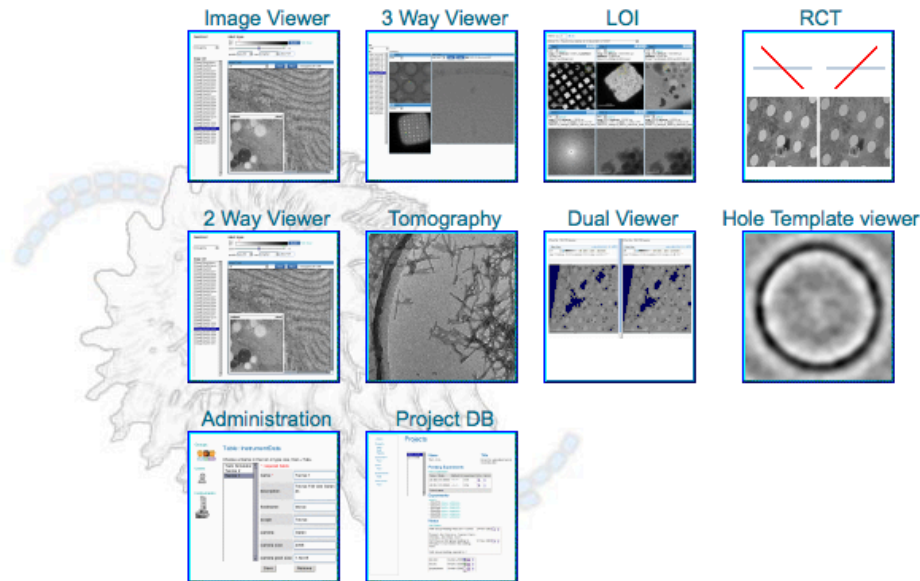


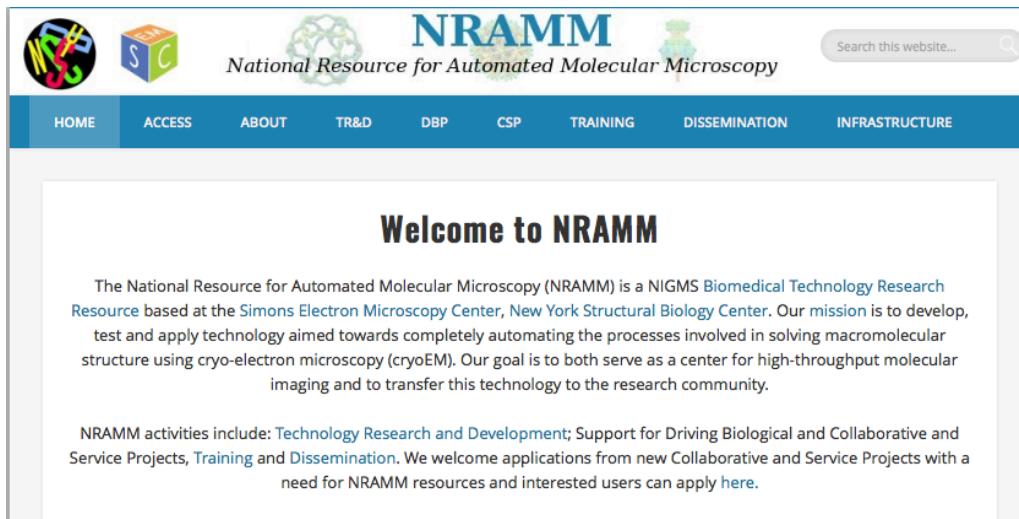
Appion and Leginon DB Tools



Introduction to Appion and Leginon tools

Chi-yu Fu (ICOB)

NRAMM/AMI at New York Structural Biology Center



The screenshot shows the NRAMM website homepage. At the top, there is a navigation bar with icons for NRAMM and S-C, and a search bar. Below the navigation bar, the text reads "Welcome to NRAMM". The main content area contains a paragraph about the National Resource for Automated Molecular Microscopy (NRAMM) and its mission. Below this, there is a section for NRAMM activities, including Technology Research and Development, Support for Driving Biological and Collaborative and Service Projects, Training and Dissemination, and a link to apply for resources.

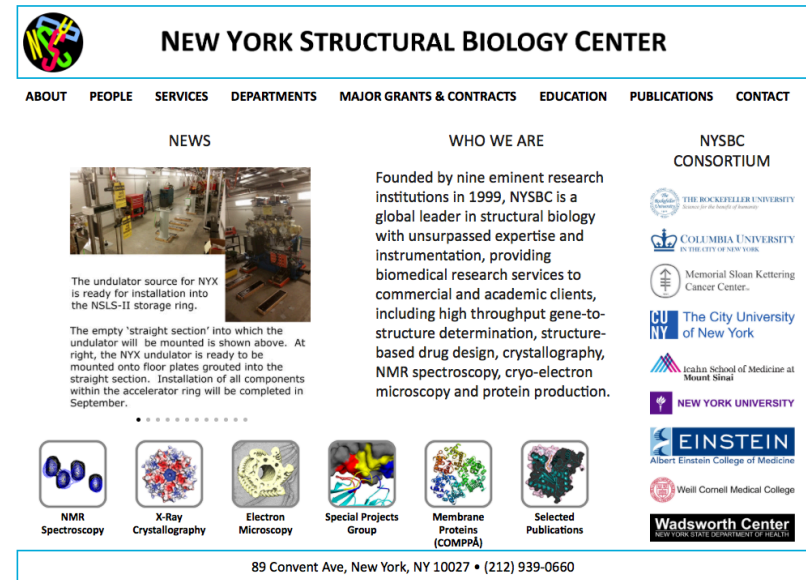
Welcome to NRAMM

The National Resource for Automated Molecular Microscopy (NRAMM) is a NIGMS Biomedical Technology Research Resource based at the Simons Electron Microscopy Center, New York Structural Biology Center. Our mission is to develop, test and apply technology aimed towards completely automating the processes involved in solving macromolecular structure using cryo-electron microscopy (cryoEM). Our goal is to both serve as a center for high-throughput molecular imaging and to transfer this technology to the research community.

NRAMM activities include: [Technology Research and Development](#); Support for Driving Biological and Collaborative and Service Projects, [Training and Dissemination](#). We welcome applications from new Collaborative and Service Projects with need for NRAMM resources and interested users can apply [here](#).

http://emg.nysbc.org/redmine/projects/legion/wiki/Leginon_Homepage

http://emg.nysbc.org/redmine/projects/appion/wiki/Appion_Home



The screenshot shows the New York Structural Biology Center website. At the top, there is a navigation bar with icons for the center and a search bar. Below the navigation bar, the text reads "NEW YORK STRUCTURAL BIOLOGY CENTER". The main content area is divided into three columns: NEWS, WHO WE ARE, and NYSBC CONSORTIUM. The NEWS column features a photo of the undulator source and a text block. The WHO WE ARE column contains a paragraph about the center's history and services. The NYSBC CONSORTIUM column lists various partner institutions.

NEW YORK STRUCTURAL BIOLOGY CENTER

NEWS

The undulator source for NYX is ready for installation into the NSLS-II storage ring.

The empty 'straight section' into which the undulator will be mounted is shown above. At right, the NYX undulator is ready to be mounted onto floor plates grouted into the straight section. Installation of all components within the accelerator ring will be completed in September.

WHO WE ARE

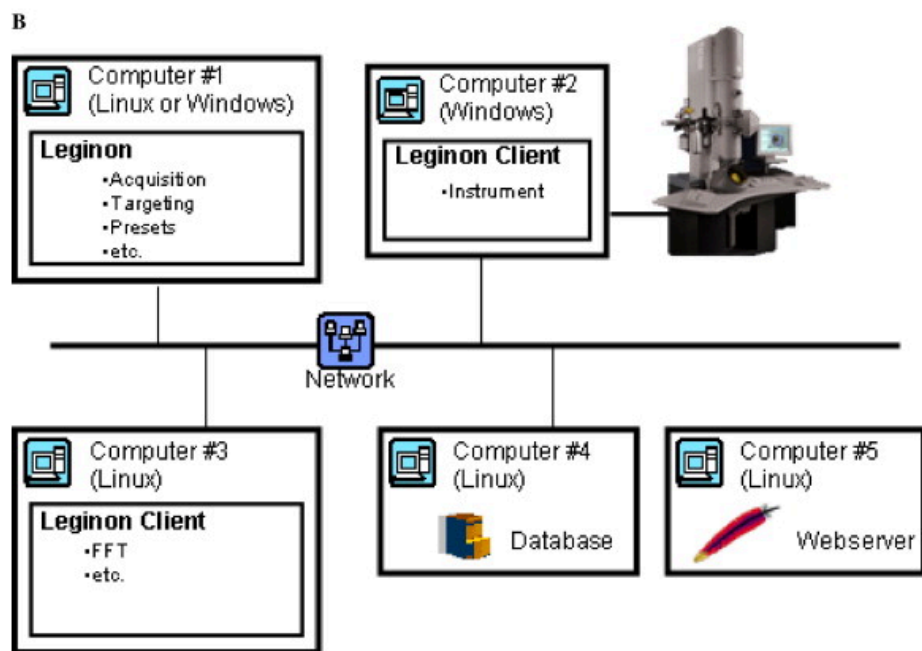
Founded by nine eminent research institutions in 1999, NYSBC is a global leader in structural biology with unsurpassed expertise and instrumentation, providing biomedical research services to commercial and academic clients, including high throughput gene-structure determination, structure-based drug design, crystallography, NMR spectroscopy, cryo-electron microscopy and protein production.

