Remote access to eBIC systems for data collection, analysis and session monitoring

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Introduction

This document is intended as a guide containing eBIC specific instructions to help you:

1) Access eBIC microscopes using NoMachine (NX)
   - o Using nx-cloud.diamond.ac.uk
2) Initiate on-the-fly data analysis in SynchWeb
3) Monitor your data collection remotely using:
   - o SynchWeb
   - o NoMachine (nx.diamond.ac.uk)
4) Download your data following your session

The guide is principally aimed at an eBIC remote user but is applicable to on-site sessions. **Please consult the additional documentation for guidance on the set up of your data collection session: "Remote EPU operation guide" or "Remote TOMO5 operation guide"**

The user is ultimately responsible for their use of eBIC and Diamond systems. If you are in doubt about an action you need to perform or are unable to progress, then please reach out to the eBIC Local Contact assigned to your session for assistance. Additionally, please report any errors in this guide to your Local Contact or kyle.morris@diamond.ac.uk.

Information box colour key

Information boxes are presented in green	Optional action instructions are presented in yellow
Terminal commands are presented in violet	

Getting prepared

- You need to be using a high speed and stable internet connection

- You are advised to check with your institute IT department that the traffic from NoMachine will not be blocked by any corporate firewall

- Download (or update to the latest version) and set up the following:
   - ☐ Microsoft Teams
   - ☐ NoMachine

- Check you know your FedID
   - ☐ https://www.diamond.ac.uk/Users/Experiment-at-Diamond/IT-User-Guide.html

- If you need to change your FedID password
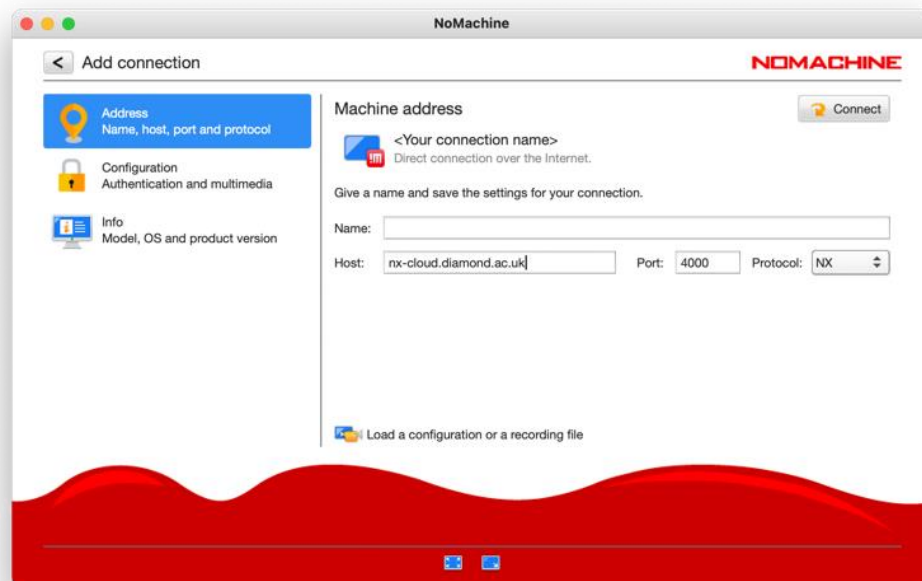   - ☐ https://access.stfc.ac.uk

Contents

# 1   Access eBIC microscopes using NoMachine

1.1   New nx-cloud connection

☐ Click "Add" to create a new connection for using nx-cloud
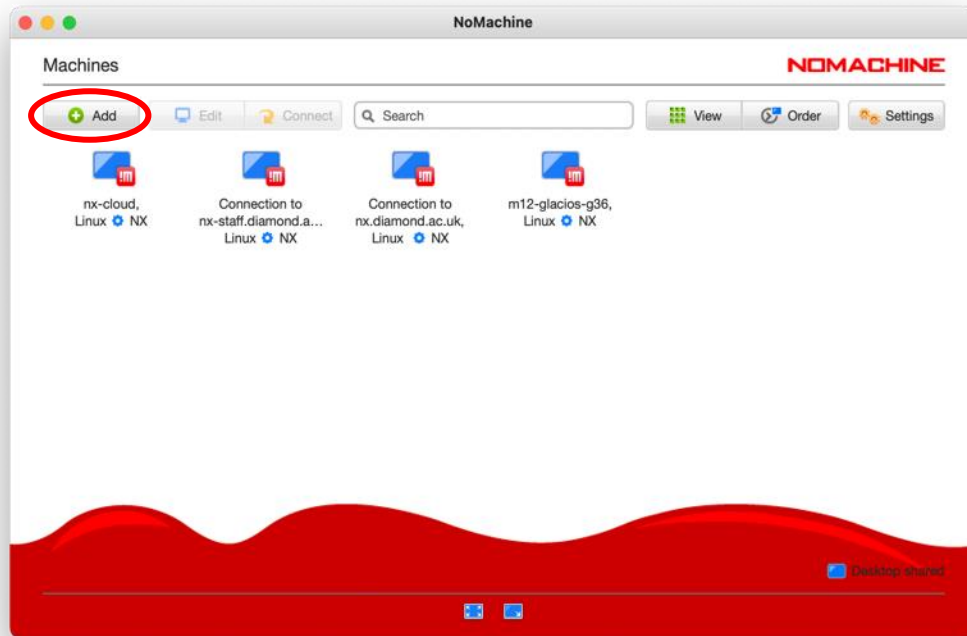
☐ Enter the host name "nx-cloud.diamond.ac.uk"
☐ Check the Port and Protocol settings
      If NX does not progress to authentication it is likely that your firewall is blocking the port
☐ Click 'Connect'

☐ Enter your FedID and password
You must enter the suffix "@fed.cclrc.ac.uk" (i.e. 'rtg01234@fed.cclrc.ac.uk')
☐ For convenience, we suggest selecting 'Save this password in the connection file'
☐ Click 'Login'
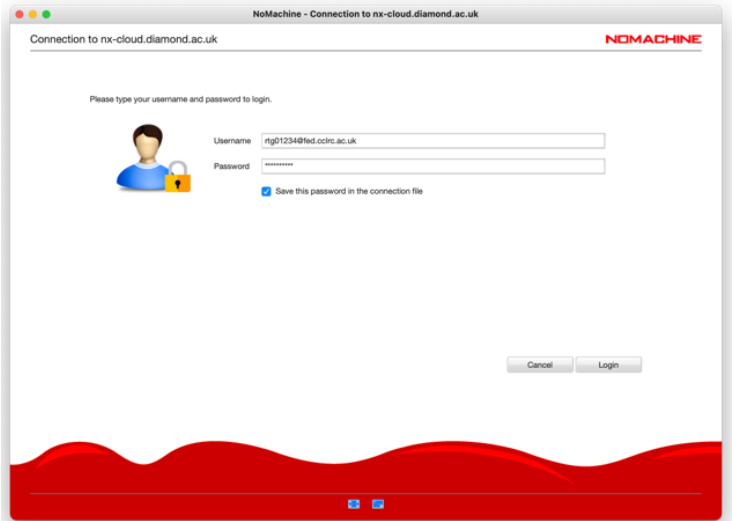
Troubleshooting authentication errors:
Note that your account will be locked after 5 failed attempts, it will then unlock after 30 minutes. You may manually type your password into the Username field to confirm it is correct, before manually typing into the Password field. This is particularly important for passwords containing special characters and users who have non-UK keyboards.

1.2 Connect to the remote support PC

☐ Double-click the remote support PC of the microscope you want to connect to
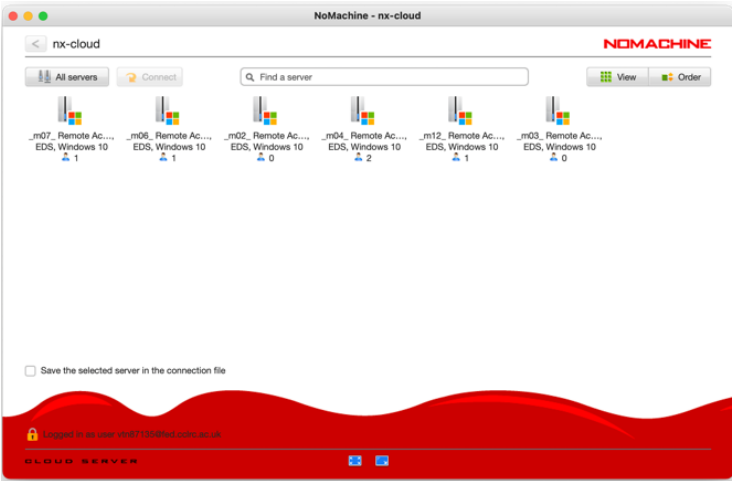
Each remote support PC is associated with a microscope. You will only see the remote support PC of the microscope that is scheduled for your session during your session. The names of the machines are as follows:

Krios I:	m02		Krios III:	m06		Talos:	m04
Krios II:	m03		Krios IV:	m07			

1.3 Log in to the remote support PC

> After a few seconds you should be able to see a windows login screen.
>
> If you are asked to 'Press Ctrl + Alt + Delete to unlock' then use NX to send this command to the remote machine.

☐ Press Ctrl + Alt + 0 (win) or Ctrl + Option + 0 (apple) on your keyboard to access NX options
☐ Alternatively, hover your mouse in the top right corner and click to access the NX options
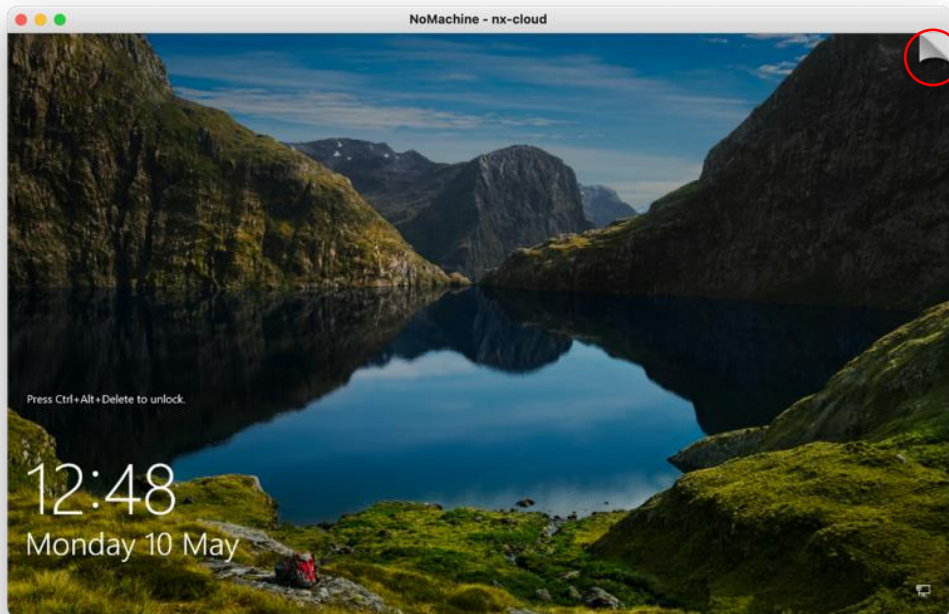
☐ Click on (1) the special sequences button and send (2) the Ctrl + Alt + Del sequence to the remote machine, then (3) to return to the remote machine screen.

