
Figure 4-5 SWATH™ Processing Dialog



Note: If the data files are not available, then download them to the local computer from the Data Store.

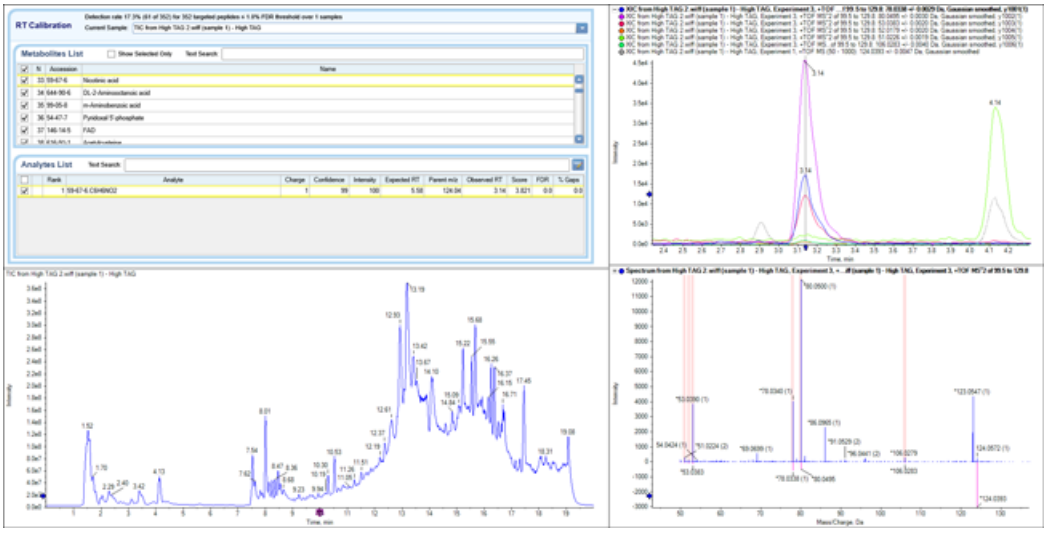
3. Click **OK**.

Figure 4-6 Open Dialog



4. Browse to and select the required data file, and then click **Open**.

Figure 4-7 Session File



The user can interact with the tabulated results to show the chromatographic and spectral data.

Note: For metabolomics results, metabolite information is shown. For proteomics results, protein and peptide information is shown.

Ion Libraries

CloudConnect can download and open large protein or peptide ion libraries. These libraries contain protein, peptide, and peptide fragment information. The libraries can be revised and uploaded for use in OneOmics™ Suite.

Note: Ion libraries can also be extracted from results files, edited, and then uploaded for use in OneOmics™ Suite.

Note: Ion library functionality applies to protein results only.

Note: Before working with ion libraries, configure the data storage option. Refer to Configure the Data Destination.

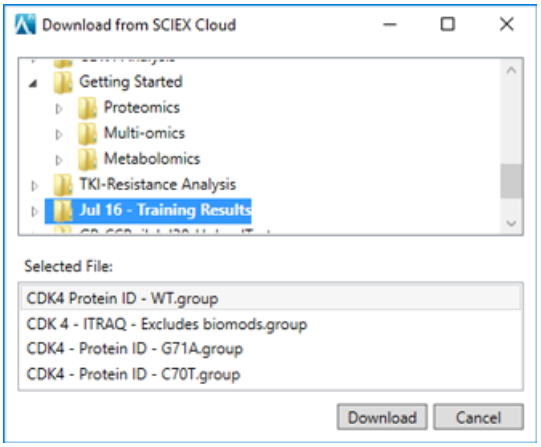
View and Edit an Ion Library

1. Click **CloudConnect > Download > Load Ion Library**.

   Note: The menu item is not available if a session is already open in the PeakView® Software.

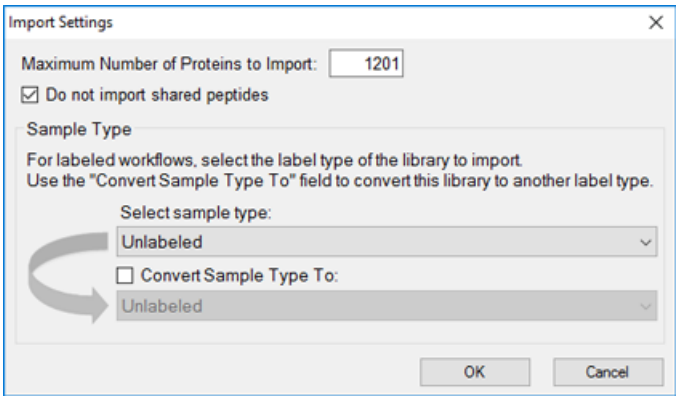
   Tip! If the user is not logged in to OneOmics™ Suite, then this menu command is not available. Complete steps 2 to 4 of Log In to OneOmics™ Suite and then return to this procedure.

Figure 4-8 Download from SCIEX Cloud Dialog



2. Browse to and select the destination folder and a library file (group or txt), and then click **Download**.

Figure 4-9 Import Settings Dialog



Note: For txt libraries, the **Maximum Number of Proteins to Import** field is unavailable. This field is only available for ProteinPilot™ Software group files.

3. Specify the import settings.

Table 4-1 Import Settings

Field	Description
Maximum Number of Proteins to Import	Specify the maximum number of proteins to be imported.
Do not import shared peptides	Select to exclude shared peptides from the import.
Sample Type	
Note: Labeled workflows are not available for OneOmics™ Suite.	

4. Click **OK**.

   After the library is loaded, the software prompts for the data files.