NYSBC CONSORTIUM

THE ROCKEFELLER UNIVERSITY
COLUMBIA UNIVERSITY
Memorial Sloan Kettering Cancer Center
The City University of New York
Leahurst School of Medicine at Mount Sinai
NEW YORK UNIVERSITY
EINSTEIN
Albert Einstein College of Medicine
Weill Cornell Medical College
Wadsworth Center
NEW YORK STATE DEPARTMENT OF HEALTH

89 Convent Ave, New York, NY 10027 • (212) 939-0660

Leginon/Appion pipeline

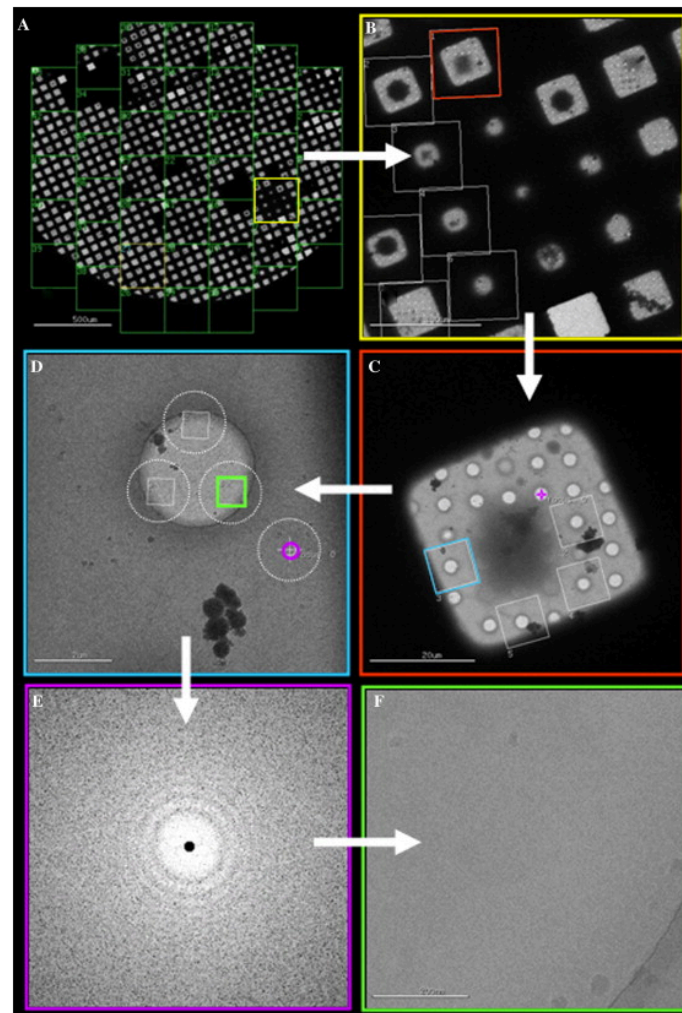


Installed in cryoEM core

Special thanks to

Anchi Cheng (AMI)

Shin-bo Cheng (ICOB computer center)



Atlas collection

The screenshot displays a software interface for 'Leginon: 17feb25a'. The main window has a menu bar (File, Application, Launcher, Node, Events, Others, Help) and a toolbar. On the left is a sidebar with a tree view of components: Presets_Manager, Grid_Targeting (highlighted), Grid, Square_Targeting, Square, Hole_Targeting, Hole, Preview, Exposure_FFT, Z_Focus, Exposure_Targeting, Exposure, Focus, Focus_FFT, Beam_Tilt, Drift_Monitor, N2_Filling, Fix_Beam, Correction, Target_Adjustment, and Navigation.

A log window in the center shows the following messages:

Level	Time	Message
Info	10:39:44 AM	Atlas targets published
Info	10:39:42 AM	Press 'Publish Atlas' to continue
Info	10:39:43 AM	Calculated Atlas with size 7000x7000 pixels from 11 target(s)

A 'Grid Targeting Setup' dialog box is open, showing 'Image Acquisition' settings: Preset: gr, Label: 1, and Radius: 0.0009 m. It has OK, Cancel, and Apply buttons.

An 'Image viewer - Mozilla Firefox' window is open, displaying a grid of images. The browser address bar shows 'localhost.localdomain/myamiweb/imageviewer.php'. The page title is '[Home][summary] [processing] [make jpgs]'. The main view shows a grid of images with a scale bar of 100µm. The selected image is '17feb25a_1_00004gr.mrc' with parameters: mag: 120 defocus: -2000.00 µm pixelsize: 2885.56 Å dose: none.

The main application window on the right shows a grid of images with a scale bar of 100µm. The selected image is '17feb25a_1_00004gr.mrc' with parameters: mag: 120 defocus: -2000.00 µm pixelsize: 2885.56 Å dose: none.

Square targeting

The screenshot displays a software interface for square targeting. The main window shows a grid of squares, with a green crosshair and a red starburst marker indicating a target. The interface includes a menu bar (File, Application, Launcher, Node, Events, Others, Help), a toolbar, and a status bar. A left sidebar lists various modules, with 'Square_Targeting' selected. A central panel shows a message log with the following entries:

Lev	Time	Message
1	1:37:04 PM	Acquisition targets submitted
1	1:37:04 PM	Submitting targets...
1	1:36:43 PM	discovered 3 targets (1 doc)

Below the message log, a statistics panel displays the following data:

Mean:	729.107
Min.:	-12.0157
Max.:	5059.16
Std. dev.:	1061.48

A control panel on the left side of the main window lists various actions:

- preview
- acquisition
- focus
- reference
- done
- position
- Image
- Filtered
- Thresholded

The main window also features a toolbar with a magnifying glass, a zoom level of 2x, and two sliders with values -12.0157 and 5059.16. The main image area shows a grid of squares, with a green crosshair and a red starburst marker indicating a target.

Hole targeting

The screenshot displays a software application window with the following components:

- Menu Bar:** File, Application, Launcher, Node, Events, Others, Help
- Toolbar:** Includes icons for file operations and a zoom level of 2/3x.
- Log Window:**

Lev	Time	Message
	1:46:32 PM	Waiting for user to check targets...
	1:46:32 PM	[beep]
	1:46:32 PM	[f...]
- Statistics Panel:**

Mean:	1669.27
Min.:	81.3489
Max.:	4041.23
Std. dev.:	451.399
- Process List:**
 - Original
 - Template
 - Threshold
 - Blobs
 - Lattice
 - acquisition
 - focus
 - preview
 - done
- Main Image Area:** A circular grayscale image of a holey carbon grid. Several holes are highlighted with green bounding boxes, and a blue crosshair is positioned at the bottom center of the image.

Exposure targeting

The screenshot displays a software interface for exposure targeting. The main window is titled "Exposure Targeting" and features a menu bar with "File", "Application", "Launcher", "Node", "Events", "Others", and "Help". Below the menu bar is a toolbar with icons for file operations and a "2/3x" zoom indicator. A status bar at the top shows a level indicator and a message: "1:49:25 PM Waiting for user to check targets...".

On the left side, there is a vertical toolbar with various tools, including "Presets_Manager", "Grid_Targeting", "Grid", "Square_Targeting", "Square", "Hole_Targeting", "Hole", "Exposure_Targeting" (highlighted in red), "Exposure", "Exposure_FFT", "Preview", "Focus", "Focus_FFT", "Z_Focus", "Beam_Tilt", "Drift_Monitor", "N2_Filling", "Fix_Beam", "Correction", "Target_Adjustment", and "Navigation".

In the center-left, a statistics panel displays the following data:

Mean:	1947.55
Min.:	924.866
Max.:	3603.51
Std. dev.:	254.126

Below the statistics panel is a list of processing steps with corresponding icons:

- Original
- Template
- Threshold
- Blobs
- Lattice
- acquisition
- focus
- preview
- done

The main image area shows a grayscale micrograph of a textured surface. Several circular regions are highlighted with green boxes, each containing a green crosshair. A blue crosshair is also visible in the center of the image. The interface includes a zoom control set to "2/3x" and two numerical readouts: "924.866" and "3218.18".

Alignment of different resets

Legion: 17feb25a

File Application Launcher Node Events Others Help

Levi Time Message

- 11:35:00 AM Parked at preset "en"
- 11:35:00 AM Returned to original camera dimensions
- 11:35:00 AM Acquiring alignment images

Presets (Cycle Order)

- gr
- sq
- hl
- fc
- fa
- en
- en_dd

Most Recent Calibrations

Pixel size	2016-04-28
Image shift	2016-12-09
Stage	2015-09-15
Beam shift	None
Modeled stage	x: 2015-09-15
Modeled stage (mag. only)	x: None, y: None
Beam tilt - Defocus	2017-02-25

Preset Parameters

TEM:	Tecnai
Magnification:	5000
Defocus:	-0.00015
Random Defocus Range:	None
Spot size:	6
Intensity:	0.566914
Image shift:	(-1.44172e-07, 2.13739e-08)
Beam shift:	(-9.77063e-07, -6.81858e-07)
Energy filtered:	No
Energy filter width:	None
Skip when cycling:	No

