

# Cryo-EM DAQ & Data Management

Yee-Ting Li, January 2019  
Cryo-EM Training Workshop, SLAC

# Agenda

1. Remote Access: **FastX**
2. Experimental Metadata: **eLogbook**
3. Data Acquisition: **Pre-processing Pipeline**
4. Where is my data? **Data Transfer**

***How do we provide the best  
experience for users of  
Stanford-SLAC's Cryo-EM  
Facility?***

# Remote Access

SLAC

Remote  
control of  
Microscope  
and Camera

Web Browser  
access to  
Remote  
Terminals

The screenshot displays a web browser window at the URL <https://fastx.slac.stanford.edu:3443>. The interface is divided into several sections:

- My Sessions:** A sidebar on the left lists four sessions: Cryo-EM TEM1, Cryo-EM TEM2, Cryo-EM TEM3, and Cryo-EM TEM4. The Cryo-EM TEM4 session is selected and highlighted.
- Search Bookmarks:** A search bar with the text "@slac\_public\_login Cryo-EM LSST-Camera Global Bookmarks My Bookmarks".
- Terminal View:** The main area shows a live feed from the selected Cryo-EM TEM4 session. The feed displays a dark, noisy image of a sample, likely a carbon grid, with a red circle indicating the area of interest. Below the feed, technical parameters are displayed: "SA 11500 x EFNano probe", "High tension: 200 kV", "Screen: 0.000 nA", "Focus step: 3", "Defocus: -1.98  $\mu\text{m}$ ", and "Ceta cooling: Stable Spot size: 6".
- Scale Bar:** A scale bar labeled "2  $\mu\text{m}$ " is visible in the bottom right corner of the live feed.
- Desktop Client:** At the bottom of the browser window, a "Desktop Client" window is visible, showing the system's taskbar and desktop environment.

Enable Secure Remote Control of TEMs

# Microscope Management and Experiment Tracking

SLAC

**Problem:** How to track usage and 500+ experiments for 4 microscopes each year

**Solution:** “elogbook” Web based logging and tracking tool

Assign Experiments to TEMs

Operator dashboard								
Instrument	Station	Experiment	PI	Leader Account	Current Sample	Description	Switched at	Switched by
TEM1	0	20181106-CS07	Brunger, Axel (brunger@stanford.edu)	brunger	20180918_Jeremy_ISV	Brunger Lab CryoEM Time	Nov/6/2018	eam
TEM2	0	20181108-C038	Sudha Chakrapani (chakrapani@casewestern.edu)	megmayer		Chakrapani	Nov/8/2018	megmayer
TEM3	0	Standby					Oct/29/2018	bushnell
TEM4	0	Standby					Nov/5/2018	bushnell

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Reports of Experiment

ID	Instrument	Date	Station	Experiment	PI	Leader Account	Current Sample	Description	Switched at	Switched by
20180919-C023	TEM4	Sep/19/2018	Sep/19/2018	Chiu, Wah (wahc@stanford.edu)	kmzhang	sample				
20180919-C019	TEM4	Sep/19/2018	Sep/20/2018	Andrzej (andrzej@anl.gov)	kmzhang	chaprone-substrate				
20180918-CR06	TEM2	Sep/18/2018	Sep/20/2018	Morais, Marc (mmorais@UTMB.EDU)	kmzhang	Marc Morais Consortium Proposal				
20180918-C042	TEM3	Sep/18/2018	Sep/19/2018	Chiu, Wah (wahc@stanford.edu)	kmzhang	smallRNA				
20180917-CS07	TEM1			Brunger, Axel (brunger@stanford.edu)	brunger	Brunger Lab CryoEM Time				
20180916-C000	TEM2	Sep/16/2018	Sep/18/2018	Wah Chiu (wahc@stanford.edu)	kmzhang	small RNA				
20180913-C038	TEM2	Sep/13/2018	Sep/16/2018	Sudha Chakrapani (chakrapani@casewestern.edu)	megmayer	Chakrapani				
20180913-C017	TEM3	Sep/13/2018	Sep/17/2018	Chiu, Wah (wahc@stanford.edu)	suzm	MaRRE232and351				
20180913-C000	TEM3			Summers, Michael (summers@hmsi.umbc.edu)	suzm	RRE232, RRE351				
20180912-C001	TEM1	Sep/12/2018	Sep/16/2018	Skinotis, Georgios (yiorgeof@stanford.edu)	qgh	Skinotis Lab CryoEM Time				
20180911-C032	TEM2	Sep/11/2018	Sep/13/2018	Yu, Edward	Yu, Edward	Lipid Transporter				
20180910-CS08	TEM1			Moemes, William (pdahlb@stanford.edu)	pdahlb	Caulobacter Correlative Cryo-Super-Resolution				
20180909-C016	TEM3			Jin, Jing (jinjing913@gmail.com)	djchmiel	Chikungunya Virus Budding				
20180908-C042	TEM2	Sep/8/2018	Sep/11/2018	Chiu, Wah (wahc@stanford.edu)	suzm	T-box full				
20180908-C038	TEM2			Sudha Chakrapani (chakrapani@casewestern.edu)	megmayer	Chakrapani				
20180908-C000	TEM3			Chiu, Wah	Chiu, Wah	3d electron crystallography of micro protein crystal				
20180907-C001	TEM1	Sep/7/2018	Sep/10/2018	Skinotis, Georgios (yiorgeof@stanford.edu)						
20180907-C042	TEM2			Chiu, Wah (wahc@stanford.edu)						
20180907-C024	TEM2			Boothroyd, John (jboothr@stanford.edu)						
20180906-CS09	TEM3	Sep/6/2018	Sep/8/2018	Bushnell, David (bushnell@stanford.edu)						
20180906	TEM2			Ann, Arvin (arvinam@stanford.edu)						
20180905-C057	TEM3			Ann, Arvin (arvinam@stanford.edu)						
20180905-C000	TEM2			Chiu, Wah (wahc@stanford.edu)						
20180904	TEM1	Sep/4/2018	Sep/7/2018	Bushnell, David (bushnell@stanford.edu)						
20180902-C028	TEM2	Sep/2/2018	Sep/4/2018	Evans, James (James.Evans@psnl.gov)	djchmiel	Structure determination of PDX				
20180902-C017	TEM3			Summers, Michael (summers@hmsi.umbc.edu)	suzm	RRE232, RRE351				

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Make Data Management Easy and Consistent

# Live Experimental Feedback for Users

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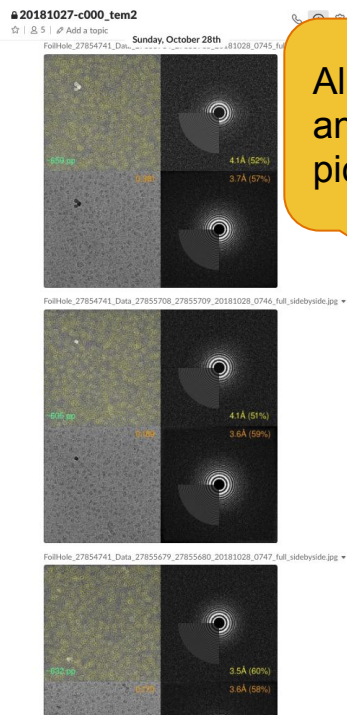
https://cryoem-logbook.slac.stanford.edu...

Name	Param Name	Param Value	Actions
m2_02	imaging_method	single-particle	✕ +
m2bar	imaging_software	SerialEM	✕ +
gcg_vpp	imaging_format	.tif	✕ +
gcg02	apix	1.06	✕ +
gcg1	imdose	1.24	✕ +
gcg8	preprocess/enable	1	✕ +
M2R_CoA	preprocess/convert_gainref	1	✕ +
FL	preprocess/apply_gainref	1	✕ +
	preprocess/align/motioncor2/throw	0	✕ +
	energy_filter/slit_size	20	✕ +
	particle_size	160	✕ +
	preprocessing/particle_pick/enable	1	✕ +
	superres	0	✕ +
	phase_plate	0	✕ +
	objective_aperture/inserted	1	✕ +
			✕ +

Update

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Mandatory and custom experimental parameters



Alignment, CTF and particle picking previews

Summary of Pre-processing data



Provide Data Logbook; Markup with Metadata; Provide Near Real-Time Feedback

# 0. Prerequisites

- Access to everything described here requires:
  - SLAC Unix Account
    - Request for yourself and all collaborators
    - Contact: [lisa@slac.stanford.edu](mailto:lisa@slac.stanford.edu)
  - An internet connection

Contact [yti@slac.stanford.edu](mailto:yti@slac.stanford.edu) for any compute/storage issues

# 1. Remote Access

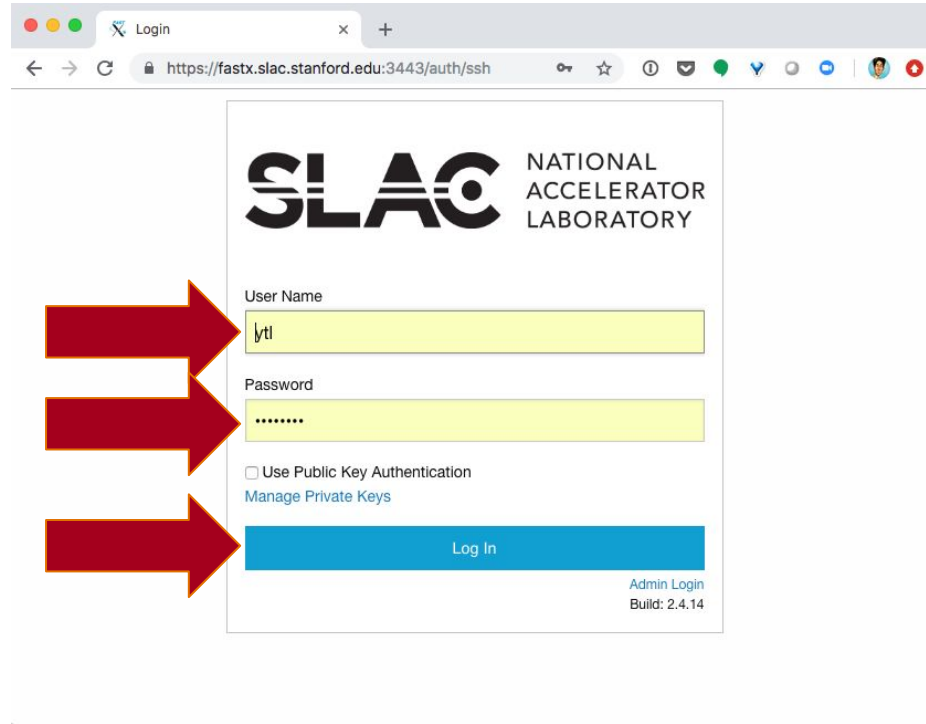
- Why?
  - Remotely control microscope to setup/change parameters, monitor live
- How?
  - Log onto website, or
  - Download 'fastx client'
- Where?
  - <https://fastx.slac.stanford.edu:3443>