5. If the SWATH® Acquisition data files are available on the computer, browse to and select them, and then click **OK**. Otherwise, click **Cancel**.

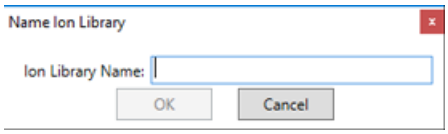
If the data files are available, then the user can view the alignment of chromatographic peaks between the data files and the ion library. If the data files are not available, then the user can still view the library file, but without the associated sample data.

6. (Optional) Make changes to the ion library, as required:
   - Exclude a protein by clearing the check box beside the protein.
   - Exclude a peptide by clearing the check box beside the peptide.
   - Limit the number of peptides shown for each protein in the Processing Settings dialog.

     Tip! To open this dialog, click **Processing Settings**.

   - Increase or decrease the number of transitions shown for each peptide in the Processing Settings dialog.
   - Build a retention time calibration protein by selecting each peptide to be used as a calibration peptide and then clicking (**Add RT-Cal**). Refer to Add Retention Time Calibration Peptides to the Ion Library.
7. (Optional) If the library has been changed, then upload it by following these steps:
   a. Click **Upload**.

   Figure 4-10 Name Ion Library Dialog

   b. Specify a name for the library, and then click **OK**.
   c. Browse to and select the destination folder, and then click **OK**.

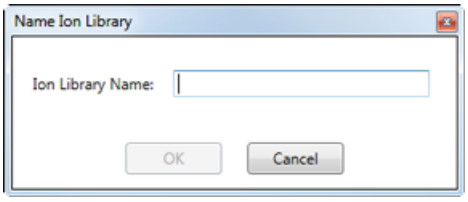
      The Upload Queue And Status dialog opens. Refer to Show the Upload Queue.
   d. Click **OK**.

Upload the Current Session Ion Library File to SCIEX Cloud

Prerequisites
• Open a local or imported session file in the PeakView® Software. Refer to *Download a Session File* or Load a Local Session.

1. Click the **Upload** button.

Figure 4-11 Name Ion Library Dialog



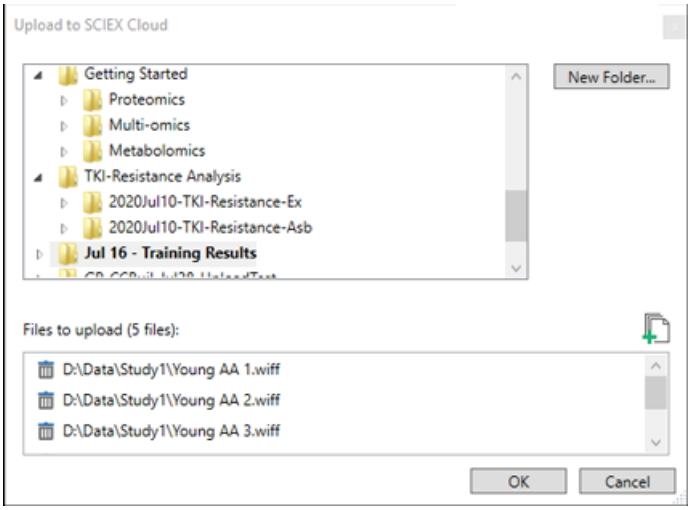
2. Type the name of the library in the **Ion Library Name** field.

   This name is used as the library name in the SCIEX Cloud.

> **Note:** Only use legal characters. Otherwise, the **OK** button is not available. A txt extension is automatically added by the system if the extension is not provided.

3. Click **OK**.

Figure 4-12 Upload to SCIEX Cloud Dialog



4. Select the destination folder, and then click **OK**.

> **Tip!** To create a new folder, click **New Folder**. Folder names can contain alphanumeric characters and the following special characters: @ ^ ( ) - _ = [ ] ` ~ $ % ; ' , !

The Upload Queue And Status dialog opens, showing the progress of the upload. Refer to Show the Upload Queue.

5. Click **OK**.

The Upload Queue And Status dialog closes. The uploads continue in the background.

Add Retention Time Calibration Peptides to the Ion Library

CloudConnect can download and open large protein or peptide ion libraries. These libraries contain protein, peptide, and peptide fragment information. Each peptide has an associated expected retention time. Because of variations in the LC system configuration and chromatographic gradient lengths, the same peptide might be detected at different retention times. During the cloud processing, the calibration peptides are used to correct the retention times of all other peptides of interest. CloudConnect allows the user to create a calibration protein by adding calibration peptides. If the **Use RT calibration protein** option is selected on the Extract page in the Proteomics app, then the Extractor automatically recalibrates the data when the calibration peptides are found.