Align Presets

Overall Reference Preset: en Full Camera

Current Reference Preset: en

Current Preset To Adjust: hl

42 1/4x 1503.27 614.089

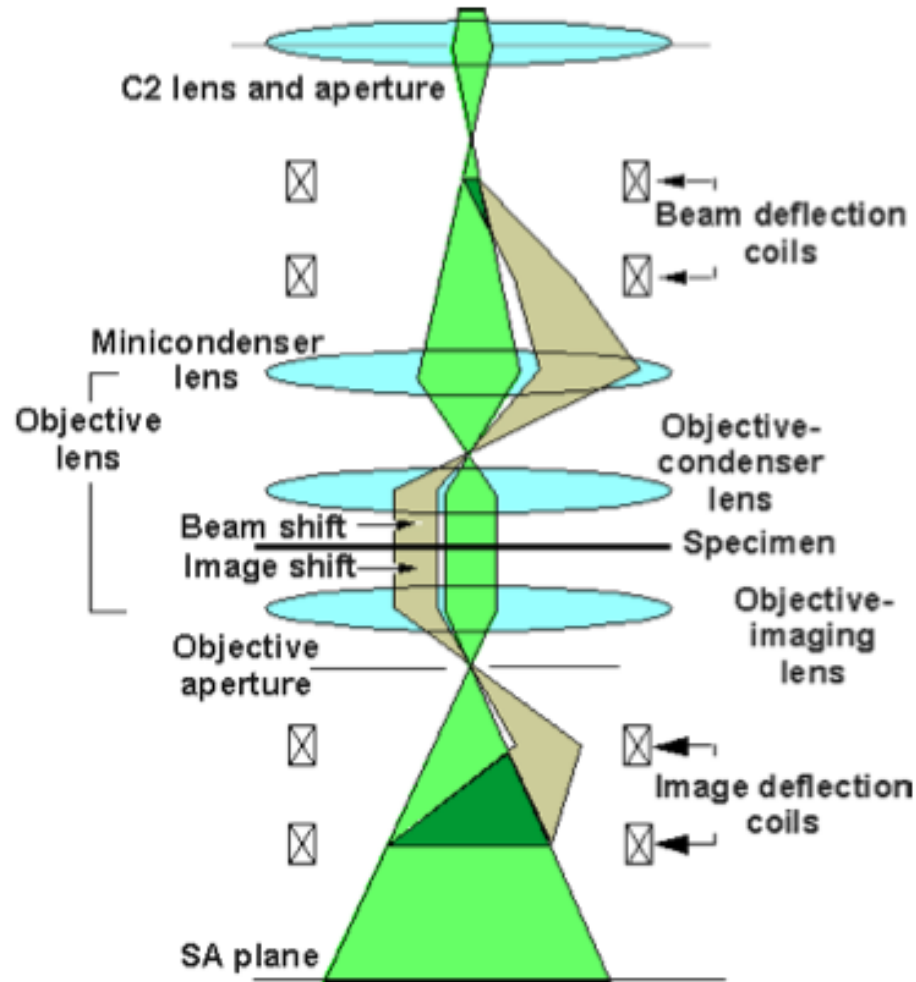
7380.59 4139.62

Mean: 4330.05
Min.: 1503.27
Max.: 9782.65
Std. dev.: 610.107

Mean: 2336.27
Min.: 614.089
Max.: 6921
Std. dev.: 360.671

Start Continue Done

Beam shift and image shift in preset alignment



Z-focusing

The screenshot displays a software interface for Z-focusing. The main window, titled "Leginon: 17feb25a", features a menu bar (File, Application, Launcher, Node, Events, Others, Help) and a toolbar. A left sidebar lists various modules, with "Z_Focus" highlighted. The central area shows a microscope image of a grid of particles. Above the image, a status bar displays "2/3x" and two sliders with values "-1049.1" and "4233.88". A statistics box on the left of the image shows: Mean: 1592.39, Min.: -12171.2, Max.: 5374.78, Std. dev.: 528.298. A message log at the top shows timestamps and messages like "Preset change to 'hl' completed." and "Requesting preset change to 'hl'...".

The "Focus Sequence (Z Focus)" dialog box is open, showing the following settings:

- Focus sequence:
- Enabled
- Preset: sq
- Focus method: Stage Tilt
- (Autofocus Only)
- Tilt: 1 degrees
- Image registration: phase correlation
- Fit limit: 5000
- Correct for delta Defocus/Z between 0 and 0.0002 meters
- Correction type: Stage Z
- Wait for drift to be less than 3e-10 m/s

Buttons for "OK" and "Cancel" are at the bottom of the dialog.

Focusing

The main window displays a log of events:

Lev	Time	Message
1	4:22:51 PM	Preset change to 'fa' completed.
1	4:22:50 PM	Requesting preset change to 'fa'...
1	4:22:50 PM	Processing focus setting 'Defocus1'...
1	4:15:25 PM	Done with simulated target, status: ok (repeat will not be honored)
1	4:15:25 PM	processing: Processing complete
1	4:15:25 PM	output: Image displayed
1	4:15:25 PM	output: Displaying image...

Statistics for the main image:

Mean:	19558.9
Min.:	12830.7
Max.:	47462.4
Std. dev.:	1326.82

Manual Focus windows show:

- Top: Mean: 13.5762, Min.: 12.2962, Max.: 16.0512, Std. dev.: 0.736404
- Bottom: Mean: 13.4212, Min.: 12.3147, Max.: 15.5694, Std. dev.: 0.584462

Coma-free alignment

The screenshot displays a software interface for beam alignment. The main window is titled "Beam-Tilt Coma" and contains several panels:

- Left Panel (Presets Manager):** A list of alignment tools including Presets_Manager, Grid_Targeting, Grid, Square_Targeting, Square, Hole_Targeting, Hole, Preview, Exposure_FFT, Z_Focus, Exposure_Targeting, Exposure, Focus, Focus_FFT, **Beam_Tilt** (highlighted), Drift_Monitor, N2_Filling, Fix_Beam, Correction, Target_Adjustment, and Navigation.
- Log Panel (Top Right):** A table of messages with columns for Level, Time, and Message.

Levl	Time	Message
?	4:18:37 PM	defocus: 3.365 um, zast: 0.264 um
?	4:18:30 PM	eparams a:195.453, b:182.266, alpha:0.072
?	4:18:30 PM	tableau defocus: 3.190 um, zast: 0.222 um
?	4:18:28 PM	defocus: 3.190 um, zast: 0.222 um
?	4:18:22 PM	Setting beam tilt back
?	4:18:21 PM	eparams a:199.240, b:178.572, alpha:-1.443
?	4:18:21 PM	tableau defocus: 3.206 um, zast: 0.350 um
- Statistics Panel (Middle Left):** A box displaying statistical data for the current image.

Mean:	13.3434
Min.:	11.4702
Max.:	16.7675
Std. dev.:	0.423016
- Image Panel (Bottom Right):** A 3x3 grid of diffraction patterns. The top row shows three patterns with values 1023, 1164, and 1190. The bottom row shows two patterns with values 1216 and 154585. The patterns consist of concentric rings around a central spot.
- Control Panel (Top Right):** Includes a zoom level of 2/3x, a color calibration icon, and two sliders for image processing.

Camera gain correction

The screenshot shows a software interface for camera gain correction, split into two panels: 'Bright' and 'Corrected'.

Left Panel (Bright):

- Mean: 36208.5
- Min.: 17848.7
- Max.: 56309.7
- Std. dev.: 1556.69

Right Panel (Corrected):

- Mean: 30055.2
- Min.: 19200
- Max.: 45860.3
- Std. dev.: 2467.03

Both panels show a grayscale image of a detector with a red dot indicating a bad pixel. The 'Corrected' panel shows a significantly darker and more uniform image compared to the 'Bright' panel.

Appion

Image assessment

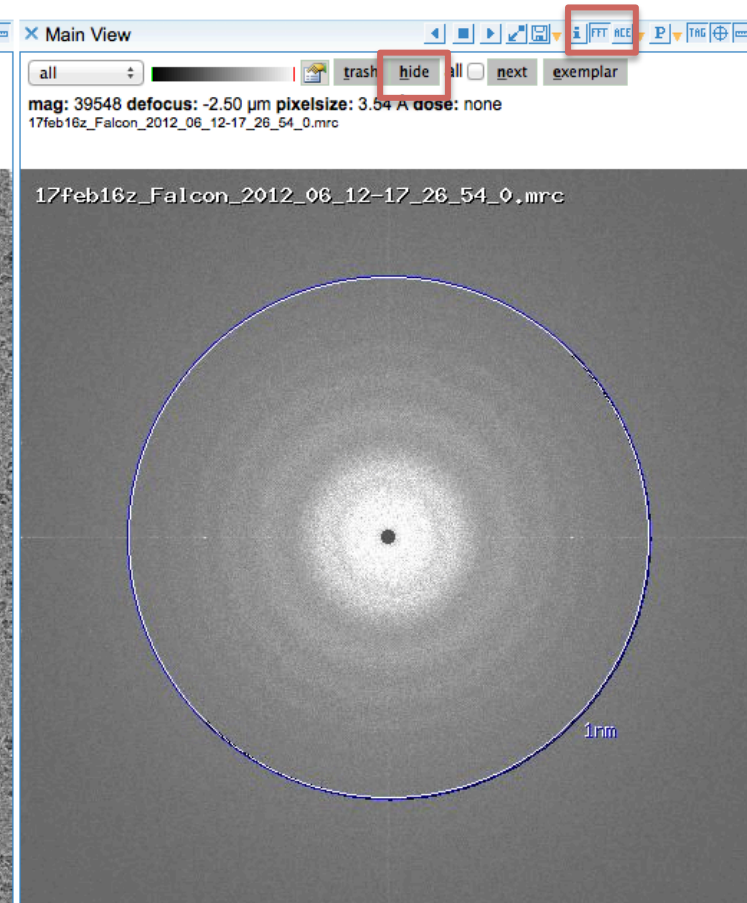
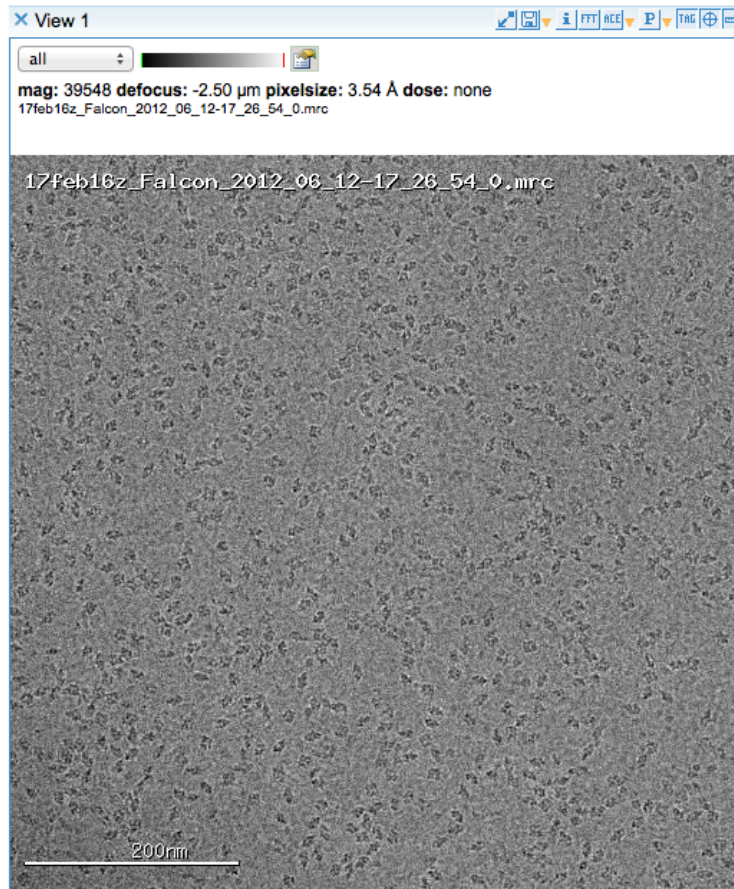
[Home][summary] [processing] [make jpgs]

