

CloudConnect 1.8 Release Notes

Introduction

CloudConnect for PeakView software 2.2 is a companion application installed within the PeakView software. It is used to migrate data to and from a cloud storage solution supported by the OneOmics suite. 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

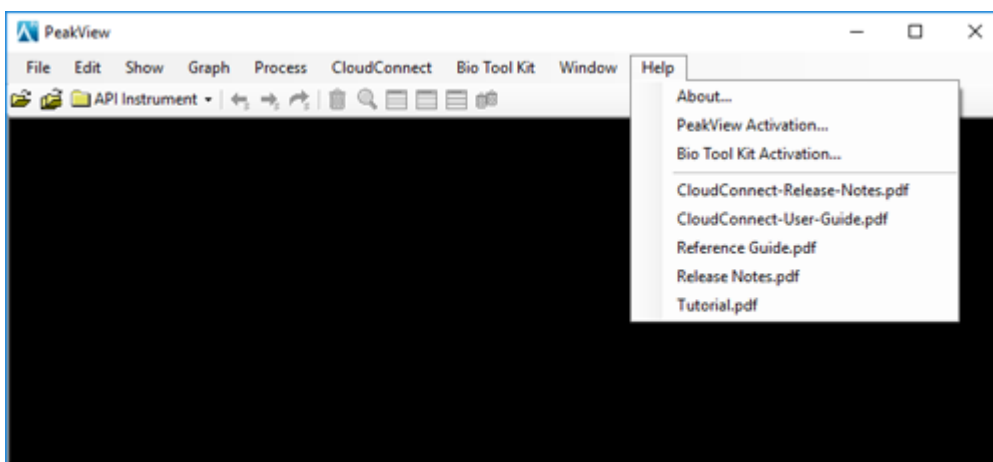
Get Help

The user documentation is part of the CloudConnect installation.

To access the documentation, click **Help > CloudConnect-User-Guide.pdf** in the PeakView software menu bar.

Note: The latest versions of the user documentation is available on the SCIEX website, at sciex.com/customer-documents.

Figure 1 Help Menu



New in Version 1.8

Note: For information about changes in an earlier version of the software, refer to the document: *Release Notes* for that version.

- Compatibility with the OneOmics 3.3 suite

Installation

Requirements

Recommended Hardware

- Intel Core i5-8500 CPU @ 3.00GHz
- 32 GB of RAM
- 100 Mbps Network Interface Card (NIC)

Operating System

- Microsoft Windows 10 Enterprise (64-bit) (English (US))

Software

- Microsoft .NET Framework 4.6.1
- PeakView software, version 2.2
- An active user account in the OneOmics suite

Note: For information about registering and activating an account, refer to the document: *OneOmics Suite User Account Setup Guide*.

Install CloudConnect

Prerequisites
<ul style="list-style-type: none">• If a version of CloudConnect earlier than 1.5 is installed on the computer, then remove it. <hr/> <p>Note: CloudConnect 1.5 or later can be upgraded to version 1.8.</p> <hr/>

1. Go to [sciex.com/software-support/software-downloads](https://www.sciex.com/software-support/software-downloads) and then select **CloudConnect 1.8** under **OneOmics** in the software list.
 2. Save the zip file to the computer desktop.
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3. After the zip file is downloaded, right-click the file and then extract all of the files to the computer.
4. After the extraction completes, browse to and then double-click the **CloudConnect.exe** file.
5. Click **Install** and then follow the on-screen instructions.
6. Open the PeakView software, version 2.2.

Note: To use CloudConnect, register for a user account on the OneOmics suite. Refer to the document: *OneOmics Suite User Account Setup Guide*.

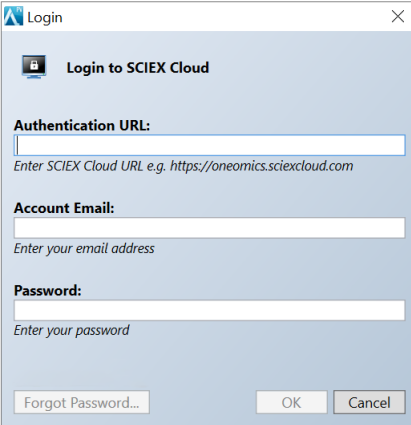
(Optional) For BaseSpace storage, register for an Illumina account and then link it to the OneOmics suite account. Refer to the document: *OneOmics Suite User Account Setup Guide*.