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☐ Enter your FedID and FedID password

If 'Sign in to: CLRC' is displayed as highlighted, then enter only your FedID

If not, then enter the prefix "clrc\", then your FedID (i.e. 'clrc\rtg01234')

Some users may be required to enter your FedID in its long form (i.e. 'rtg01234@fed.cclrc.ac.uk')
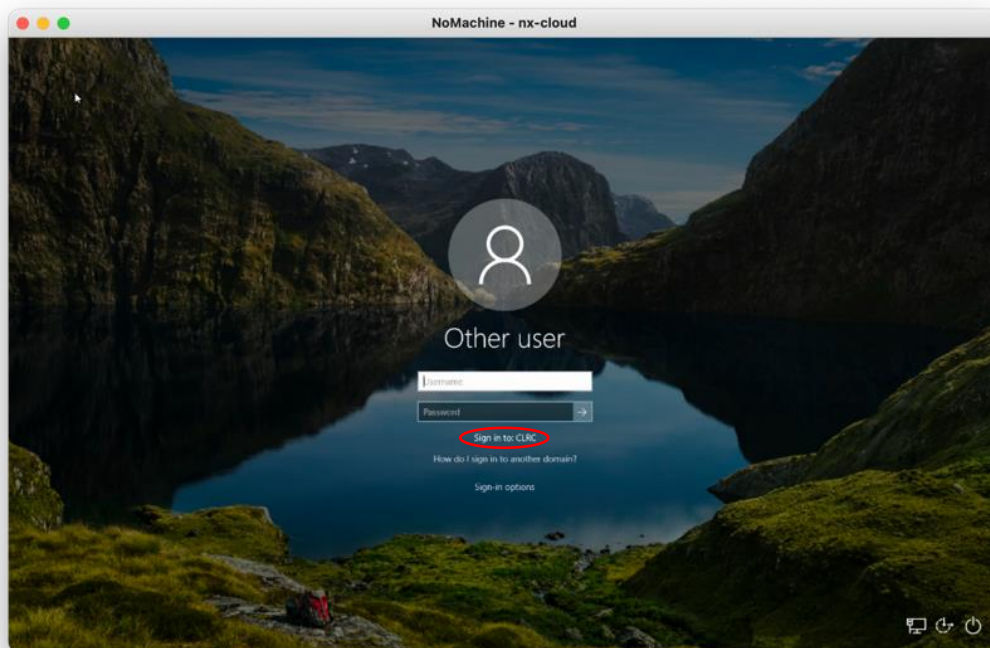
A keyboard can be accessed via the 'Ease of Access' button should you have a different keyboard layout to the remote machine. This can also be accessed once logged in via:
Start > Settings > Ease of Access > Keyboard
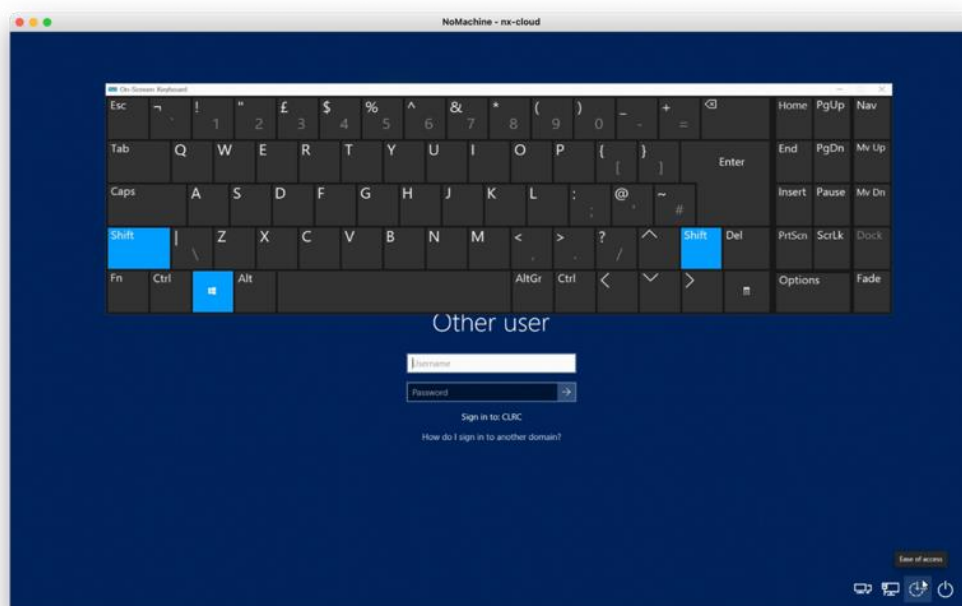
1.4 Connect to the microscope using TeamViewer

You are now connected to a windows virtual support PC via NoMachine. This machine has TeamViewer installed.

From the windows virtual support PC, you can now connect to your microscope using TeamViewer.
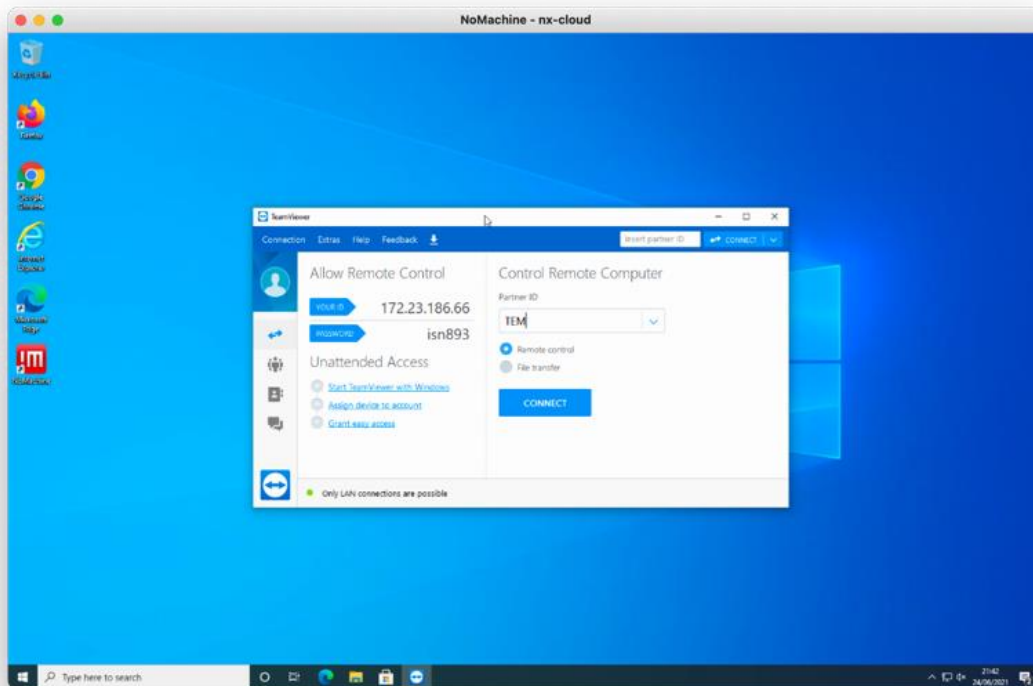
☐ Start TeamViewer, enter "TEM" as the Partner ID and press Connect
☐ Enter the TeamViewer password. Check the table below for each instruments password.

Instrument	TeamViewer user	TeamViewer password
Krios I (m02)	TEM	diamondkrios1
Krios II (m03)	TEM	diamondkrios2
Krios III (m06)	TEM	diamondkrios3
Krios IV (m07)	TEM	diamondkrios4

You will now be connected to the TEM user interface at the microscope on monitor 1. You may use TeamViewer to switch to monitor 2 where EPU or TOMO will be started.
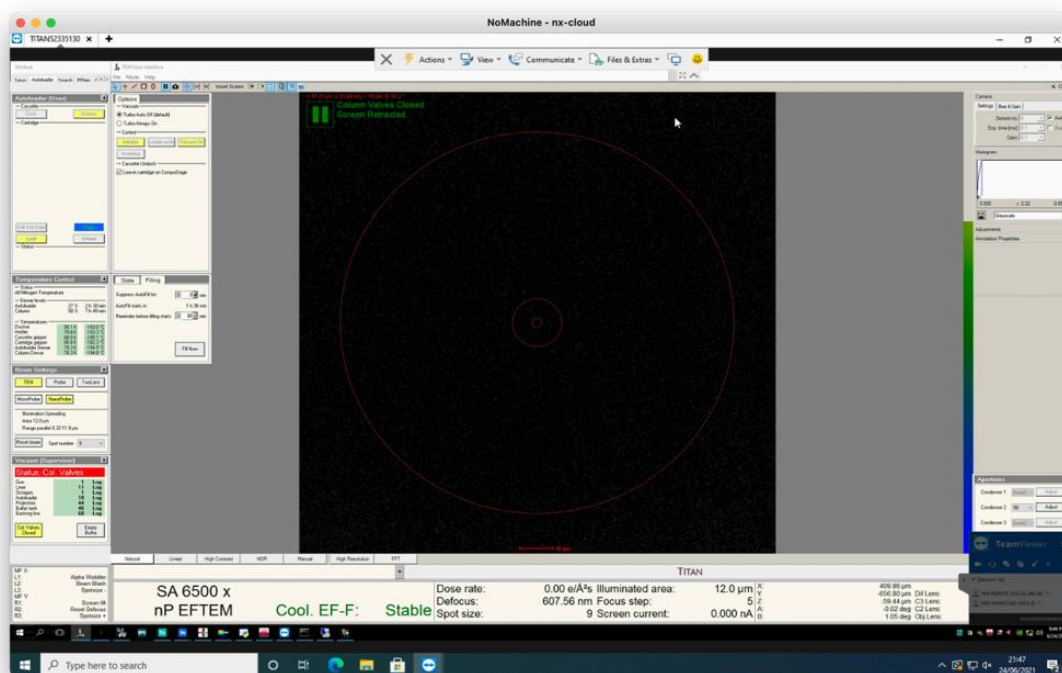
☐ Set TeamViewer to "Best Fit" under the "View" tab

☐ Switch between the TEM PC and EPU/TOMO monitors using the "Monitor:1/2" highlighted buttons (🖥️🖥️) under the "View" tab or using the highlighted button (🖥️)
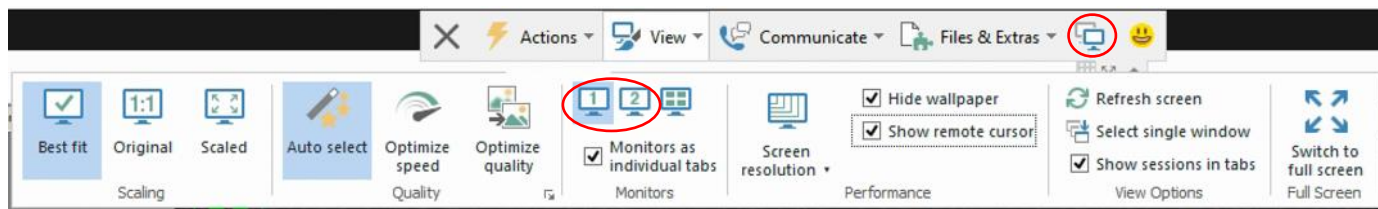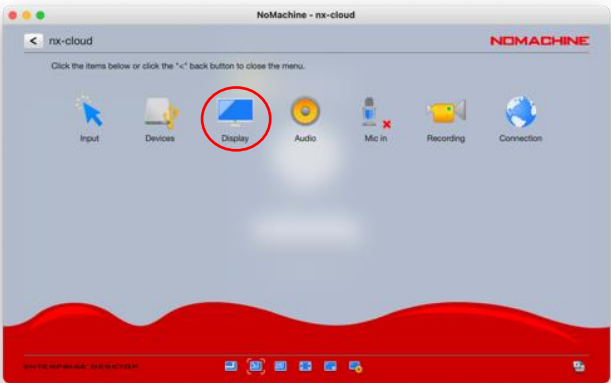

> To closely inspect on-screen elements and data you may find "Scaling: Original 1:1" and "Quality: Optimize quality" useful.

