

MXCuBE user manual Proxima1



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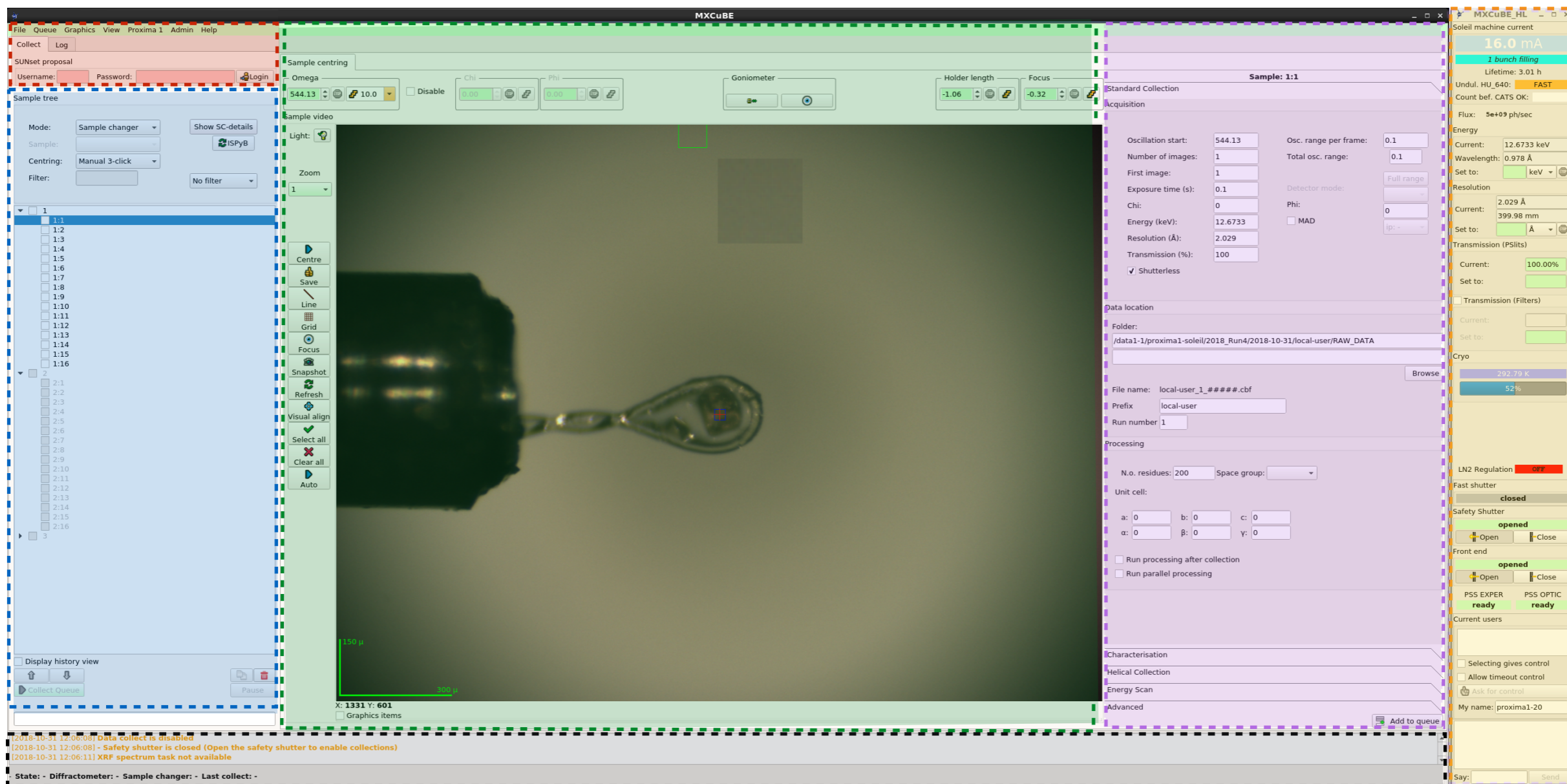
MXCuBE user manual

Proxima1

Part I: The Graphical User Interface (GUI) Description

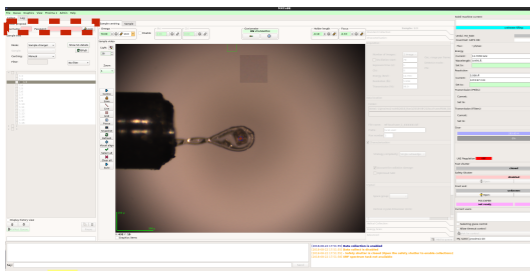


GUI: The “Main” page

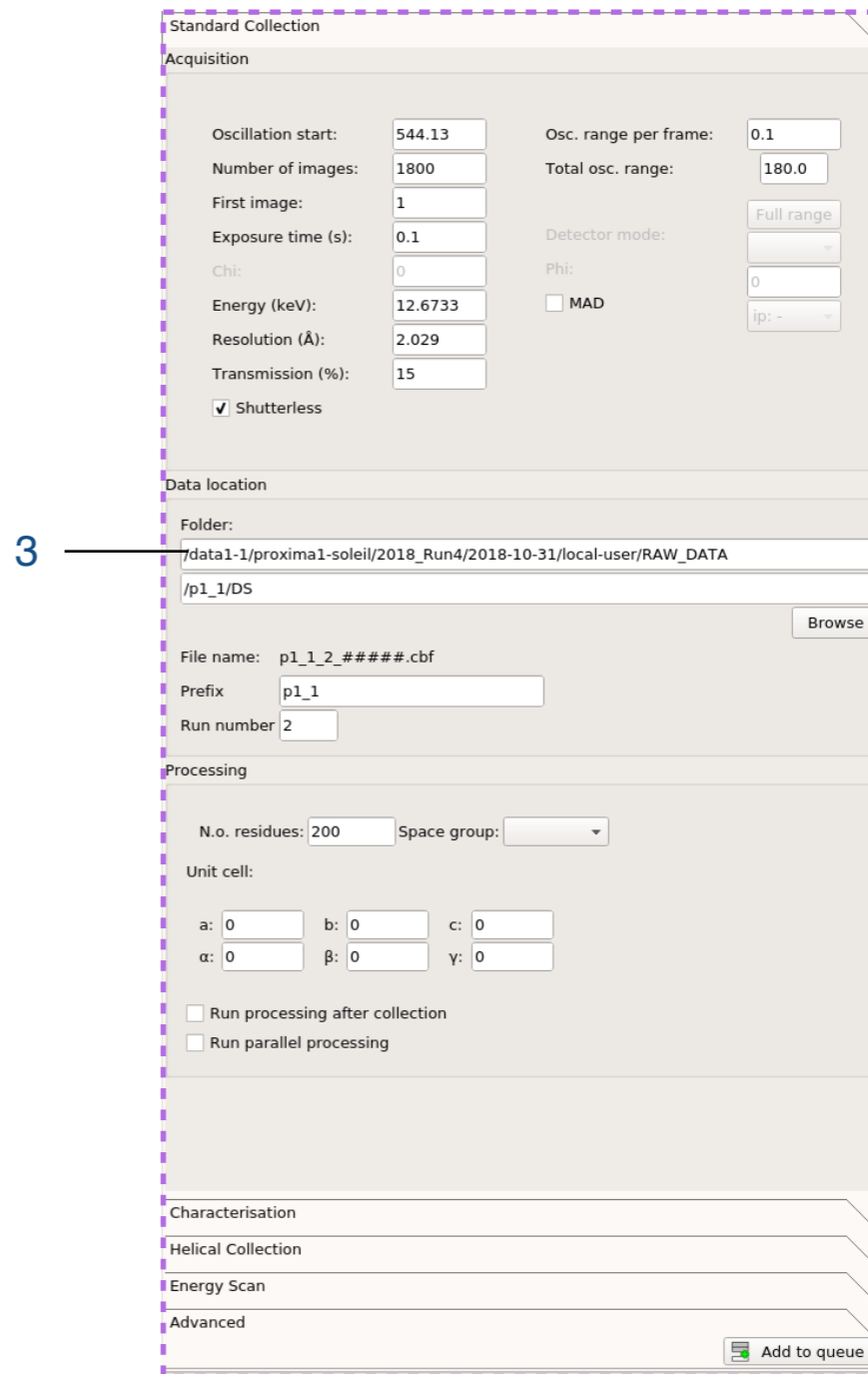
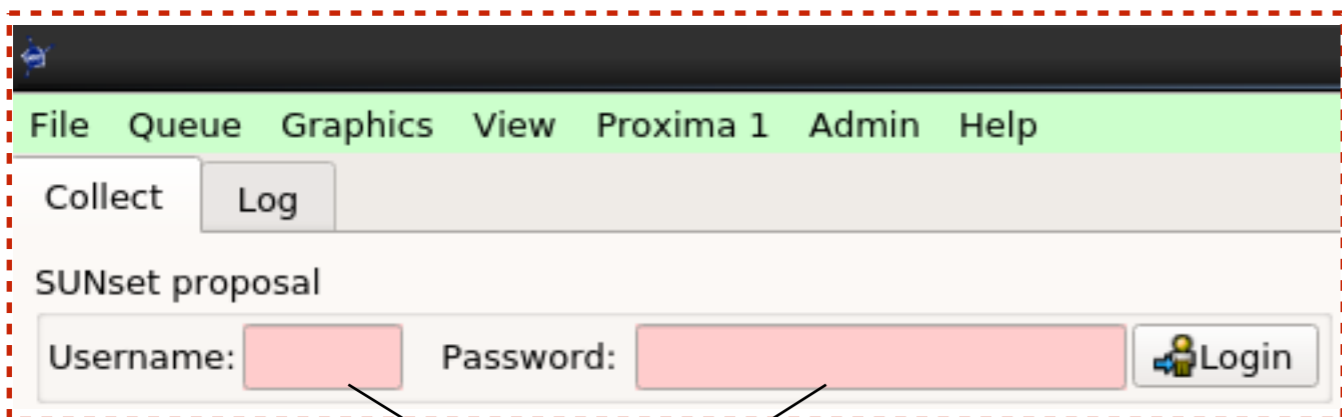
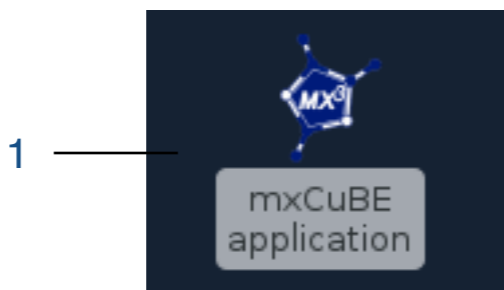


The MxCuBE graphic user interface (GUI) operational areas:

- Login
- Sample tree and data collection queue
- Sample centring
- Collection method
- Machine status
- Dialogue box



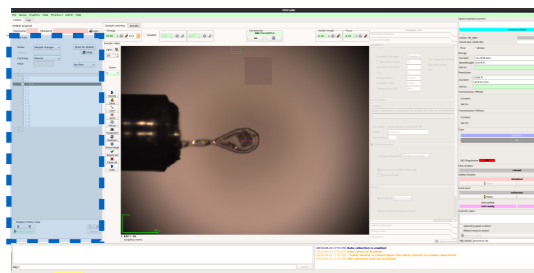
GUI: The "Main" page The login area



1. Click on the mxCuBE icon on the computer Desktop to open the application
2. Enter your login (proposal number) and password, then click on « Login »
2. The path where your data will be stored will appear in the collection method area

GUI: The “Main” page

The sample tree and queue area (1)



1

Sample tree

Mode: **Manually mounted**

Sample changer

Hide SC-details

Sample:

ISPyB

Centring: Manual

Filter: No filter

Sample tree

Mode: Sample changer

Sample:

ISPyB

Centring: **Manual**

Filter: No filter

2

Sample tree

Mode: Sample changer

Sample:

ISPyB

Centring: Manual

Filter: No filter

3

No filter

Star

Sample name

Protein name

Basket index

Executed

Not executed

OSC

Helical

Charaterisation

Energy Scan

XRF Spectrum

Advanced

1

2

3

Sample tree

Mode: Manually mounted

Show SC-details

Sample: ISPyB

Centring: Manual

Filter: No filter

4

manually-mounted

Display history view

Collect Queue

Pause

Sample tree

Mode: Sample changer

Show SC-details

Sample: ISPyB

Centring: Manual

Filter: No filter

5

1:1 Centring done 1

1:2

1:3

1:4

1:5

1:6

1:7

1:8

1:9

1:10

1:11

1:12

1:13

1:14

1:15

1:16

2

3

7

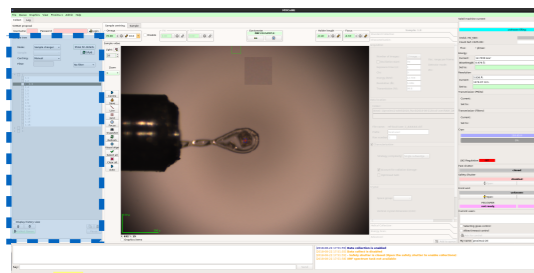
8

Display history view

Collect Queue

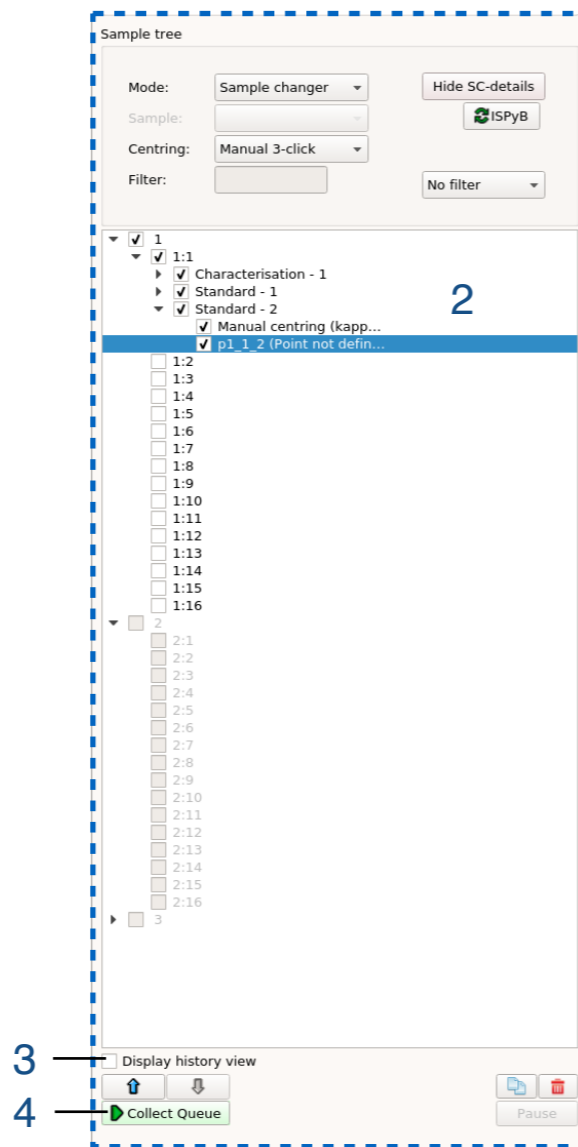
Pause

1. Select the sample-mounting mode
2. Choose the sample-centring mode
3. Choose the queue-filtering mode
4. Synchronize with ISPyB database to display a sample list. This mode is not implemented for BAGs yet
5. Show sample changer (SC) details
6. In sample changer mode: sample list is sorted by puck (sample:puck = 1:1)
7. Delete selected collections
8. Pause the running chain of tasks



GUI: The “Main” page

The sample tree and queue area (2)



1. Sample tree
2. Tick the box corresponding to:
 - ▶ A puck: to collect all tasks corresponding to this puck when collecting on Collect queue
 - ▶ First line: to collect all tasks corresponding to this sample when collecting on Collect queue
 - ▶ A particular task: to collect only this task when collecting on Collect queue

Sample status color code:

- ▶ No color= not selected
- ▶ Blue= selected

Task status color code:

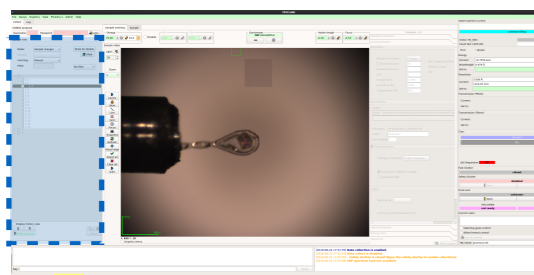
- ▶ No color= not selected
- ▶ Green= collected
- ▶ Red= collection failed

3. Select 'Display history view' to see the history of the tasks performed

4. Collect queue starts data collection

GUI: The “Main” page

The sample tree and queue area (3)



The screenshot shows the main GUI interface with the following numbered callouts:

- 1**: Points to the 'Sample changer' button in the 'Sample centring' section.
- 2**: Points to the 'Load' button in the 'Contents' section.
- 3**: Points to the 'Unload' button in the 'Contents' section.
- 4**: Points to the 'Wash' button in the 'Contents' section.
- 5**: Points to the 'Power On' button in the 'Arm Power' section.
- 6**: Points to the 'Power Off' button in the 'Arm Power' section.
- 7**: Points to the 'Regulation On' button in the 'LN2 Regulation' section.
- 8**: Points to the 'Clear Memory' button in the 'Actions' section.
- 9**: Points to the 'Dry & Soak' button in the 'Actions' section.
- 10**: Points to the 'Home/Open' button in the 'Actions' section.
- 11**: Points to the 'Safe' button in the 'Actions' section.
- 12**: Points to the 'CATS message' section showing 'doors opened'.
- 13**: Points to the 'CATS Status' section showing 'Number of sample before the next dry and soak command : 10'.
- 14**: Points to the 'Display history view' checkbox at the bottom left.
- 15**: Points to the 'Collect Queue' button at the bottom left.

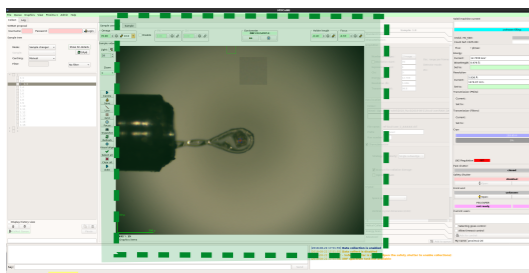
1. The SC-details window allows you to control the sample changer loading:

- ▶ Green= Collected samples
- ▶ Black= Not collected samples

2. Load selected sample
3. Unload selected sample
4. Wash sample. This will unload the sample and quickly reload it. This procedure is often very efficient to get rid of ice
5. Power ON the robot
6. Power OFF the robot
7. Power ON the N2 automatic regulation of the robot dewar
8. ‘Clear Memory’, for the Local Contact
9. ‘Dry and Soak’ dries and cools down the tong of the robot
10. ‘Home/Open’ pulls out of the dewar the arm of the robot and opens the lid of the dewar
11. ‘Safe’ button to recover after soft collision *
12. Error messages form the robot
13. Status messages of the robot. If the key is not in remote mode you will find a message here
14. Display tasks history
15. Collect the queue tasks

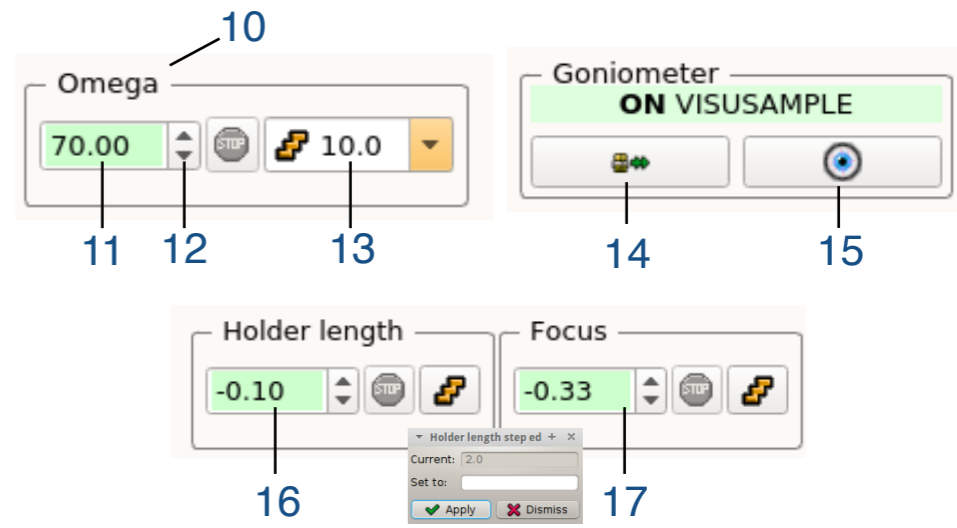
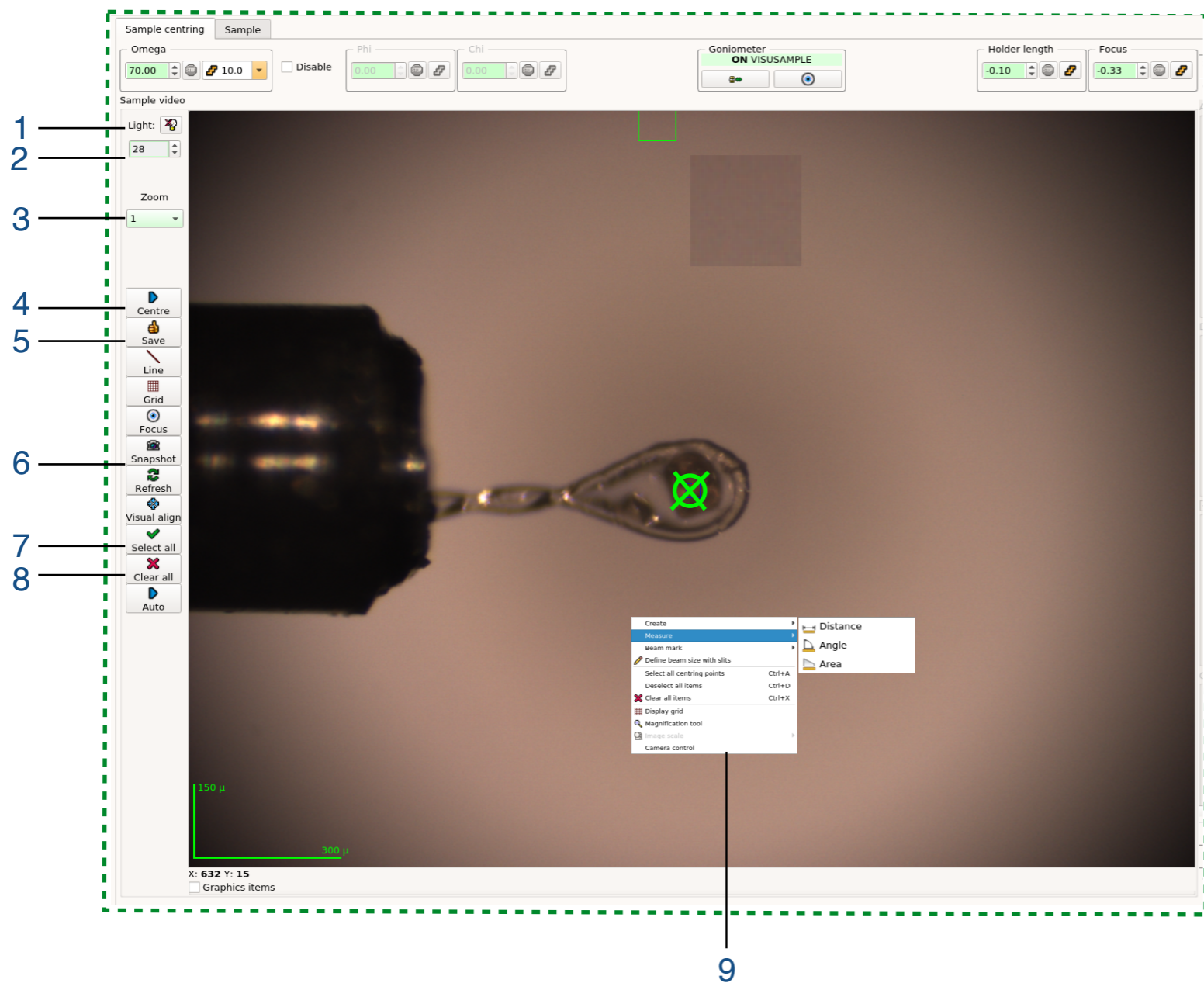
* A soft collision implies that the robot is still power ON after the collision

** Attention: This interface is not meant to load the sample. Please see the section ‘[Load and unload a sample](#)’. Double click on a sample will load it!