- Remote control software similar to NoMachine, TeamViewer etc.
- No software install required (just a standard browser)
- Client App allows microscope software windows to appear like normal windows on your Desktop

# FastX - Logon

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A screenshot of a web browser window showing the SLAC FastX login page. The browser's address bar displays the URL `https://fastx.slac.stanford.edu:3443/auth/ssh`. The page features the SLAC logo and the text "NATIONAL ACCELERATOR LABORATORY". Below this, there are two input fields: "User Name" containing the text "lytl" and "Password" containing seven dots. A checkbox labeled "Use Public Key Authentication" is present, with a link "Manage Private Keys" below it. A blue "Log In" button is at the bottom of the form. Three large red arrows point from the left towards the "User Name" field, the "Password" field, and the "Log In" button. In the bottom right corner of the form, the text "Admin Login" and "Build: 2.4.14" is visible.

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User Name  
lytl

Password  
.....

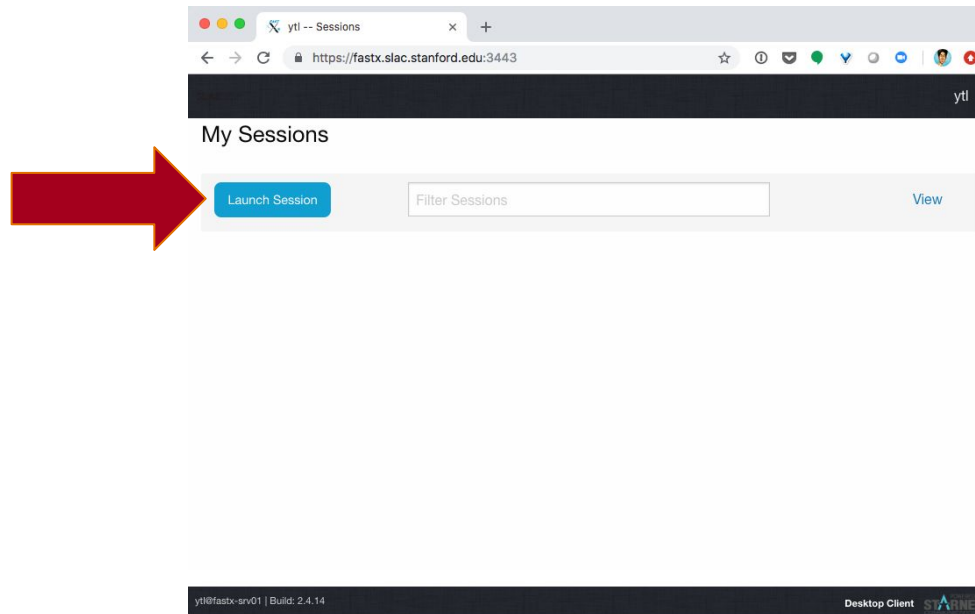
☐ Use Public Key Authentication  
[Manage Private Keys](#)

Log In

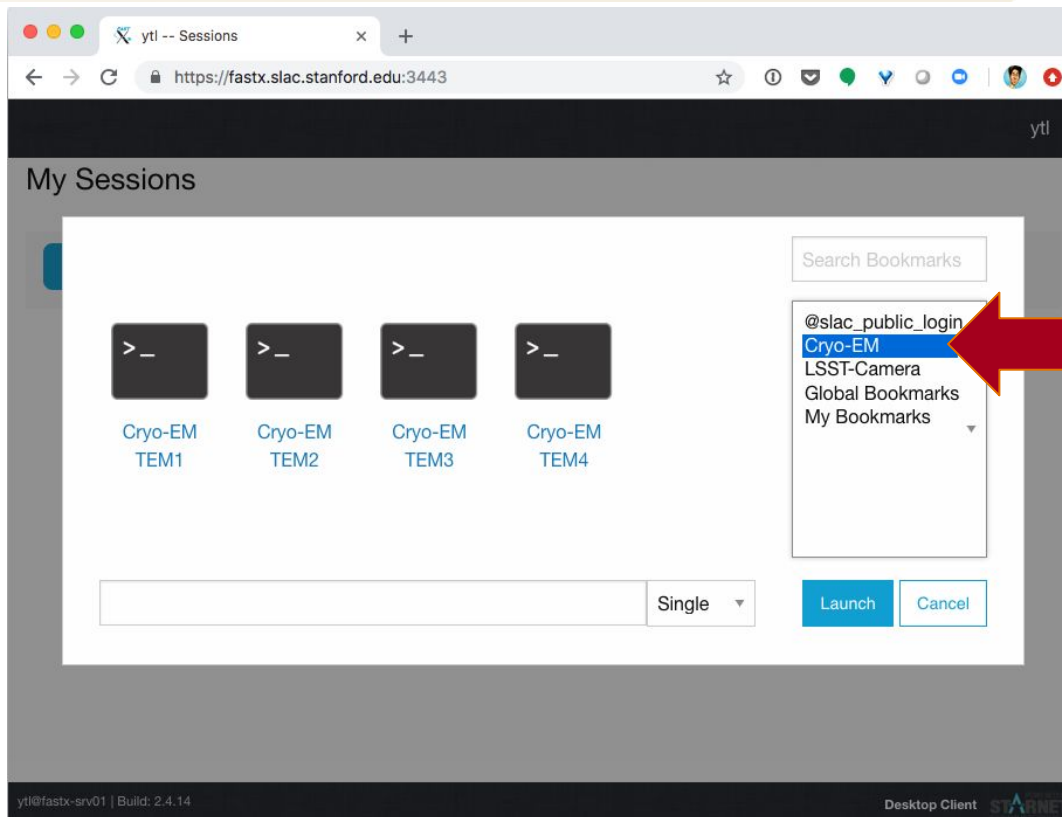
Admin Login  
Build: 2.4.14

<https://fastx.slac.stanford.edu:3443>

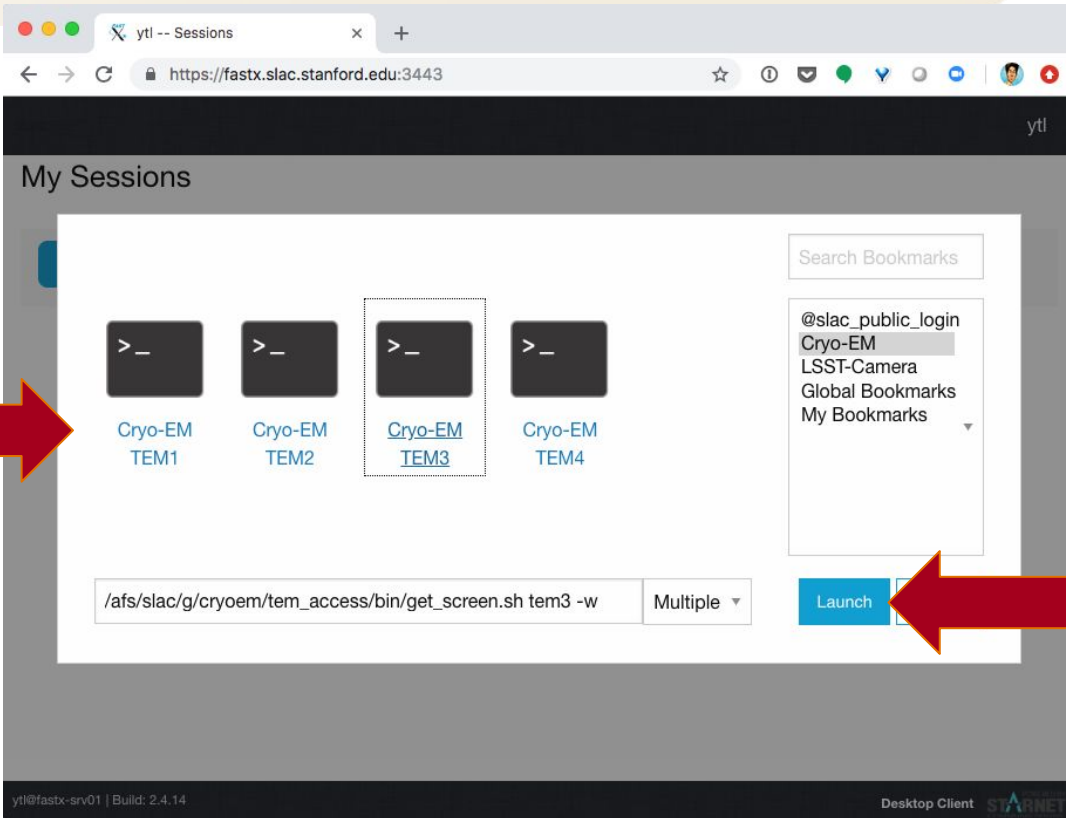
# FastX - Click 'Launch Session'