all (all) 17feb16z - Demo

Select Demo project

#images :15

- Falcon_2012_6_12-17_26_54_
- Falcon_2012_6_12-17_23_32_
- Falcon_2012_6_12-17_17_5_
- Falcon_2012_6_12-17_14_17_
- Falcon_2012_6_12-17_2_43_
- Falcon_2012_6_12-16_59_12_
- Falcon_2012_6_12-16_55_40_
- Falcon_2012_6_12-16_44_7_
- Falcon_2012_6_12-16_26_22_
- Falcon_2012_6_12-15_56_10_
- Falcon_2012_6_12-15_53_9_
- Falcon_2012_6_12-15_41_22_
- Falcon_2012_6_12-15_14_1_
- Falcon_2012_6_12-14_57_34_
- Falcon_2012_6_12-14_33_35_



DD frame alignment



Create a Direct Detector Frame Stack

Project: Demo (83)

Session: **17feb16z** - Demo

Image Path: /myamimages/leginon/17feb16z/rawdata

Hide | Expand | Contract

▶ Object Selection : 2

▶ CTF Estimation

▶ Stacks : 3

▶ Particle Alignment

▶ Refine Reconstruction

▶ Helical Processing

▼ Direct Detector Tools

Create frame stack

Launch Alignment Catchup

Launch DE Frame Alignment

▼ Import tools

Upload more Images

Upload particles

Upload template

Upload stack

Upload reconstruction

PDB to Model

EMDB to Model

Upload model

1 available

▼ Img Assessment

Web Img Assessment

Multi Img Assessment

Run Image Rejector

▼ Region Mask Creation

Run Manual Masking

Run Automated Masking

▼ Synthetic Data

Synthetic Dataset Creation

Run name

ddstack1

Output directory

/myamimages/17feb16z/ddstack/

Description

Preset: upload

Wait for more images after finishing

[Show Advanced_Loop_Options](#)

Test these settings on image:

Just Show Command

Make DD stack params:

align

defer gpu processing

remove generated stack after uploading aligned sum image

binning

append label to aligned image

frame offset

b factor in motioncorr

CC search boxsize in motioncorr

Frames used for sum image after alignment:


start frame total frames



If you find this software useful please cite:

"Appion: an integrated, database-driven pipeline to facilitate EM image processing." (2009) Lander GC, Stagg SM, Voss NR, et al. J Struct Biol. v166(1). PMID: 19263523 Free text: PMC2775544 DOI: 10.1016/j.jsb.2009.01.002

CTF correction

 **CTF Estimation by CtfFind** Username:

Project: Demo (83)
Session: 17feb16z - Demo
Image Path: /myamilimages/leginon/17feb16z/rawdata

Hide | Expand | Contract

▼ Object Selection : 2

DoG Picking
2 complete

Template Picking

Manual Picking
1 running

Repeat from other session

▼ **CTF Estimation**

Estimate the CTF
1 complete

Repeat from other session

▼ Stack creation

Stack creation
2 complete

more stack tools

▼ Particle Alignment

Run Alignment

Template Stacks

▼ Refine Reconstruction

Run Single-Model Refinement
1 jobs ready to run

Run Multi-Model Refinement

▼ Helical Processing

Helical Image Processing (PHOELIX)

▼ Direct Detector Tools

Create frame stack

Launch Alignment Catchup

Launch DE Frame Alignment

▼ Import tools

Upload more images

Upload particles

Upload template

Upload stack

Run name

Output directory

Preset: upload
 Wait for more images after finishing

[Show Advanced Options](#)

Run CtfTilt , instead of CtfFind

Medium:
 carbon ice

Amplitude Contrast:
 Carbon
 Ice

Pre-Binning

Use best values from DB is not available (1 ctf runs)
Override nominal defocus set in experiment:
Set to: (in μm , i.e. 2.0)

CtfFind Values


Field Size (pixels)
 Minimum Resolution (Ångstroms)
 Maximum Resolution (Ångstroms)

Defocus search step size (Ångstroms)
 Number of steps to search
Search range: $\pm 2.5\mu\text{m}$

Expected astigmatism (Ångstroms)

PRESET VALUES:

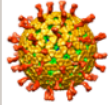
CTF correction

 **Just Show ctfestimate.py Command** Username: Password:

Project: Demo (83)
Session: **17feb16z** - Demo
Image Path: /myamimages/eginon/17feb16z/rawdata

Hide | Expand | Contract

- Object Selection : 2
 - DoG Picking
 - 2 complete
 - Template Picking
 - Manual Picking
 - 1 running
 - Repeat from other session
 - CTF Estimation
 - Estimate the CTF
 - 1 complete
 - Repeat from other session
 - Stacks : 2
 - Stack creation
 - 2 complete
 - more stack tools
 - Particle Alignment
 - Run Alignment
 - Template Stacks
 - Refine Reconstruction
 - Run Single-Model Refinement
 - 1 jobs ready to run
 - Run Multi-Model Refinement
 - Helical Processing
 - Helical Image Processing (PHOELIX)
 - Direct Detector Tools
 - Create frame stack
 - Launch Alignment Catchup
 - Launch DE Frame Alignment
 - Import tools
 - Upload more images
 - Upload particles
 - Upload template
 - Upload stack



The Grigorieff Lab
at Brandeis University

If you find this software useful please cite:
"Accurate determination of local defocus and specimen tilt in electron microscopy." (2003) Mindell, JA, Grigorieff N. J Struct Biol. v142(3). PMID: 12781660

Copy and paste this ctfestimate.py command into a terminal:

```
ctfestimate.py --runname=ctffindrun2 --rundir=/myamimages/17feb16z/ctf/ctffindrun2 --commit --
preset=upload --projectid=83 --session=17feb16z --no-rejects --no-wait --continue --
ampcarbon=0.15 --ampice=0.07 --fieldsize=512 --medium=ice --bin=2 --resmin=100 --
resmax=10 --defstep=1000 --numstep=25 --dast=500 --expid=105 --jobtype=ctfestimate
```

ampcarbon	0.15
ampice	0.07
bin	2
--commit	<i>flag enabled</i>
--continue	<i>flag enabled</i>
dast	500
defstep	1000
expid	105
fieldsize	512
jobtype	ctfestimate
medium	ice
--no-rejects	<i>flag enabled</i>
--no-wait	<i>flag enabled</i>
numstep	25
preset	upload
projectid	83
resmax	10
resmin	100
rundir	/myamimages/17feb16z/ctf/ctffindrun2
runname	ctffindrun2
session	17feb16z

CTF correction

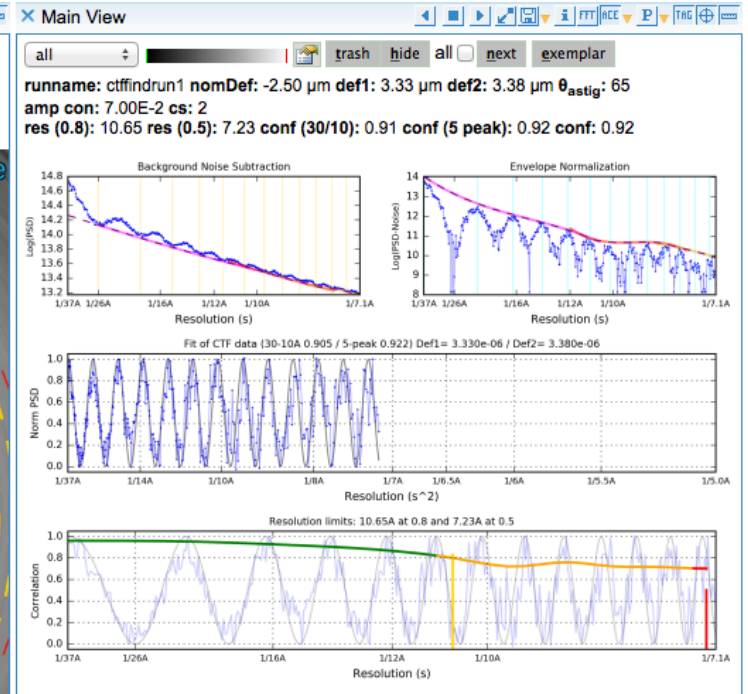
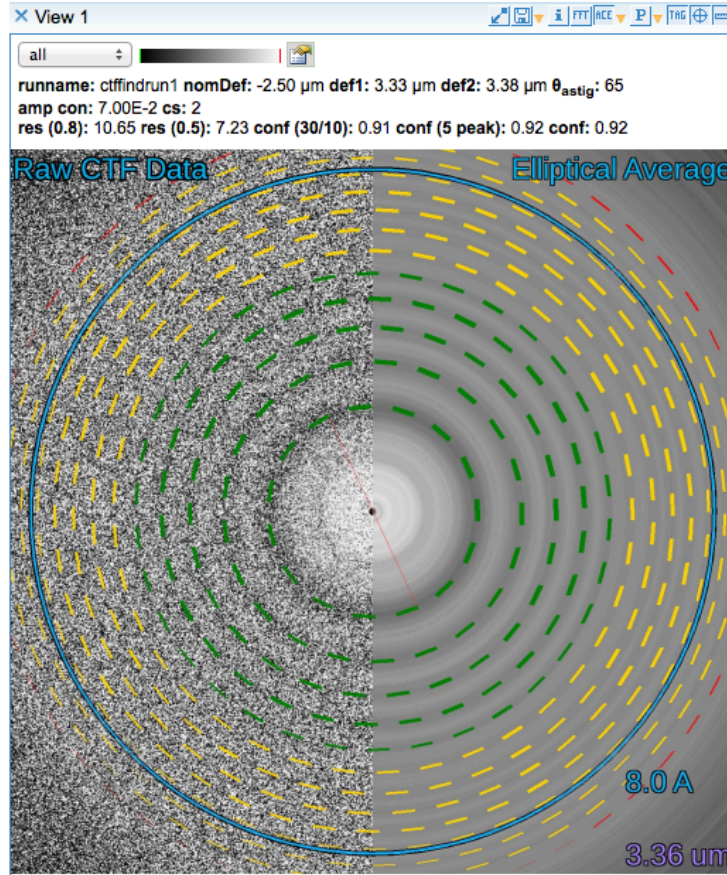
[Home][summary] [processing] [make jpgs]