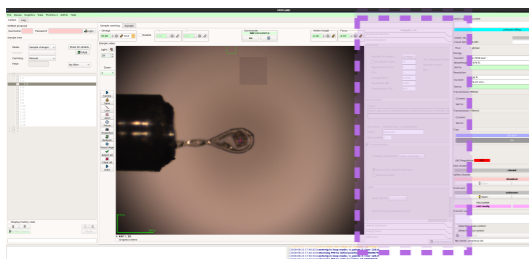
GUI: The "Main" page

Sample centering and video area



1. Tick to switch the light on
2. Intensity of the light
3. Zoom of the camera
4. Centre the sample
5. Save the centring position
6. Take snapshot of the crystal
7. Select all centring positions
8. Delete all centring positions
9. Measurements tool box (right click)

10. Parameter
11. Current value of parameter
12. Tune up and down the parameter by the step defined in 13
13. Tuning step
14. Enter the hutch and manual mounting of the sample
15. Activate the centring mode
16. Holder length (click on ladder, insert value and Apply)
17. Focus (click on ladder, insert value and Apply)



GUI: The “Main” page Collection method area

p1_1_2 (Point not defined)

Standard Collection

Acquisition

Oscillation start: 544.13 Osc. range per frame: 0.1
 Number of images: 1800 Total osc. range: 180.0
 First image: 1
 Exposure time (s): 0.1 Detector mode: Full range
 Chi: 0 Phi: 0
 Energy (keV): 12.6733 MAD ip: -
 Resolution (Å): 2.029
 Transmission (%): 15
 Shutterless

Data location

Folder:
 /data1-1/proxima1-soleil/2018_Run4/2018-10-31/local-user/RAW_DATA
 /p1_1/DS 2

File name: p1_1_2_#####.cbf
 Prefix: p1_1
 Run number: 2

Processing

N.o. residues: 200 Space group:
 Unit cell:
 a: 0 b: 0 c: 0
 α: 0 β: 0 γ: 0
 Run processing after collection
 Run parallel processing

Characterisation
 Helical Collection
 Energy Scan
 Advanced

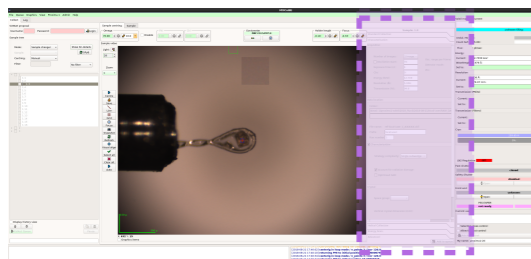
3

1. Collection methods (Characterisation, Energy Scan, Standard Collection, Helical Collection)
2. Pathway for your data. Diffraction images will typically be stored in a subdirectory of your choice under RAW_DATA:

 The pathway is automatically filled once you are logged in with your Proposal number and password. Fill in the subdirectory name

 Fill in the prefix of the sample

 The Run number is automatically incremented at the end of each experiment of the same type
3. For each collection method, « Add to queue » will add the collection to the selected samples and display it in the sample tree and queue area



GUI: The “Main” page Collection method area « Characterisation »

Sample: 1:1

Standard Collection

Characterisation

Acquisition

1 — Number of images: 4 Image ▾

Oscillation start: 0

2 — Exposure time (s): 1

Chi: 0

Energy (KeV): 12.6733

Resolution (Å): 2.897

Transmission (%): 14.9

Osc. range per frame: 1

Detector mode: ▾

Phi: 0

Data location

Folder: /data1-1/proxima1-soleil/2018_Run4/2018-11-06/local-user/RAW_DATA

/test Browse

File name: ref-pos1_1_#####.cbf

Prefix: pos1

Run number: 1

3 — Characterisation

Strategy complexity: Single subwedge ▾

Account for radiation damage

Optimised SAD

4 — Crystal

Space group: ▾

Vertical crystal dimension (mm):

Helical Collection

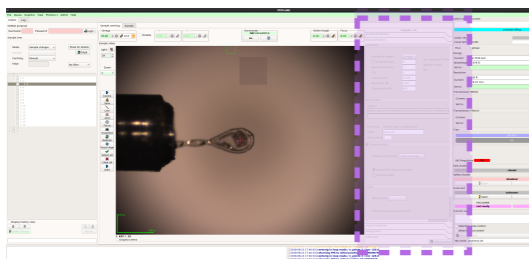
Energy Scan

Advanced

Add to queue

Use the Characterisation method when you want to test the diffraction of your crystal or run a data collection strategy with xdsme

1. Number of images taken to characterize the crystal (1, 2 or 4) corresponding to the angles: (0° , $0^\circ - 90^\circ$, $0^\circ - 90^\circ - 180^\circ - 270^\circ$).
2. The value of Chi used in the Characterisation is the same as that used for sample centring
- 3, 4. Not implemented yet



GUI: The “Main” page « Standard Collection »

Sample: 1:1

Standard Collection

Acquisition

Oscillation start: Osc. range per frame:

Number of images: Total osc. range:

First image:

Exposure time (s): Detector mode:

Chi: Phi:

Energy (keV): MAD

Resolution (Å):

Transmission (%):

Shutterless

Data location

Folder:

File name:

Prefix

Run number

Processing

N.o. residues: Space group:

Unit cell:

a: b: c:

α : β : γ :

Run processing after collection

Run parallel processing

Characterisation

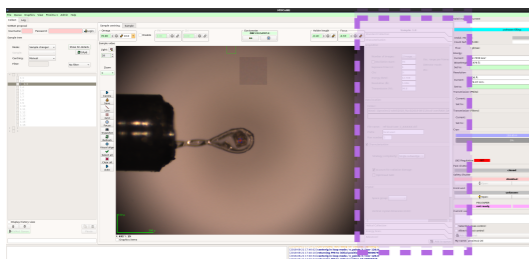
Helical Collection

Energy Scan

Advanced

Use the Standard Collection to collect a complete data set of your crystal based onto the xds data collection strategy plan

1. Data collection parameters obtained from the strategy plan
2. Tick if you want to collect MAD dataset at the energies of peak, inflection point and remote from an Energy Scan
3. Directory where the images will be stored.
Processing information will be automatically filled if a isample list is synchronized from ISPyB (not implement for BAGs yet)



GUI: The “Main” page « Energy Scan »

Sample: 1:1

Standard Collection

Characterisation

Helical Collection

Energy Scan

1 — Zn — Edge: K — 2

Data location

3 — Folder: /data1-1/proxima1-soleil/2018_Run4/2018-10-31/local-user/RAW_DATA

/Escan_Zn

File name: p1_1_1_#####.raw

Prefix: p1_1

Run number: 1

Parameters

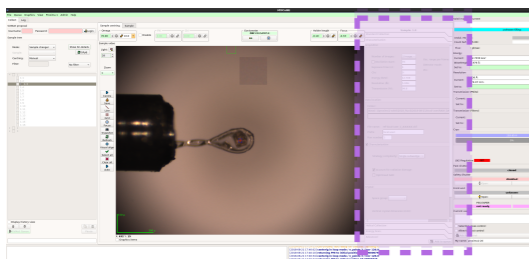
Adjust transmission

Maximum transmission: 20

Advanced

Use the Energy Scan if your crystal contains anomalous scatterers (Fe, Cu, Zn...)

1. List of the anomalous scatterers
2. List of the absorption Edges
3. Directory where the images will be stored



GUI: The “Main” page « Helical Collection »

2

Sample: manually-mounted

Standard Collection
Characterisation
Helical Collection

Line

Name	Start point	End point
Line 1	1	2

Display overlay Swap point

Acquisition

Oscillation start: Osc. range per frame:

Number of images: Total osc. range:

First image:

Exposure time (s): Detector mode:

Chi: Phi:

Energy (keV): MAD

Resolution (Å):

Transmission (%):

Shutterless

Data location

Folder:

File name: local-user_1_####.h5

Prefix:

Run number:

Processing

N.o. residues: Space group:

Unit cell:

a: b: c:

α : β : γ :

Run processing after collection

Run parallel processing

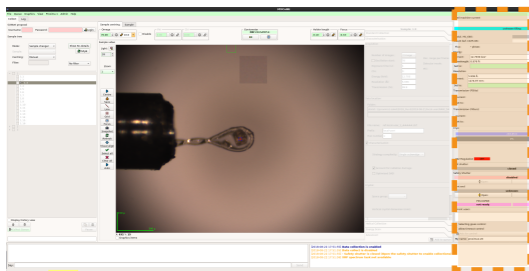
Energy Scan
Advanced

1

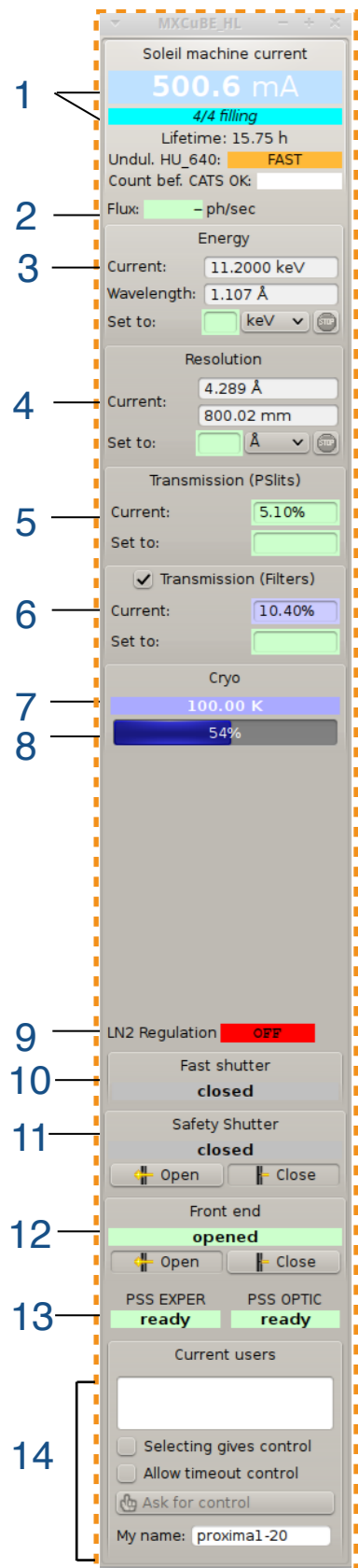
Use the Helical Collection if you want to collect your sample along a straight line (recommended for samples in the shape of rods)

1. Data collection parameters
2. Helical collection task
3. Directory where the images will be stored.

3



GUI: The “Main” page Machine status



1. Machine current and filling mode
2. Flux of photons at sample position
3. Beamline energy. Nominal energy of the beamline is 12.67 keV.
To tune the energy beamline enter a value in the « Set to » box and press enter then select the corresponding units (Å or keV)
4. Maximum resolution (recorded at the edge of the detector).
To change resolution enter the new value in the « Set to » box and press enter then select the corresponding units (Å or keV)
5. Beam Transmission by the primary slits (PSlits).
To adjust the transmission of the beam, enter a new value in the « Set to » box and press enter
6. Beam Transmission by the Filters.
Change only when doing XRF scans or energy scans (please ask the Local Contact)
7. Cryogenic stream temperature at the sample position
8. N2 level in the CryoCane dewar
9. N2 regulation of the robot dewar
10. Open/Close the Fast shutter
11. Open/Close the Safety shutter
12. Open/Close the Front end
13. State of the PSS of Experimental and Optical hutch (green= PSS is running, red= PSS is not running)
14. Remote access menu (for the Local Contact)