☐ It is not normally necessary to adjust the TeamViewer Screen resolution. Optimal settings for your display can normally be found using the NoMachine display configuration.

1.5 Configure the NoMachine display

☐ Press Ctrl+Alt+0 (win) or Ctrl+Option+0 (apple) on your keyboard to access NX options
☐ Alternatively, hover your mouse in the top right corner to access the NX options

☐ Display > Scale to window
☐ Display > Change settings > Best Quality
☐ Display > Change settings > Set resolution appropriate to your system

> To closely inspect on-screen elements and data, you may find selecting "Enable viewport mode" to view the remote desktop at 1:1 scaling helpful.

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Selecting 1920 x 1200 works well on a 13-inch screen with a resolution of 2560 x 1600 pixels.
Selecting "Disable client side image post-processing" can improve image quality.
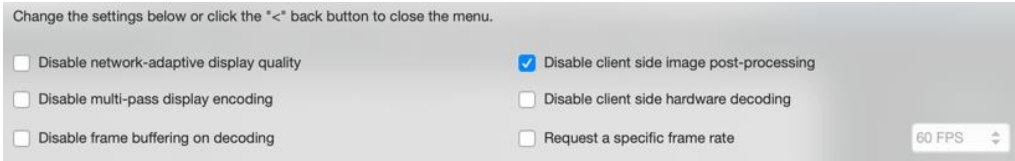
2 Set up your data collection

2.1 EPU and TOMO set up guides

eBIC actively maintain operation guides that are designed to complement your training. You may find them helpful to follow for guidance in setting up your data collection session:

https://www.diamond.ac.uk/Instruments/Biological-Cryo-Imaging/eBIC/User-Guide/User-guide-downloads.html

Single particle analysis: Remote_EPU_operation_guide.pdf
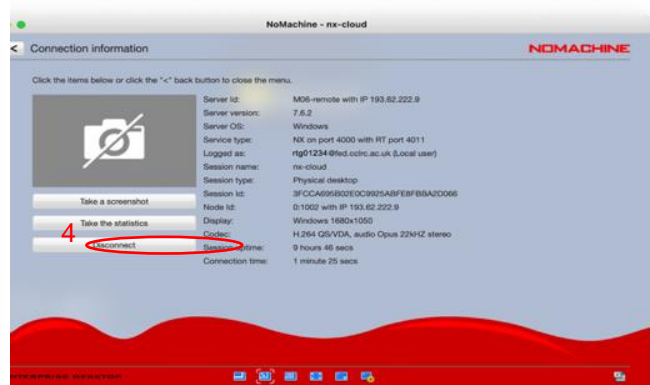**Tomography:**   Remote_TOMO5_operation_guide.pdf

Set up your data collection and work with your local contact to start the collection and data transfer.

2.2 At the end of your session

☐ Click on (1) the highlighted cross to close TeamViewer
  (Take care that you do not accidentally close the "TEM User Interface")
☐ Click on (2 and 3) to sign out of the remote support PC
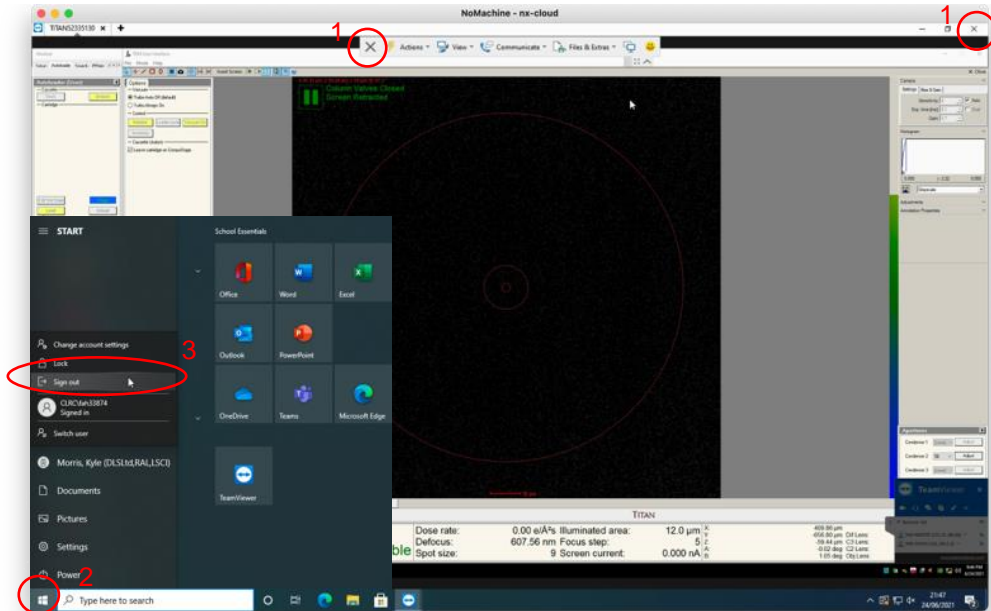
☐ Press Ctrl+Alt+0 (win) or Ctrl+Option+0 (apple) on your keyboard to access NX options
☐ Click on (3) "Connection"
☐ Click on (4) "Disconnect" to disconnect from the NoMachine nx-cloud session

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3 On-the-fly data analysis for EPU/SPA via SynchWeb

This assumes you have set up your EPU data collection, informed your local contact who will have initiated the data transfer and are thus ready to submit an on-the-fly data analysis job.
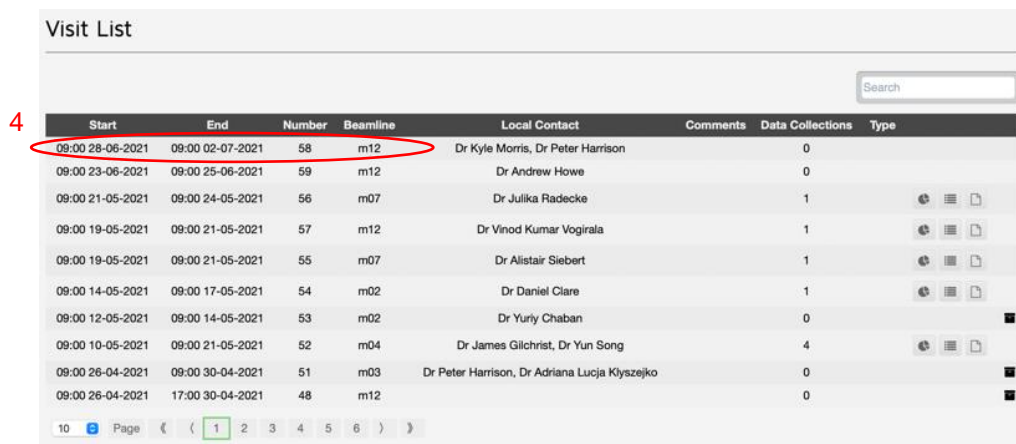
3.1 Initiate on-the-fly data analysis via SynchWeb

3.1.1 Log in to SynchWeb and find your experiment

☐ Log in to SynchWeb using your FedID and password: https://ispyb.diamond.ac.uk/
     Your active visit should be found on the front page, otherwise:

☐ Click on (1) Proposals, enter your (2) Proposal ID and click on (3) the Proposal
     Your Proposal ID is the prefix of your Experiment ID

☐ Click on (4) the Visit associated with your experiment

☐ Click on (5) "Add data Collection"

☐ Enter your acquisition software and the name of raw directory (i.e. raw, raw1, raw2, etc)
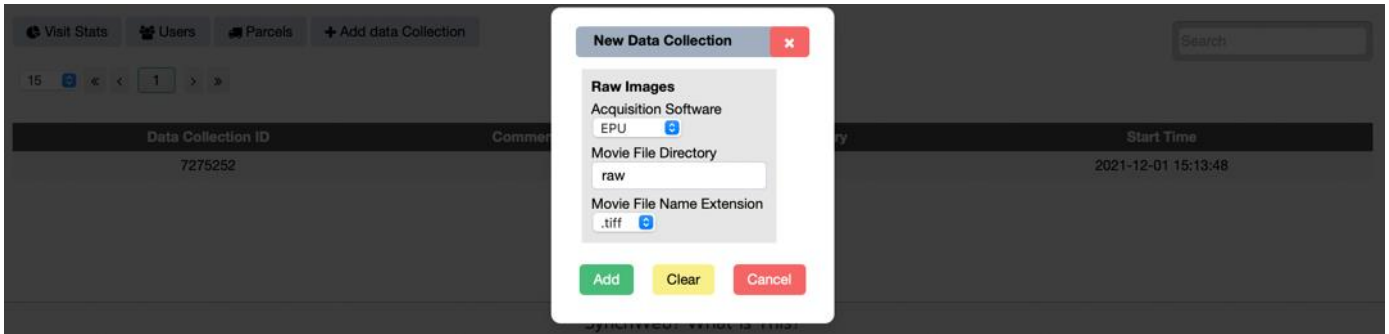
3.1.2 Add an on-the-fly analysis job

