

How to Download Your Project Data via SFTP

This document describes how to access and download your data delivery from Xpress Genomics.

Credentials

You will receive from us the following credentials:

- Host: [sftp.yourserver.com](#)
- Username: [your_username](#)
- Password: [your_password](#)

Windows (GUI)

The easiest way to connect on Windows is with a free graphical client like **FileZilla**.

1. **Download and Install:** Get the FileZilla Client from the [official website](#) and install it.
2. **Connect:** Open FileZilla and use the "Quickconnect" bar at the top. Enter the **Host**, **Username**, and **Password** from above and click **Quickconnect**.
3. **Download Your Project Folder:**
 - On the left side (**Local site**), navigate to the folder on your computer where you want to save your project (e.g., your Desktop or Downloads folder).
 - On the right side (**Remote site**), you will see your project folder(s).
 - Drag your entire project folder from the right panel and drop it into the desired location on the left panel. The download will begin.
 - Resume an interrupted download: If the connection drops, reconnect and drag the same folder over again. FileZilla will detect partially downloaded files and ask whether to overwrite or resume. Choose resume.

macOS & Linux (Command Line)

macOS and most Linux distributions have a built-in command line tool for SFTP.

1. **Open Terminal:**

- macOS: Open the "Terminal" app.
- Linux: Open your "Terminal" or "Console" application.

2. **Connect:** Type the following command and press Enter.

`sftp your_username@sftp.yourserver.com`

3. **Enter Password:** You will be prompted for your password. Note: Your typing will not be visible. Type the password and press Enter.

4. **Download Your Project Folder:** Once you see the sftp> prompt, follow these steps:

- (Optional) Set your download location so files save to a known directory (otherwise they save where you started):
`lcd ~/Downloads`
- Find your project folder on the server:
`ls`
- Download the folder with resume enabled and recursively include all files:
`get -aR Your_Project_Folder_Name`
Replace Your_Project_Folder_Name with the actual folder name. The -aR flag enables resume and recursive download. If the download is interrupted, run the same command again to resume.
- Disconnect when finished:
`exit`

For questions, please contact us at service@xpress-genomics.com.