Link CloudConnect to OneOmics Suite

To register for a OneOmics suite account, refer to the document: *OneOmics Suite User Account Setup Guide*.

1. Open the PeakView software.
2. Click **CloudConnect > Login**.

Figure 2 Login Dialog



3. In the **Authentication URL** field, type <https://oneomics.sciexcloud.com>.
4. Type the **Account Email** and **Password** for the OneOmics Suite account.
5. Click **OK**.
The OneOmics suite account is now linked to CloudConnect.

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Note: The next time that the user logs in to the SCIEX cloud from this computer, the **Authentication URL** is retained.

Troubleshooting

Symptom	Corrective Action
CloudConnect upload and download files 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 shown.	<ul style="list-style-type: none">• 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:<ul style="list-style-type: none">• C:\ProgramData\AB SCIEX\CloudConnectUploader\log\CloudConnectLog.log• C:\ProgramData\AB SCIEX\CloudConnectPlugin\CloudConnectPlugin.log <hr/> <p>Note: If the ProgramData folder is not visible in File Explorer, then set the View options for File Explorer to show Hidden Items.</p> <hr/>

Known Issues and Limitations

Note: The numbers in parentheses are reference numbers to each issue or feature in the SCIEX internal tracking system.

Batch upload stops if a wiff2 file is open in SCIEX OS while the batch is in progress

If one or more of the acquisition data files are open in SCIEX OS at the time of the upload, then the current upload and any subsequent uploads might be interrupted.

Workaround: Avoid opening the files of interest in SCIEX OS when an upload is in progress. (OOM-2663)

Files are missing from the list of files to upload

When the user adds files to the upload list with the **Add files to upload** option, the list of files to upload does not show the added files. However, the files are shown in the upload queue. (OOM-2512)

(BaseSpace) Multiple RNA or ion library files cannot be uploaded under a single analysis

When multiple RNASeq or ion library (txt or group) files are selected for upload to a BaseSpace Project, the **Analysis** and **Files to Upload** fields in the Upload to BaseSpace dialog are missing.

Workaround: Upload each file individually to an **Analysis** under the BaseSpace Project. (OOM-2413)

Charge state is not shown for negative polarity metabolites

For metabolomics results for negative ion mode, the charge field is blank for each metabolite. (OOM-2363)

(BaseSpace) Some qresult files are not available for download

On the Download from BaseSpace dialog, only a subset of qresults files is available to download for an analysis within a project.

Workaround: Follow these steps:

1. In Google Chrome, go to the Illumina BaseSpace Sequence Hub URL, and then log on.
2. Browse to the location of the qresult file and then download the file.
3. Change the file extension from qresult to swath.
4. Click **CloudConnect > Import > Load Session (local)**.
5. Open the downloaded file.

(OOM-1463)

(BaseSpace) An error is shown when a qresult file is opened

When a user opens a session (qresult) file using the **CloudConnect** menu (**CloudConnect > Download > Load Session (BaseSpace)**), the following error message is shown: `the process cannot access the file C:\Users\computername\AppData\Local\Temp\filename.qresult because it is in use by another process.`

Workaround: Browse to the `Temp` folder specified in the message and then delete the appropriate qresult file. If this does not resolve the issue, then close and open the PeakView software.

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To avoid this issue, users can download the qresult file from BaseSpace and then open the file using CloudConnect. The SWATH acquisition data must be available on the local hard drive of the computer where CloudConnect is installed. (OOM-50)

Data upload speeds vary

Data upload speeds vary based on the maximum connection speeds and internet traffic in the location of the user. Actual speeds and total time to move and process data vary. We recommend a minimum connection speed of 4 MB/s to make efficient use of CloudConnect.

(BaseSpace) Downloading data files from BaseSpace using CloudConnect is not supported

To retrieve data, we recommend downloading directly from BaseSpace.

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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>.

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

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(GEN-IDV-09-10816-D)

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