# FastX - Select 'Cryo-EM'

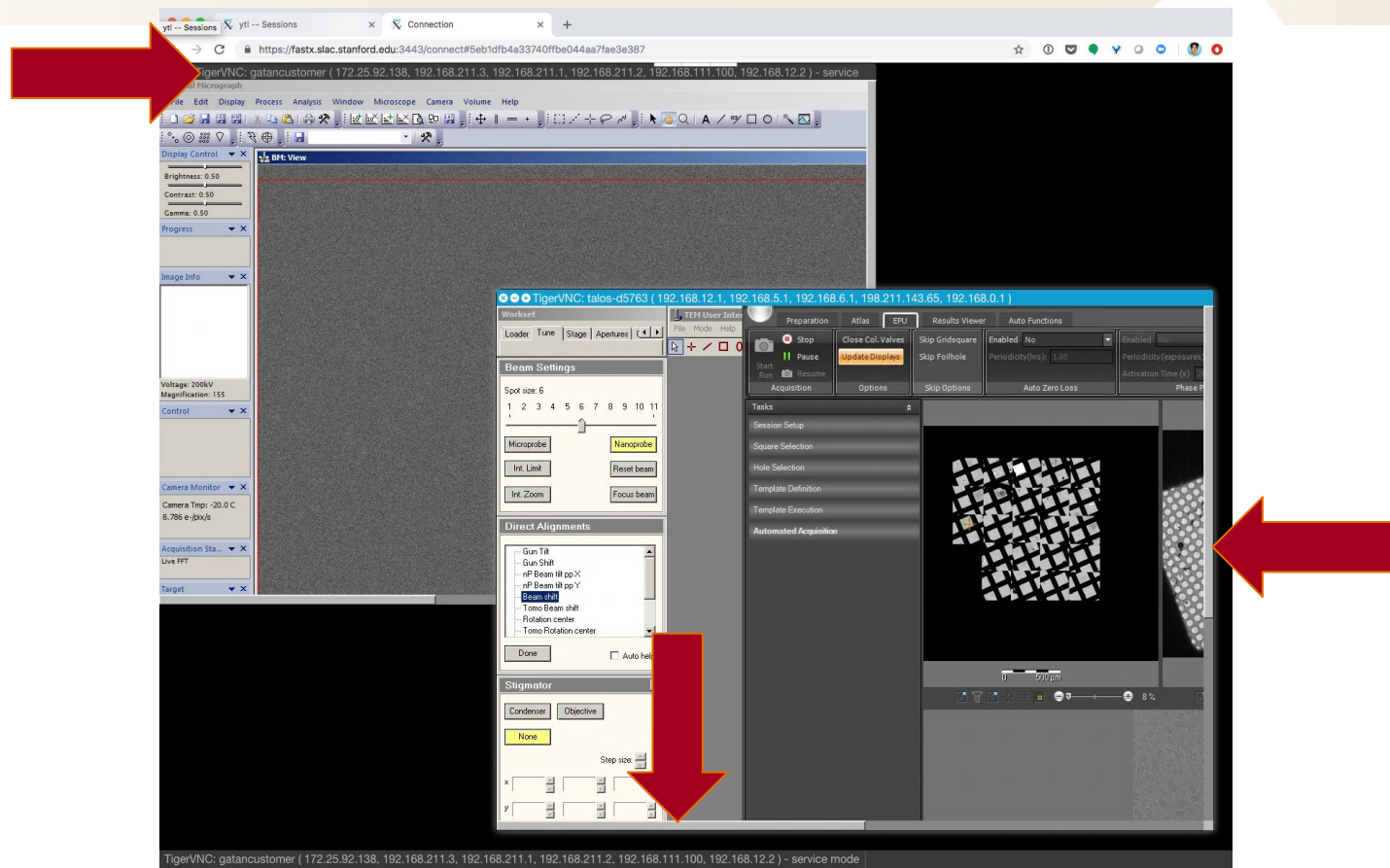


# FastX - Select assigned TEM and 'Launch'



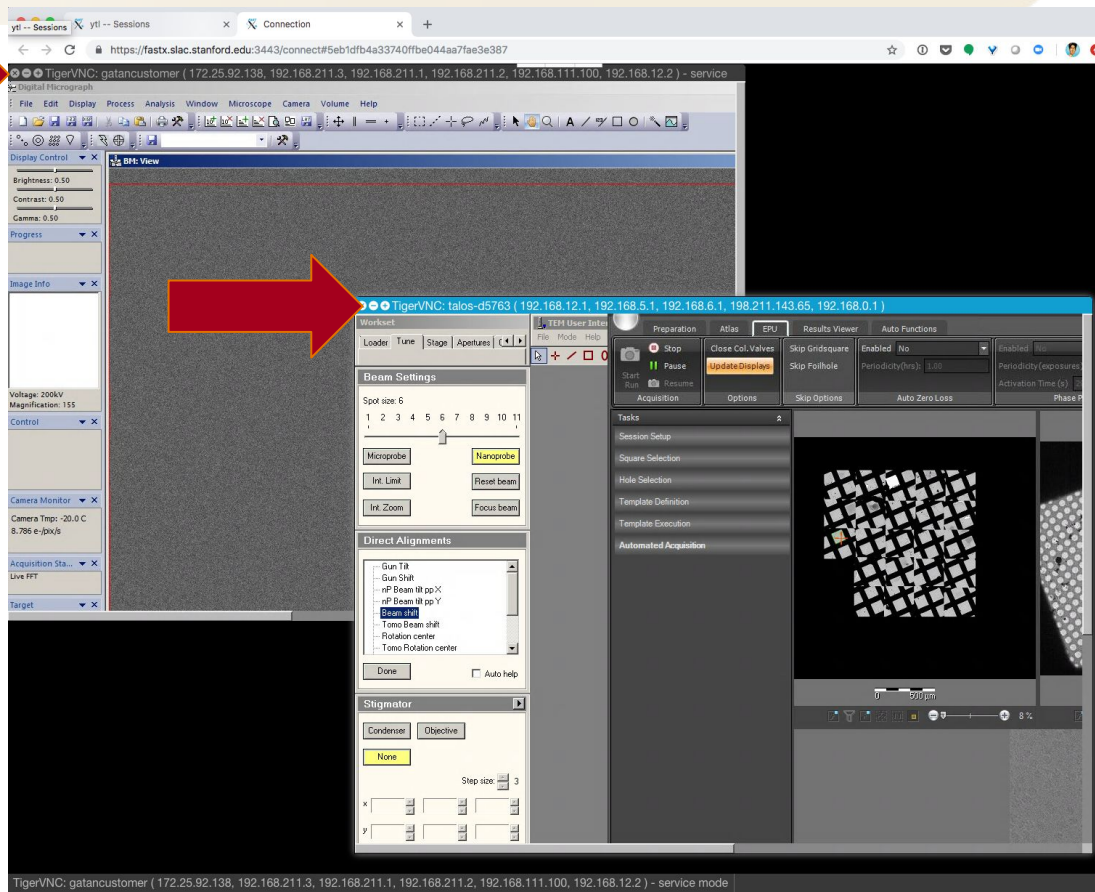
The screenshot shows a web browser window with the URL `https://fastx.slac.stanford.edu:3443`. The page title is "My Sessions". It displays four session cards, each with a terminal icon and the text "Cryo-EM TEM1", "Cryo-EM TEM2", "Cryo-EM TEM3", and "Cryo-EM TEM4". A red arrow points to the "Cryo-EM TEM3" card, which is highlighted with a dashed border. To the right of the session cards is a "Search Bookmarks" section with a dropdown menu showing options: "@slac\_public\_login", "Cryo-EM", "LSST-Camera", "Global Bookmarks", and "My Bookmarks". Below the session cards is a command input field containing `/afs/slac/g/cryoem/tem_access/bin/get_screen.sh tem3 -w` and a "Multiple" dropdown. A red arrow points to the "Launch" button next to the command field. The bottom status bar shows "ytl@fastx-srv01 | Build: 2.4.14" and "Desktop Client STARNET".

# FastX - Two Windows (K2/3 & EPU/SerialEM)



- Session persists if you close your browser window
  - i.e. you will still be logged on
- Need to explicitly terminate session...

# FastX - Exiting (option 1)





# FastX - Exiting (option 2)

The screenshot shows a web browser window with two tabs: 'ytl -- Sessions' and 'Connection'. The address bar shows 'https://fastx.slac.stanford.edu:3443'. The page title is 'ytl' and the main heading is 'My Sessions'. Below the heading, there is a 'Launch Session' button, a 'Filter Sessions' input field, and a 'View' link. An 'Actions' dropdown menu is open, showing a 'Terminate Session' option. A red arrow points to this option. Below the menu, there is a session card for 'Cryo-EM TEM3' with a play button icon and a '1' in a blue circle. At the bottom of the page, there is a status bar with 'ytl@fastx-srv01 | Build: 2.4.14', 'Desktop Client', and the STARNET logo.