all (all) 17feb16z - Demo

Select Demo project

#images :15

- Falcon_2012_6_12-17_26_54_
- Falcon_2012_6_12-17_23_32_
- Falcon_2012_6_12-17_17_5_
- Falcon_2012_6_12-17_14_17_
- Falcon_2012_6_12-17_2_43_
- Falcon_2012_6_12-16_59_12_
- Falcon_2012_6_12-16_55_40_
- Falcon_2012_6_12-16_44_7_
- Falcon_2012_6_12-16_26_22_
- Falcon_2012_6_12-15_56_10_
- Falcon_2012_6_12-15_53_9_
- Falcon_2012_6_12-15_41_22_
- Falcon_2012_6_12-15_14_1_
- Falcon_2012_6_12-14_57_34_
- Falcon_2012_6_12-14_33_35_



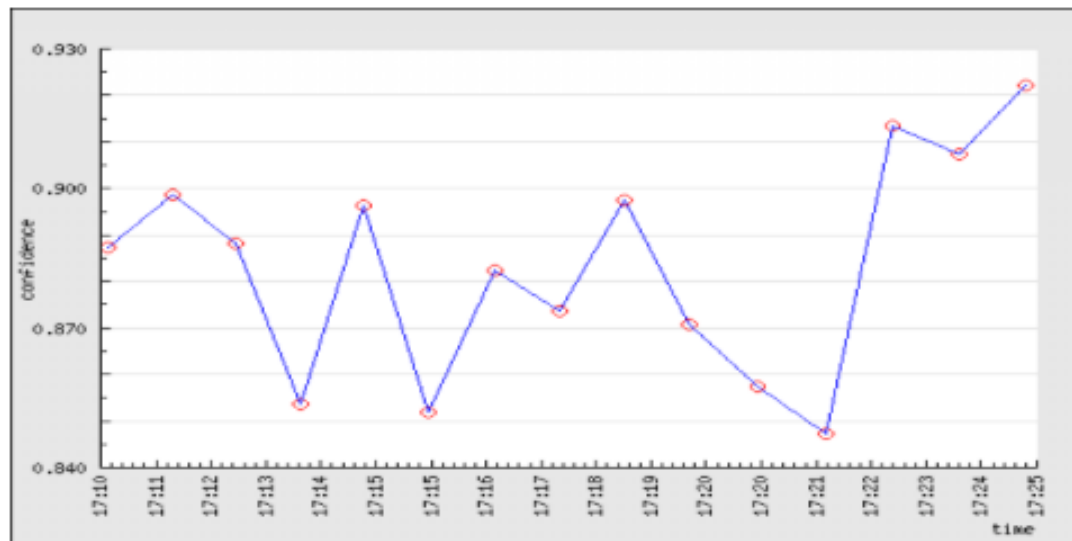
Ctf Run: 1 [ctffindrun1](#) [hide](#) [delete](#) ([download ctf data](#))

Time: 2017-02-16 17:52:10


Path: /myamilimages/appion/17feb16z/ctf/ctffindrun1

	nb	min	max	avg	stddev
defocus1	15	2.02 μm	3.41 μm	2.73 μm	0.43 μm
defocus2	15	2.03 μm	3.44 μm	2.77 μm	0.44 μm
angle_astigmatism	15	-87.290	85.000	27.654	43.560
amplitude_contrast	15	7.000×10^{-2}	7.000×10^{-2}	7.000×10^{-2}	0
confidence_30_10	15	0.823	0.913	0.872	2.626×10^{-2}
confidence_5_peak	15	0.767	0.922	0.872	3.774×10^{-2}
resolution_80_percent	15	8.674	13.737	11.261	1.393
resolution_50_percent	15	7.198	9.457	8.024	0.784

Confidence values during run



Particle picking


 **Automated Particle Selection with DoG Picker** Username:

Project: Demo (83)
Session: 17feb16z - Demo
Image Path: /myamiImages/leginon/17feb16z/rawdata

Hide | Expand | Contract

- Object Selection : 2
- DoG Picking**
 - 2 complete
- Template Picking
- Manual Picking
 - 1 running
- Repeat from other session
- CTF Estimation
- Stacks : 2
- Particle Alignment
- Refine Reconstruction
- Helical Processing
- Direct Detector Tools
- Import tools
- Img Assessment
- Region Mask Creation
- Synthetic Data

DoG Picker



Run name

Output directory

Preset: upload
 Wait for more images after finishing

[Show Advanced Options](#)

Test these settings on image:

Particle Diameter:
 Particle diameter for filtering (in Angstroms)

Peak thresholds:
 Minimum threshold
 Maximum threshold
 Max number of particles allowed per image

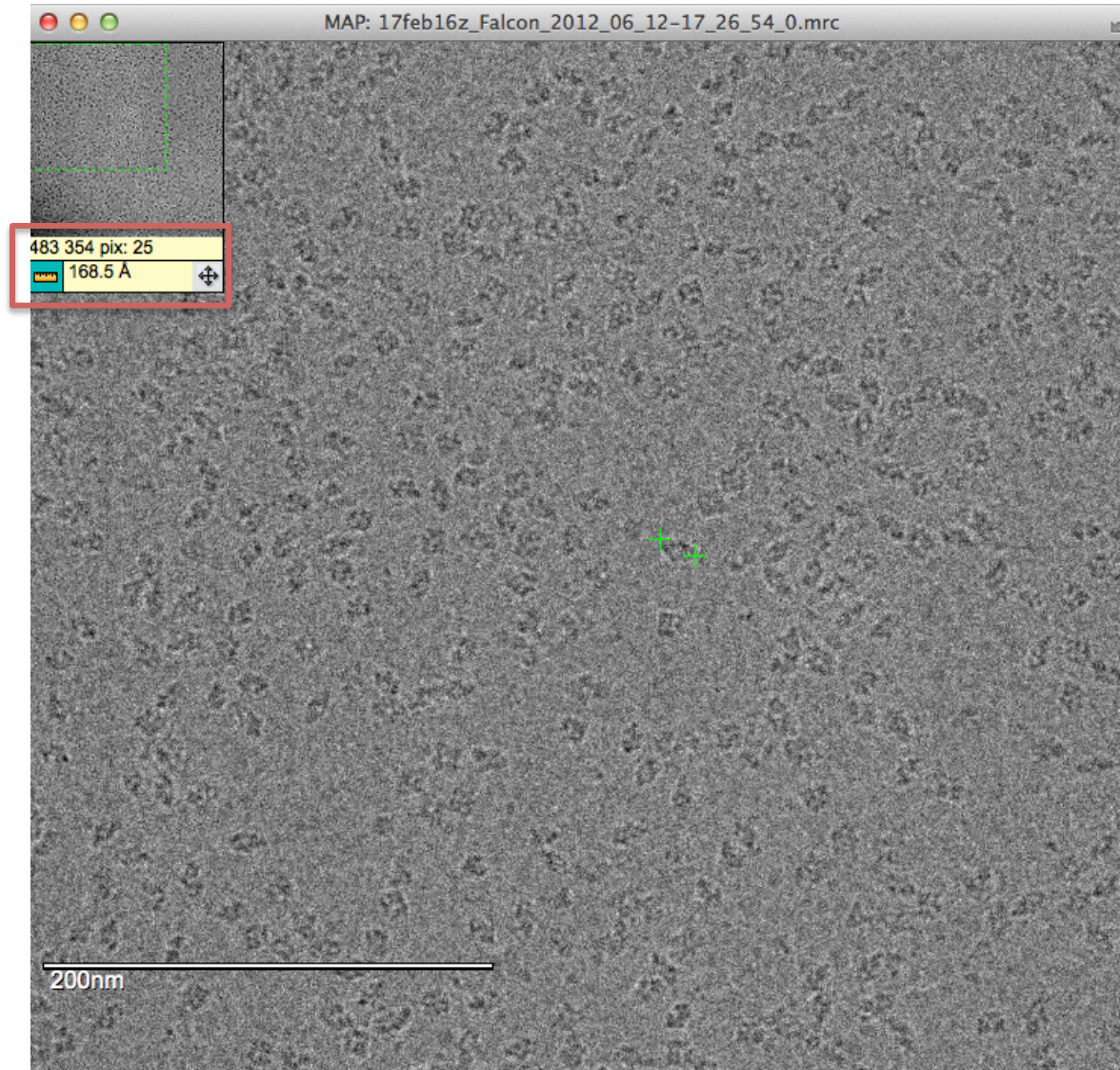
Filter Values:
 Low Pass (in Angstroms; 0 = off)
 High Pass (in Angstroms; 0 = off)
 Median (in pixels; 0 = off)
 Pixel Limit (in Standard Deviations; 0 = off)
 Binning (power of 2)
 Plane regression

