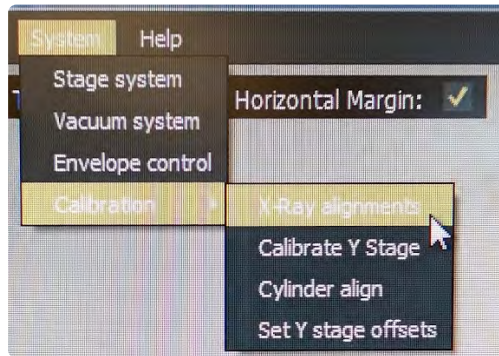


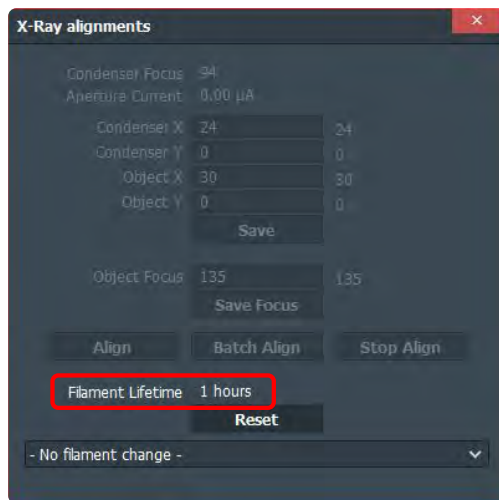
Heliscan MicroCT (Mark II) Basic Quick Guide

Starting up



!!!Before starting your scan!!!

1. On your computer your cell phone go to **FBS system** and **START** your session.
2. In FoxtrotUI navigate to **System > Calibration > X-Ray Alignments** .
3. In the popup window, locate the "**Filament Lifetime**".
4. Record the "**Filament Lifetime**" in the logbook and close the popup window.
5. At the end of your scan, return to the "**Filament Lifetime**" and record it in the logbook again and **STOP** your session on the **FBS system**.



LSU Shared Instrument Facility (SIF)

Thermo Fisher HeliScan X-ray microCT LogBook

Date:	Operator:	Sample Description:
Start Time:	PI/Company:	Power:
End Time:	Department:	Comments:
	Account:	

X-ray generation and safety indicators



Enable and unable X-ray generation

To enable X-ray: close all system doors and press the X-ray Arm button

To unable X-ray: press the X-ray Disarm button and you can open the doors if needed.