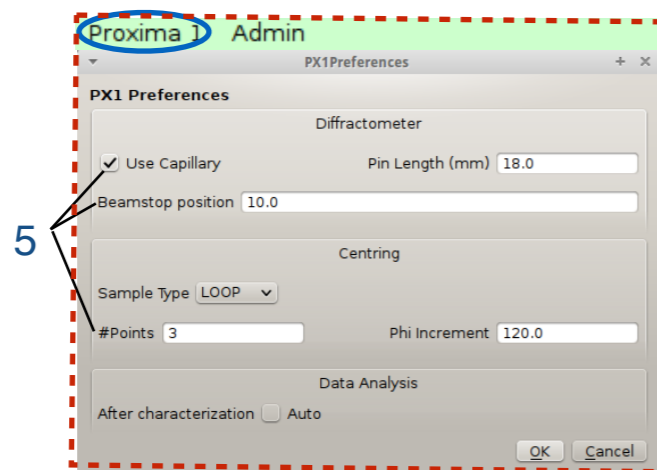
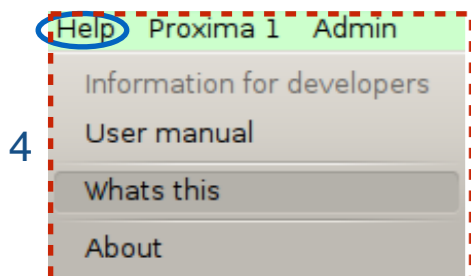
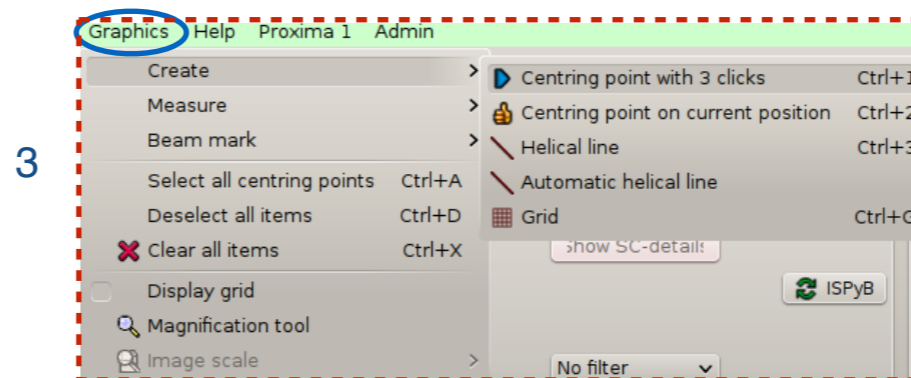
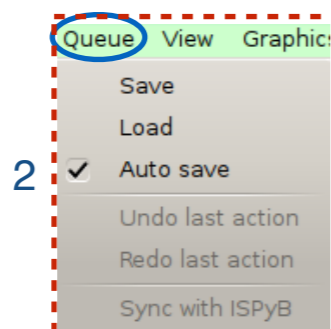
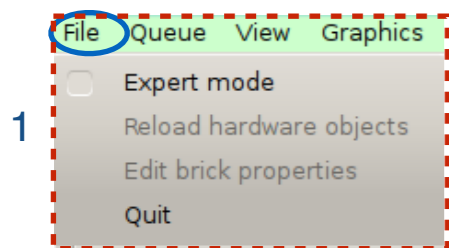
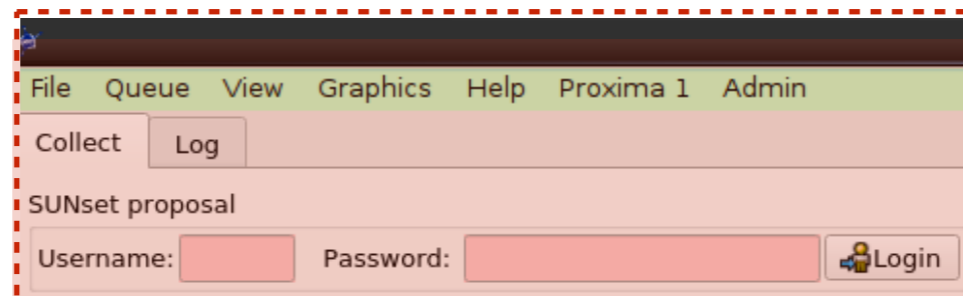
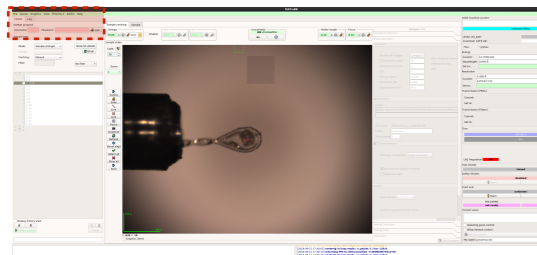
Open/Close color code:

grey= closed
green=opened

PSS color code:

green= PSS is running
red= PSS is not running

GUI: The “Main” page Sub-menus



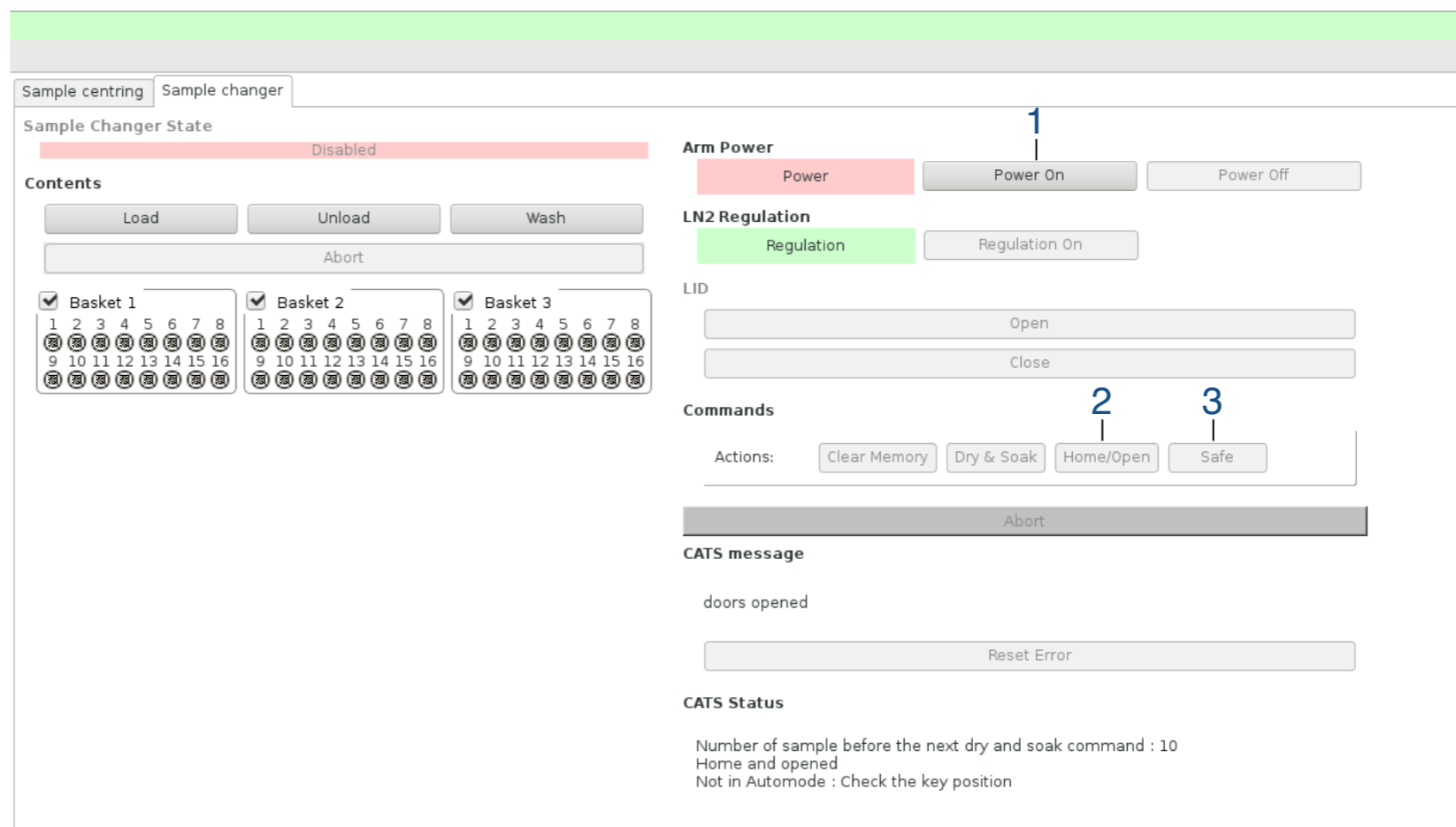
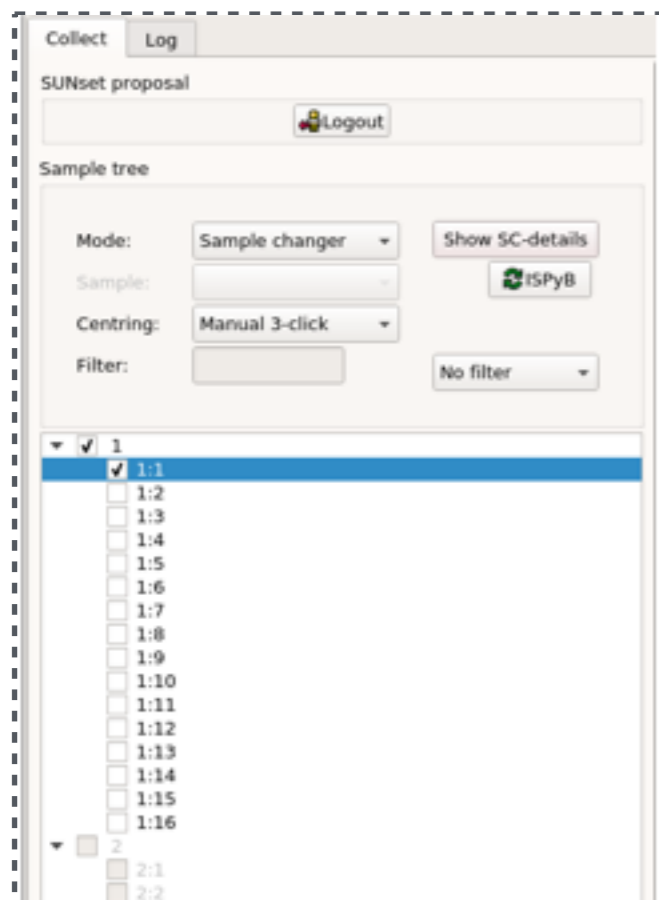
1. Expert mode (for the local contact)
2. Sample tree mode
3. Centring, measurement and item selection tools
4. Access to MXCuBE manual and Information for Developers
5. Go in Proxima1 -> Edit Preferences to access the following options:
 - Use capillary: Ticked by default. Untick if you don't want to use the capillary
 - Beamstop position: Default value is 10mm but you can move it up to 30 mm to collect the low resolution
 - #Points: Select the number of points used for centring and the corresponding Phi angle increment