☐ Click on (6) the gear cog to "Run relion Processing"
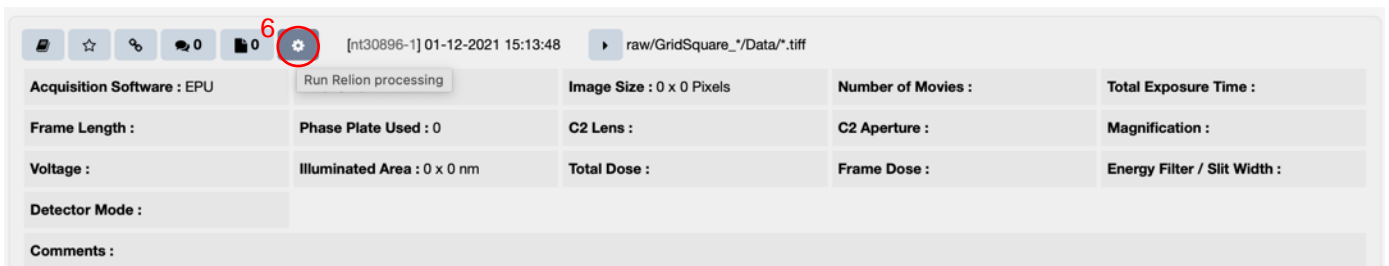
☐ Enter parameters specific to your data collection and click (7) "Process"
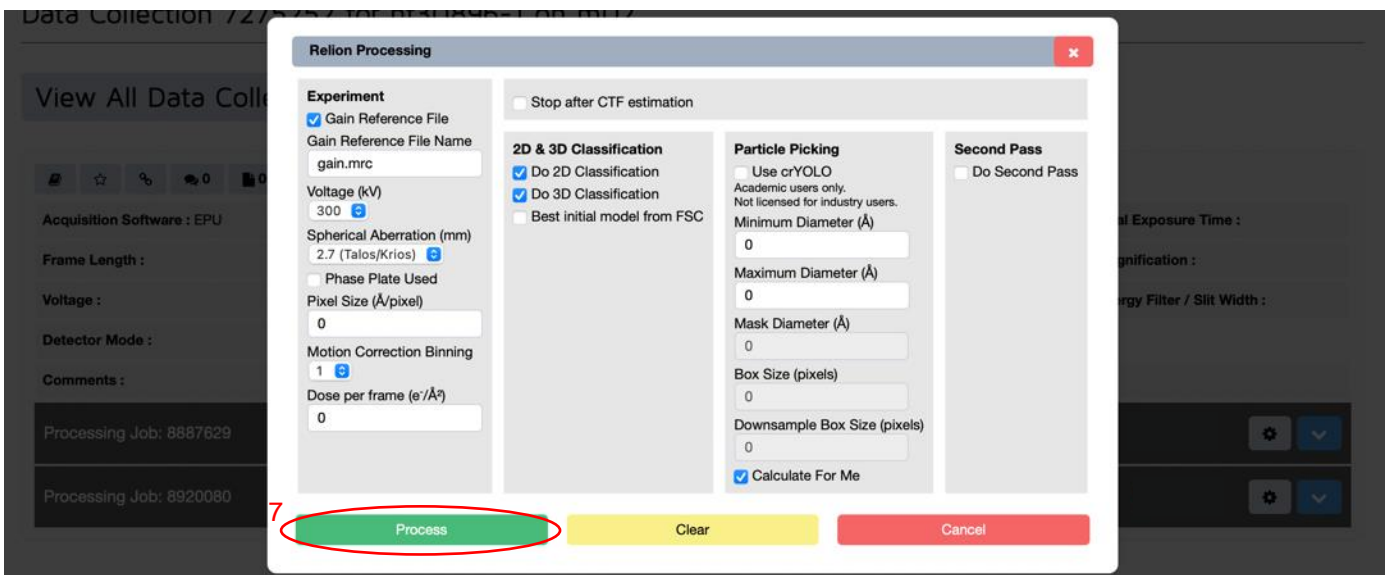
Check with your Local Contact what the "Raw Folder" and "Gain Reference File Name" are called for your current data collection.

If you are performing multiple data collections in one session you should pay particular attention to what the Movie File Directory (i.e. raw) folder is called.
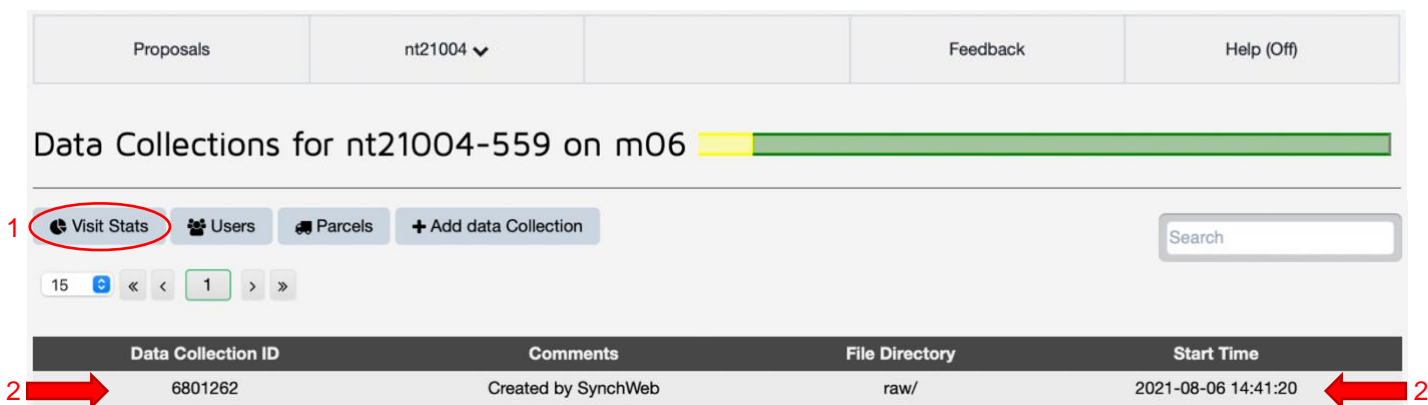
If you have used EPU 2-fold binning from super-resolution counted images, in this case enter the magnified pixel size and set "Motion Correction Binning" to "1". Otherwise, enter the super-resolution pixel size and "Motion Correction Binning" at "2".

3.2 Monitor your on-the-fly data analysis via SynchWeb

> This assumes you have initiated the eBIC data analysis pipeline in SynchWeb as described in 3.1.
>
> The on-the-fly data analysis pipeline is being actively developed at eBIC. The reporting interface will show increasing amounts of information and analysis as this development progresses. In the meantime, the following sections will help you learn how to inspect your data analysis results.

☐ Navigate to your visit in SynchWeb as in 3.1.1

On the visit landing page, you will find a list of all Data Collections / processing jobs you have submitted
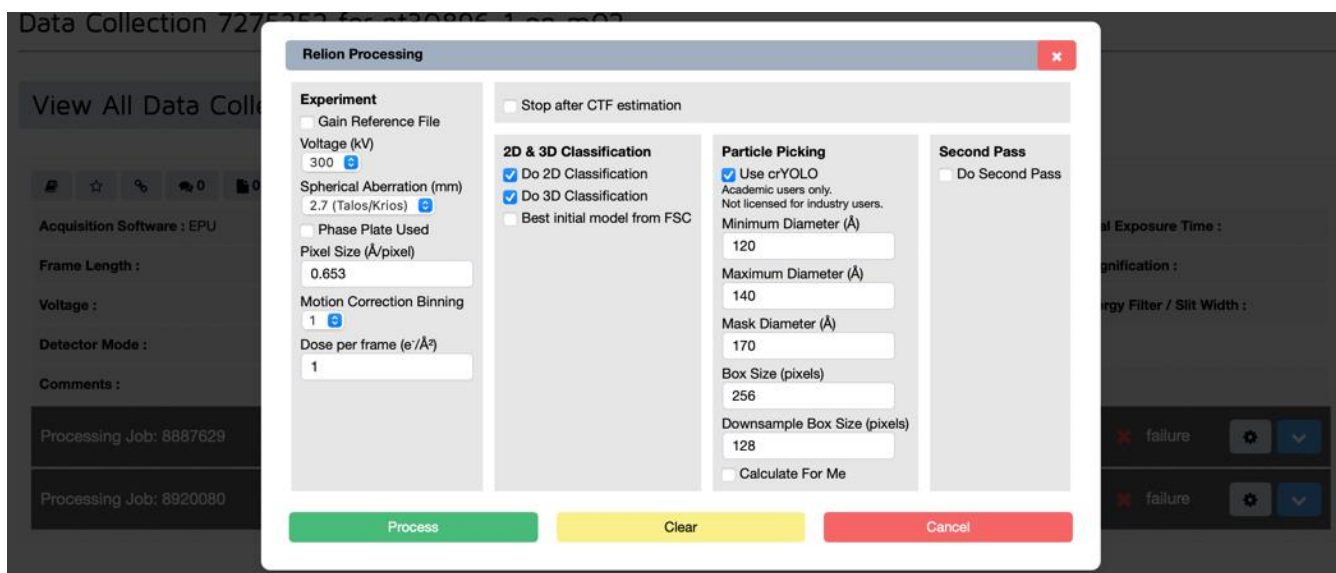
☐ Click on (1) Visit Stats to view collection statistics from all on-the-fly analysis results

Expected output in 3.2.1

☐ Click on (2) a Data Collection ID to view on-the-fly analysis results for that collection

Expected output in 3.2.2 – 3.2.3

☐ Click on (3) to view a Processing Job's parameters

3.2.1 Visit statistics

☐ Click on (4) to return to the Data Collections landing page

3.2.2 Auto Processing results summary

☐ Click on the drop-down arrow to view the Processing Job results

☐ Click on a summary graph to expand and inspect results
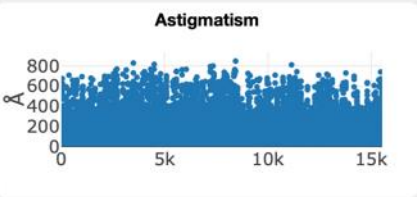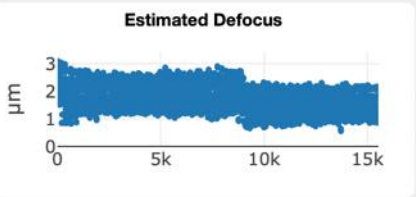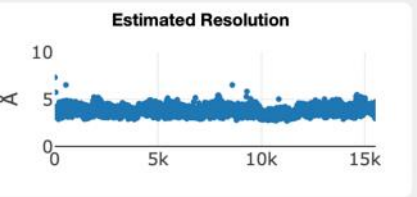
☐ Click-drag to zoom on individual data points
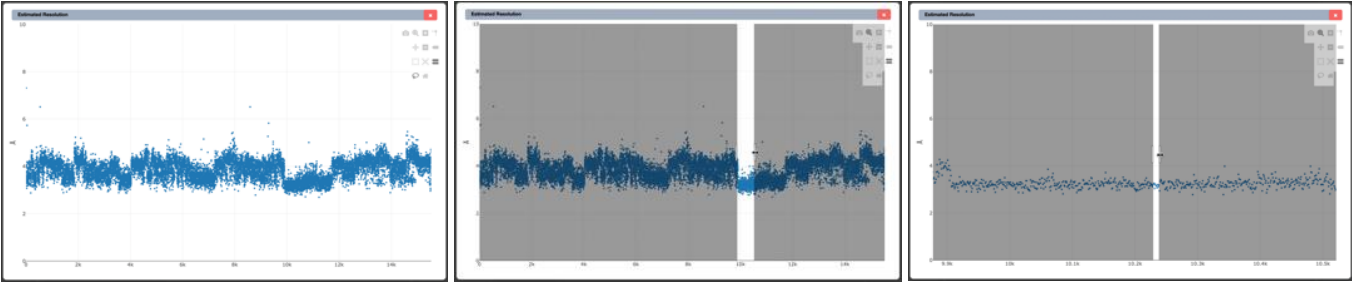
☐ Hover over a data point to view its time stamp and result
☐ You may click that data point to load and inspect its analysis results