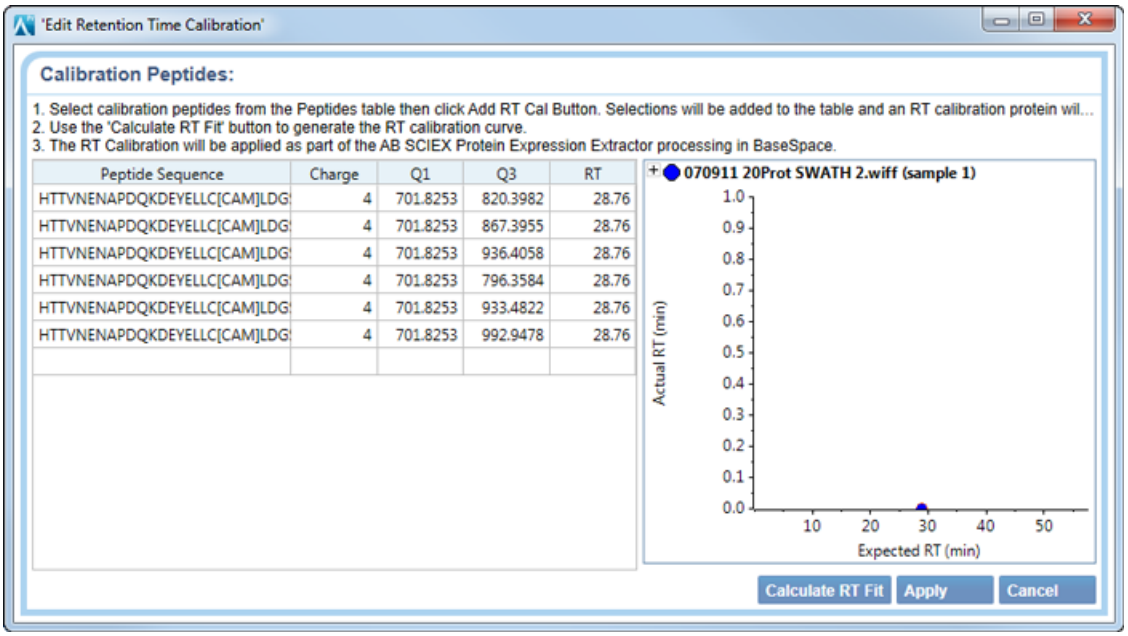
1. In the Peptides table, select each peptide to be used for calibration, and then click  (**Add RT-Cal**).

   A Retention time calibration protein is added as the first entry in the Protein Table. The peptides of this protein are the chosen peptide calibrants.

2. To view and generate the calibration fit, click  (**Edit-RT Cal**).

   The 'Edit Retention Time Calibration' dialog opens. The peptides selected in step 1 are shown in the Calibration Peptides table.

Figure 4-13 "Edit Retention Time Calibration' Dialog



3. To make sure that the peptides are distributed across the gradient, ideally 2 every 10 minutes, view the graph.
4. To generate the retention time calibration curve, click **Calculate RT Fit**.
5. (Optional) To remove a peptide from the calibration process, select a peptide in the table on the left and then press **Delete**.
6. Click **Apply** to update and save the retention time calibration list.

   This list is used in the Protein Expression Extractor application to calibrate the ion library.

Tip! Click the + symbol in the top left corner of the Calibration Peptides graph to expand the list of SWATH® Acquisition samples and review the fit for each sample (each sample has a unique color).

Illumina BaseSpace Sequence Hub 5

Data Files

Users can upload data files. Files can be uploaded from a network drive or from any type of removable media, such as a USB drive. Files can also be uploaded from the active session in the PeakView® Software.

Note: When uploading from removable media, make sure that the media is accessible until the upload is complete.

Users can upload files to a shared folder if they have the required read and write access to the target folder.

Note: Before uploading data files, configure the data storage option. Refer to Configure the Data Destination.

Upload Data Files to BaseSpace

This feature is not available when the CloudConnect Uploader Service, installed with CloudConnect, is not available or not responding. Refer to Troubleshooting.

Note: Make sure that the file names of the files being uploaded are valid. File names can contain alphanumeric characters, plus the following special characters: @ ^ . ( ) - _

1. Click **CloudConnect > Upload > Upload files**.

   Tip! If the user is not logged in to OneOmics™ Suite, then this menu command is not available. Complete steps 2 to 4 of Log In to OneOmics™ Suite and then return to this procedure.

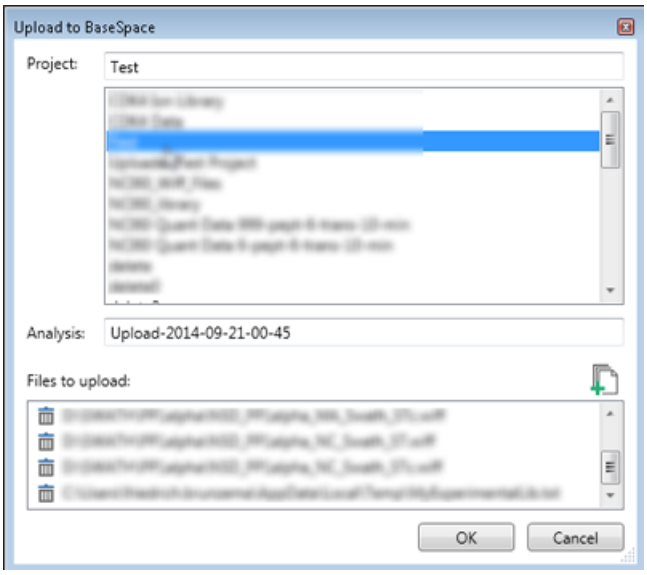
   The Open dialog opens.

2. Browse to and then select the file to be uploaded.

Note: By default, files of type **Wiff Files (*.wiff)** are shown. To upload other file types, select **All files (*.*)**.

3. Click **Open**.

Figure 5-1 Upload to BaseSpace Dialog



4. Select an existing project from the **Project** list or type a name in the **Project** field to create a project.

Tip! Project names can contain alphanumeric characters and the following special characters: @ ^ ( ) - _

If a new project name is provided, then the application creates the project in BaseSpace.

5. (Optional) Type a name for the session in the **Analysis** field.

A default name is provided.

Tip! Analysis names can contain alphanumeric characters and the following special characters: @ ^ ( ) - _

If a new name is provided, then the application adds this name to BaseSpace.