MXCuBE user manual

Part II: Practical guidelines

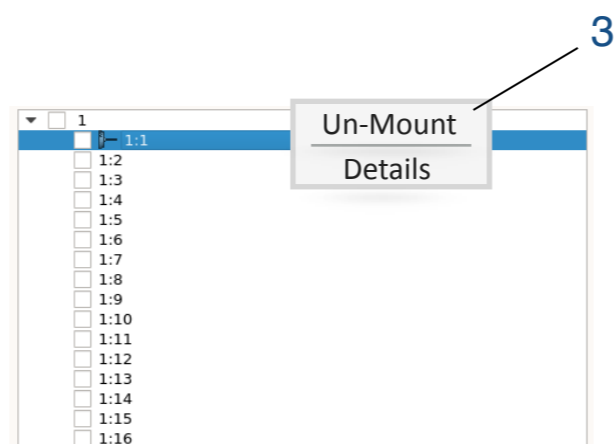
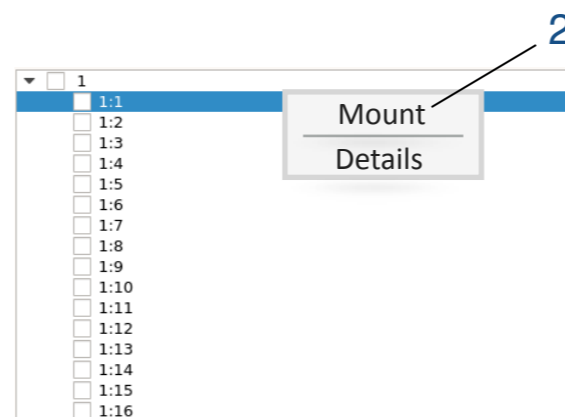
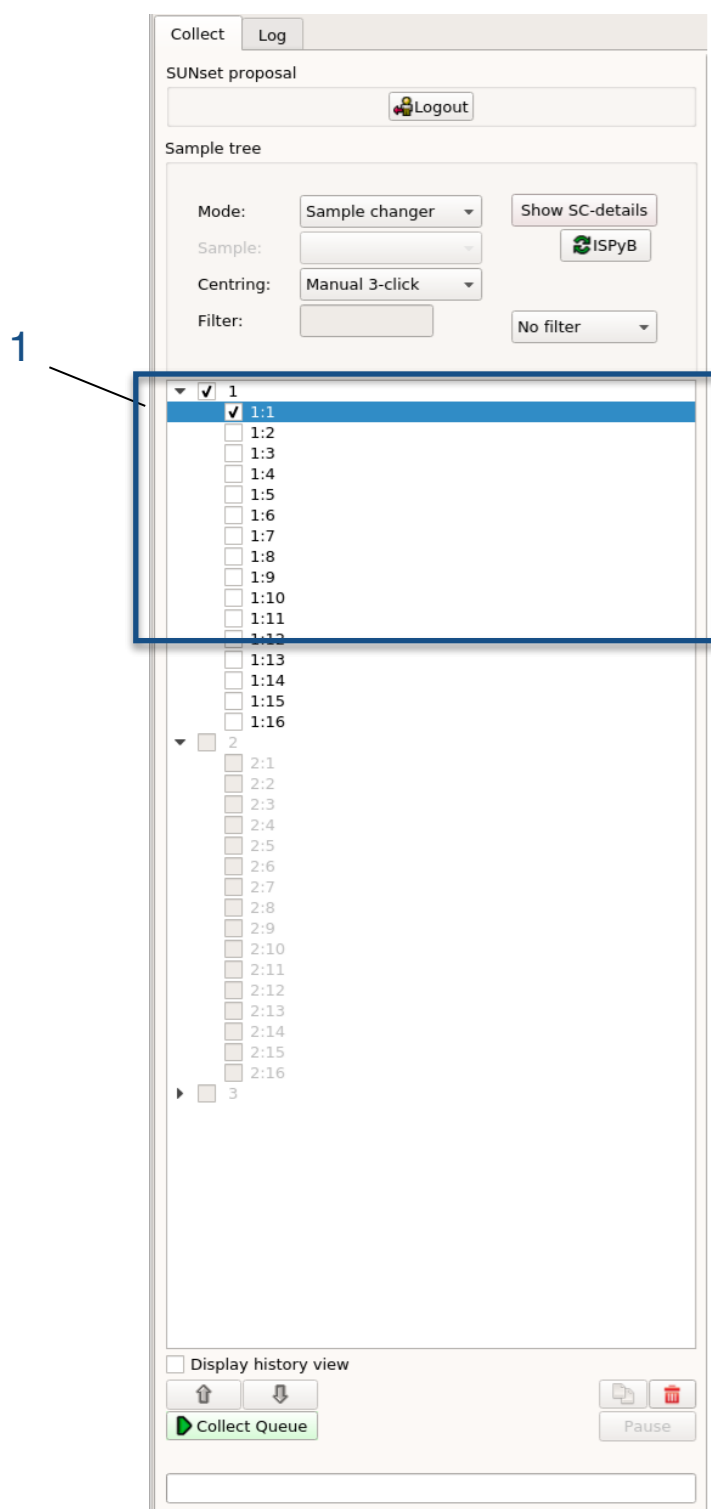


Practical guidelines: Prepare the robot for sample charging



1. Click on the « Show SC-details » to access to the
2. Click on Power ON to switch the robot ON
3. Click on Dry & Soak to dry and cool down the arm of the robot before charging the first sample.
 - The dry and soak procedure is mandatory the first time after loading the pucks. Afterwards it is automatically performed every 10 samples and after a Safe procedure
 - At the end of the dry and soak the lid of the dewar is closed and the arm of the robot plunges inside the dewar
4. Load the sample
5. Centre the sample and save
6. Select « Characterisation » and run the task (please see section [Run a task associated to a position on a sample](#))

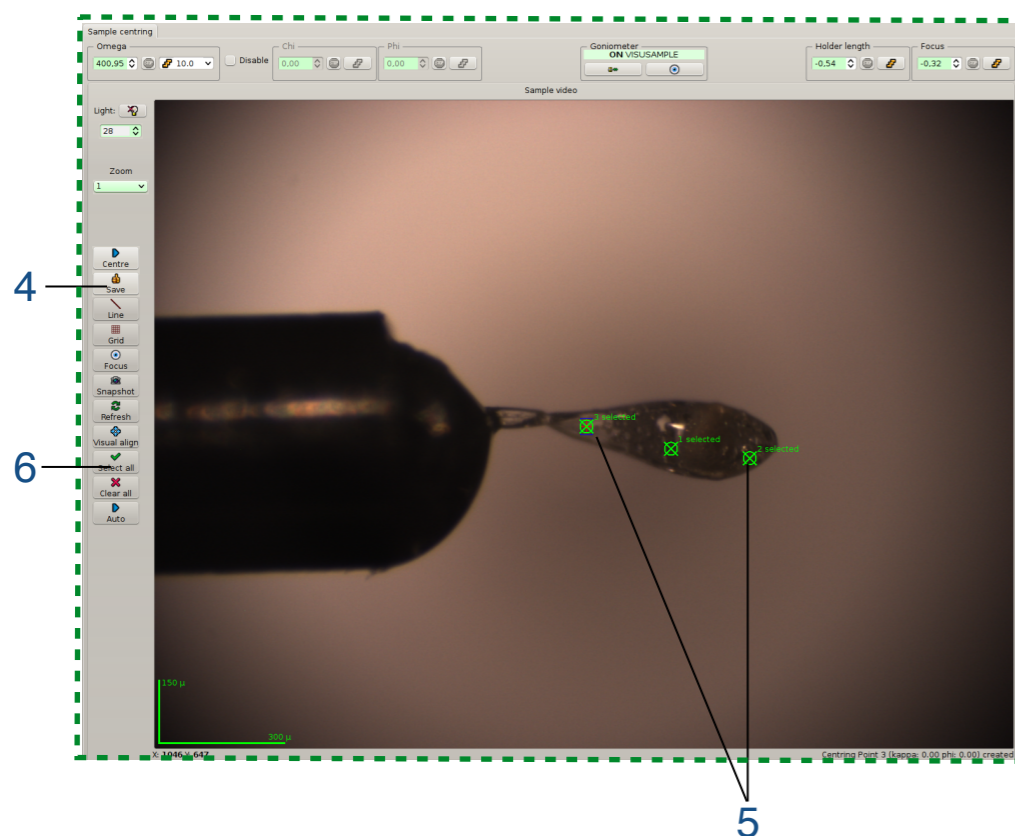
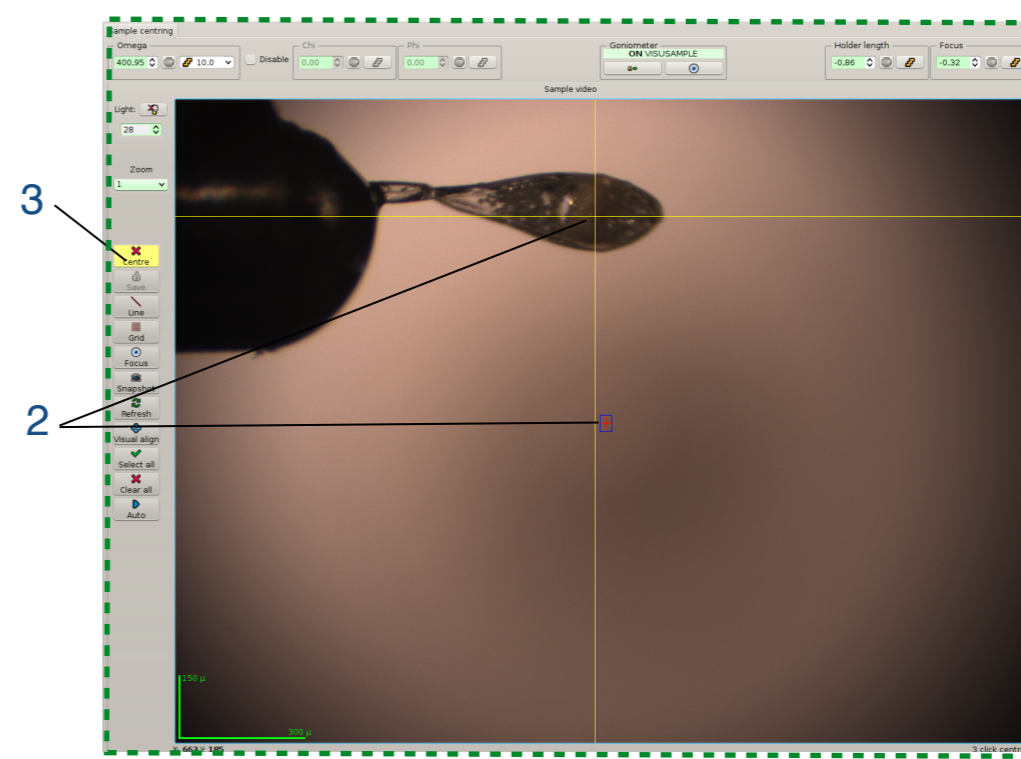
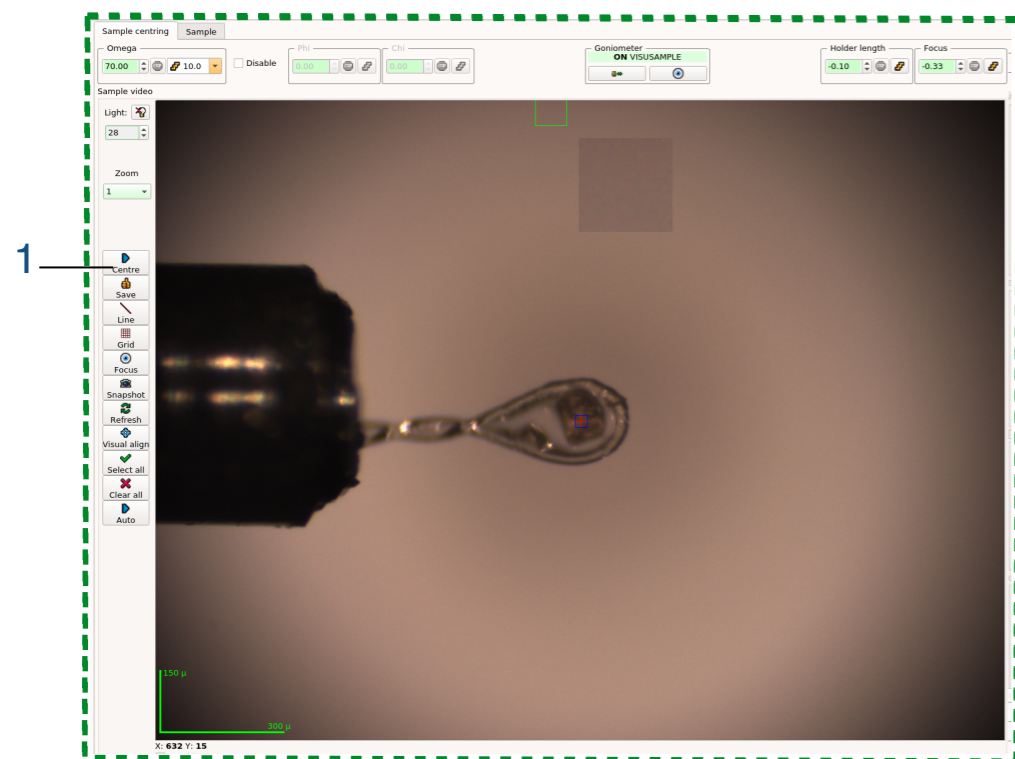
Practical guidelines: Load and unload a sample



To load/un-load a sample the Sample changer mode must be selected

1. Click on a sample. The sample will be highlighted in blue
2. To mount a sample: right click on sample name to open to the sample changer menu and click on Mount
3. To unmount a sample: right click to open to the sample changer menu and click on Un-Mount

Practical guidelines: Centre the sample and save one (or more) position(s)