My Sessions

Launch Session Filter Sessions View

Actions

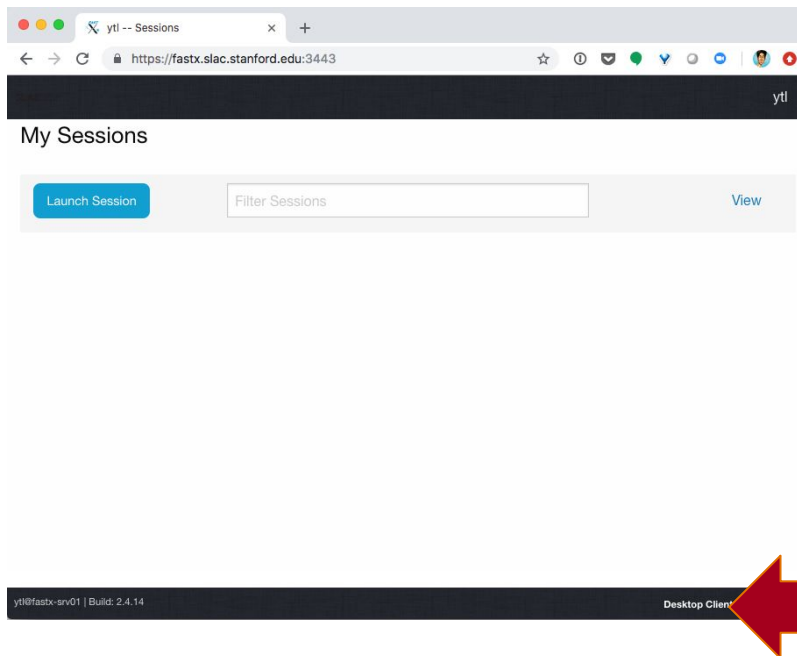
Terminate Session

Cryo-EM TEM3 1

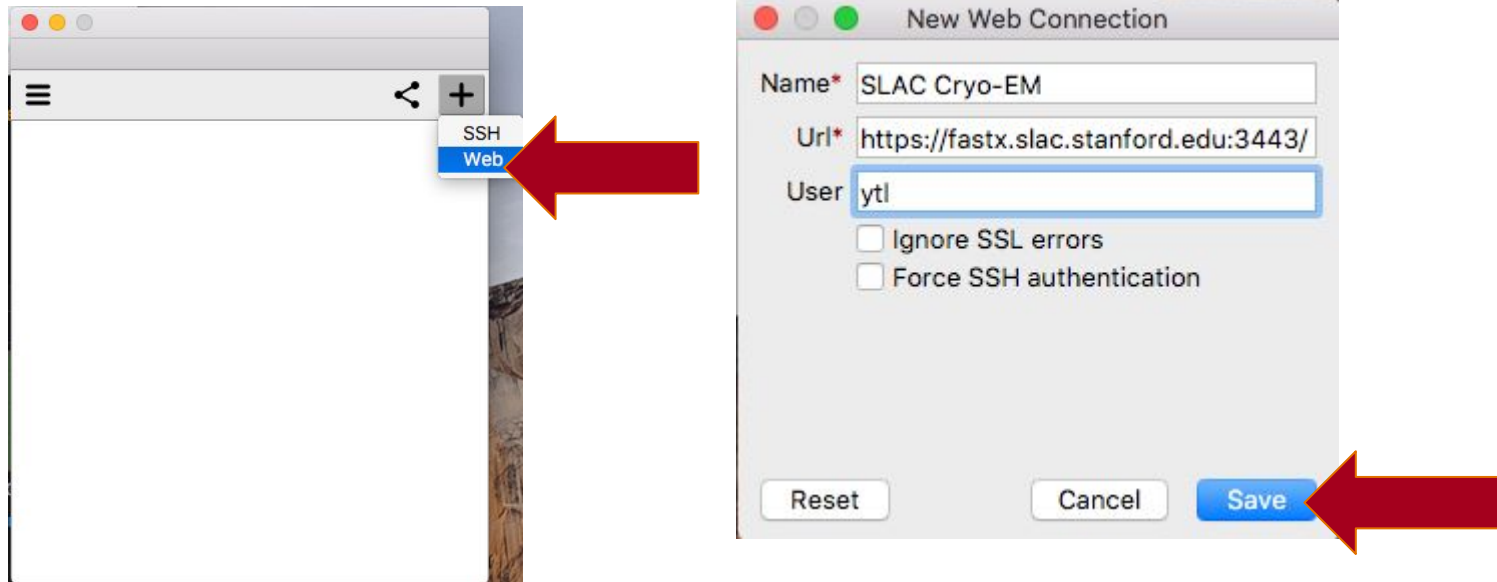
Cryo-EM TEM3 show

ytl@fastx-srv01 | Build: 2.4.14 Desktop Client STARNET

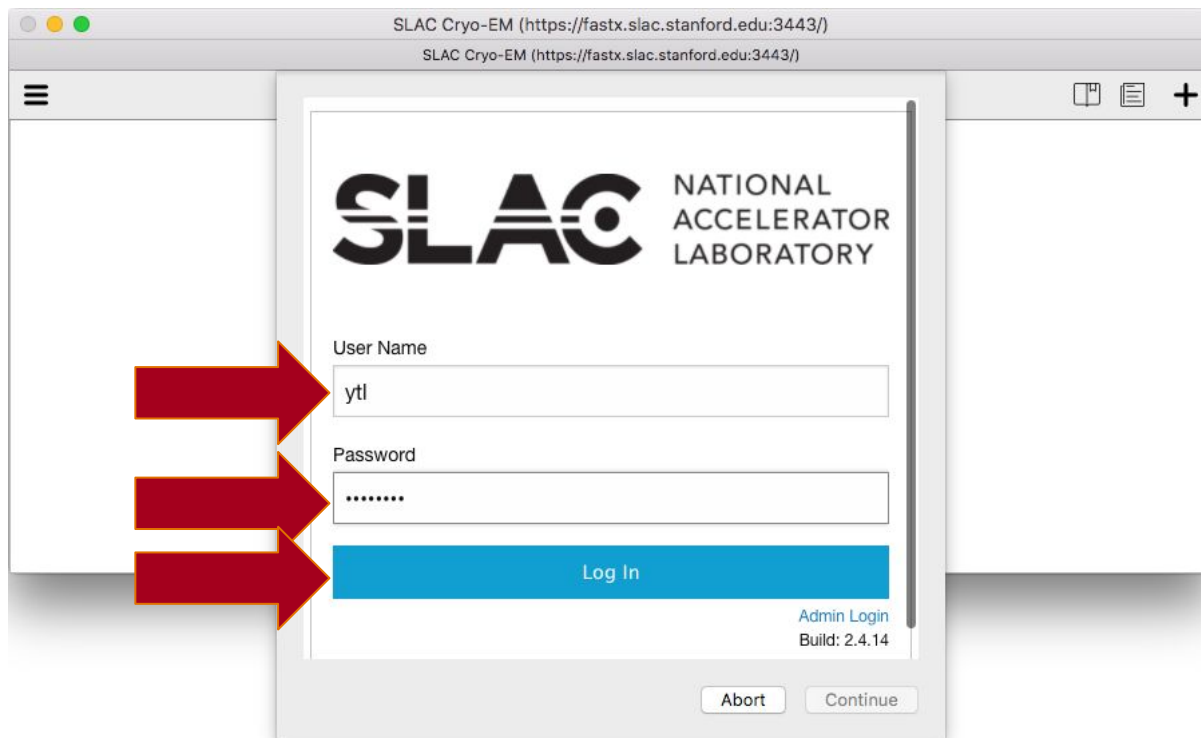
# FastX - Download Native Client



# FastX - Configuring Native Client (1)



# FastX - Configuring Native Client (2)



SLAC Cryo-EM (https://fastx.slac.stanford.edu:3443/)

SLAC Cryo-EM (https://fastx.slac.stanford.edu:3443/)

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User Name

yti

Password

\*\*\*\*\*

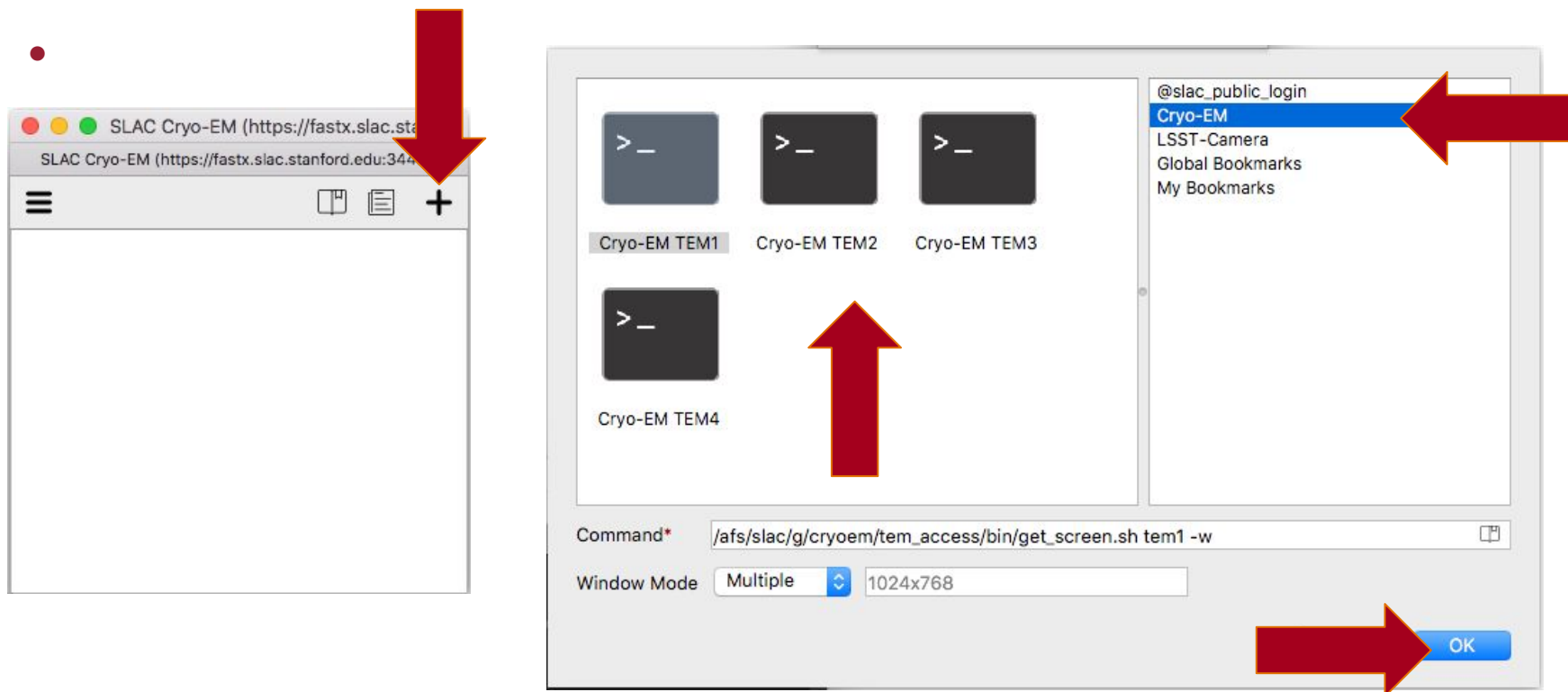
Log In

Admin Login  
Build: 2.4.14

Abort Continue

The image shows a web browser window displaying the SLAC Cryo-EM login page. The page has a header with the SLAC logo and the text 'NATIONAL ACCELERATOR LABORATORY'. Below the header, there are two input fields: 'User Name' and 'Password'. The 'User Name' field contains the text 'yti'. The 'Password' field is masked with asterisks. Below the password field is a blue 'Log In' button. At the bottom right of the login form, there is a link for 'Admin Login' and the text 'Build: 2.4.14'. At the very bottom of the browser window, there are two buttons: 'Abort' and 'Continue'. Three large red arrows are pointing from the left towards the 'User Name', 'Password', and 'Log In' fields, indicating the sequence of steps for logging in.