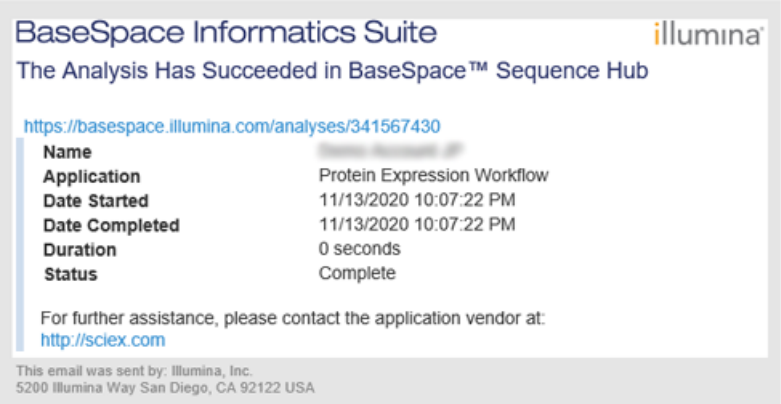
6. Click **OK**.

The Upload Queue And Status dialog opens, showing the progress of the upload. Refer to Show the Upload Queue.

7. Click **OK** to close the Upload Queue And Status dialog.

Note: When the upload is complete, an e-mail is received from BaseSpace, indicating that the task has been completed.

Figure 5-2 BaseSpace E-mail



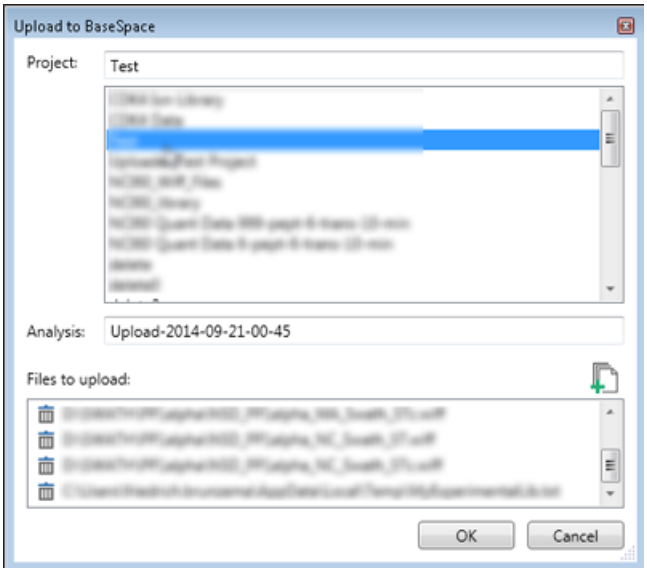
Upload Active Data Files to BaseSpace

Prerequisites
• Open samples in the PeakView® Software. Refer to the *PeakView® Reference Guide*.

1. Click **CloudConnect > Upload > Upload Active Wiff files**.

Tip! If the user is not logged in to OneOmics™ Suite, then this menu command is not available. Complete steps 2 to 4 of Log In to OneOmics™ Suite and then return to this procedure.

Figure 5-3 Upload to BaseSpace Dialog



2. Select an existing project from the **Project** list or type a name in the **Project** field to create a project.

   Tip! Project names can contain alphanumeric characters and the following special characters: @ ^ ( ) - _

   If a new project name is provided, then the application creates the project in BaseSpace.

3. (Optional) Type a name for the session in the **Analysis** field.

   A default name is provided.

   Tip! Analysis names can contain alphanumeric characters and the following special characters: @ ^ ( ) - _

   If a new name is provided, then the application adds this name to BaseSpace.

4. (Optional) Click the **Remove from the list** icon to the left of the file name in the **Files to upload** list to remove a file from the upload job.

5. (Optional) Click the **Add files to upload** icon to the right of the **Files to upload** list to add extra files, such as ion library files, to the upload job.

6. Click **OK**.

The Upload Queue And Status dialog opens, showing the progress of the upload. Refer to Show the Upload Queue.

7. Click **OK** to close the Upload Queue And Status dialog.

Note: When the upload is complete, an e-mail is received from BaseSpace, indicating that the task has been completed.

Results Files

Note: Before working with results files, configure the data storage option. Refer to Configure the Data Destination.

Download a Session File

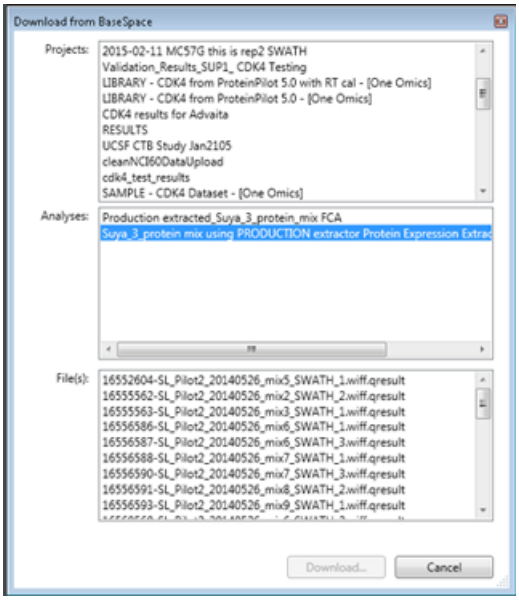
Follow this procedure to download the extraction results for a SWATH® Acquisition from the Proteomics or Metabolomics apps.

1. Click **CloudConnect > Download > Load Session**.

Tip! If the user is not logged in to OneOmics™ Suite, then this menu command is not available. Complete steps 2 to 4 of Log In to OneOmics™ Suite and then return to this procedure.