Indicator statuses

X-ray lamp statuses

Signal

Green ●

Green and Yellow ●●

Green, Yellow and Red blinking ●●●

Green, Yellow and Red ●●●

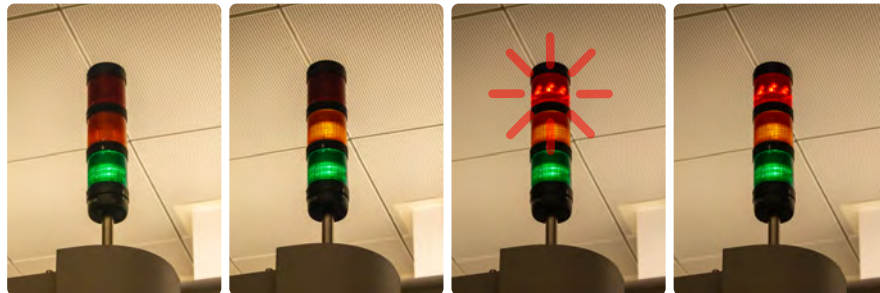
Description

System is powered

X-ray generation is enabled

X-ray is starting to be generated

X-ray is generated



Control panel LED

Status

LED is off

LED is on

LED is blinking

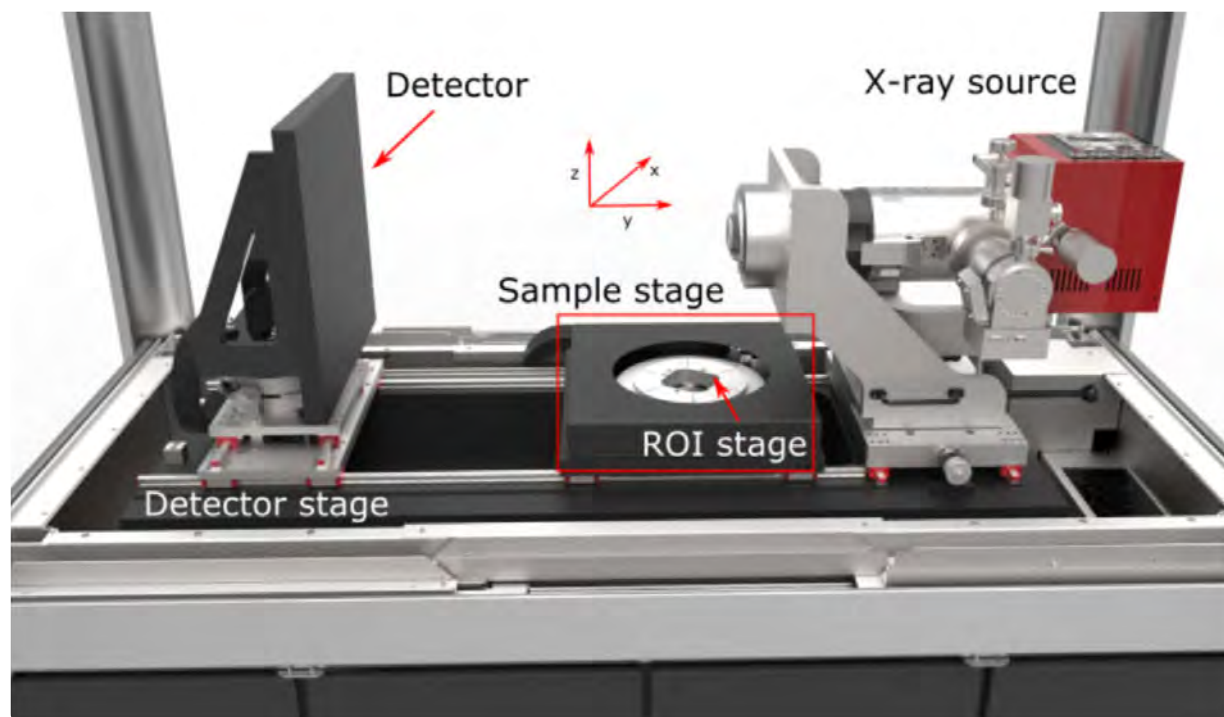
Meaning

X-ray generation is enabled and doors are locked

X-ray generation is disabled

X-ray generation is disabled and doors are locked

Motion System



Motion System

Max load	15 kg
Z axis travel	195 mm
R axis	360° continuous rotation
Y stage travel	400 mm
Y detector travel	830 mm
X detector travel	100 mm
ROI X travel	-20 mm – 20 mm
ROI Y travel	-20 mm – 20 mm

FoxtrotUI layout

The screenshot shows the FoxtrotUI interface with several key components labeled:

- Live image widget:** The large central area displaying a grayscale image of a specimen.
- Shortcuts:** A vertical toolbar on the right side of the image area containing icons for Auto focus, Bright view, Dark view, Snapshot, Live View, and Auto rotate.
- Acquisition panel:** A central panel containing settings for Acquisition, Darkfields/Clearfields, Geometry, and Trajectory.
- Opened project:** A panel on the right side showing X-RAY parameters (Tube Voltage, Tube Current, etc.) and Detector status.
- Hardware control panel:** A panel on the far right side showing X-RAY status (Warmup, Turn On, etc.) and Detector status.
- Image histogram:** A small window at the bottom left showing a histogram of the image data with statistics like Avg, Mean, Min, and Max.

