

CloudConnect 1.6 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 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:

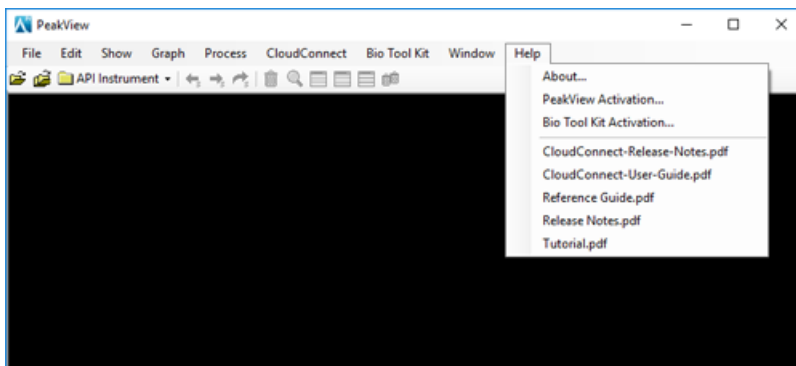
- Inspection of peak groups within SWATH[®] Acquisition data files processed by the Proteomics and Metabolomics apps in the OneOmics[™] Suite
- Definition of retention time calibration peptides within an ion library for use in the Proteomics app in the OneOmics[™] Suite

Get Help

The user documentation is part of CloudConnect installation.

To access the documentation, click **Help > CloudConnect-User-Guide.pdf** in the PeakView[®] Software menu bar.

Figure 1 Help Menu



New in Version 1.6

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

- Compatibility with OneOmics™ 3.1 Suite powered by SCIEX Cloud.
- Support for IDA and SWATH® Acquisition data acquired by the ZenoTOF™ 7600 LC-MS/MS System.
- Small usability fixes and improvements.

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)

Software

- Microsoft .NET Framework 4.6.1
- PeakView® Software, version 2.2
- An active user account in the OneOmics™ Suite powered by SCIEX Cloud

Note: For information about registering and activating an account, refer to the *Release Notes* for the OneOmics™ Suite.

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.
Note: CloudConnect 1.5 can be upgraded to version 1.6.

- Go to sciex.com/software-support/software-downloads and then select **CloudConnect 1.6** under **OneOmics** in the software list.
- Save the zip file to the computer Desktop.
- After the zip file is downloaded, right-click the file and then extract all of the files to the computer.
- After the extraction completes, browse to and then double-click the **CloudConnect.exe** file.
- Click **Install** and then follow the on-screen instructions.
- Open the PeakView[®] Software, version 2.2.

Note: To use the CloudConnect, register for a user account on the OneOmics[™] Suite. Refer to the *Release Notes* for the OneOmics[™] Suite.

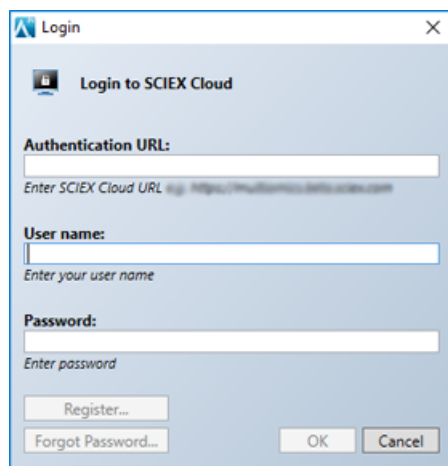
(Optional) For BaseSpace storage, register for an Illumina account and then link it to the OneOmics[™] Suite account. Refer to the *Release Notes* for the OneOmics[™] Suite.

Link CloudConnect to SCIEX Cloud

To register for a OneOmics[™] Suite account, refer to the *Release Notes* for the OneOmics[™] Suite.

- Open the PeakView[®] Software.
- Click **CloudConnect > Login**.

Figure 2 Login Dialog



3. In the **Authentication URL** field, type <https://oneomics.sciexcloud.com>.
4. Type the **User name** and **Password** for the OneOmics™ Suite account.
5. Click **OK**.

The SCIEX Cloud account is now linked to CloudConnect.

Note: The next time that the user logs in to the SCIEX Cloud from this computer, the **Authentication URL** is retained. The **User name** and **Password** are the user name and password of the logged on user.

Troubleshooting

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, <i>Unable to connect to the remote server</i> , might be received.	<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 brackets are reference numbers to each issue or feature in the SCIEX internal tracking system.

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. To resolve this issue, 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. To resolve this issue, navigate 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.

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 your location. 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.

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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.

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