Note: The menu item is not available if a session is already open in the PeakView® Software.

Figure 5-4 Download from BaseSpace Dialog

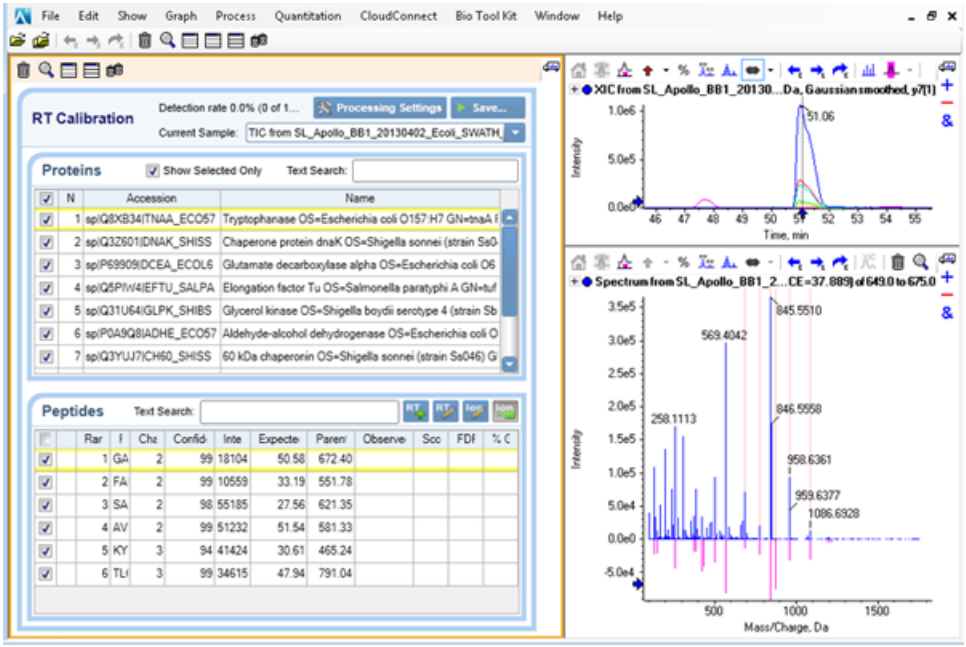


2. Select a project, session (Analyses) and a qresult session file, and then click **Download**.

   The session file is downloaded to a temporary location on the local computer and is then opened in the CloudConnect.

> **Note:** While opening the session file, the system might prompt the user to re-associate the wiff data files with the session. If the wiff files are not available, then they must be downloaded to the local computer using the BaseSpace web site.

Figure 5-5 Session File



Ion Libraries

CloudConnect can download and open large protein or peptide ion libraries. These libraries contain protein, peptide, and peptide fragment information. The libraries can be revised and uploaded for use in OneOmics™ Suite.

Note: Ion libraries can also be extracted from results files, edited, and then uploaded for use in OneOmics™ Suite.

Note: Ion library functionality applies to protein results only.

Note: Before working with ion libraries, configure the data storage option. Refer to Configure the Data Destination.

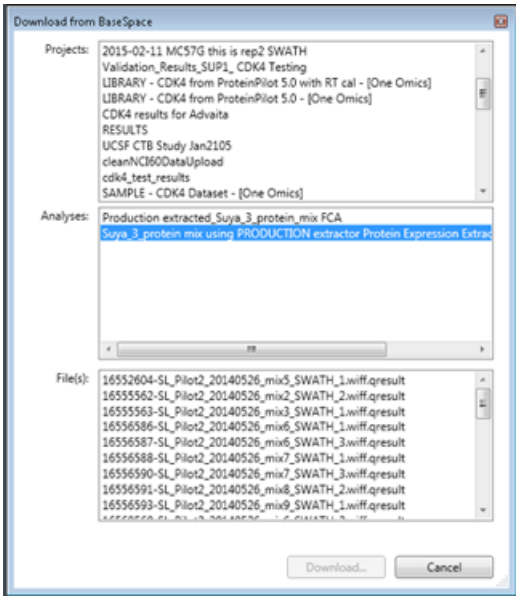
View and Edit an Ion Library

1. Click **CloudConnect > Download > Load Ion Library**.

Note: The menu item is not available if a session is already open in the PeakView® Software.

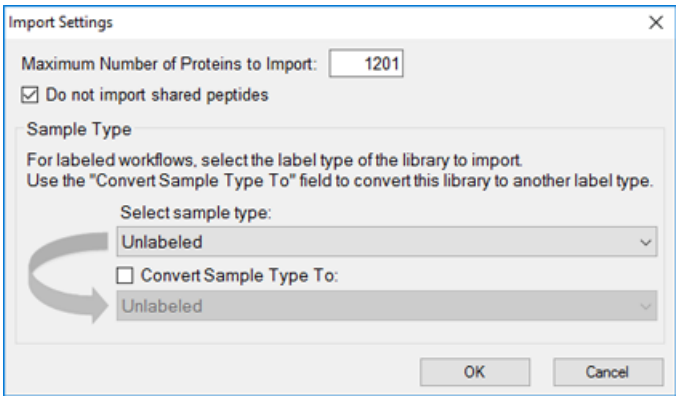
Tip! If the user is not logged in to OneOmics™ Suite, then this menu command is not available. Complete steps 2 to 4 of Log In to OneOmics™ Suite and then return to this procedure.