Acquisition Settings:

- Mode: 3040x3040 px
- Exposure time: 0.380 s
- Detector X Start Position: 0.00 mm
- Averaging: 3
- Turn off X-Ray after tomogram:
- Warmup Time: 5 min
- Key Field Spacing: 90
- Do Offset Calibration:
- Set Starting Rotation Position: 0.00°

Detector Status:

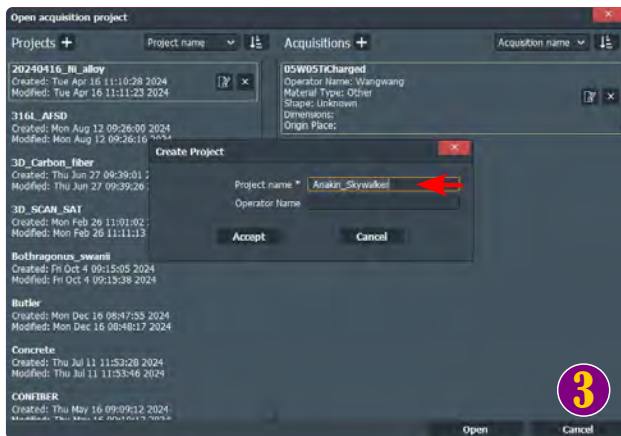
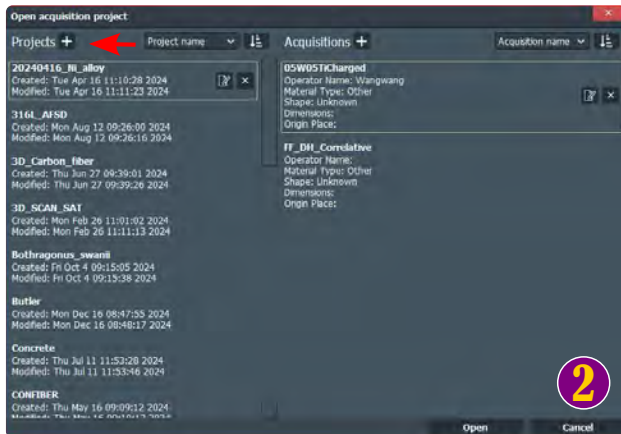
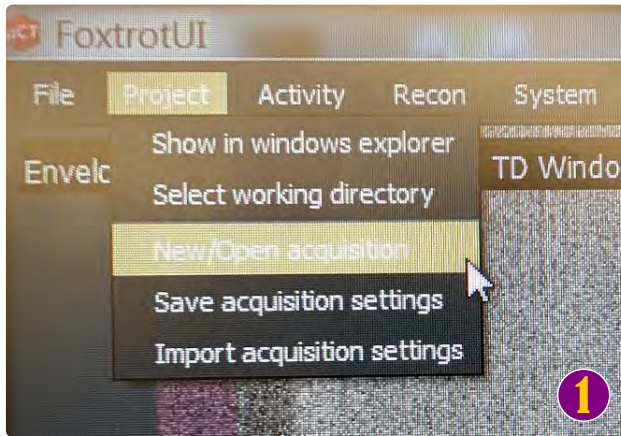
- Mode: 3040x3040 px
- Exposure Time: 0.250 s
- Averaging: 1
- Frame Rate: 0 fps
- Status: Stopped

Image Statistics:

- 3040 x 3040 px
- Depth: 65536
- Min: 0
- Max: 170.997
- Avg: 70.8015
- Mean: 70.8015
- Autocorrect:

Image histogram

Creating a new project/file



1. Go to **Project > New/Open acquisition**.

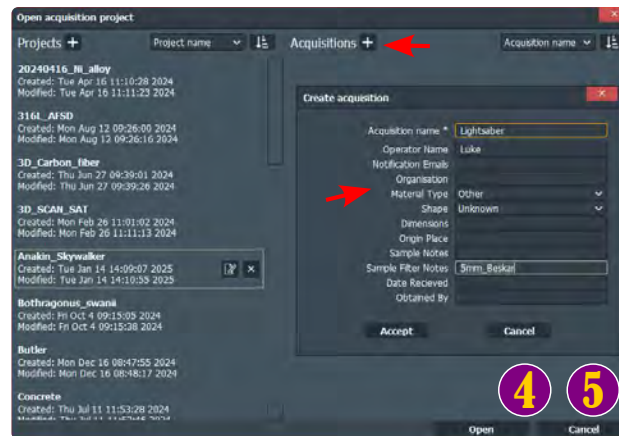
2. In the "Open acquisition project" window, click the + sign on the right side of "Projects".