Defocal pairs:
 Calculate shifts for defocal pairs

Advanced options:
 Maximum peak area multiple
 Minimum peak overlap distance multiple
Peak extraction type
 Center of mass (default)
 Maximum position
 Pick only doubles
 Invert image density
 K-factor (slopeiness)

Multi-scale dogpicker:
 Number of Slices (number of sizes)
 Size Range (in Angstroms)

Assess particle sizes



Particle picking

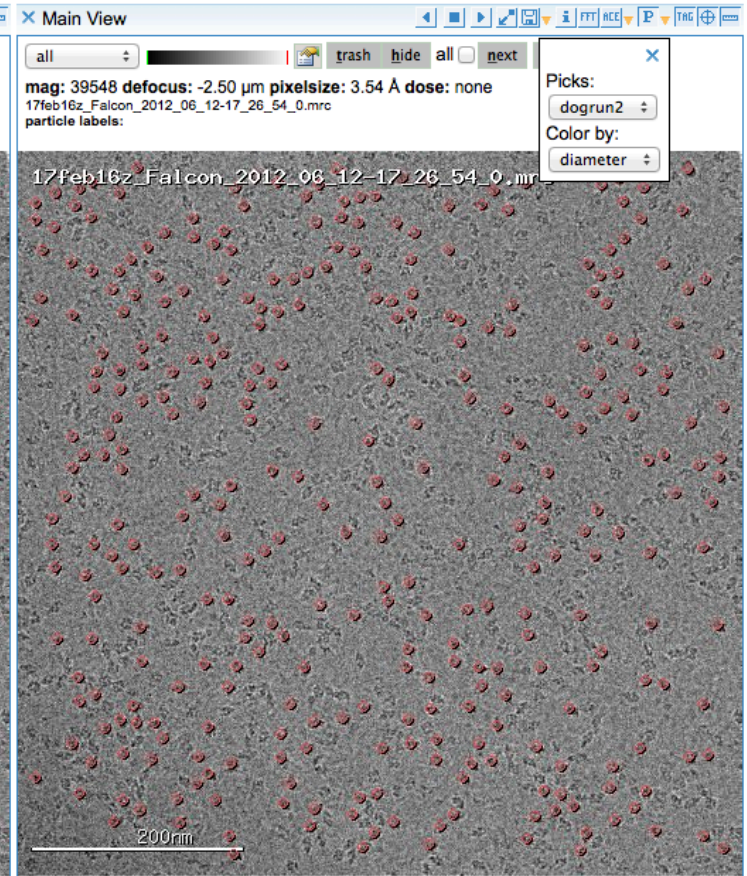
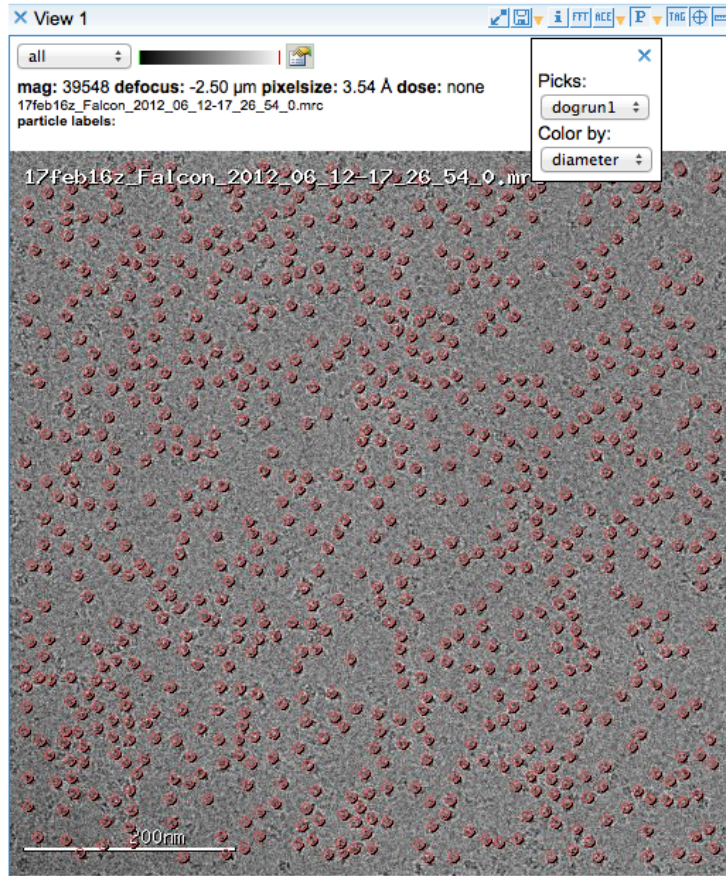
[\[Home\]](#) [\[summary\]](#) [\[processing\]](#) [\[make jpgs\]](#)

all (all) 17feb16z - Demo

Select Demo project

#images :15

Falcon_2012_6_12-17_26_54_
Falcon_2012_6_12-17_23_32_
Falcon_2012_6_12-17_17_5_
Falcon_2012_6_12-17_14_17_
Falcon_2012_6_12-17_2_43_
Falcon_2012_6_12-16_59_12_
Falcon_2012_6_12-16_55_40_
Falcon_2012_6_12-16_44_7_
Falcon_2012_6_12-16_26_22_
Falcon_2012_6_12-15_56_10_
Falcon_2012_6_12-15_53_9_
Falcon_2012_6_12-15_41_22_
Falcon_2012_6_12-15_14_1_
Falcon_2012_6_12-14_57_34_
Falcon_2012_6_12-14_33_35_



Manual picking

Hide | Expand | Contract

- ▼ Object Selection : 2
 - DoG Picking
2 complete
 - Template Picking
 - Manual Picking**
1 running
 - Repeat from other session
- ▼ CTF Estimation
 - Estimate the CTF
1 complete
 - Repeat from other session
- ▼ Stacks : 3
 - Stack creation
3 complete
 - more stack tools
- ▼ Particle Alignment
 - Run Alignment
 - Run Feature Analysis
 - Run Particle Clustering
 - Run MaskItOn
 - Template Stacks
- ▼ Refine Reconstruction
 - Run Single-Model Refinement
1 jobs ready to run
 - Run Multi-Model Refinement
- ▼ Helical Processing
 - Helical Image Processing (PHOELIX)
- ▼ Direct Detector Tools
 - Create frame stack

Run name

Output directory

Preset: upload
 Wait for more images after finishing

[Show Advanced Options](#)

Particle Labels

Label:

Edit Particle Picks:

Particle Diameter:
 Particle diameter for result images (in Angstroms)

Picking Icon
(only for visual purposes, does not affect data):
 Picking icon shape
 Picking icon diameter (in pixels; 0 = autosize)
16 pixels is best

Helical Parameters:
 Pick along helices
 Step size for Helical Insert (in Angstroms)
 Percent overlap (%)

Filter Values:
 Low Pass (in Angstroms; 0 = off)
 High Pass (in Angstroms; 0 = off)
 Median (in pixels; 0 = off)
 Pixel Limit (in Standard Deviations; 0 = off)
 Binning (power of 2)
 Plane regression

Defocal pairs:
 Calculate shifts for defocal pairs

Advanced options:
 Do NOT create summary peak jpegs
 Invert image density

Submission will NOT run, only output a command that you can copy and paste into a unix shell

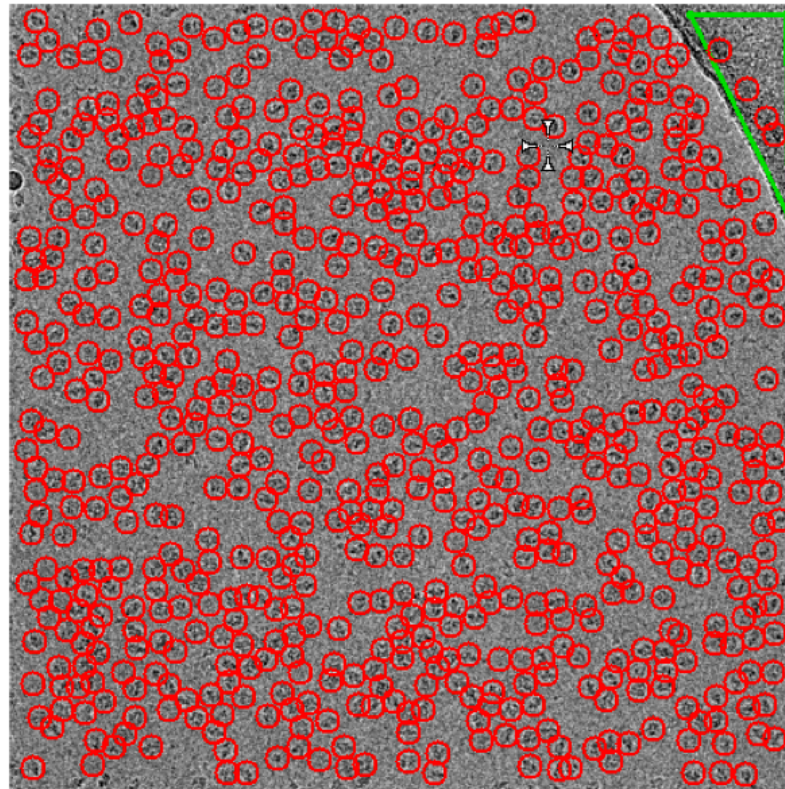
Clean up particle picks

Vital Stats: Image 1 of 15, inserted 0 picks, image name: 17feb16z_Falcon_2012_06_12-14_33_35_0