1. Load the sample and click on Centre
2. To centre click 3 times on the point of the sample you want to centre in the beam (the beam is represented by the red cross)
3. To reject the position click on Centre
4. To save the position click on Save (mandatory to start the data collection). The yellow circle becomes bold green and a number appears beside (selected position)
5. Repeat point 2, 3 and 5 to save additional positions.
6. To select all the centring points click left and drag or click on Select all

Practical guidelines: Run a task associated to a position on a sample

Collect Log

SUNset proposal

Logout

Sample tree

Mode: Sample changer Show SC-details

Sample: ISPyB

Centring: Manual 3-click

Filter: No filter

1:1 (selected)

1:2

1:3

1:4

1:5

1:6

1:7

1:8

1:9

1:10

1:11

1:12

1:13

1:14

1:15

1:16

2

2:1

2:2

2:3

2:4

2:5

2:6

2:7

2:8

2:9

2:10

2:11

2:12

2:13

2:14

2:15

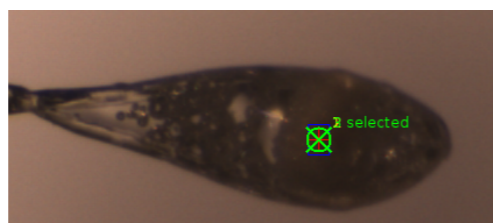
2:16

3

Display history view

Collect Queue

Pause



Standard Collection

Sample: 1:1

Acquisition

Oscillation start: -0.33 Osc. range per frame: 0.1

Number of images: 1800 Total osc. range: 180.0

First image: 1

Exposure time (s): 0.1 Detector mode: Full range

Chi: 0 Phi: 0

Energy (keV): 12.6733 Resolution (Å): 2.897

Transmission (%): 14.9

Shutterless

Data location

Folder: /data1-1/proxima1-soleil/2018_Run4/2018-11-06/local-user/RAW_DATA

/test

File name: pos1_1_####.cbf

Prefix: pos1

Run number: 1

Processing

N.o. residues: 200 Space group:

Unit cell:

a: 0 b: 0 c: 0

α: 0 β: 0 γ: 0

Run processing after collection

Run parallel processing

Characterisation

Helical Collection

Energy Scan

Advanced

Add to queue

The sample and a saved position must be selected (please see section Centre the sample and save the position)

1. Fill in the parameters in the collection method associated to that position and click on « Add to queue »
2. The data collection is added to the sample list. Click on « Collect queue »

A confirmation message will appear, click on « Continue »

Please remember that each task is associated to the corresponding selected position

Practical guidelines

Collection mode: Characterisation

1. Username: Password: Login

2. Mode: Sample changer

3. Sample tree: 1:1

4. Centre

5. Characterisation

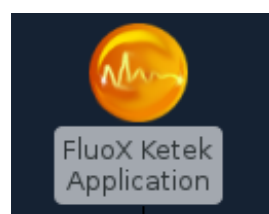
6. Collect Queue

1. Log-in using your Proposal number and Password
2. Choose the charging mode
3. Load the sample
4. Centre the sample and save
5. Select « Characterisation » and run the task (please see section [Run a task associated to a position on a sample](#))

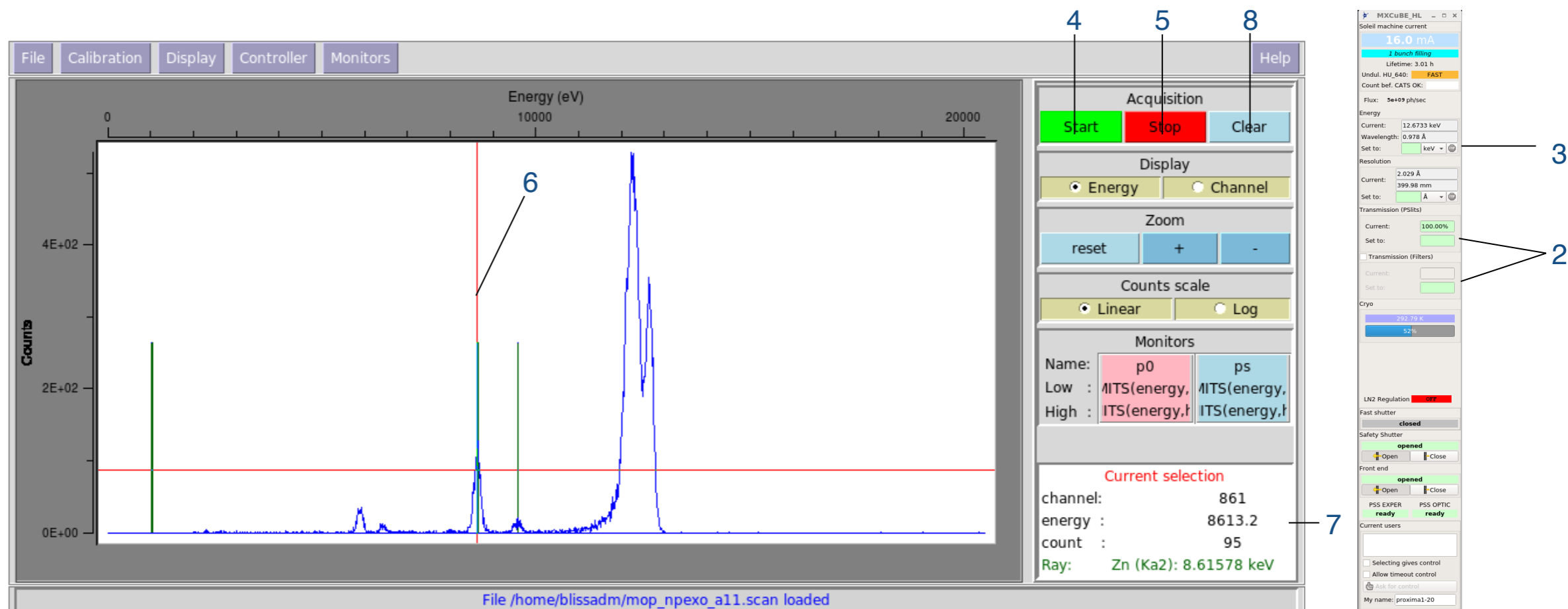
Default parameters for sample Characterisation:

Numb. of images = 1, 2 or 4
 Oscillation start = 0°
 Oscillation range per frame = 1°
 Exposure time = 1 sec
 Transmission = 10 - 15%

Practical guidelines: Measure a XRF spectrum



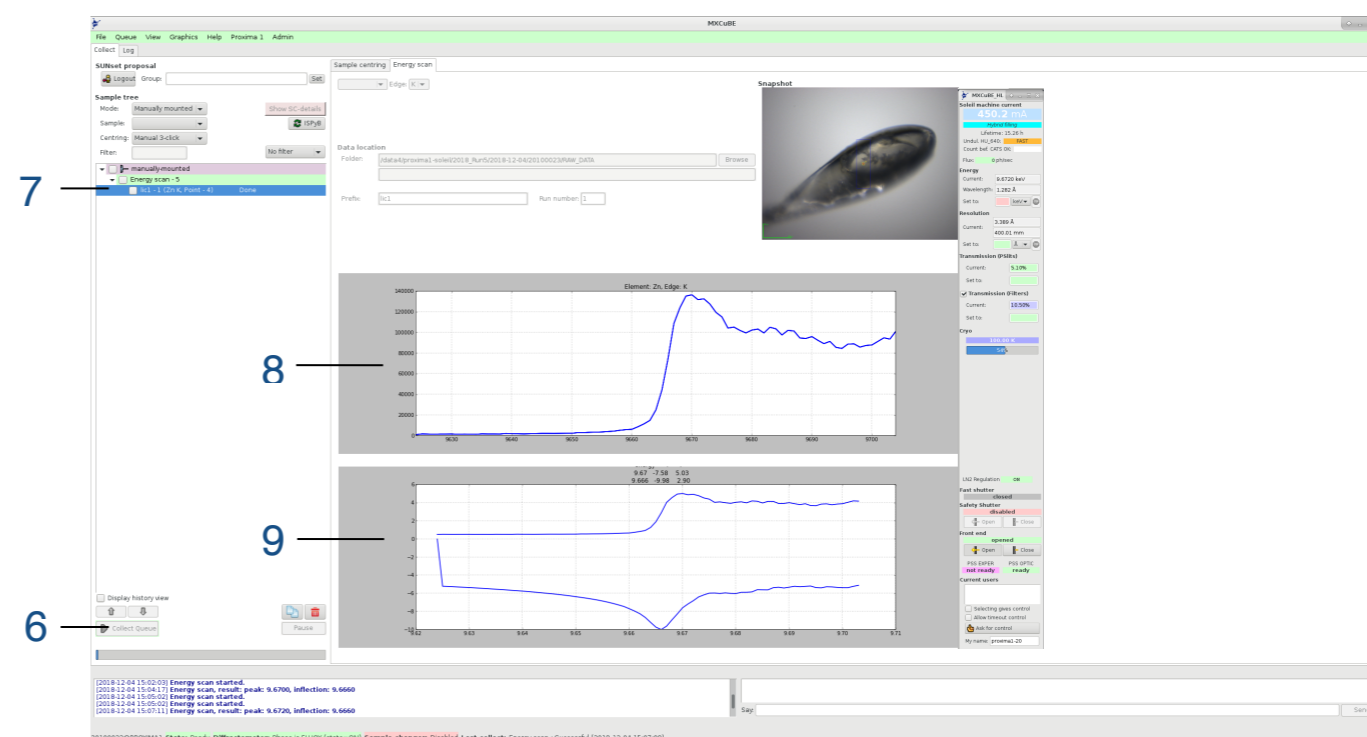
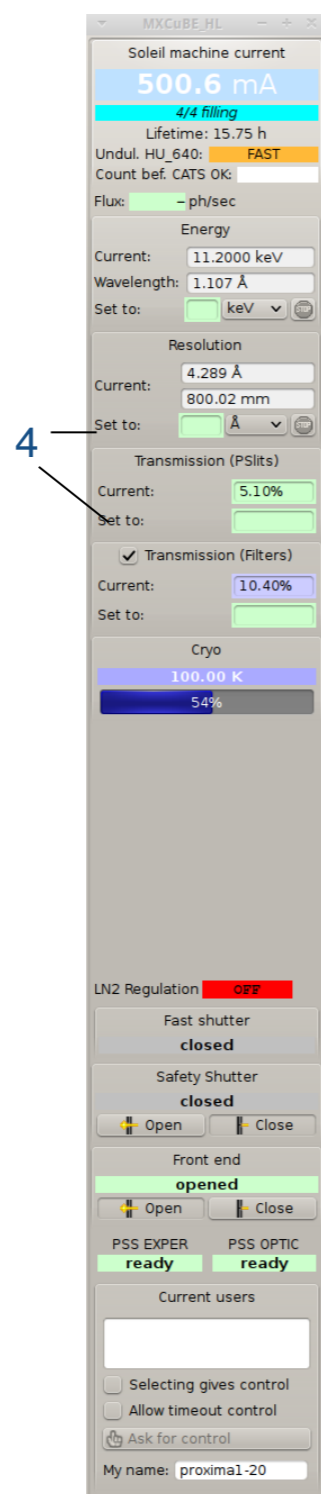
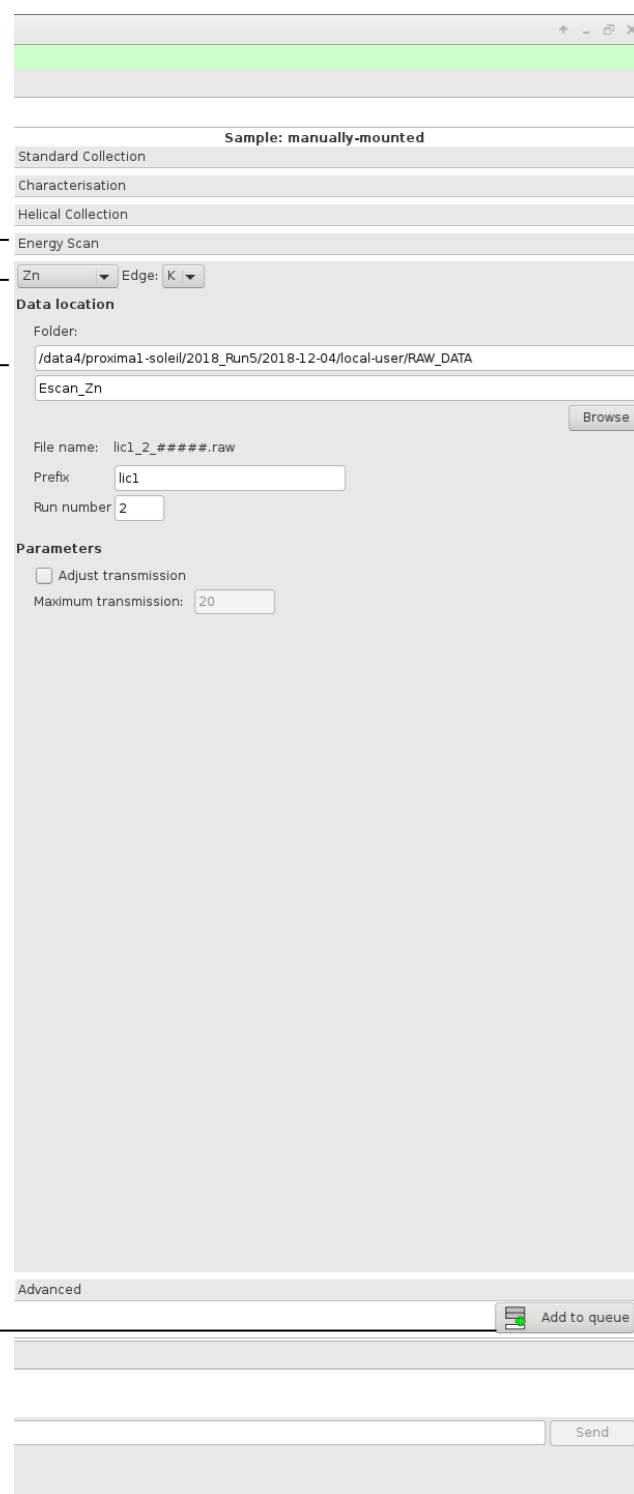
1