3. In the "Create Project" window, enter your PI's name (laboratory), if it doesn't already exist, and click **Accept**.

4. Once the project is created, in the "Open acquisition project" window, select the project and click the + sign on the right side of "Acquisitions".

5. In the "Create acquisition" window, fill in the fields "Acquisition name", "Operator Name", and "Sample Filter Notes" and click **Accept**.

6. Your scan will then be ready to acquire and save within your laboratory's folder (project).



Setting acquisition

X-RAY

Tube Voltage: 92 kV 0 kV
 Tube Current: 95 µA 0 µA
 Focus Mode: S
 Target Current: 0.00 µA Limiter Off
 Filament status: Ok
 Filament mode: Tungsten
 Interlock: Opened
 Vacuum: 2.3e-5 Pa
 Status: Not Ready

Reset Turn On Warmup

DETECTOR

Mode: 3040x3040 px
 Exposure Time: 0.250 s
 Averaging: 1
 Frame Rate: 0 fps
 Status: Stopped

Calibrate Start

SAMPLE STAGE

Autorotate:
 Rotation Speed: 35.00 °/s
 Rotation: 90.000 ° 0.000 °
 Position Y: 60.000 mm 60.000 mm
 Position Z: 135.000 mm 135.000 mm
 Stage status: Ready
 Envelope status: Unprotected

Abort

DETECTOR STAGE

Position X: 0.000 mm 0.000 mm
 Position Y: 330.000 mm 330.000 mm
 Stage status: Ready

Abort

ROI STAGE

ENVELOPE INFO

ROI STAGE

Position X: -0.300 mm -0.300 mm
 Position Y: -0.200 mm -0.200 mm
 Stage status: Ready
 Envelope status: Unprotected

Abort

Acquisition panel

Scan Setup

X-ray

Select Tube Voltage and focus mode based on sample composition, thickness and desired voxel size

Adjust Tube current to optimize the target current

Detector

Select Mode (number of pixels on the detector)

Select Start to get a live view

Sample Stage

Lower position Z to 1 mm to get a Clearfield

Detector Stage

Move detector Y position to 330 mm (unless higher magnification is required)

Increase the exposure time to get the maximum number of counts at the detector without over-saturating it.

- Clearfield with Optimum Counts (~45,000 max)
- Oversaturated Clearfield (~>55,000)

Sample Stage

Move the sample closer to the source using **Position Y**. **Autorotate** the sample while adjusting Y stage and use the **Horizontal Margin** to ensure there is Clearfield all around the sample

Select **Z Start position** by moving the sample lower using **Position Z**. Use the **TD window** as a guide to ensure the sample will transition through the middle region.

ROI Stage

Centralize the sample by setting Position X and Y using the rotation on the **Sample Stage** settings.

- Position X: 0° and 180°
- Position Y: 90° and 270°

Sample Stage

- Autorotate
- Select Z End Position by moving the sample higher using Position Z. Use the TD window as a guide to ensure the sample will transition through the middle region.

Setting acquisition

Acquisition

ACQUISITION SETTINGS

Mode: 3040x3040 px

Exposure time: 1.000 s

Detector X Start Position: 0.00 mm

Averaging: 2

Turn off X-Ray after tomogram:

Warmup Time: 5 min

Key Field Spacing: 90

Do Offset Calibration:

Set Starting Rotation Position:

Starting Rotation Position: 0.00 °

DARKFIELDS / CLEARFIELDS

ClearFields: 10

DarkFields: 5

Specify Exposure Time:

Exposure Time: 1.000 s

Z position: 1.00 mm

Type: Both

Do detector X shift:

Detector X shift columns: 9

GEOMETRY

Specimen Distance: 60.000 mm

Detector Length: 330.000 mm

Voxel Size: 25.273 µm

Field of View (X): 65.709 mm

Field of View (Y): 65.709 mm

Field of View (Z): -25.273 mm

TRAJECTORY

Trajectory: Double Helix

Auto ClearFields/DarkFields:

Projections per Revolution: 1800

Converted Proj./Rev.: 1800

Z Start Position: 138.000 mm

Z End Position: 160.000 mm

Same Z Direction:

Total Projections: 1102

Dataset Size: 19.71 GB

Z Stage Init Steps: 100

Z Stage Init via CF Pos:

Double Helix Pitch Multiplier: 0.95000

Pitch: 71.98727 mm

Review of all Acquisition Settings

ACQUISITION SETTINGS

- Detector Mode: matching the one selected during live view
- Exposure time: matching the one selected during clearfield live view
- Averaging: Increasing the number of projections to average will reduce noise in the image while spending more time acquiring the tomogram
- Turn off X-ray after tomogram: Selected in most cases to prolong the filament lifetime acquiring images rather than remaining idle
- Warmup Time: Recommended if the source has been off for a while

DARKFIELDS / CLEARFIELDS

- Clearfields: 10 (Recommended)
- Darkfields: 5 (Recommended)
- Exposure time: Matching the projection acquisition exposure time, unless a different exposure time want to be acquired to avoid oversaturating the detector (application specific)
- Z Position: 1 mm usually
- Type: Both (Recommended)
- Do detector X-shift: Yes, to avoid helical/circular artifacts
- Detector X-Shift Columns: 9 (recommended)

TRAJECTORY

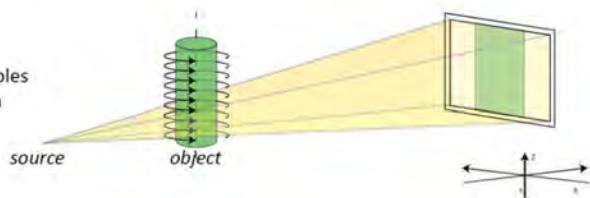
- Select Trajectory
- Auto Clearfields/Darkfields: Yes, unless the sample does not allow it

Review **Estimate Time** and **Start** Acquisition

Trajectories

Trajectories:

Circular trajectory
scanning of tall samples
At a $<10^\circ$ conebeam



Circular scanning mode: This trajectory is based on rotating the sample through 360 degrees of projections at fixed vertical position with respect to the X-ray source.

Benefit: a small number of projections are required.

Drawback: the reconstruction algorithm to work, an assumption that all the X-ray paths from the source that reach the detector are parallel must hold true.

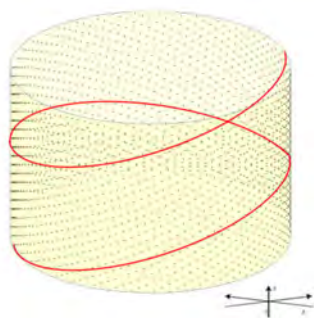
Helical trajectory
scanning of tall samples
at a $<110^\circ$ conebeam



Double Helix scanning mode: During helical scan the sample is simultaneously rotated and moved up to the next position at which the projection image of the X-rays passing through the sample is acquired. This allows to image a longer object – with diameter vs height aspect ratio up to 10 (AR:10) – within a single scan or to scan several objects, mounted on top of each other, without a need for re-mounting the samples between every scan.

Benefit: (1) It allows the detector to be moved very close utilizing as much X-ray flux as possible (i.e. better signal to noise ratio); (2) all reconstructed points have travelled through the mid-plane of the detector allowing for a theoretically exact reconstruction of the data and (3) very tall sample can be scanned resulting in tall tomograms.

Drawback: requires a much more precise knowledge of system geometry for the reconstruction to work and has 6 degrees of freedom that need to be known accurately. A helical trajectory also required more projections for the same final tomogram volume as a single circular scan.