# FastX - Configuring Native Client (3)



# 1. Experimental Metadata

- Why?
  - Keep information about the experimental setup and image quality
- How?
  - Use an Electronic Notebook to store, and view information about experiment
- Where?
  - <https://cryoem-logbook.slac.stanford.edu>

Cryo-EM elogbook is the portal to your experiment at SLAC

- Provide portal for all Cryo-EM experimental data
  - Assign samples
  - Annotate new metadata
  - Preview results
  - Set permissions for data on disk
  - Summary of image preprocessing
  - Initiate pre-processing pipeline

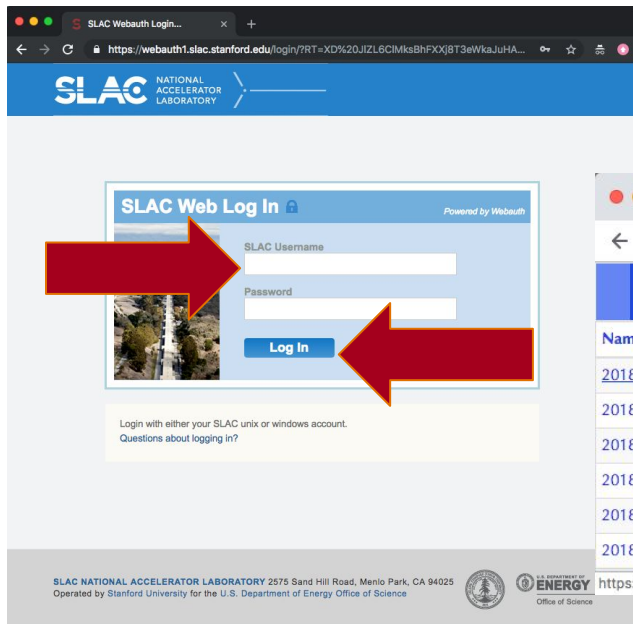
# When should I use it?

- Upon new data for a new sample
- To register a change in sample during an experiment
- To allow collaborators access to data (on disk)
- To allow collaborators access to Remote Access to TEM
- To take notes/annotate the experiments (text, pictures etc)
- Obtain statistics about data quality
- To setup pre-processing



# Accessing the eLogbook

SLAC



Select Experiment

https://cryoem-logbook.slac.stanford.edu/igbk/experiments

My Experiments	Active	TEM1	TEM2	TEM3	TEM4	Unassigned	
Name	First Run	Last Run	Contact	Description			
<a href="#">20181218-C060</a>	Dec/17/2018	Dec/19/2018					
<a href="#">20181215-C000</a>	Dec/15/2018	Dec/17/2018					
<a href="#">20181214-C000</a>	Dec/14/2018	Dec/15/2018					
<a href="#">20181213-C043</a>	Dec/13/2018	Dec/14/2018					
<a href="#">20181212-C061</a>	Dec/12/2018	Dec/13/2018					
<a href="#">20181016-C061</a>	Dec/12/2018	Dec/12/2018					

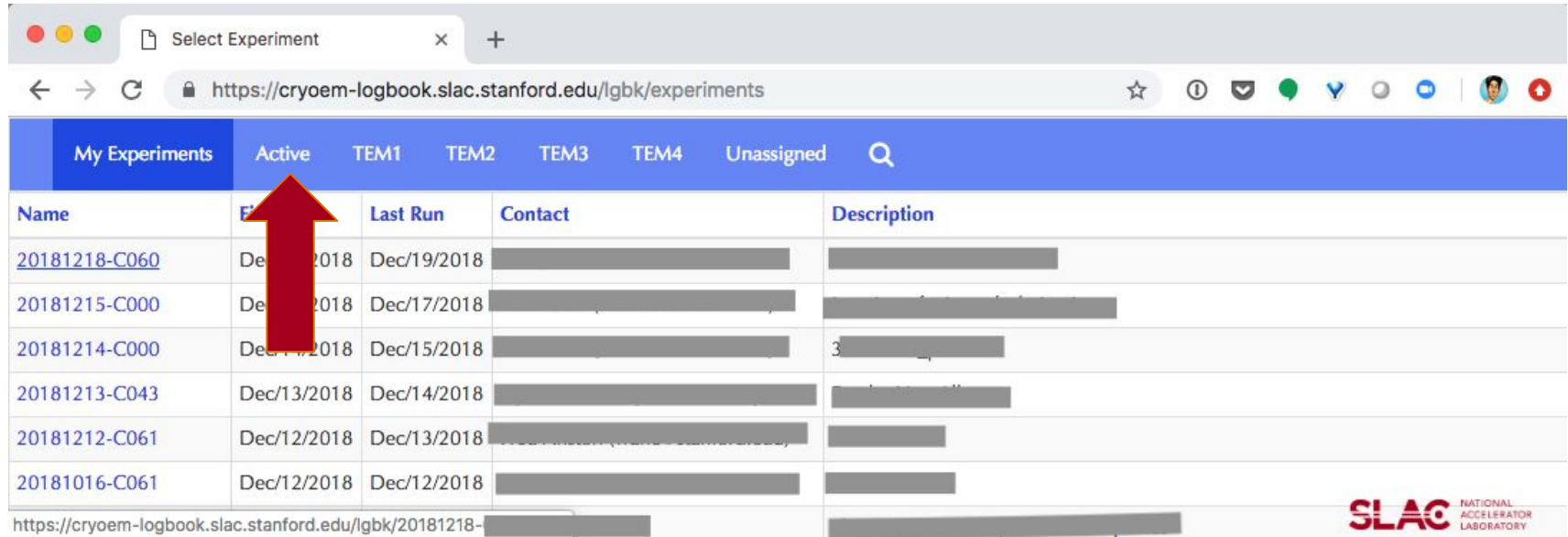
https://cryoem-logbook.slac.stanford.edu/igbk/20181218-

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<https://cryoem-logbook.slac.stanford.edu> - use SLAC account

- What is a 'Sample'?
  - A set of data (movies) collected under identical specimen and experimental (microscope) parameters.
- When should I create a new 'Sample'?
  - When you either change specimen or EPU/SerialEM settings
- Data for each new Sample is copied to new directory (see later)

# Is my experiment active?



The screenshot shows a web browser window with the URL <https://cryoem-logbook.slac.stanford.edu/lgbk/experiments>. The page has a blue header with tabs: "My Experiments", "Active", "TEM1", "TEM2", "TEM3", "TEM4", and "Unassigned". A red arrow points to the "Active" tab. Below the header is a table with columns: "Name", "First Run", "Last Run", "Contact", and "Description". The table lists several experiments, with the first one being "20181218-C060".

Name	First Run	Last Run	Contact	Description
<a href="#">20181218-C060</a>	Dec/18/2018	Dec/19/2018	[REDACTED]	[REDACTED]
<a href="#">20181215-C000</a>	Dec/15/2018	Dec/17/2018	[REDACTED]	[REDACTED]
<a href="#">20181214-C000</a>	Dec/14/2018	Dec/15/2018	[REDACTED]	3 [REDACTED]
<a href="#">20181213-C043</a>	Dec/13/2018	Dec/14/2018	[REDACTED]	[REDACTED]
<a href="#">20181212-C061</a>	Dec/12/2018	Dec/13/2018	[REDACTED]	[REDACTED]
<a href="#">20181016-C061</a>	Dec/12/2018	Dec/12/2018	[REDACTED]	[REDACTED]

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If your experiment is not Active, then you will not be able to Remote Access!

# Create a new Sample

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The screenshot shows the SLAC Experiment Logbook web application. A large red arrow points to the 'Samples' tab in the top navigation bar. A red speech bubble points to a '+' icon in the top right corner, labeled 'Create New Sample'. Another red speech bubble points to a pencil and copy icon in the 'Actions' column of a sample row, labeled 'Edit/Clone a Sample'. The sample row is highlighted in yellow. The table has columns for Name, Description, and Actions. The description for the highlighted sample is '130K, 2/1'. The SLAC logo is in the bottom right corner.