Use the XRF external application when you want to detect the presence of metals in your sample

1. Click onto the « FluoX Ketek » icon on the computer Desktop to open the XRF Program
2. Set up the suitable beam line energy (the value of the energy should be above the absorption edge of the metal you want to detect)
3. Set up the suitable attenuation for the Primary Slits (PSlits) and the Filters in the Machine Status panel (roughly 5% and 10% respectively)
4. Click Start
5. You can Stop your XRF measurement at any time
6. Left click on a peak to display the corresponding characteristic X-ray, energy and fluorescent element
7. The result of the XRF spectrum is displayed in the bottom right window
8. Click on « Clear » before starting a new measurement

Practical guidelines: Energy Scan (SAD or MAD)



1. Select « Energy Scan »
 2. Select the anomalous scatterer present in your sample and the desired absorption edge
 3. Enter the sample name
 4. Select the suitable primary slits and filters attenuation (please ask your Local Contact)
 5. Click on Add to queue
 6. Click on Collect Queue in the sample list menu
 7. Double click on the prefix name in the sample list to display the Energy scan
 8. Energy scan for the selected element
 9. Result of the CHOOCH program with computed Energy, f' , f'' values for the peak and inflection point
- At the end of CHOOCH the Beam line Energy will automatically be set up at the peak value

Practical guidelines

Collection mode: Standard Collection

The screenshot shows the MXCuBE software interface. The main window displays a sample image with a diffraction pattern. The interface is divided into several panels:

- Top Left:** Login fields (Username, Password, Login) and a 'Collect' button.
- Top Center:** Goniometer controls (Omega, Chi, Phi) and Goniometer buttons.
- Top Right:** Sample centring controls (Holder length, Focus).
- Left Panel:** Sample tree with a list of sample positions (1:1 to 2:16).
- Center:** Sample video window showing the sample and diffraction pattern.
- Right Panel:** Acquisition parameters for 'Standard Collection' (Oscillation start, Number of images, Exposure time, Energy, Resolution, etc.).
- Bottom Left:** 'Collect Queue' button.
- Bottom Right:** Status and control panels (Current, Wavelength, Resolution, etc.).

Numbered annotations (1-6) point to specific elements in the interface:

- 1: Login fields (Username, Password, Login)
- 2: Mode dropdown (Sample changer)
- 3: Sample tree list
- 4: Centre button
- 5: Standard Collection acquisition parameters
- 6: Collect Queue button

1. Log-in using your Proposal number and Password
2. Choose the charging mode
3. Load the sample
4. Centre the sample and save
5. Select « Standard Collection » and run the task (please see section Run a task associated to a position on a sample)

Standard parameters for Collection:

Oscillation start = Suggested by the strategy plan
 N. of Images = Suggested by the strategy plan
 Oscillation range per frame = 0.1°
 Total oscillation range = 0.1°
 Exposure time = 0.0125 sec
 Transmission = 60%

Practical guidelines

Collection mode: Helical Collection

The screenshot shows the MXCuBE software interface. The top menu bar includes File, Queue, View, Graphics, Help, Proxima 1, and Admin. The main window is divided into several sections:

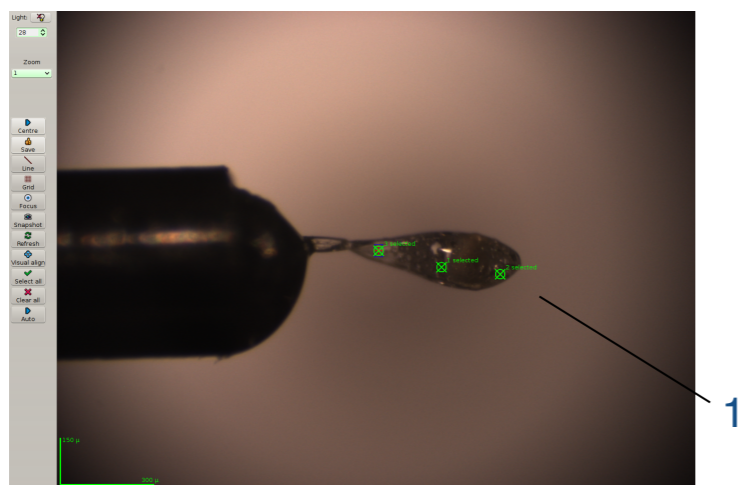
- Top Panel:** Contains controls for Omega (56.55), Chi (0.00), Phi (0.00), Goniometer (ON VISUSAMPLE), Holder length (-0.59), and Focus (-0.30).
- Left Panel (Sample tree):** Shows Mode (Manually mounted), Sample, Centring (Manual 3-click), and Filter (No filter). A checkbox for 'manually-mounted' is checked.
- Center Panel (Sample video):** Displays a live video of the sample. A green line is drawn across the sample, with two points marked. The status bar at the bottom indicates 'Line (points: 1, 2) kappa: 0.00 phi: 0.00 created'.
- Right Panel (Helical Collection):** Contains a table for Helical Collection with columns Name, Start point, and End point. Below the table are sections for Acquisition (Oscillation start, Number of images, Exposure time, etc.) and Data location (Folder, File name, Prefix, Run number, etc.).

Numbered callouts in the image point to the following elements:

1. SUNset proposal (circled in blue)
2. Sample tree
3. Sample tree filter
4. Centre button
- 5a. Line button
- 5b. Helical Collection section
6. Helical Collection table

1. Log-in using your Proposal number and Password
2. Choose the charging mode
3. Load the sample
4. Centre the sample in one end of the line (point1) and save the position
Centre the sample in the second end of the line (point2) and save the position
5. Select both the centring points and click on the button Line (5a). A green line will appear connecting the two centring points as well as a description of the task (5b)
6. Select « Helical Collection » and run the task (please see section [Run a task associated to a position on a sample](#))

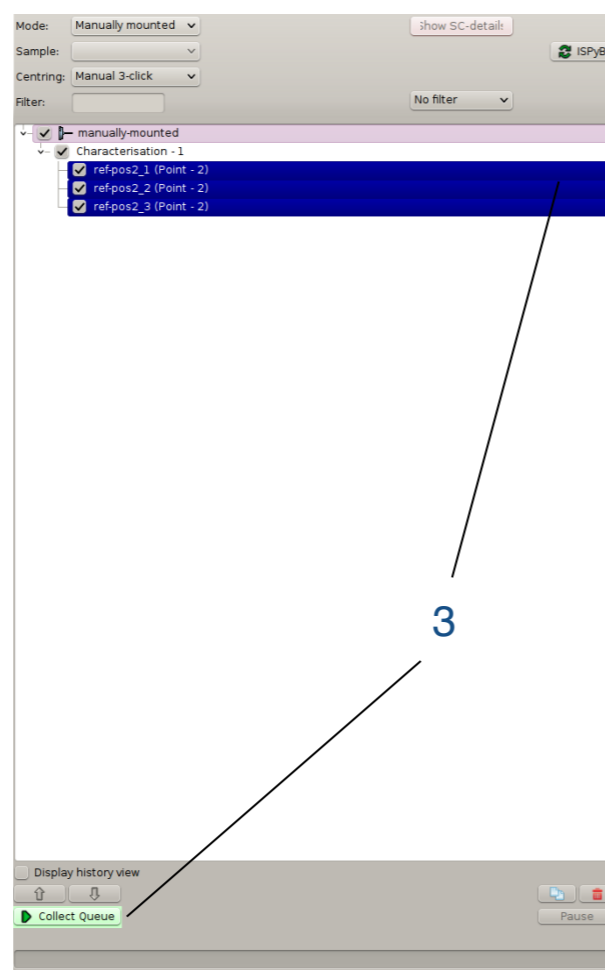
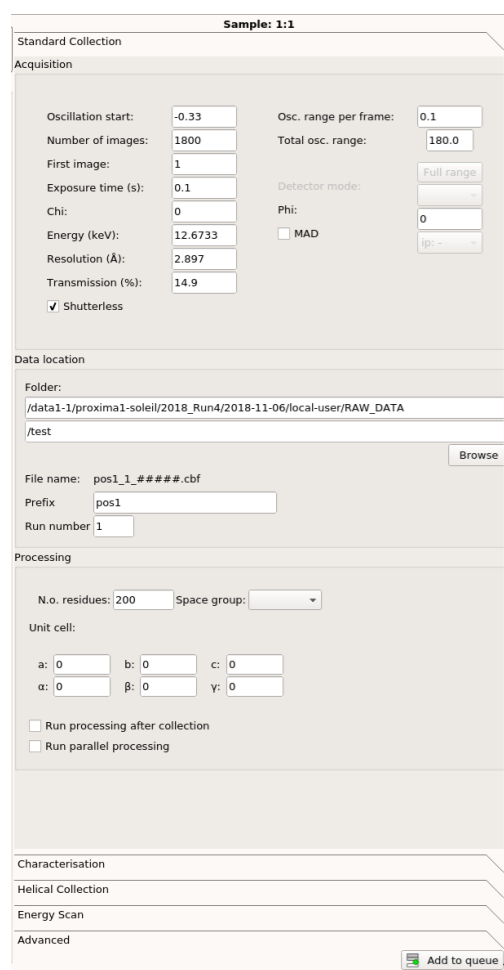
Practical guidelines: Run the same collection method on multiple positions on the same sample



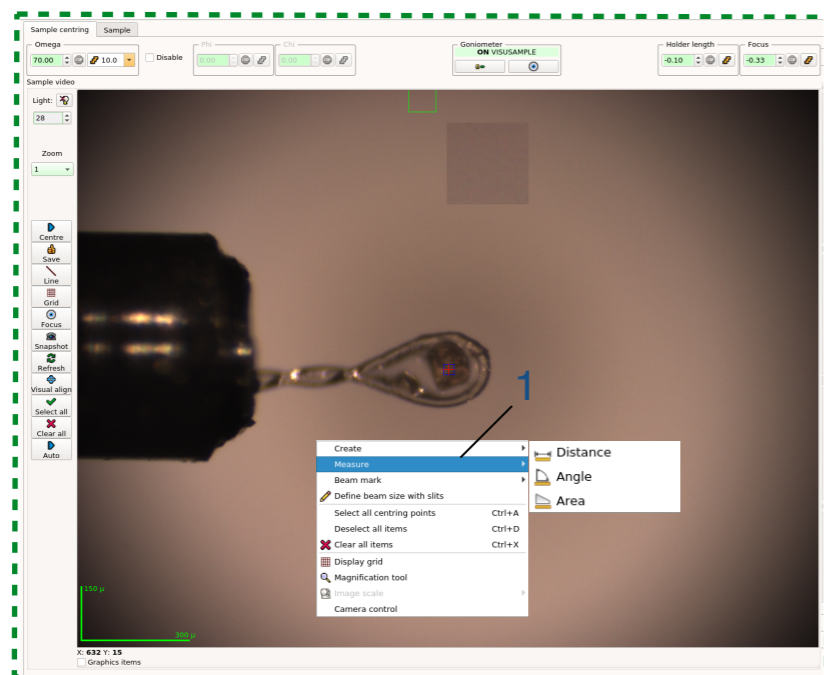
Follow these guidelines to perform for example a Characterisation on multiple centred positions on the same sample