Figure 5-6 Download from BaseSpace Dialog



2. Select a project, session (Analyses), and a library file (group or txt), and then click **Download**.

Figure 5-7 Import Settings Dialog



Note: For txt libraries, the **Maximum Number of Proteins to Import** field is unavailable. This field is only available for ProteinPilot™ Software group files.

3. Specify the import settings.

Table 5-1 Import Settings

Field	Description
Maximum Number of Proteins to Import	Specify the maximum number of proteins to be imported.
Do not import shared peptides	Select to exclude shared peptides from the import.
Sample Type **Note:** Labeled workflows are not available for OneOmics™ Suite.	

4. Click **OK**.

   After the library is loaded, the software prompts for the data files.

5. If the SWATH® Acquisition data files are available on the computer, browse to and select them, and then click **OK**. Otherwise, click **Cancel**.

   If the data files are available, then the user can view the alignment of chromatographic peaks between the data files and the ion library. If the data files are not available, then the user can still view the library file, but without the associated sample data.

6. (Optional) Make changes to the ion library, as required:
   - Exclude a protein by clearing the check box beside the protein.
   - Exclude a peptide by clearing the check box beside the peptide.
   - Limit the number of peptides shown for each protein in the Processing Settings dialog.

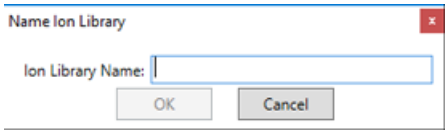
     Tip! To open this dialog, click **Processing Settings**.

   - Increase or decrease the number of transitions shown for each peptide in the Processing Settings dialog.

- Build a retention time calibration protein by selecting each peptide to be used as a calibration peptide and then clicking  (**Add RT-Cal**). Refer to Add Retention Time Calibration Peptides to the Ion Library.

7. (Optional) If the library has been changed, then upload it by following these steps:
   a. Click **Upload**.

Figure 5-8 Name Ion Library Dialog



   b. Specify a name for the library, and then click **OK**.
   c. Browse to and select the destination folder, and then click **OK**.

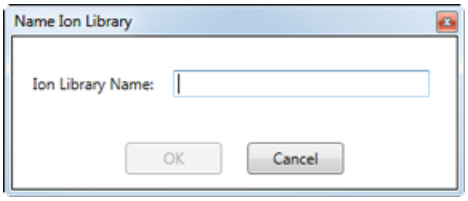
      The Upload Queue And Status dialog opens. Refer to Show the Upload Queue.
   d. Click **OK**.

Upload the Current Session Ion Library File to BaseSpace

Prerequisites
• Open a local or imported session file in the PeakView® Software. Refer to Download a Session File or Load a Local Session.

1. Click the **Upload** button.

Figure 5-9 Name Ion Library Dialog



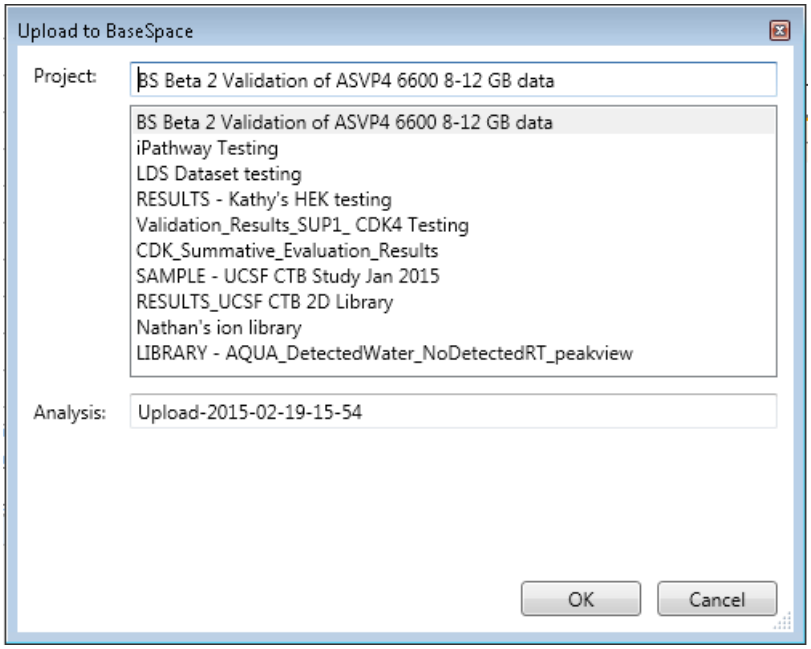
2. Type the name of the library in the **Ion Library Name** field.

   This name is used as the library name in BaseSpace.

> **Note:** Only use legal characters. Otherwise, the **OK** button is not available. A txt extension is automatically added by the system if the extension is not provided.

3. Click **OK**.

Figure 5-10 Upload to BaseSpace Dialog



4. Select an existing project from the **Project** list or type a name in the **Project** field to create a project.

> **Tip!** Project names can contain alphanumeric characters and the following special characters: @ ^ ( ) - _

If a new project name is provided, then the application creates the project in BaseSpace.

5. (Optional) Type a name for the session in the **Analysis** field.

   A default name is provided.

> **Tip!** Analysis names can contain alphanumeric characters and the following special characters: @ ^ ( ) - _

If a new name is provided, then the application adds this name to BaseSpace.

6. Click **OK**.

   The Upload Queue And Status dialog opens, showing the progress of the upload. Refer to Show the Upload Queue.

7. Click **OK** to close the Upload Queue And Status dialog.

Note: When the upload is complete, an e-mail is received from BaseSpace, indicating that the task has been completed.

Load a Local Session 6

Use this procedure to open a SWATH® Acquisition session file that was saved on the local computer.