42 1x 2.55e-05
 255


Mean: 128.301
Min.: 2.55e-05
Max.: 255
Std. dev.: 30.7417

- Region to Remove
- particle_w/o_label



Forward **Remove Region** Clear Revert Image Assessment: None **Keep** Reject

Stack creation



Create an Image Stack

Username:

Project: Demo (83)
Session: 17feb16z - Demo
Image Path: /myamilimages/leginon/17feb16z/rawdata

Hide | Expand | Contract

- Object Selection : 2
 - DoG Picking
 - 2 complete
 - Template Picking
 - Manual Picking
 - 1 running
 - Repeat from other session
- CTF Estimation
 - Estimate the CTF
 - 1 complete
 - Repeat from other session
- Stacks : 2
 - Stack creation
 - 2 complete
 - more stack tools
- Particle Alignment
 - Run Alignment
 - Template Stacks
- Refine Reconstruction
 - Run Single-Model Refinement
 - 1 jobs ready to run
 - Run Multi-Model Refinement
- Helical Processing
 - Helical Image Processing (PHOELIX)
- Direct Detector Tools
 - Create frame stack
 - Launch Alignment Catchup
 - Launch DE Frame Alignment

Run name:

Output directory:

Description:

Preset: upload
 Wait for more images after finishing

[Show Advanced Options](#)

Density modifications:
 Invert image density
[Show Advanced Stack Options](#)

Just Show Command

Particles: dogrun2 (4,040 parts) ▾

Stacks: None ▾

Box Size (Unbinned, in pixels)
 (override boxsize)

Binning


Fast Insert

Ctf Correct Particle Images

CTF Confidence Cutoff
Use Values Above: (between 0.0 - 1.0)

[Show Advanced CTF Options](#)

[Show Advanced Stack Options](#)



If you find this software useful please cite:
"Appion: an integrated, database-driven pipeline to facilitate EM image processing." (2009) Lander GC, Stagg SM, Voss NR, et al. J Struct Biol. v166(1). PMID: 19263523 Free text: PMC2775544 DOI: 10.1016/j.jsb.2009.01.002

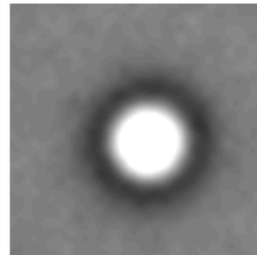
Stack creation

Hide | Expand | Contract

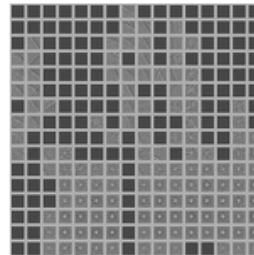
- ▼ Object Selection : 2
 - DoG Picking
 - 2 complete
 - Template Picking
 - Manual Picking
 - 1 running
 - Repeat from other session
 - ▼ CTF Estimation
 - Estimate the CTF
 - 1 complete
 - Repeat from other session
 - ▼ Stacks : 3
 - Stack creation
 - 3 complete
 - more stack tools
 - ▼ Particle Alignment
 - Run Alignment
 - Template Stacks
 - ▼ Refine Reconstruction
 - Run Single-Model Refinement
 - 1 jobs ready to run
 - Run Multi-Model Refinement
 - ▼ Helical Processing
 - Helical Image Processing (PHOELIX)
 - ▼ Direct Detector Tools
 - Create frame stack
 - Launch Alignment Catchup
 - Launch DE Frame Alignment
 - ▼ Import tools
 - Upload more Images
 - Upload particles

[Show original stack summary page]

Stack Info: **stack3** (ID: 3) [hide](#) [delete](#) ([download particles data](#)) [list per-particle CTF info](#) [bake recipe](#)



averaged stack image
[Center Particles]
[Sort Junk]
[Create Substack]
[Mask Particles with Box]

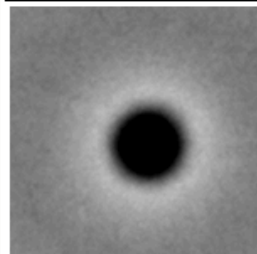


mean/stdev montage
[Filter by Mean/Stdev]

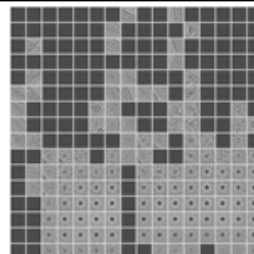
date time: 2017-02-22 16:55:40
session id: 17feb16z
description: bin_ctf_inverted
particles: 3,978
images used: 15
file size: 15.5 MB
path: /myamilimages/17feb16z/stacks/stack3
stack file: [start.hed](#) [hed](#) [img](#)
box size: 32 pixels
pixel size: 10.62 Å/pixel
ctf correct: yes, ace2image
selection run: dogrun2 (2)

Stack Info: **stack2** (ID: 2) [hide](#) [delete](#) (no particles)

Stack Info: **stack1** (ID: 1) [hide](#) [delete](#) ([download particles data](#)) [list per-particle CTF info](#) [bake recipe](#)



averaged stack image
[Center Particles]
[Sort Junk]
[Create Substack]
[Mask Particles with Box]



mean/stdev montage
[Filter by Mean/Stdev]

date time: 2017-02-17 09:43:10
session id: 17feb16z
description: dog
particles: 10,856
images used: 15
file size: 381.7 MB
path: /myamilimages/17feb16z/stacks/stack1
stack file: [start.hed](#) [hed](#) [img](#)
box size: 96 pixels
pixel size: 3.54 Å/pixel
ctf correct: no
selection run: dogrun1 (1)

[Show original stack summary page]

Assessment of particle picks

stack: /myamiImages/17feb16z/stacks/stack1/start.hed

#images: 10856

from: 0 to: 40 binning: 1 quality: jpeg 50 info: scale bar: Load

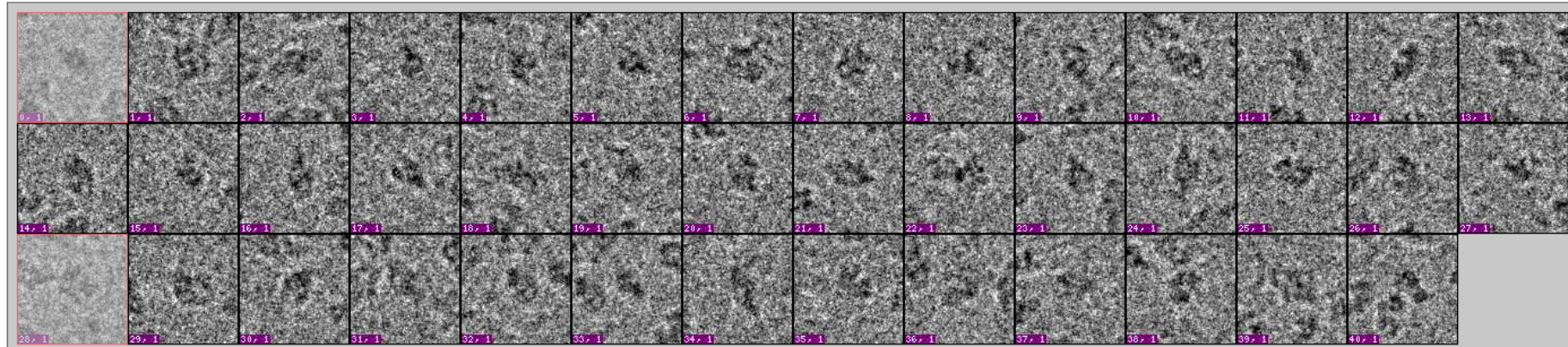
Selection mode: **exclude**

Selected images:

Select:

Excluded images:

Exclude:



2D classification and 3D refinement


Particle Alignment Selection Page

Project: Demo (83)
Session: 17feb16z - Demo
Image Path: /myamlimages/loginon/17feb16z/rawdata






Hide | Expand | Contract

- Object Selection : 2
 - DoG Picking
 - 2 complete
 - Template Picking
 - Manual Picking
 - 1 running
 - Repeat from other session
- CTF Estimation
 - Estimate the CTF
 - 1 complete
 - Repeat from other session
- Stacks : 2
 - Stack creation
 - 2 complete
 - more stack tools
- Particle Alignment
 - Run Alignment
 - Template Stacks
- Refine Reconstruction
 - Run Single-Model Refinement
 - 1 jobs ready to run
 - Run Multi-Model Refinement
- Helical Processing
 - Helical Image Processing
- Direct Detector Tools
 - Create frame stack
 - Launch Alignment Catchup
 - Launch DE Frame Alignment
- Import tools
 - Upload more images
 - Upload particles
 - Upload template
 - Upload stack
 - Upload reconstruction
 - PDB to Model
 - EMDB to Model
 - Upload model
 - 1 available
- Img Assessment
 - Web Img Assessment
 - Multi Img Assessment
 - Run Image Receptor
 - Receptor Mark Creation

Particle Alignment Procedures



Particle alignment consists of shift, rotation, and mirror transformations for all particles in a stack to a common orientation or template. The reference free methods are great methods to create a template for particle picking or reference-based alignments.