Logbook for [redacted]

Name	Description	Actions
[redacted]	130K, 2/1	[edit] [clone]

Yellow highlighted sample is Active

- Keep track of experimental parameters for each sample as key-value pair
- Keys
  - Selectable from a list (pre-defined)
  - Free form keys (user definable)
- Some keys are mandatory
- Most important keys:
  - fmdose, apix, superres, phase\_plate

# Edit a Sample

Sample details

Sample Name:

Sample Description:

130K, 2/1


Param Name	Param Value	Actions
imaging_method	single-particle	✕ +
imaging_software	EPU	✕ +
imaging_format	.mrc	✕ +
apix	1.07	✕ +
frmdose	0.99	✕ +
preprocess/enable	1	✕ +
preprocess/apply_gainref	1	✕ +
preprocess/convert_gainref	1	✕ +
preprocess/align/motioncor2/throw	0	✕ +
preprocess/align/motioncor2/outst	0	✕ +
preprocess/align/motioncor2/patch	5 5	✕ +
phase_plate	0	✕ +
superres	0	✕ +
objective_aperture/inserted	0	✕ +
energy_filter/slit_size	20	✕ +
		✕ +

Update

Free  
form text

Fields of  
experimental  
parameters

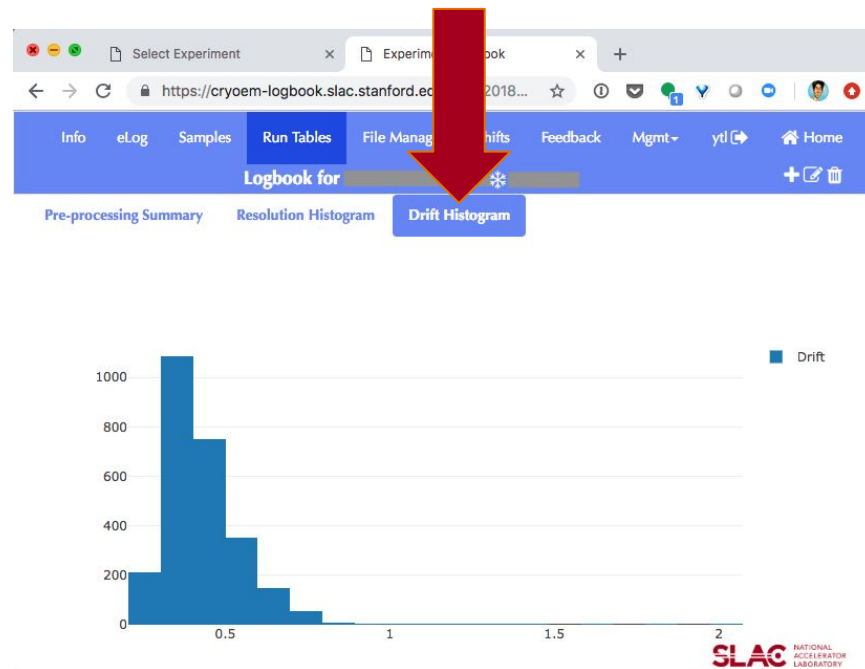
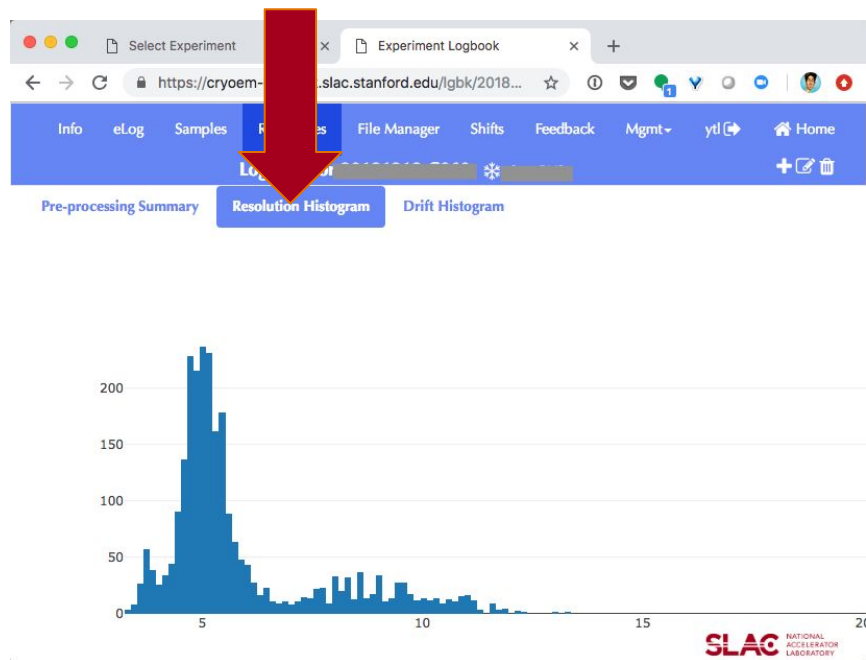
# Run Tables



Browser interface showing the 'Run Tables' tab selected. The URL is <https://cryoem-logbook.slac.stanford.edu/lgbk/20181218-C060/#runTables>. The interface includes a navigation bar with tabs: Info, eLog, Samples, Run Tables (selected), File Manager, Shifts, Feedback, and Mgmt. Below the navigation bar is a 'Logbook for' section with a dropdown menu. The main content area displays a table with columns: Num, Sample, Unaligned Resolution, Drift, Defocus 2, Cross Correlation, and Defocus 1. The table contains 15 rows of data.

Num	Sample	Unaligned Resolution	Drift	Defocus 2	Cross Correlation	Defocus 1
FoilHole_19622422_Data_19621643_19621644_20181219_1247	5c1839d9afcba2000e47a49e	6.233913	5.431061	0.32999077213416983	15298.352539	13231.825195
FoilHole_19622422_Data_19621637_19621638_20181219_1247	5c1839d9afcba2000e47a49e	10.542647	5.157554	0.5864216168933571	15509.198242	13398.279297
FoilHole_19622422_Data_19621628_19621629_20181219_1248	5c1839d9afcba2000e47a49e	4.910274	3.939011	0.27112073633871814	14832.755859	12893.351562
FoilHole_19622421_Data_19621643_19621644_20181219_1245	5c1839d9afcba2000e47a49e	11.029231	7.878022	0.5375809892059968	16145.301758	14831.040039
FoilHole_19622421_Data_19621637_19621638_20181219_1245	5c1839d9afcba2000e47a49e	10.7	9.432895	0.47696019910810594	16217.693359	15414.990234
FoilHole_19622421_Data_19621628_19621629_20181219_1246	5c1839d9afcba2000e47a49e	9.956945	4.978472	0.3119474355642209	16702.605469	14630.331055
FoilHole_19622420_Data_19621643_19621644_20181219_1243	5c1839d9afcba2000e47a49e	9.956945	8.434118	0.37180790196485675	13534.121094	13239.767578
FoilHole_19622420_Data_19621637_19621638_20181219_1242	5c1839d9afcba2000e47a49e	716.900024	8.146591	0.6759940021221882	14827.082031	13663.527344
FoilHole_19622420_Data_19621628_19621629_20181219_1243	5c1839d9afcba2000e47a49e	9.956945	12.150848	0.3970782587524496	12936.891602	12726.240234
FoilHole_19622419_Data_19621643_19621644_20181219_1240	5c1839d9afcba2000e47a49e	5.472519	4.685621	0.5254111708452334	16073.761719	14015.852539
FoilHole_19622419_Data_19621637_19621638_20181219_1240	5c1839d9afcba2000e47a49e	5.35	4.168023	0.4184625075081815	17132.792969	14940.836914

# Run Tables





# Adding Collaborators

The screenshot shows the SLAC Experiment Logbook interface. The 'Collaborators' tab is selected, displaying a table of collaborators. Two red arrows point to the 'Collaborators' button and the list of collaborators.

Id	Full Name	Permissions
[redacted]	[redacted]	[edit] [delete] [add] [trash]
[redacted]	[redacted]	[edit] [delete] [add] [trash]
[redacted]	[redacted]	[edit] [delete] [add] [trash]
[redacted]	[redacted]	[edit] [delete] [add] [trash]

<https://cryoem-logbook.slac.stanford.edu/lgbk/20181213-C043/#collaborators>

The screenshot shows the 'Add a collaborator' dialog box. A red arrow points to the 'Add' button.

Search for id's:

yti

Id	Name	Select
yti	Yee Ting Li	<input checked="" type="checkbox"/>

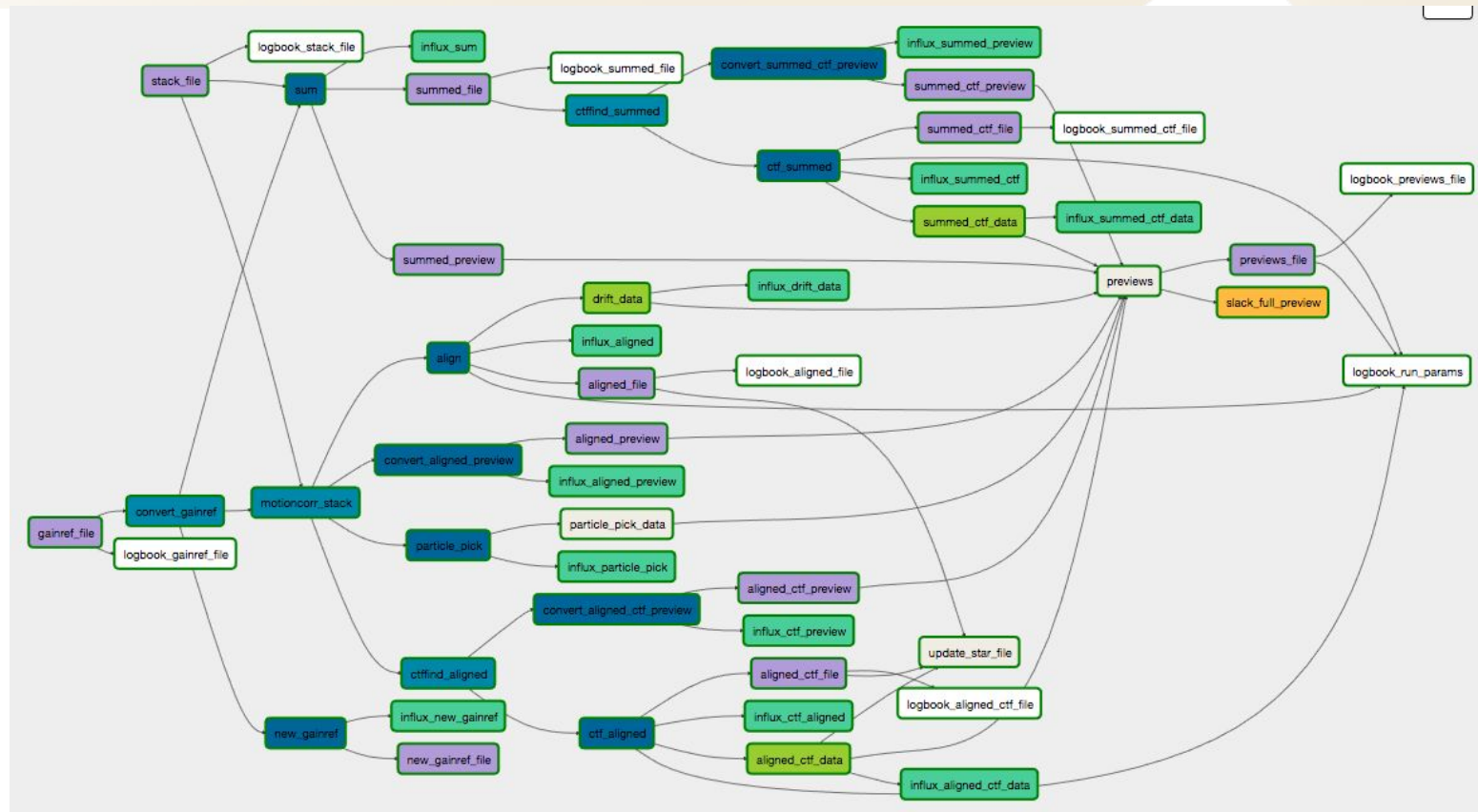
Add

Added Collaborators will have Remote Access & Data Access to Experiment

# 1. Pre-Processing

- Why?
  - Common tasks required prior to 2D classification; we provide aligned images and CTF ‘out-of-the-box’
- How?
  - As we stream the movies from the microscopes, we also do pre-processing and logging at the same time.
- Where?
  - Pre-processed data in the `./aligned` directory.