1. Click **CloudConnect > Import > Load Session (local)**.

Tip! If the user is not logged in to OneOmics™ Suite, then this menu command is not available. Complete steps 2 to 4 of Log In to OneOmics™ Suite and then return to this procedure.

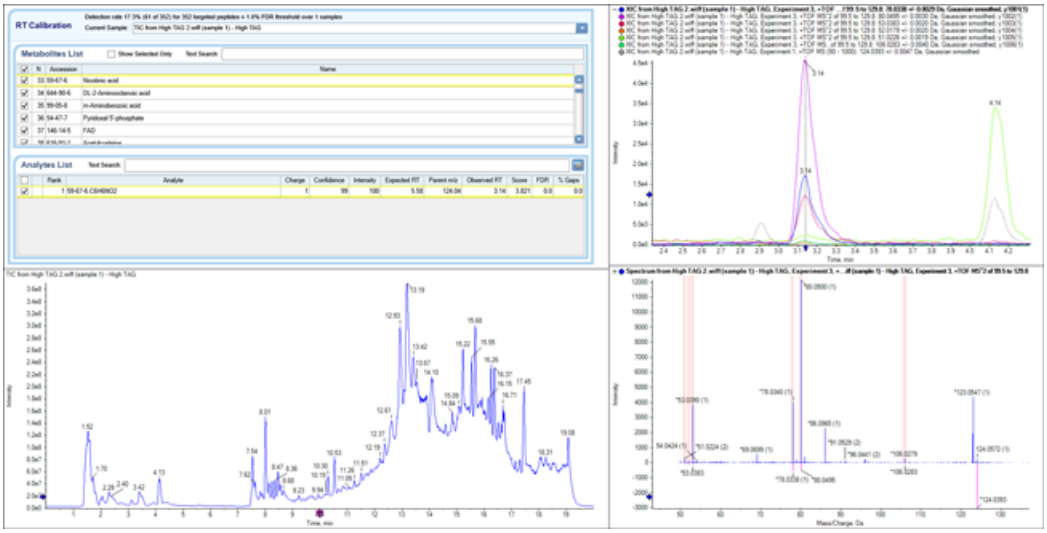
Note: The menu item is not available if a session is already open in the PeakView® Software.

The Load Session dialog opens.

2. Browse to and select the required file, and then click **Open**.

The selected session opens in CloudConnect.

Figure 6-1 Loaded Local Session



Load a Local Ion Library 7

1. Click **CloudConnect > Import > Load Ion Library (local).**

Tip! If the user is not logged in to OneOmics™ Suite, then this menu command is not available. Complete steps 2 to 4 of Log In to OneOmics™ Suite and then return to this procedure.

Note: The menu item is not available if a session is already open in the PeakView® Software.

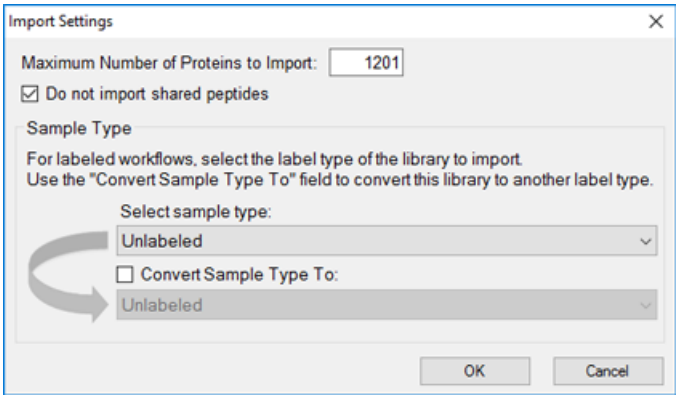
The Import Ion Library dialog opens.

2. Browse to and select the ion library file, and then click **Open**.

Tip! By default, the file type is set to group. To open a txt file, change the file type to txt.

The Import Settings dialog opens.

Figure 7-1 Import Settings Dialog



3. Specify the import settings, and then click **OK**.
4. Click **OK**.

   After the library is loaded, the software prompts for the data files.
5. If the SWATH® Acquisition data files are available on the computer, browse to and select them, and then click **OK**. Otherwise, click **Cancel**.

If the data files are available, then the user can view the alignment of chromatographic peaks between the data files and the ion library.

Show the Upload Queue 8

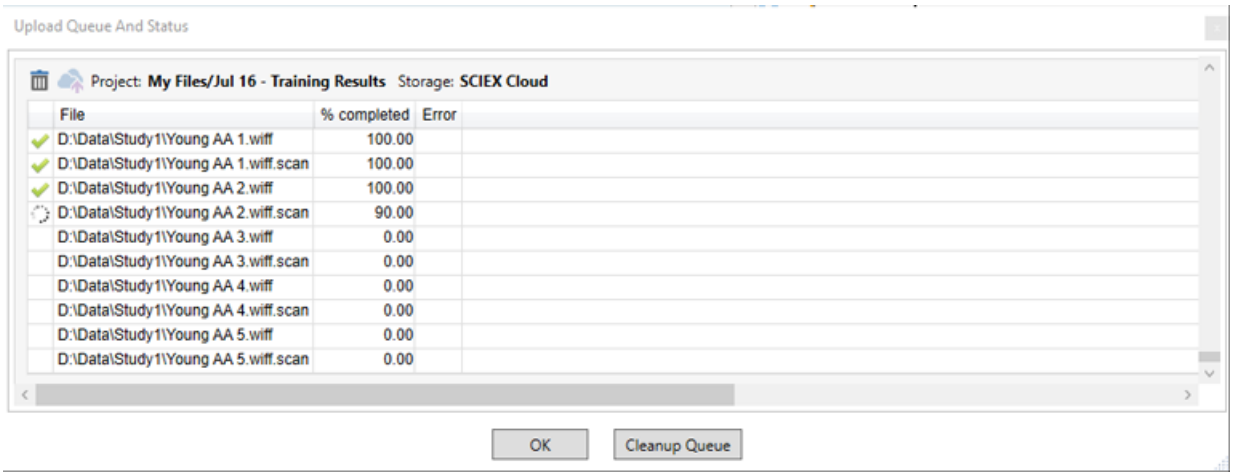
After the user submits a job for upload, the upload progress is shown on the Upload Queue and Status dialog. Large jobs can take up to 45 seconds to be shown in the dialog.