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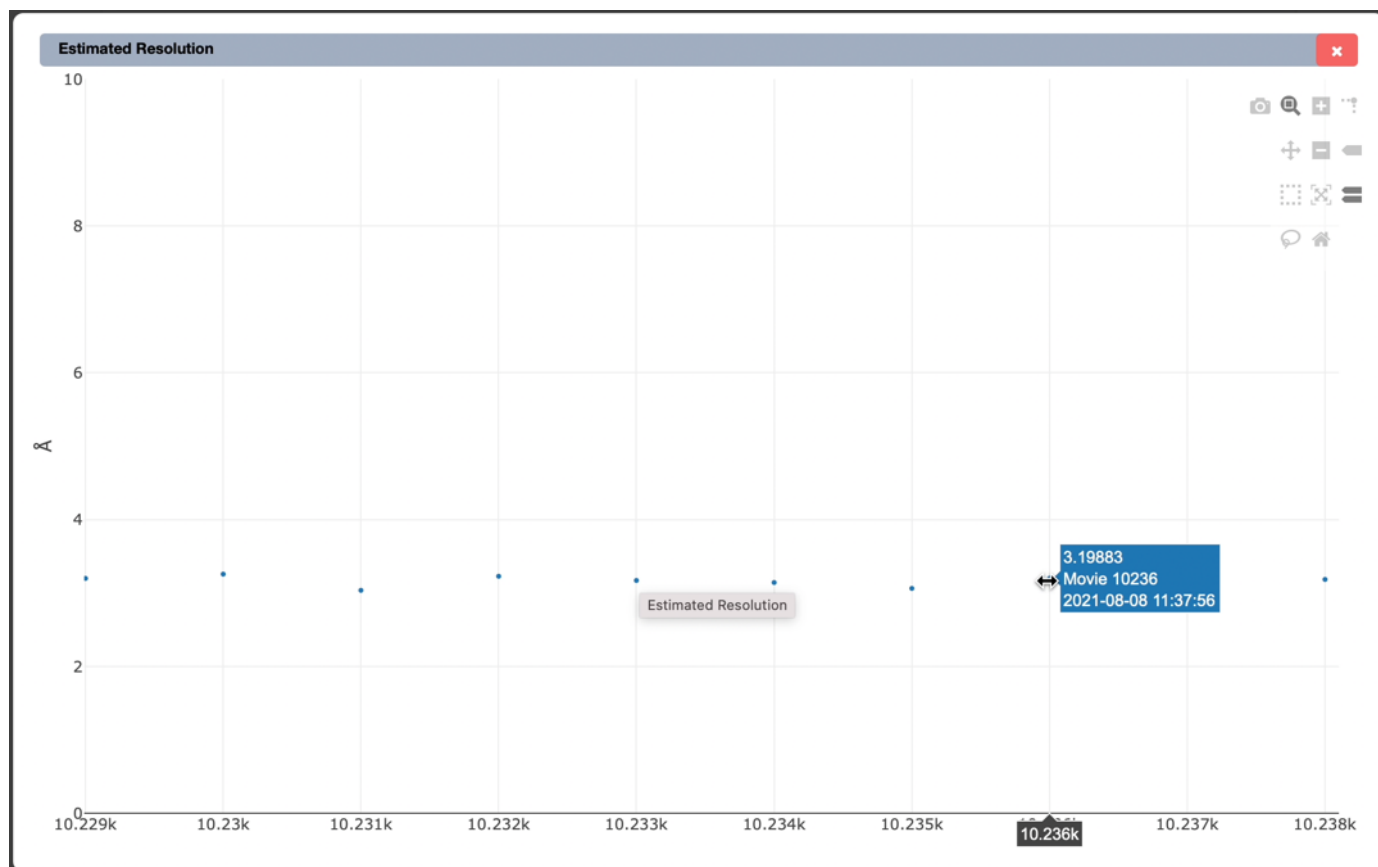
3.2.3 Auto Processing results in detail

☐ View the analysis results for a micrograph you have selected in the summary or by typing its collection index in the Images box.
☐ Note all images are clickable thumbnails

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Summary

Processing Job Parameters

Motion Correction

Image: « ‹ 1887 › » Show most recent ☐

Image Number : 1887	**Movie Time Stamp :** 2021-12-01 15:14:29
First Frame :	**Last Frame :**
Dose Per Frame : 1 e⁻/Å²	**Dose Weight :**
Total Motion : 18.1 Å	**Average Motion / Frame :** 0.35 Å
Patches Used : 5 X 5	
Comments :	

Micrograph Snapshot

Drift

CTF Estimation

Image: « ‹ 1887 › » Show most recent ☐

Image Number : 1887	**Movie Time Stamp :** 2021-12-01 15:14:29
Box size : 512 µm x 512 µm	**Resolution :** 30 Å - 5 Å
Defocus : 5000 Å - 50000 Å	**Defocus Step Size :** 500 Å
Astigmatism : 34.8277 nm	**Astigmatism Angle :** 0.9 °
Estimated Resolution : 4.35 Å	**Estimated Defocus :** 2.10031 µm
Amplitude Contrast : 0.1	**CC Value :** 0.09519
Comments :	

FFT Theoretical

Particle Picking

Image: « ‹ 1496 › » Show most recent ☐

Image Number : 1496	**Movie Time Stamp :** 2021-11-16 23:28:44
Number of Particles : 305	**Particle Diameter :** 21.2 nm

Summary Image

2D Classification

Sort by: Particles Per Class ☐ Page 1 of 193 « ‹ › »

13 - 19 (4982) 20 - 31 (4645) 14 - 34 (4474) 2 - 21 (4386) 10 - 50 (4352) 20 - 38 (4323) 3 - 22 (4141)

Type : 2D	**Batch Number :** 13
Classes Per Batch : 50	**Particles Per Batch :** 20000
Symmetry : C1	**Class Number :** 19
Class Distribution : 0.24659	**Particles Per Class :** 4982
Rotation Accuracy : 2.6	**Translation Accuracy :** 1.42588 Å
Estimated Resolution : 6.43103	**Overall Fourier Completeness :** 0.97451
Resolution :	**Number of Particles :**

13 - 19

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4 Monitor your session and view analysis via NoMachine

4.1 Connect to a Linux machine via NX

For the duration of your session, you may also log in to a remote Linux machine to inspect your on-the-fly data analysis results and monitor the progression of your data collection.

☐ Follow section 1.1 to create a new NX connection but enter the following host name: "nx.diamond.ac.uk"
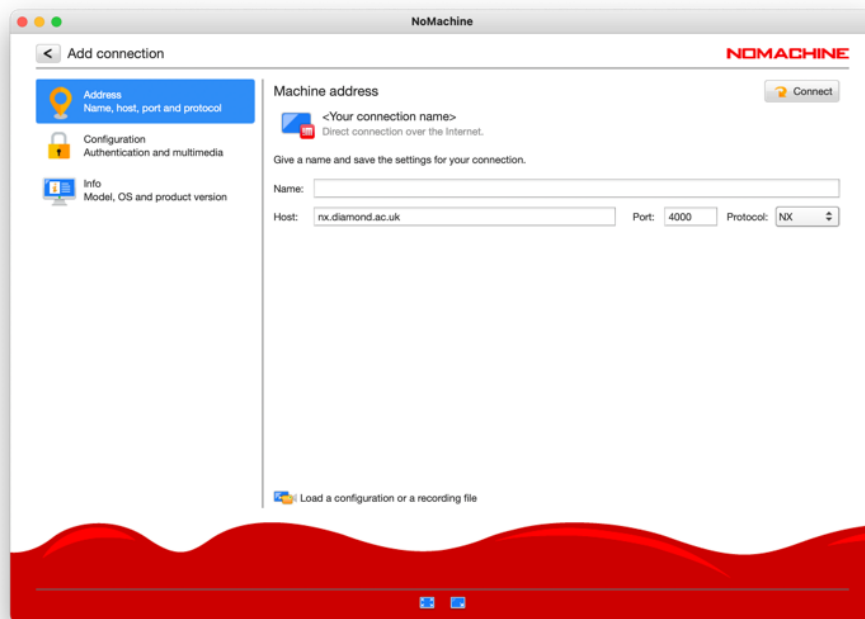
☐ Double-click on "Create a new virtual desktop"
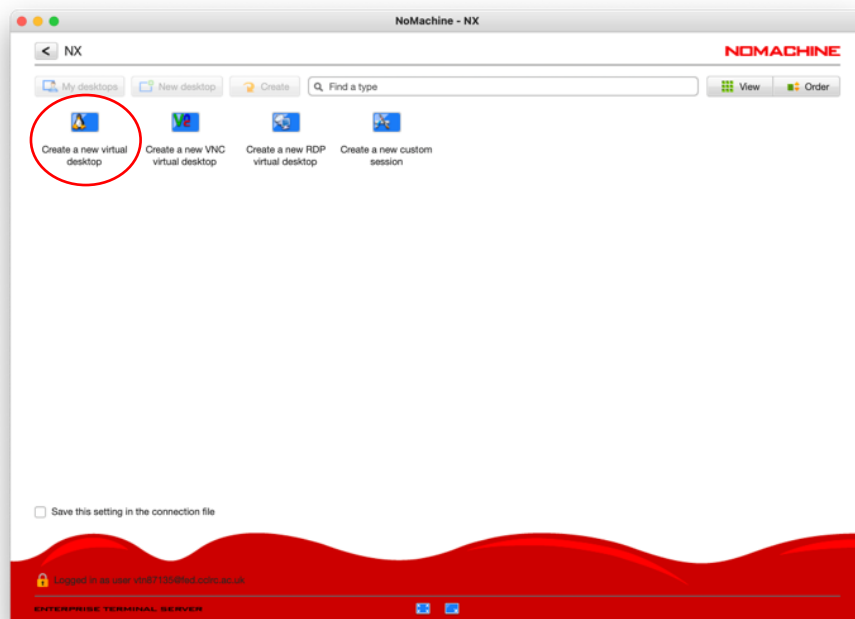
☐ Follow section 1.5 to configure the display for your computer
☐ Click on (1) the applications menu, (2) search for "Terminal" and (3) launch a terminal

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4.2 EPU: Check data is being written to your visit directory

> Atlas, EPU and raw directories are located in your visit directory, a typical structure is shown below:
> ./*_Atlas | Images that make up the grid overview
> ./*_EPU | Images collected during EPU setup and acquisition
> ./raw | Movie frames, organised in the same directory structure as in the EPU directory
>
> All directories are protected from accidental modification, but you can still execute commands to inspect the data. The following present several different ways you can monitor your incoming data.