Schematic visualization of the X-ray beam trajectory with respect to the scanned sample (yellow cylinder) during:

- **Helical scan** (red line) – projections are acquired in a continuous trajectory curve with a progressive increment of the rotation angle and vertical travel

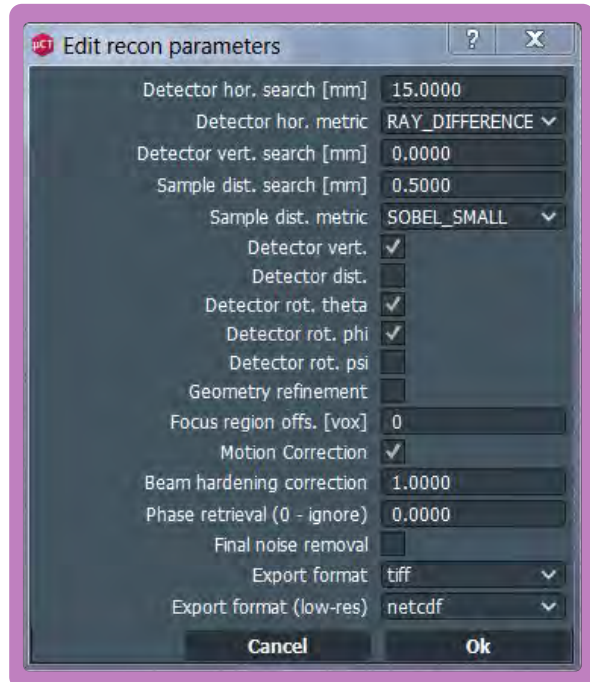
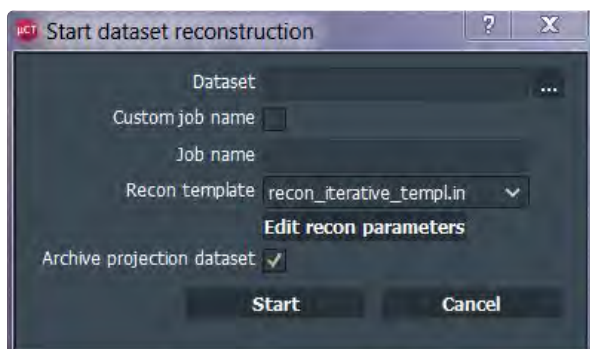
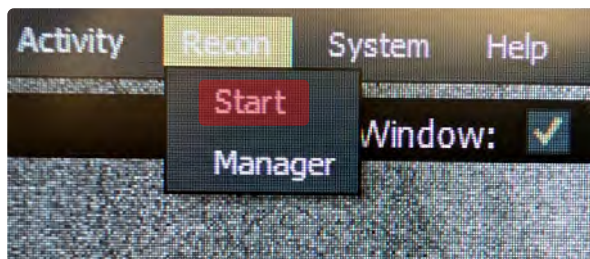
- **Space-Filling scan** (dark dots) – acquisition of the mutually independent projections is evenly spread with respect to the sample volume across whole vertical travel

Space-filling mode: This allows generating high-quality images with reduced amount of the acquired projections.

Benefit: (1) High cone-angle imaging; (2) entire detector area is fully utilized; (3) half the overscan required in comparison with Double Helix; (4) More uniform sampling of the object reducing the artifacts e.g., non-uniform magnification, helical filtering, streaking around high-density inclusions and secondary source.

Drawback: (1) May result in a lower signal-to-noise ratio (SNR) and (2) increased computational complexity for reconstruction.

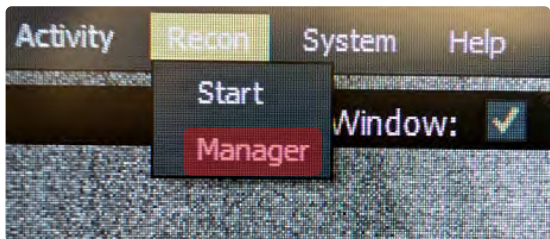
Reconstruction



Reconstruction

1. Once the scan is complete, navigate to **Recon > Start** and select the full-frame dataset that was just acquired.
 2. Choose the appropriate reconstruction template:
 - **Space filling** → recon_iterative_tmpl.in
 - **Double Helix** → recon_FBP_tmpl.in
 - **Circular** → recon_FBP_circular.in
- Note:** If necessary, click on “**Edit recon parameters**” and adjust the “**Beam hardening correction**” value. The range is **0.7 to 2.0**, with recommended starting values at **1.4**, increasing in increments of **0.2** until you achieve a satisfactory result.
3. Ensure that the “**Archive projection dataset**” box is checked to automatically save the reconstruction once completed.
 4. Click **Start** to begin the reconstruction.