Centre the sample and save several positions (please see Centre the sample and save one (or more) position(s))

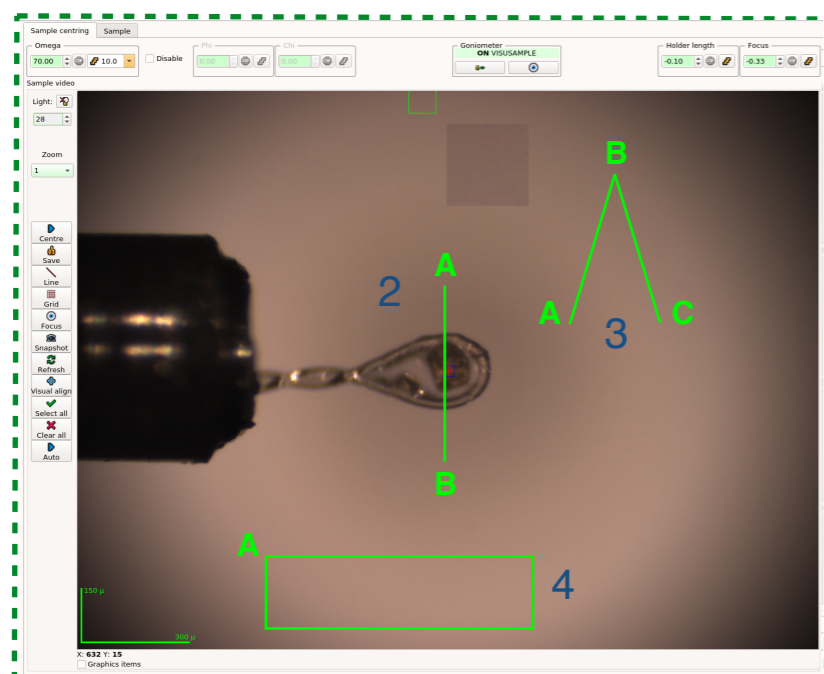
1. Select all saved position: left click and drag or click on Select all
2. Select a collection method (ex. Characterisation), fill the parameters, click on Add to queue
3. All the tasks will appear in the Sample tree, click on Collect Queue



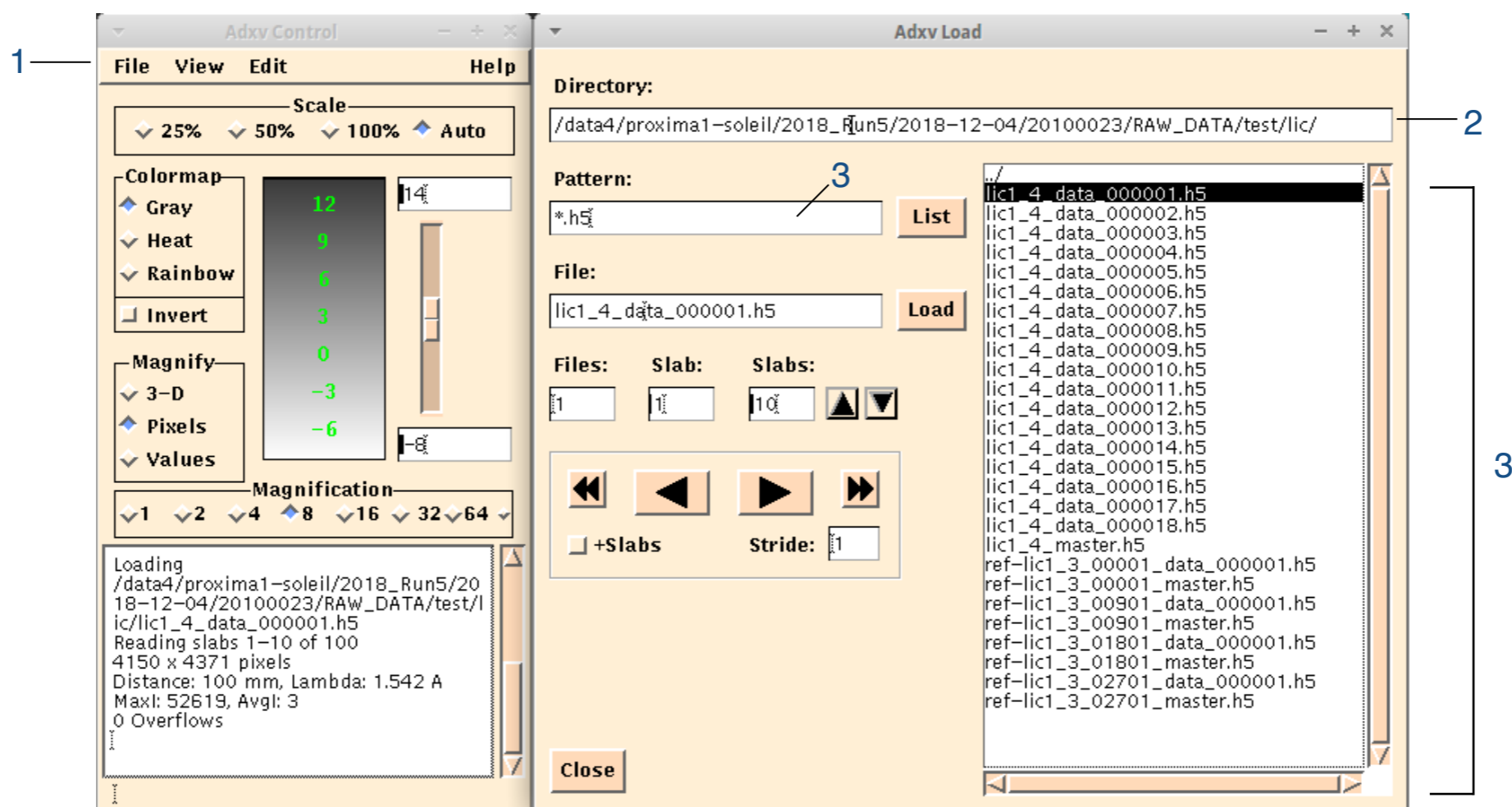
Practical guidelines: Measure distances, angles and areas



1. Right click on the sample view to open the measure menu
Click on the measure you want to perform (distance, angle, area)
 2. Measure distances: Click on the starting point (A) and the ending point (B)
 3. Measure angles: click on the end of the first branch (A), then on the peak of the angle (B) and finally on the end of the second branch (C)
 4. Measure areas: click on the first point (A) and draw the desired polygon
- ▶ The value of the measurement will appear beside the measure on the sample view (not for area measurements)
 - ▶ To delete a measurement double click on the sample view



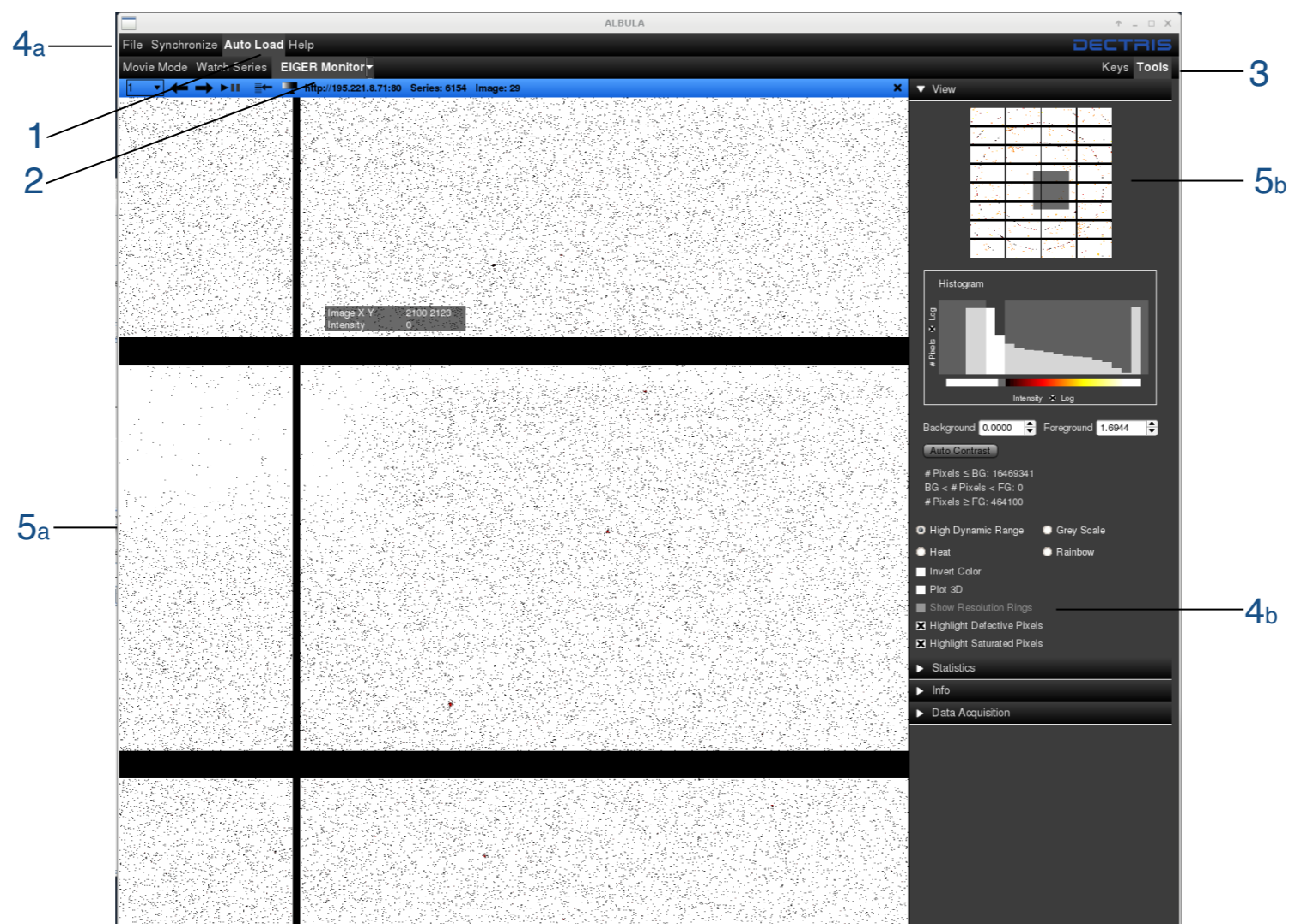
Practical guidelines: Visualise the diffraction images with ADXV



Use ADXV to inspect the diffraction images: (You won't be able to follow the progression of the diffraction images during the data collection)

1. Click on File, then click on Load
2. Retrieve your diffraction images directory
3. List diffraction images by sorting the h5 files
4. To load an image from the sample Characterisation:
Click on the corresponding ref-XXX_master.h5 file, then click on the corresponding data_?????.h5 file and insert Slabs value = 10
5. To load an image from the sample Standard Collection:
Click on the corresponding XXX_master.h5 file, then click on the corresponding data_?????.h5 file

Practical guidelines: Visualise the diffraction images with ALBULA



Use ALBULA to inspect diffraction images: (You will be able to follow the progression of the diffraction images during the data collection)

1. Click on Auto Load
2. Click on EIGER Monitor
3. Click on Tools to open up the right panel
4. To show the resolution rings click on « File » (4a) then on « Show Resolution Rings » (4b)
Please remember to scroll on the image to refresh the resolution rings values
5. To move on the diffraction image click left and drag on the diffraction image (5a) or click left and drag on the small window (5b)

Most frequent BUGs