☐ Use the terminal to navigate to your visit directory

```
$ cd /dls/{beamline}/data/{year}/{visit number}
        e.g. /dls/m04/data/2021/bi23047-52/
```

```
vtn87135@cs05r-sc-serv-02:/dls/m04/data/2021/bi23047-52                        ✕

File  Edit  View  Search  Terminal  Help
[vtn87135@cs05r-sc-serv-02 bi23047-52]$ ll
total 8
drwxrws---+   5 gda2 bi23047_52 4096 Jun 21 10:33 processed
drwxrws---+   6 root bi23047_52 4096 May 11 15:58 raw
drwxrws---+   3 root bi23047_52 4096 May 12 16:05 raw2
drwxrws---+   5 root bi23047_52 4096 May 12 15:54 supervisor_20210512_111920_BI23047-52_Atlas
drwxrws---+   4 root bi23047_52 4096 May 13 09:23 supervisor_20210512_131245_BI23047-52_EPU
drwxrws---+  12 root bi23047_52 4096 May 17 17:55 supervisor_20210517_121108_BI23047-52_Atlas
drwxrws---+   4 root bi23047_52 4096 May 18 00:05 supervisor_20210517_153323_BI23047-52_EPU
drwxrws--T+   3 gda2 bi23047_52 4096 Jun 25 09:32 tmp
drwxrws---+   2 gda2 bi23047_52 4096 May  7 00:03 xml
[vtn87135@cs05r-sc-serv-02 bi23047-52]$ █
```
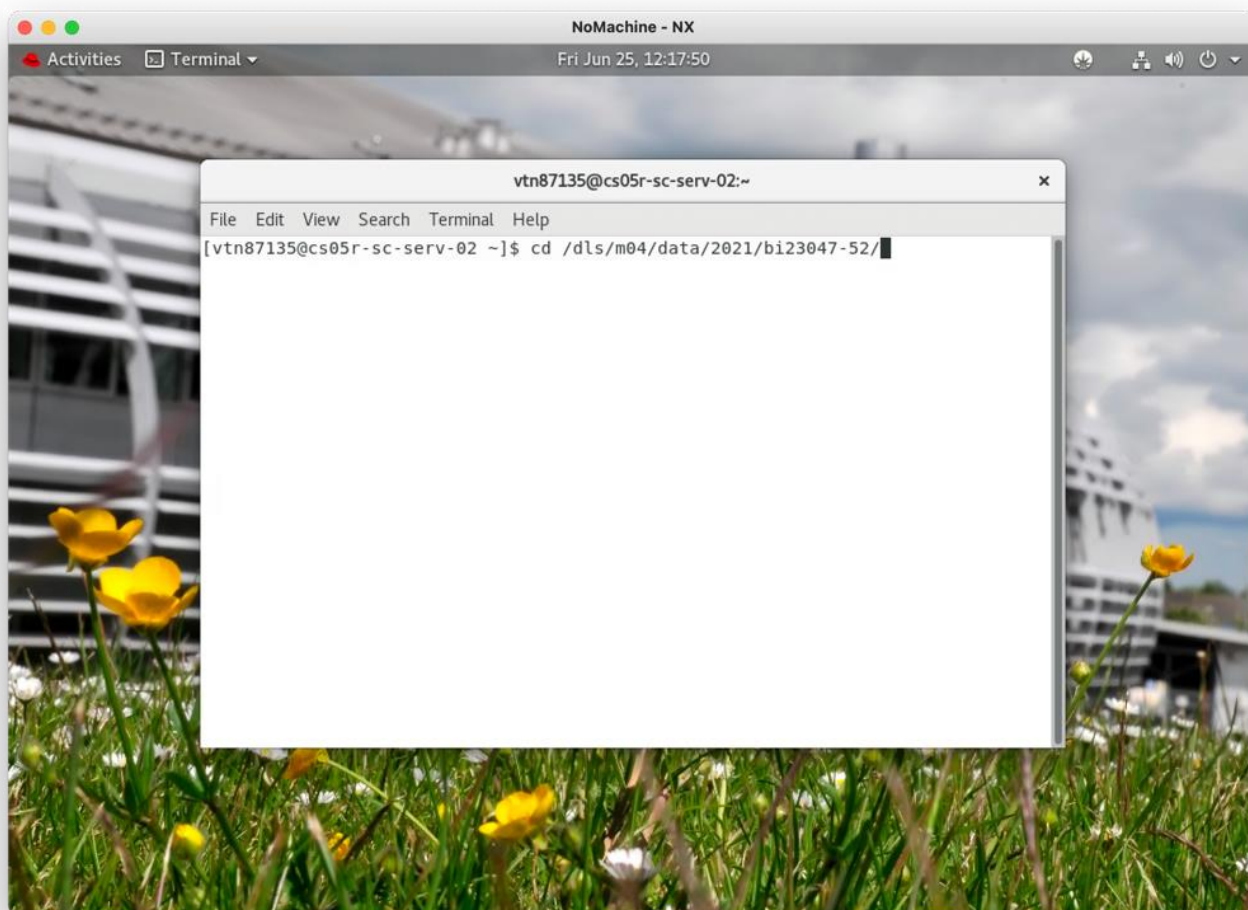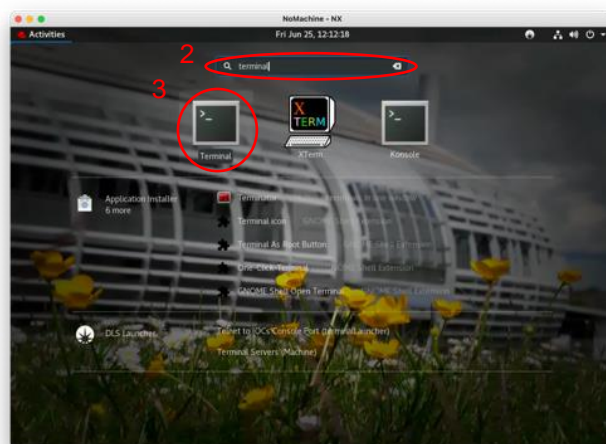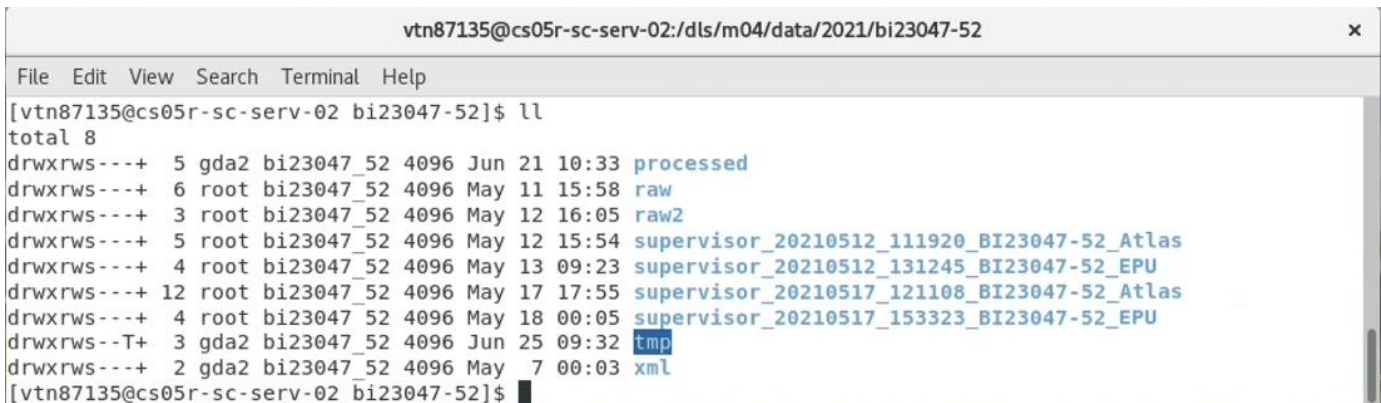
4.2.1 Check data is still being collected and transferred via a terminal

```
# To count the movies in the raw directory
$ find ./raw/GridSquare*/Data -name "*fractions.tiff" -printf '%T@ %Tc %p\n' | wc -l

# To list the recent movies in the raw directory
$ find ./raw/GridSquare*/Data -name "*fractions.tiff" -printf '%TF %TR 1 %p\n' | sort -n | cat -n | tail

# To monitor the number of movies in the raw directory at a 5 sec interval
$ watch -n 5 "find ./raw/GridSquare*/Data -name "*fractions.tiff" -print0 -printf '\n' | wc -l"

# To monitor several useful parameters at a 0.5 sec interval
$ export command="find ./raw/GridSquare*/Data -name "*fractions.tiff" -printf '%T@ %Tc %p\n' | sort -n"

$ watch -n 5 'export mic=$(eval $command | tail -n 1) && echo Latest micrograph: && echo $mic && echo ""
&& echo Total micrographs collected: && eval $command | wc -l'
```

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4.2.2 View the most recent unaligned movie frame average in imod

```
# Load the imod module (you only need to do this once per session)
$ module load imod

# Return the name and path of the most recent unaligned movie frame average
$ ls -ltr ./{EPU_session_directory}/Images-Disc1/GridSquare*/Data/*.mrc | tail -n 1

# Open the most recent unaligned movie frame average
# You may copy and paste the path from the previous command output
$ 3dmod ./{file_path}/{filename}
```

A 3dmod control window and micrograph will load. Please remember to close this window after you have finished checking your micrograph. Please keep in mind that this micrograph will NOT be motion corrected.

4.2.3 View the list of files being written by EPU in a file browser

```
# Use the Linux file browser, Nautilus, to open the EPU directory
$ nautilus ./{EPU_session_directory}/Images-Disc1/
```
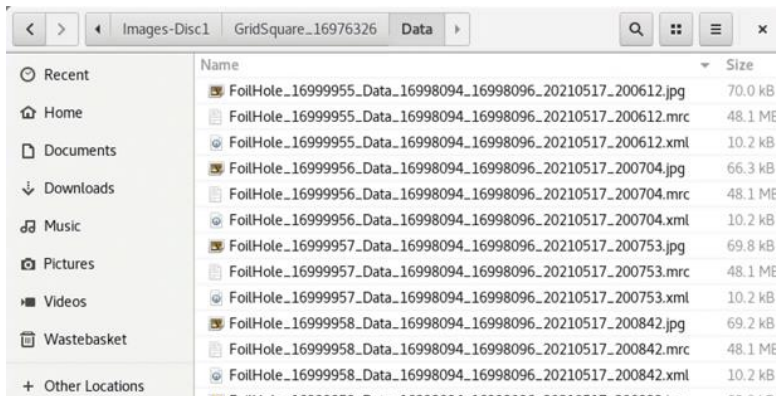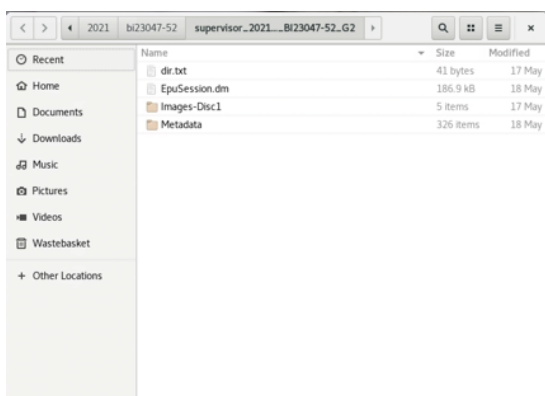

4.2.4 View the compressed *.jpgs of the unaligned movie frame averages

```
# Use the Linux image browser, eye of gnome, to browse the movie frame averages
$ eog ./{EPU_session_directory}/Images-Disc1/GridSquare*/Data/*jpg
```

4.2.5 Monitor your data collection session

☐ **Verify that new micrographs are being collected during your session**
☐ **In particular, follow 4.2.1 and ensure that new files appear in the list and that they have a recent time stamp.**

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> **!**
>
> Please note that EPU will pause collecting images (for all sessions) when LN2 is being refilled, or if you use a K3 camera, when GIF ZLP is being adjusted. However, this should not last longer that 15-20 minutes. Additional time might be required for EPU to move to a new target and acquire an image.
>
> Therefore, if after 30 minutes no new files appear from the command in section 4.2.1, please, contact your Local Contact (LC) directly during normal working hours (Monday-Friday 9am to 5pm) or Experimental Hall Coordinators (EHC) outside normal working hours (EHC contact phone number 01235 77 8787).
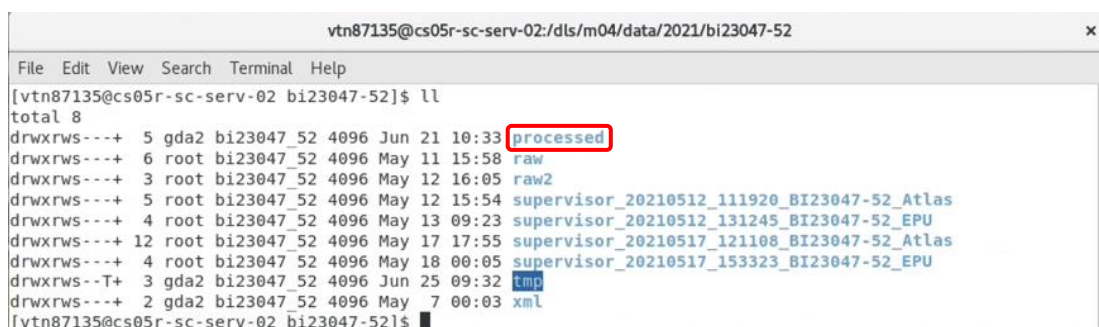
4.3 EPU: Inspect the on-the-fly data analysis results

Having navigated to your visit directory by following section 4.1, you can then use the terminal to inspect the progress of the on-the-fly analysis.