# All Movies are put into Pipeline



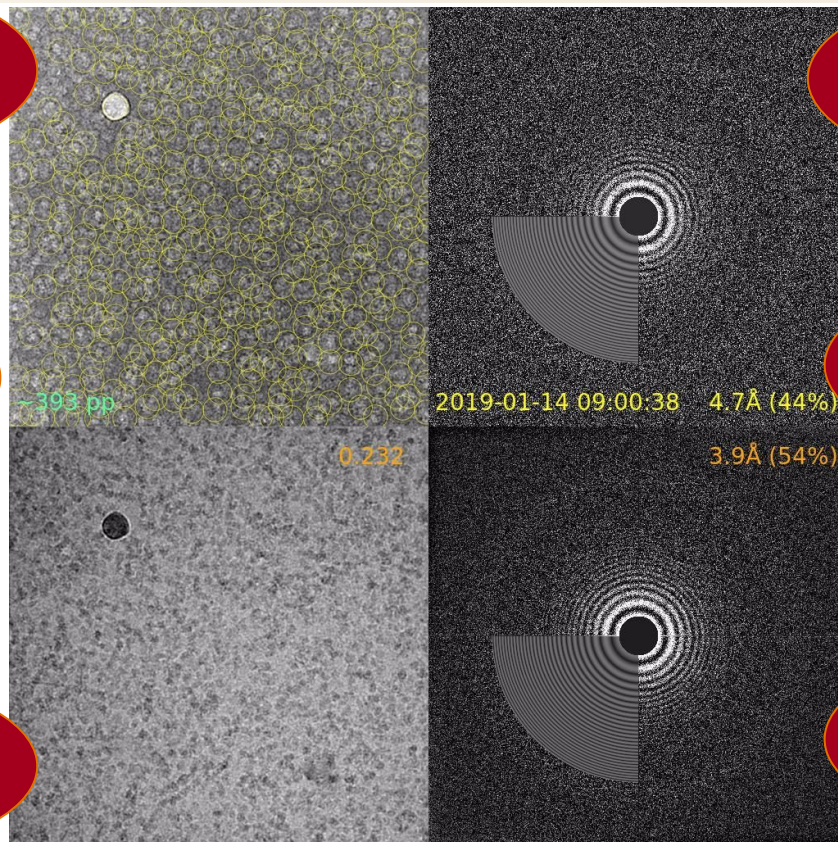
# Preview Generated

SLAC

Particle  
Picked

Num. Picked  
particles /  
RMS Drift

Aligned  
Image

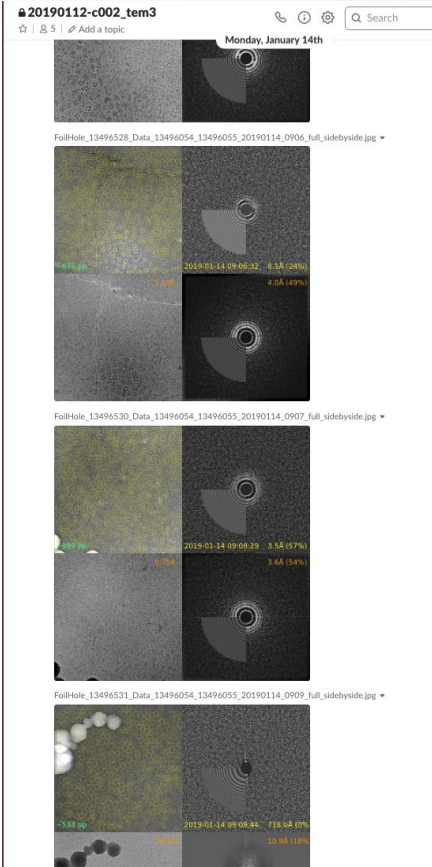


CTF Before  
Alignment

Est.  
Resolution /  
% of Nyquist

CTF After  
Alignment

# Live Stream of Previews



- Sign up at
  - [slac-cryoem.slack.com](https://slac-cryoem.slack.com)
- Use home institution email for signup
- Operator may need to invite you to experiment

### 3. Where is my data?

- Why?
  - Once your experiment is over, you want access to the raw and pre-processed data.
- How?
  - All data is kept at SLAC
  - Current plan is that data will be retained for ~5 years
- Where?
  - `/gpfs/slac/cryo/fs1/exp/`

**All experimental data kept on Long Term Storage**

# Directory Layout

- Parent Directory: `/gpfs/slac/cryo/fs1/exp/`
- Each experiment kept under:
  - `./<YYYYMM>/<YYYYMMDD>-<PROP-ID>_<TEM#>/`
- Each experiment folder has n samples:

```
# pwd
/gpfs/slac/cryo/fs1/exp/201901/20190111-CS30_TEM3
# ls -lah
...
drwxrwsr-x+  7 ytl  4.0K Jan 11 19:37 5c391d7c79c214000e33cbdd
lrwxrwxrwx   1 ytl    24 Jan 11 17:34 vista -> 5c391d7c79c214000e33cbdd
...
```



## Directory Layout (2)

- Each sample folder has:

```
$ ls -lah
total 256K
drwxrwsr-x+ 7 ytl 4.0K Jan 11 19:37 .
drwxrwsr-x+ 3 ytl 4.0K Jan 11 17:34 ..
drwxrwsr-x+ 3 ytl 4.0K Jan 11 17:41 aligned
-rw-rw-r--+ 1 ytl 139K Jan 12 07:25 images.star
drwxrwsr-x+ 3 ytl 4.0K Jan 11 17:42 particles
drwxrwsr-x+ 2 ytl 48K Jan 12 07:25 previews
drwxrwxrwx+ 6 ytl 4.0K Jan 12 12:42 raw
drwxrwsr-x+ 3 ytl 4.0K Jan 11 17:41 summed
```



- Duplication of files kept on the microscopes
  - Ensure EPU/SerialEM is configured to store all data to `X:\` drive
- Do NOT move files around on the microscope computers
  - It will cause duplication of data as its streamed onto disk

# Aligned Data: `./aligned/`

- Pre-processed data kept here
- Aligned image:
  - `./motioncor2/<version>/`
    - `<filename>_aligned.mrc`
    - `<filename>_aligned_DW.mrc`
    -
- CTFs
  - `./motioncor2/<version>/ctffind4/<version>/`
    - `<filename>_aligned_ctf.txt`
    - `<filename>_aligned_ctf.mrc`

# How do I copy my data?

- Can use standard UNIX tools
  - scp, rsync
    - `dtn01.slac.stanford.edu`
- Globus Online
  - Send [ytl@slac.stanford.edu](mailto:ytl@slac.stanford.edu) an email to enable your SLAC account
    - <https://www.globus.org/>
    - `slac#cryoem`

- Copy entire experiment:

3+ TB

```
rsync -avz \  
dtn01.slac.stanford.edu:/gpfs/slac/cryo/fs1/exp/201901/20190107-CS01_TEM4 \  
.
```

- Copy just aligned images:

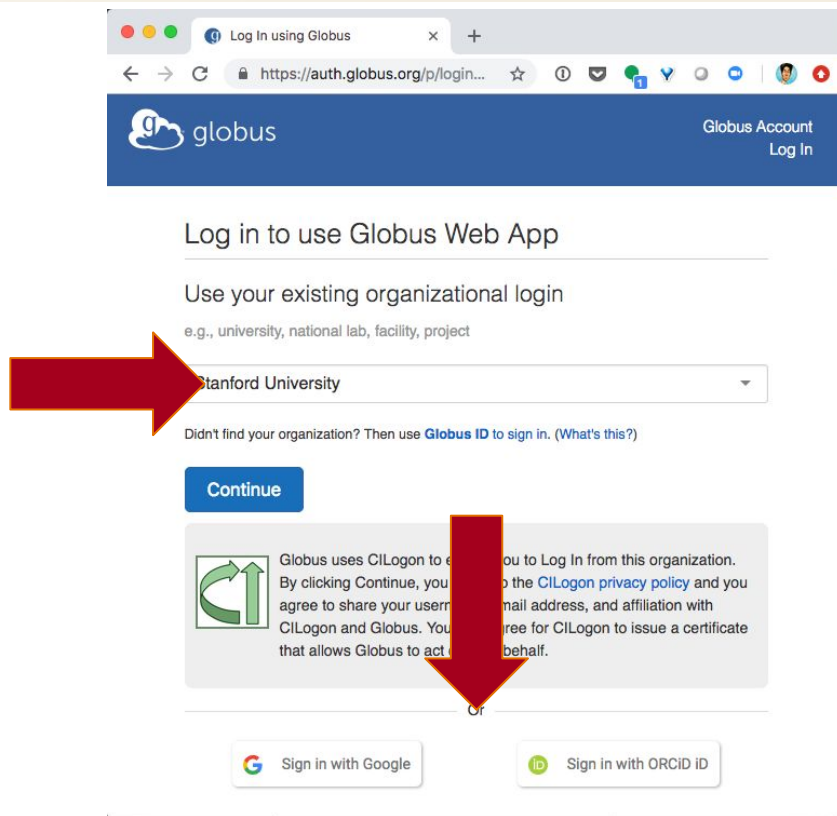
~500 GB

```
rsync -avz \  
dtn01.slac.stanford.edu:/gpfs/slac/cryo/fs1/exp/201901/20190107-CS01_TEM4/aligned \  
.
```

- Copy just raw images:

2+ TB

```
rsync -avz \  
dtn01.slac.stanford.edu/gpfs/slac/cryo/fs1/exp/201901/20190107-CS01_TEM4/raw \  
.
```



The screenshot shows the Globus login interface in a web browser. The browser's address bar displays the URL `https://auth.globus.org/p/login...`. The Globus logo is in the top left, and 'Globus Account Log In' is in the top right. The main heading is 'Log in to use Globus Web App'. Below it, the text 'Use your existing organizational login' is followed by a list of examples: 'e.g., university, national lab, facility, project'. A dropdown menu is open, showing 'Stanford University' as the selected option. A large red arrow points to this dropdown. Below the dropdown, a link says 'Didn't find your organization? Then use Globus ID to sign in. (What's this?)'. A blue 'Continue' button is present. Below the button is a grey box containing a circular arrow icon and text explaining that Globus uses CILogon for organizational login. A second large red arrow points to this text box. At the bottom, there are two buttons: 'Sign in with Google' and 'Sign in with ORCID iD', separated by an 'Or'.