Submitted jobs are uploaded in the background. The PeakView® Software need not remain open. Some fault tolerance has been built into the CloudConnect Uploader Service so that it attempts a restart of the upload jobs if the computer is restarted.

1. Click **CloudConnect > Upload > Show Upload Queue and Status.**

   On the Upload Queue And Status dialog, completed jobs are shown with a check mark, and in-process jobs are shown with a progress circle to the left of the project name.

Figure 8-1 Upload Queue And Status Dialog



   Users can stop an upload or remove the upload history. Refer to Stop an Upload and Clean Up the Upload Queue.

2. Click **OK** to close the dialog.

Stop an Upload

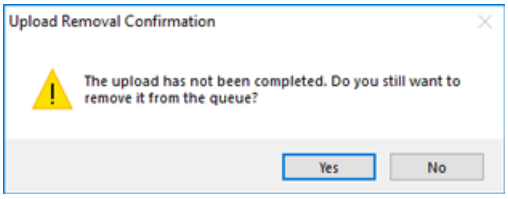
When an upload is stopped, all of the information included in the job is removed.

1. Click **CloudConnect > Upload > Show Upload Queue and Status**.

   The Upload Queue And Status dialog opens.

2. Select the job to be stopped, and then click (**Remove from the queue**).

Figure 8-2 Upload Removal Confirmation Dialog



3. Click **Yes** to stop the job.

Clean Up the Upload Queue

1. Click **CloudConnect > Upload > Show Upload Queue and Status**.

   The Upload Queue And Status dialog opens.

2. To remove selected jobs from the queue, select the jobs, and then click (**Remove from the queue**).
3. To remove all completed jobs from the queue, click **Cleanup Queue**.

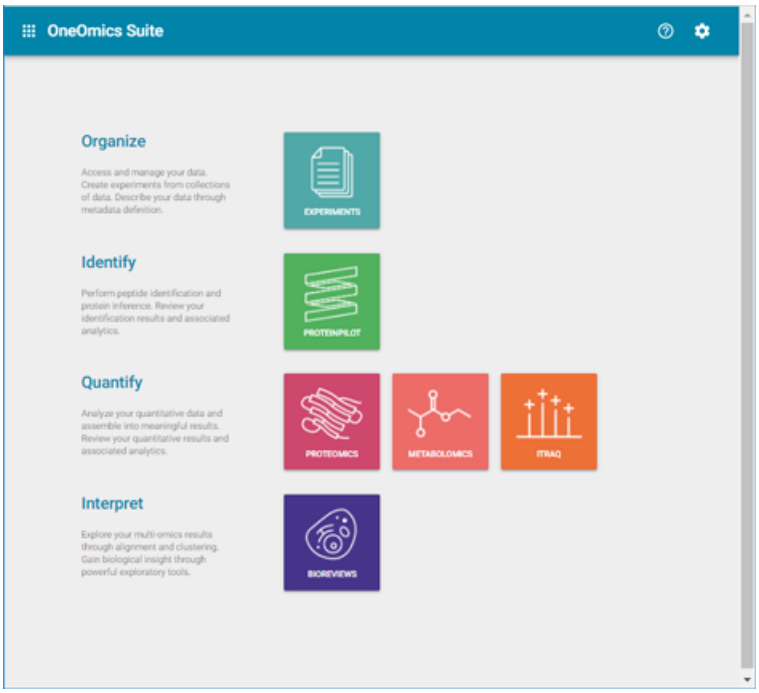
Open OneOmics™ Suite 9

- Click **CloudConnect > Open SCIEX Cloud**.

  OneOmics™ Suite opens in the default browser.

  Note: OneOmics™ Suite requires Google Chrome, so we recommend that Google Chrome be configured as the default browser.

Figure 9-1 OneOmics™ Suite



For information about using OneOmics™ Suite, refer to the *Release Notes*.

Troubleshooting 10

Symptom	Corrective Action
CloudConnect upload and options commands are not available.	Make sure that the **Status** of the CloudConnect Uploader Service is **Started** (**Start > Run > Servicesmsc**).

Files cannot be uploaded. The error message, *Unable to connect to the remote server*, might be received.	• Make sure that the **Status** of the CloudConnect Uploader Service is **Started** (**Start > Run > Servicesmsc**).
	• If the issue persists, then restart the service.
	• If the issue persists, then send the application log files to SCIEX Support:
	  • C:\ProgramData\AB SCIEX\CloudConnectUploader\log\CloudConnectLog.log
	  • C:\ProgramData\AB SCIEX\CloudConnectPlugin\CloudConnectPlugin.log
	Note: If the ProgramData folder is not visible in File Explorer, then set the View options for File Explorer to show **Hidden Items**.

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 OneOmics™ Suite User community

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.

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