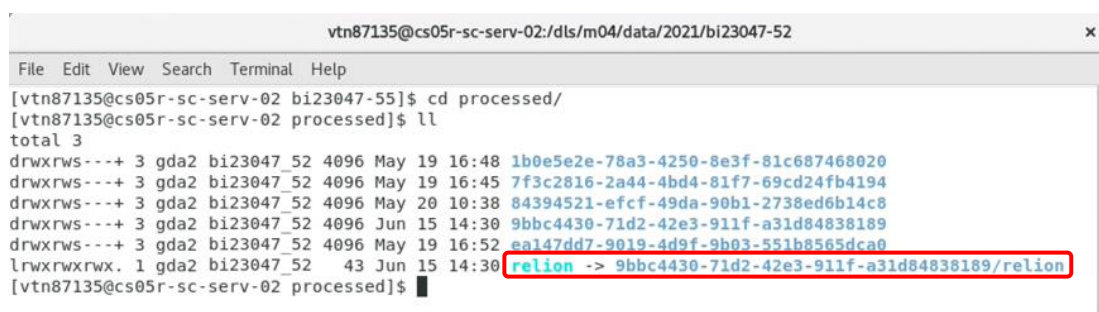Diamond provides several EM analysis software packages, which can be listed and loaded using the module system.

$ module avail EM/

The on-the-fly data analysis results will be contained in the ./processed folder of your visit directory.

Analysis jobs are given a unique identifier and a symbolic link (relion) is created pointing to the most recent analysis job:

☐ Load Relion to inspect the on-the-fly data analysis results

```
# Load the Relion module
$ module load EM/relion

# Change directory into the desired analysis job
$ cd ./processed/relion

# Load Relion in read only mode
$ relion --readonly
```

You may then use the Relion GUI to inspect the on-the-fly analysis results in the usual way. Please note, other programs such as Chimera and EMAN are available in the module system for exploring your data.

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4.4 TOMO5: Check data is being written to your visit directory

Having navigated to your visit directory by following section 4.1, you can then use the terminal to inspect the progress of the data collection. A typical TOMO5 directory structure is shown below. Follow a similar procedure to 4.2 and list the latest tomogram that was written to disk. Check the time stamp as it should be updated frequently.

```
vtn87135@cs05r-sc-serv-02:/dls/m04/data/2021/bi23047-52                    ×

File  Edit  View  Search  Terminal  Help
[vtn87135@cs05r-sc-serv-02 bi23047_5]$ ll
total 523
dr-xrws---+ 2 gda2       bi23047_5   4096 Jun 18 00:03 processing
drwxrws---+ 2 root       bi23047_5 524288 Jun 23 09:41 raw
drwxrws---+ 2 gda2       bi23047_5   4096 Jun 18 00:03 spool
drwxrwxr-x+ 6 m06detector bi23047_5  4096 Jun 21 13:46 Supervisor_20210621_BI23047-5_atlas
drwxrwxr-x+ 3 m06detector bi23047_5  8192 Jun 23 10:46 Supervisor_20210621_BI23047-5_tomo
drwxrws--T+ 2 gda2       bi23047_5   4096 Jun 18 00:03 tmp
drwxrws---+ 2 gda2       bi23047_5   4096 Jun 18 00:03 xml
[vtn87135@cs05r-sc-serv-02 bi23047_5]$
```

```
# To list the recent tilted movie frames in the raw directory
$ ls -ltr ./raw/*.mrc | tail

# To count the tilted movie frames in the raw directory
$ ls -ltr ./raw/*.mrc | wc -l

# To return the name and path of the most recent tilted movie frames
$ ls -ltr ./raw/*.mrc | tail -n 1

# To monitor the number of tilted movies in the raw directory at a 1 sec interval
$ watch -n 1 "ls -ltr ./raw/*.mrc | wc -l"
```

If you do not see the latest tomogram file being updated for longer than 20 minutes then you should reach out to your Local Contact (LC) during normal working hours (Monday-Friday 9am to 5pm) or Experimental Hall Coordinators (EHC) outside normal working hours (EHC contact phone number 01235 77 8787).

5 Download your data following your session

The data collected during your Diamond session will be moved from the microscope during your session but remain on the central filesystem for approximately 40 days. The data is then archived to tape backups and removed from the central filesystem. The archived copy remains on tape for the medium lifetime. Data can be downloaded from the archive using the topcat web interface (https://icat.diamond.ac.uk/#/my-data/DLS).

Please follow the next steps to download your data from the central filesystem. Note that Globus is significantly faster than SFTP.
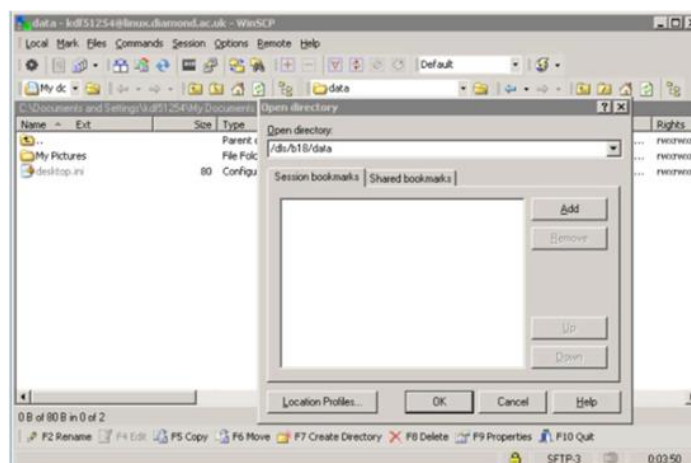
5.1 Transfer data to your home institute (SFTP)

5.1.1 Windows

☐ Start WinSCP and connect to the server 'nx.diamond.ac.uk' with your FedID
Try as CLRC\FedID if your FedID alone does not work
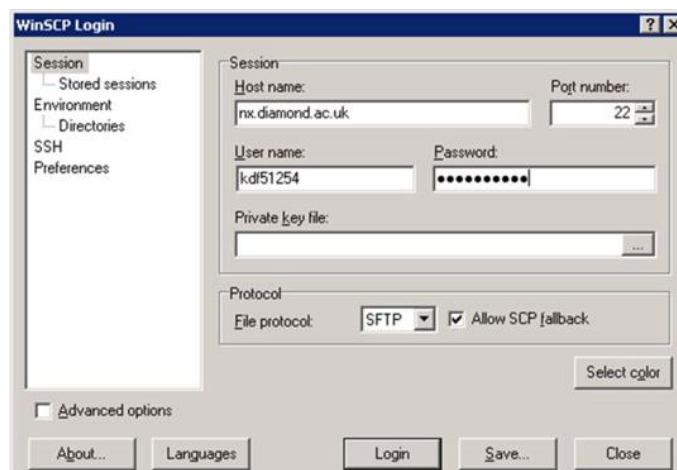
☐ Once connected, open the data directory on the beamline
/dls/{beamline}/data/2021/{visit number}

☐ Navigate to your experiment (data/2017/{visit number}) and copy the folder

5.1.2 Linux

There are numerous remote transfer clients for Linux; the shown examples are gFTP (using 'SSH2' as the protocol; the default FTP will not work), and command-line rsync.
You will have to log in using your FedID (if this does not work immediately then try adding CLRC before the FedID). Note that this drops you into your home directory (/home/{FedID}), from where you will have to navigate into the data directory from which you want to transfer. The data directory can be found as /dls/{beamline}/data/{year}/{visit number} and you can transfer data via drag and drop.
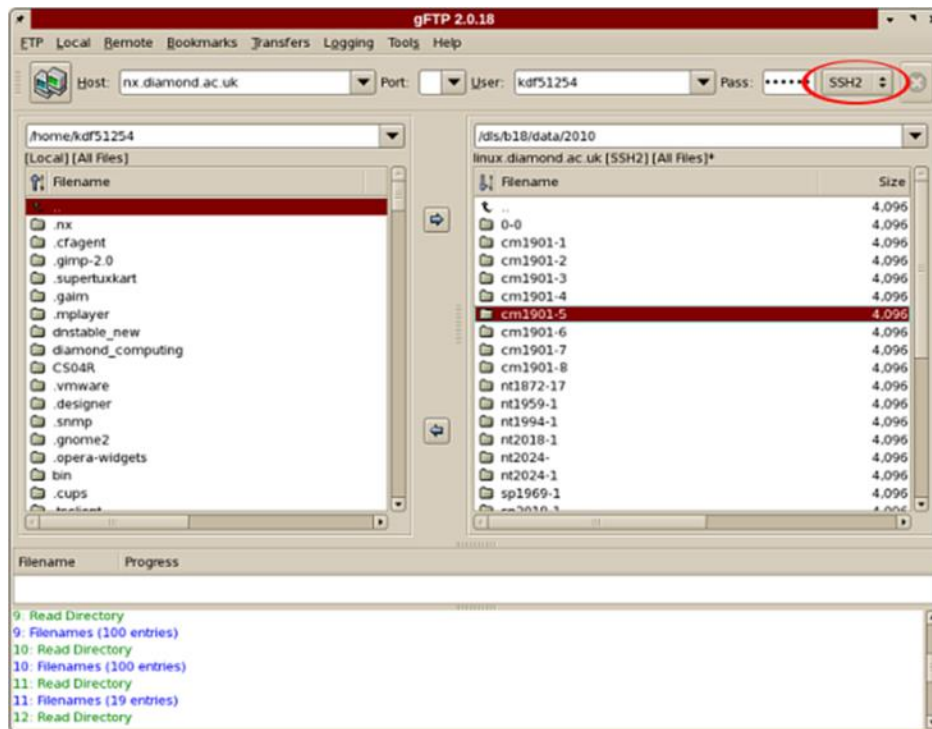
Alternatively, transfer data from your experiment using command-line rsync in a terminal window.
Navigate to the area of your local disk where you will put the data then enter the following command and authenticate with you FedID password to start the transfer.

```
$ rsync – av –e ssh {fedID}@nx.diamond.ac.uk:/dls/{beamline}/data/{year}/{visit number}/raw .
```

5.1.3 Mac OS (Apple)

There are numerous remote transfer clients for Mac; the shown example is FileZilla. The rsync transfer shown in the linux section will also work using mac terminal.