Log In using Globus

https://auth.globus.org/p/login...

globus Globus Account Log In

Log in to use Globus Web App

Use your existing organizational login

e.g., university, national lab, facility, project

Stanford University

Didn't find your organization? Then use [Globus ID](#) to sign in. (What's this?)

Continue

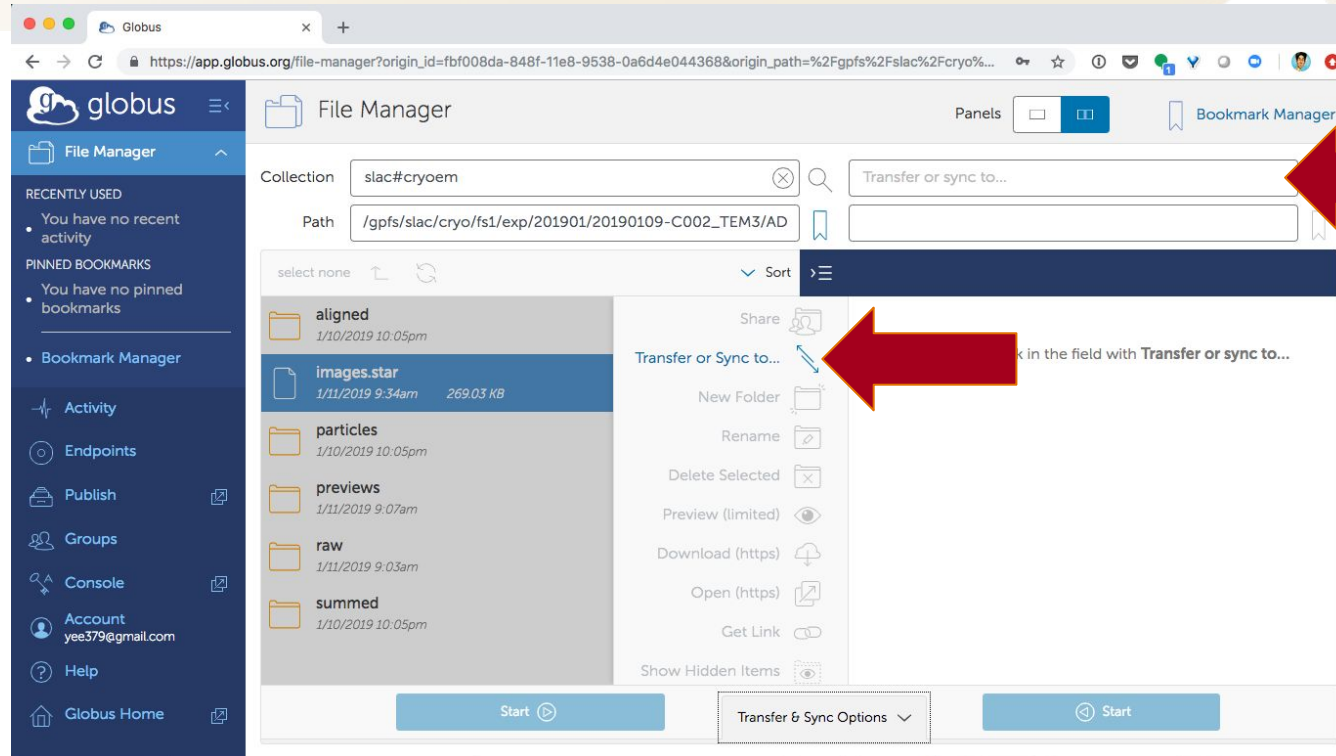
Globus uses CILogon to enable you to Log In from this organization. By clicking Continue, you agree to the [CILogon privacy policy](#) and you agree to share your username, email address, and affiliation with CILogon and Globus. You agree for CILogon to issue a certificate that allows Globus to act on your behalf.

Or

Sign in with Google Sign in with ORCID iD

# Globus Online

SLAC



**Download and Install 'Globus Personal Connect' to transfer to your Desktop**

The screenshot shows the Globus File Manager web interface. The left sidebar contains navigation links: File Manager, RECENTLY USED, PINNED BOOKMARKS, Bookmark Manager, Activity, Endpoints, Publish, Groups, Console, Account (yee379@gmail.com), Help, and Globus Home. The main content area is titled 'File Manager' and shows a 'Collection' dropdown set to 'slac#cryoem'. Below it is a 'Path' input field. A red arrow points to the 'Collection' dropdown. The main content area displays a login form with the text 'Please authenticate to access this collection'. The form includes fields for 'Login Server' (osgmyproxy2.slac.stanford.edu), 'Username' (ytl), and 'Password' (masked with dots). A red arrow points to the 'Authenticate' button. A red speech bubble with the text 'SLAC Unix Account' points to the 'Username' field. The bottom right of the form has a 'Advanced' section with a 'Deactivate' button.

File Manager | Globus

https://app.globus.org/file-manager?origin\_id=fbf008da-848f-11e8-9538-0...

File Manager

Collection: slac#cryoem

Path:

Please authenticate to access this collection

Login Server: osgmyproxy2.slac.stanford.edu

Username: ytl

Password: .....

Authenticate

SLAC Unix Account

## Other transfer tools

- CyberDuck
- WinSCP
-

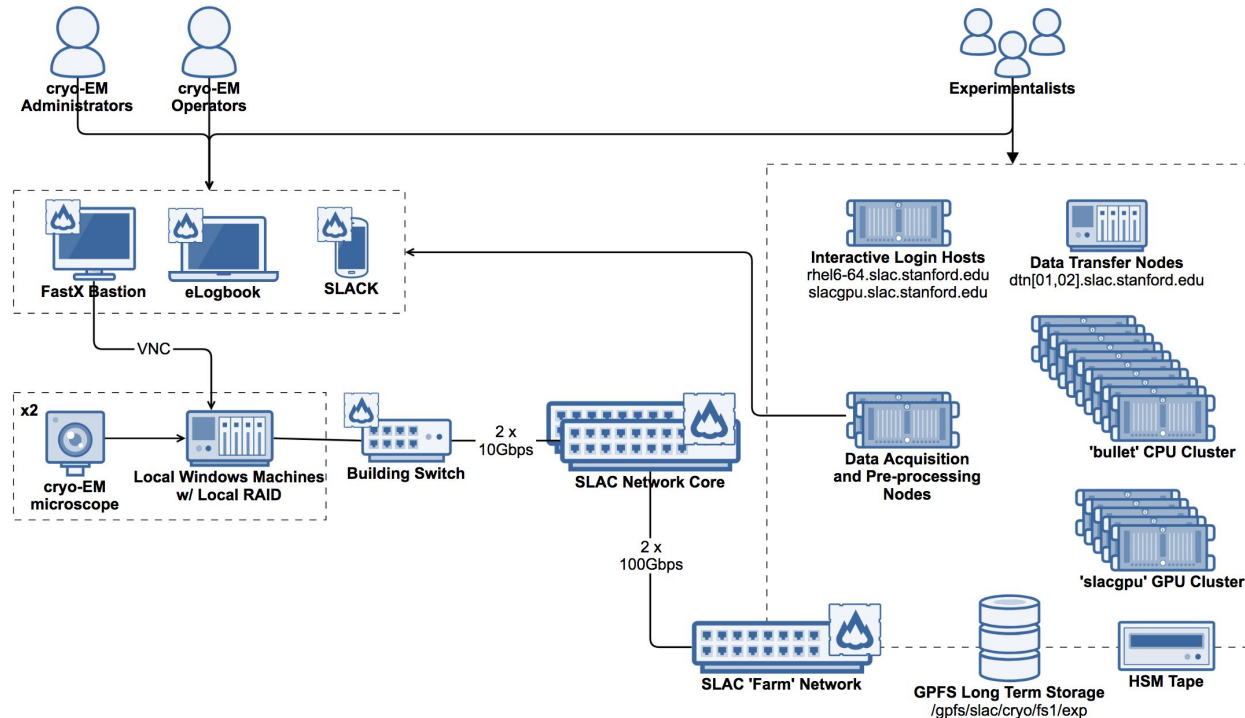


- Remote Access to TEM
  - <https://fastx.slac.stanford.edu:3443>
- Samples in eLogbook
  - **Activate new samples** for each new microscope config
- Pre-processing Pipeline and near-real-time previews
  - [slac-cryoem.slack.com](https://slac-cryoem.slack.com)
- Data Transfer
  - [slac#cryoem](#) on Globus
  - [dtn01.slac.stanford.edu](https://dtn01.slac.stanford.edu) for rsync etc.

# Questions?

-

# DAQ and Data Management Overview



Provide 'Fast Feedback' to Users