Reconstruction



5. Navigate to **Recon > Manager**.
6. The **top half** of the window will display the dataset as it uploads to the cluster. Once the upload is complete, a new job number will appear in the **bottom half** of the window. Enabling **Auto Refresh** will periodically update the status, showing the **start time, finish time, and current status** of the reconstruction.
7. Once finished, the reconstructed data will be available in the **project folder on the SIF server**.

Recon manager
✕

Datasets

Dataset filter: Actual datasets

Name	Project	Acquisition	Status	Size	Current size	Description	Actions
Bswanii_FullbodyFixAttempt_202...	Bswanii_Fullbody	Bswanii_Fullbody	Upload finished	94.7 GB	94.7 GB	4/29/2024 1:1...	▶ ▶ ✕
GRX_NON_and_HIP_2024-04-30...	SIF	GRX_NON_and...	Upload finished	286.0 GB	286.0 GB	4/30/2024 10:...	▶ ▶ ✕
20240507_W-Ti_alloy_2024-05-...	SIF	20240507_W-...	Upload finished	71.2 GB	71.2 GB	5/8/2024 11:2...	▶ ▶ ✕
Sample_3a_2024-05-08_12:47:19	Albermarle	Sample_3a	Upload finished	6.9 GB	6.9 GB	5/8/2024 12:4...	▶ ▶ ✕
Heat_EX3_tilt_2024-05-09_11:0...	SIF	Heat_EX3_tilt	Upload finished	50.7 GB	50.7 GB	5/9/2024 11:1...	▶ ▶ ✕
Heat_EX4_tilt_2024-05-09_15:0...	SIF	Heat_EX4_tilt	Upload finished	63.2 GB	63.2 GB	5/9/2024 3:10...	▶ ▶ ✕
Sand_Hg_2024-05-10_07:07:48	Albermarle	Sand_Hg	Upload finished	0.0 GB	0.0 GB	5/10/2024 7:0...	▶ ▶ ✕
Sample_1a_2024-05-10_07:10:04	Albermarle	Sample_1a	Upload finished	8.7 GB	8.7 GB	5/10/2024 7:1...	▶ ▶ ✕
20240512_05W05T_2024-05-1...	SIF	20240512_05...	Upload finished	154.2 GB	154.2 GB	5/12/2024 5:2...	▶ ▶ ✕

Recon jobs

Id	Name	Status	Result	Start	Finish	Actions
435	Tooth_2025-01-31_12:12:04	Finished	Success	1/31/2025 2:19 PM	1/31/2025 2:29 PM	
434	A_spnov_LSUMZ_91870_fullbody...	Finished	Success	1/31/2025 12:14 PM	1/31/2025 1:37 PM	
433	A_spnov_LSUMZ_98170	Finished	Killed	1/31/2025 11:50 AM	1/31/2025 12:04 PM	
432	Thrush_Full_body_2025-01-27_0...	Finished	Success	1/27/2025 11:48 AM	1/27/2025 11:58 AM	
431	Battery_DC02_2025-01-24_16:3...	Finished	Success	1/24/2025 6:48 PM	1/24/2025 7:21 PM	
430	Battery_CH92_2025-01-24_16:2...	Finished	Success	1/24/2025 6:39 PM	1/24/2025 6:48 PM	
429	Bswanii_PMA_2025-01-18_20:56...	Finished	Success	1/18/2025 11:19 PM	1/19/2025 3:23 AM	
428	Thrush_Full_body_2025-01-18_0...	Finished	Success	1/18/2025 10:25 AM	1/18/2025 10:34 AM	
427	A_muller_LSUMZ_01969_2025	Finished	Success	1/16/2025 4:57 PM	1/16/2025 6:00 PM	

76

Refresh
Auto refresh
Shutdown
Reboot