Open Filezilla and click on the site manager icon and select new site. Then enter nx.diamond.ac.uk in the host and use the SFTP protocol. Then put your FedID in as the user and then select Ask for password as logon type. Then click connect and enter your password.
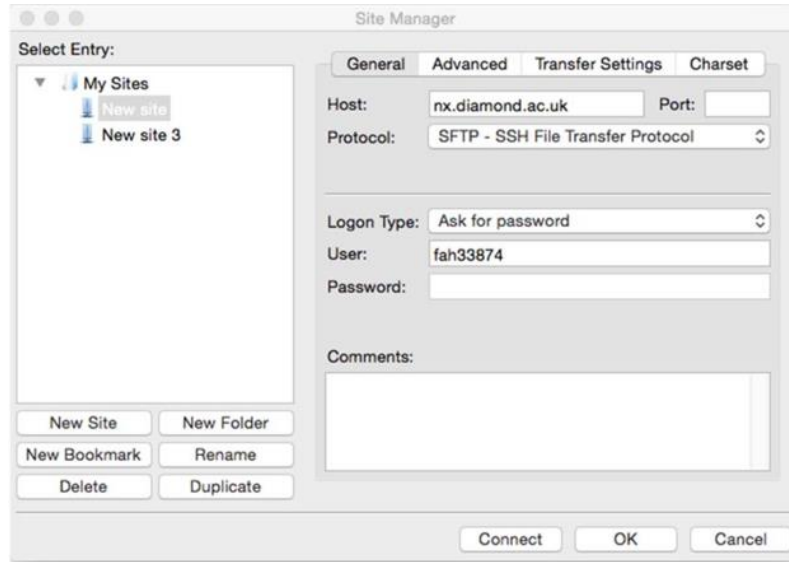
☐ Navigate to your visit folder in the left hand side of the panel and then drag the directories you require into the area on your local file system
/dls/{beamline}/data/{year}/{visit number}
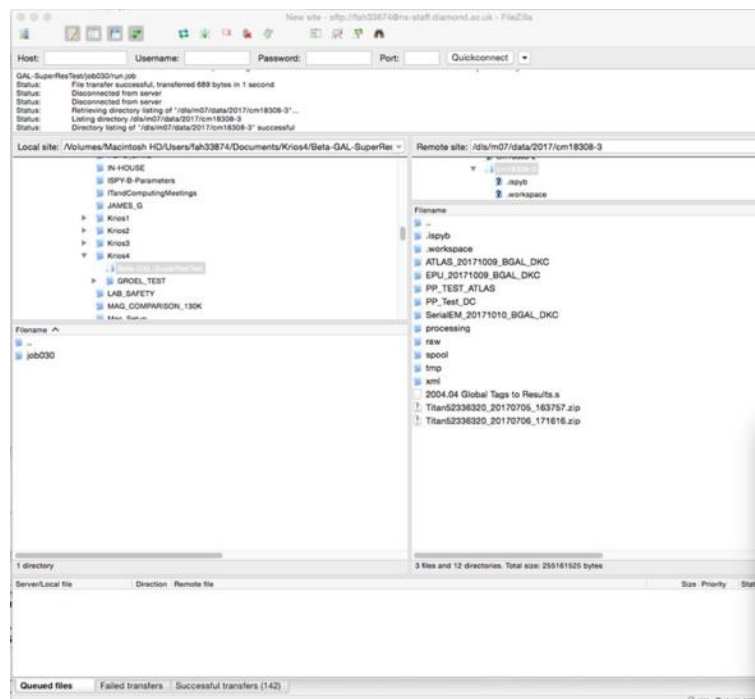
5.2 Transfer data to your home institute (Globus)

5.2.1 Introduction

This is how researchers can download large datasets from Diamond using Globus Online, a service designed to optimise the file transfer process.
1. Log in to a web interface called Globus Online 2. Log in to Diamond with your usual FedID
3. You will see a folder browser with all mounted beamlines
4. Select the files you want to transfer to your institute's Globus server
5. Click the transfer button, the file transfer is managed by Globus Online
• You may close the window and shut down your laptop - the transfer between servers will proceed and you be emailed when the transfer is complete

5.2.2 Setting up Globus

To send files using Globus Online you will need:
1. A free Globus Online account
2. Globus Connect endpoint software
• Globus Connect might already be set up at your institution
• You can set up a Globus Connect endpoint on your own server, workstation or laptop

5.2.3 Getting started

Follow steps 1, 2, 3 and 4 of the Globus 'Getting Started guide' at https://www.globus.org/researchers/getting-started

5.2.4 Seeing your file at Diamond

Diamond's Endpoint is called diamondftp#transit.diamond.ac.uk
1. Go to the Globus Transfer Files page
2. Go to the left box
3. In the 'endpoint' put diamondftp#transit.diamond.ac.uk and click Go
4. In the Username and Password boxes put your Diamond FedID and password.
5. When you click 'Authenticate' you should see a list of beamlines on the left-hand side.

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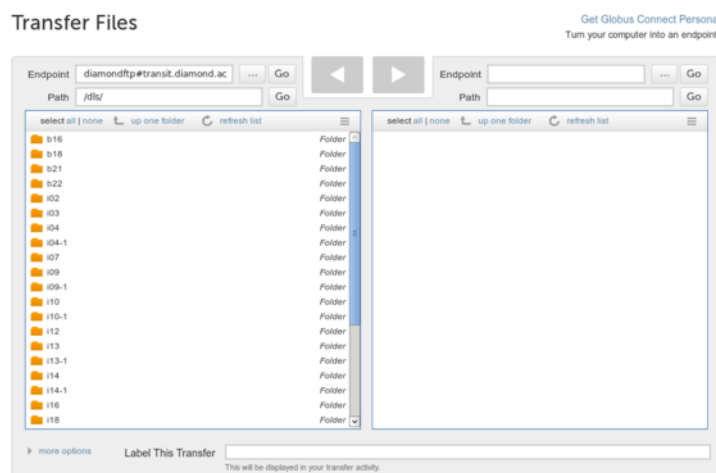
5.2.5   Finding your institution

Many campuses, research labs, and cross-site projects have already set up Globus server endpoints on their servers.

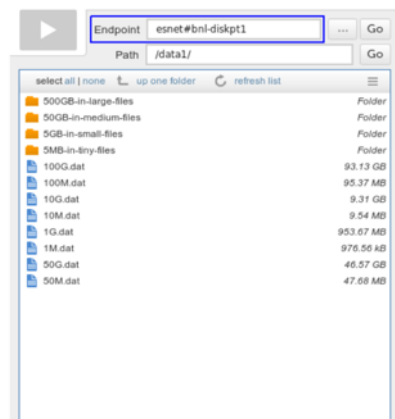### 5.2.6   Your institute already has a Globus endpoint

If your institution has already set up a Globus endpoint:
1. Enter the institute's endpoint name on the Globus Transfer Files page and click Go
2. Put in your username and password for your home institute and click Authenticate

5.2.7   Searching for your institution's endpoint

The endpoint name is a Globus-specific name that identifies a server inside the Globus Online system.

Globus endpoints are named using the format <globus-username>\#<resource-name>. For example, the XSEDE project has a Globus account under the username 'xsede' and server endpoints named xsede#stampede (for the Stampede system at Texas Advanced Computing Center).

If you don't know your institute's endpoint name, you can use the Globus Transfer Files page to search. Just enter a likely name in the Endpoint field and look for the resource in the scroll-down list. For example, 'umich', 'nersc', 'xsede', . . .
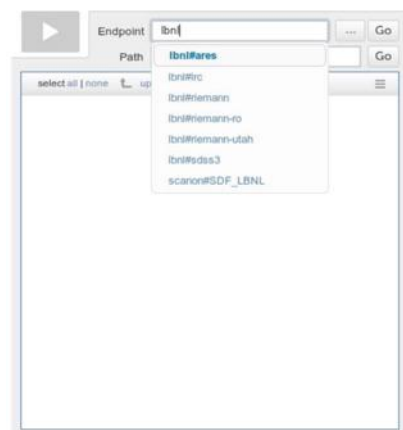
5.2.8   Your institute is not found in the list

The Globus Online software needs to be running at your institution so that we can send files to you. See the Appendix 'Installing the Globus Online software' to install Globus Online on a server, workstation or laptop.

5.2.9   Sending files

1. On the Transfer Files page Use Globus Online to log in to Diamond on one side, and log in to your institution on the other side
2. You will see a folder browser on the left with all available beamlines 3. Use the folder browser to find your visit
4. Select the files or folder you want to transfer to your institute
5. Click the transfer button to start the transfer
6. The file transfer is managed by Globus Online
• You may close your web browser; the transfer will carry on between servers
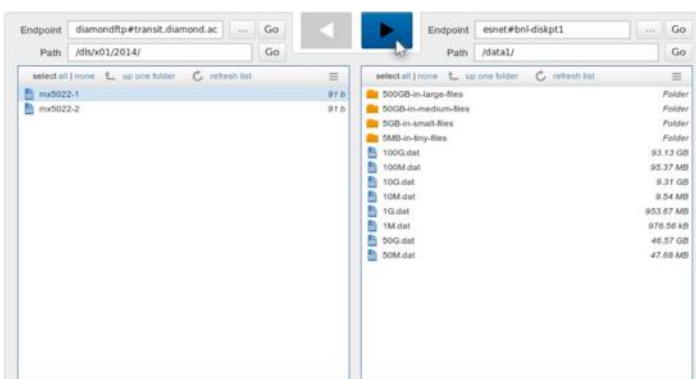
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• You will get an email when the transfer is finished

5.3 Appendix A - Installing the Globus Online software

If your institution is not set up as a Globus endpoint, you need to set up a Globus Connect endpoint on your own server, laptop or desktop.
• We recommend installing on a dedicated server if your institution has experience working with Linux systems

5.3.1 A.1 - Installing on your own desktop or laptop

This tells you how to install Globus Connect Personal on your desktop or laptop. You will need:

1. A machine running either a Windows, Linux or MacOS
2. Administrator permissions to install software on the machine
3. Access to enough free disk space for your research data

Follow the guide at: https://www.globus.org/globus-connect-personal

5.3.2 A.2 - Setting up a dedicated Globus server at your institution

This tells you how to install Globus Connect Server on a dedicated server. You will need a server with:

1. Access to enough free disk space for your research data
2. A recent version of Linux:
• (Red Hat Enterprise Linux (RHEL), CentOS, Scientific Linux, Fedora, SuSE Linux Enterprise Server, Ubuntu or Debian)

3. A reliable, fast network connection. Follow the guide at:
    https://www.globus.org/globus-connect-server
    Click 'Install Globus Connect Server'