	<h4>Xmipp Maximum Likelihood Alignment</h4> <p>this method is the most robust, but takes some time to complete. It uses the Xmipp ml_align2d program to perform alignments.</p> <p>This method is unbiased and very thorough, but also the slowest of the methods (~days). Maximum likelihood also does a coarse search, integer pixels shifts and ~5 degree angle increments, so it is best to get templates with this method and use ref-based alignment to get better alignment parameters</p>
	<h4>Xmipp 2 Clustering 2D Alignment</h4> <p>this method builds a hierarchical classification of particles It uses the Xmipp 2 cl2d program to perform alignments. It is a relatively fast method that aligns and classify the images at the same time. The method starts by estimating a few classes that are further subdivided till the desired number of classes is reached. Every time an image is compared to the class averages it is aligned before-hand. NOTE: in Xmipp 2.4 the alignment parameters are not saved in the database, and therefore this method cannot be used for RCT / OTR reconstructions.</p>
	<h4>Xmipp 3 Clustering 2D Alignment</h4> <p>this method builds a hierarchical classification of particles It uses the Xmipp 3 cl2d program to perform alignments. It is a relatively fast method that aligns and classify the images at the same time. The method starts by estimating a few classes that are further subdivided till the desired number of classes is reached. Every time an image is compared to the class averages it is aligned before-hand.</p>
	<h4>IMAGIC Multi Reference Alignment (MRA)</h4> <p>this method uses the IMAGIC m-r-a command to align your particles to the templates within a specified template stack</p>
	<h4>Iterative Stable Alignment and Clustering (ISAC)</h4> <p>Initial version. More information about ISAC is available from: sxisac - SPARX</p>

Reconstruction Refinement Procedures

Most initial models establish a preliminary sense of the overall shape of the biological specimen. To reveal structural information that can answer specific biological questions, the model requires refining. In single particle analysis, a refinement is an iterative procedure, which sequentially aligns the raw particles among their appropriate spatial orientations (Euler angles) by comparing them against the model, and then back-projects them into 3D space to form a new model. Effectively, a full refinement takes as input a raw particle stack and an initial model and is usually carried out until no further improvement of the structure can be observed.

Xmipp projection-matching refinement



This is the [Xmipp projection-matching refinement protocol](#). The classification of raw particles is done using the [angular projection matching](#) operation in Xmipp. The user is given the option of employing an algebraic reconstruction technique (ART), weighted back-projection (WBP) or Fourier interpolation method to reconstruct the computed classes from projection-matching. One big advantage to this protocol is speed. Because all Euler angle and alignment parameters are saved for each iteration of angular projection-matching, the later iterations localize the search space to an increasingly narrow region and, therefore, take significantly less cpu time to complete.

Frealign projection-matching refinement



The [Frealign](#) (Fourier REconstruction and ALIGNment) projection-matching refinement protocol has been designed to refine a stack of particles for which the alignment and classification parameters are approximately known. It therefore also relies on a good initial model. The algorithms used in the Frealign package are designed to extract as much high resolution information out of the data as possible.

Note: Unless your particle has icosahedral symmetry, Frealign requires initial Euler angles determined from other (such as Xmipp) reconstruction refinement procedures./p>

Relion regularized likelihood optimisation refinement



This is the [Relion refinement protocol](#). This procedure implements so-called gold-standard FSC calculations, where two models are refined independently for two random halves of the data to prevent overfitting. Thereby, reliable resolution estimates and clean reconstructions are obtained without compromising reconstruction quality, see (Scheres & Chen, Nature Methods, in press) for more details. Note that for cyclic point group symmetries (i.e. C_n), the two half-reconstructions are averaged up to 40 Angstrom resolution to prevent diverging orientations.

EMAN1 projection-matching refinement



This is one of the original projection-matching refinement protocols, as implemented in [EMAN](#). It has been successfully tested on many different samples. Within each iteration, the raw particles are classified according to the angular sampling of projection directions, then iteratively aligned within each class to reduce the model bias. Further classification and particle 'filtering' has been incorporated using a SPIDER protocol that identifies and removes the particles with the highest variance (and therefore least correspondence) in the class using the [CAS](#) correspondence analysis operation in spider.

Import particle stack to Frealign

Project: Demo (83)
Session: 17feb16z - Demo
Image Path: /myamimages/leginon/17feb16z/rawdata

Hide | Expand | Contract

▼ Object Selection : 2

- DoG Picking
2 complete
- Template Picking
- Manual Picking
1 running
- Repeat from other session

▼ CTF Estimation

- Estimate the CTF
1 complete
- Repeat from other session

▼ Stacks : 2

- Stack creation
2 complete
- more stack tools

▼ Particle Alignment

- Run Alignment
- Template Stacks

▼ Refine Reconstruction

- Run Single-Model Refinement
1 jobs ready to run
- Run Multi-Model Refinement

▼ Helical Processing

Helical Image Processing

▼ Direct Detector Tools

- Create frame stack
- Launch Alignment Catchup
- Launch DE Frame Alignment

▼ Import tools

- Upload more images
- Upload particles
- Upload template
- Upload stack
- Upload reconstruction
- PDB to Model
- EMDB to Model
- Upload model
1 available

▼ Img Assessment

- Web Img Assessment
- Multi Img Assessment
- Run Image Rejector
- Region Mask Creation
- Run Manual Masking

Run Automated Masking

Run name
frealign_recon2

Output directory
/myamimages/17feb16z/recon/


Description

Stack Preparation Parameters

- last particle to use (leave blank for all particles)
- binning
- Import initial orientations from completed reconstruction:
Reconstruction: no EMAN recons available to import Euler angles
- Only use CTFIND3 values
- Only use CTFtilt values
- Only create the Frealign parameter file, not the stack


Just Show Command

Stack info: stack1 (ID: 1) [hide](#) [delete](#) [download particles data](#) [list per-particle CTF info](#) [bake recipe](#)



average
[Sort Junk]

date time: 2017-02-17 09:43:10
session id: 17feb16z
descript: dog
size: 10,856 / 381.7 MB
path: /myamimages/17feb16z/stacks/stack1/start.hed [hed](#) [img](#)
box/apix: 96 pixels / 3.54 Å/pixel

Initial model: upload-upload-upload-iggFcr_model-17jan09s31-17feb09k22-17feb17k10.mrc (ID: 1) [hide](#)



date time: 2017-02-17 10:11:23
description: mock
path: /myamimages/17feb16z/models/accepted/upload_17feb17k10
filename: upload-upload-upload-iggFcr_model-17jan09s31-17feb09k22-17feb17k10.mrc ([download model](#))
symmetry: C1: Asymmetric
pixel size: 3.54 Å/pix
box size: 192 pixels

 **The Grigorieff Lab** at Brandeis University

If you find this software useful please cite:
"FREALIGN: high-resolution refinement of single particle structures." (2007)
Grigorieff, N. J Struct Biol. v157(1). PMID: 16828314
DOI: 10.1016/j.jsb.2006.05.004

```
[user1@fulab frealign_recon1]$ ls
files_to_remote_host initmodel0001.mrc note params.000.par
prepRefineFrealign.log start.mrc thread000.log thread001.log
```

```
[cyfu@pcf00243 refinement]$ ls
frealign.log mparameters pdh_2_r1.mrc pdh_2_r1.par pdh_stack.mrc scratch
```

```
1  0.00  0.00  0.00  0.00  0.00 10000.  1 34109.6 34384.8 29.41 0.00 0.00  1
2  0.00  0.00  0.00  0.00  0.00 10000.  1 34109.6 34384.8 29.41 0.00 0.00  2
3  0.00  0.00  0.00  0.00  0.00 10000.  1 34109.6 34384.8 29.41 0.00 0.00  3
4  0.00  0.00  0.00  0.00  0.00 10000.  1 34109.6 34384.8 29.41 0.00 0.00  4
5  0.00  0.00  0.00  0.00  0.00 10000.  1 34109.6 34384.8 29.41 0.00 0.00  5
6  0.00  0.00  0.00  0.00  0.00 10000.  1 34109.6 34384.8 29.41 0.00 0.00  6
```

Control parameter file to run Frealign

=====

This file must be kept in the project working directory from which the refinement scripts are launched.

Note: Please make sure that project and scratch directories are accessible by all sub-processes that are run on cluster nodes.

```
# Computer-specific setting
cluster_type      none          ! Set to "sge", "lsf", "slurm" or "pbs" when running on an SGE, LSF, SLURM or PBS cluster, otherwise set to "none".
nprocessor_ref    4              ! Number of CPUs to use during refinement.
nprocessor_rec    2              ! Number of CPUs to use during reconstruction.
mem_per_cpu      2048         ! Memory available per CPU (in MB).

# Refinement-specific parameters
MODE              1              ! 1, 2, 3 or 4. Refinement mode, normally 1. Set to 2 for additional search.
start_process    3              ! First cycle to execute. Output files from previous cycle (n-1) required.
end_process      10            ! Last cycle to execute.
res_high_refinement 35.0       ! High-resolution limit for particle alignment.
res_high_class   8.0           ! High-resolution limit to calculate class membership (OCC).
thresh_reconst   0.0           ! Particles with scores below this value will not be included in the reconstruction.
nclasses         1              ! Number of classes to use.

# Search-specific parameters
res_search       30.0          ! High-resolution limit for orientational search.
thresh_refine    70.0          ! Score threshold above which search will not be performed.
DANG             200.0         ! Angular step for orientational search.
ITMAX            200           ! Number of repetitions of grid search with random starting angles.
Bsearch          2000.0        ! B-factor filtering (when > 0) applied during search.

# Dataset-specific parameters
data_input       pdh           ! Root name for parameter and map files.
raw_images       /usr1/cyfu/frealign/examples_for_frealign_v9/refinement/pdh_stack
image_contrast   N             ! N or P. Set to N if particles are dark on bright background, otherwise set to P.
outer_radius     146.0         ! Outer radius of spherical particle mask in Angstrom.
inner_radius     0.0           ! Inner radius of spherical particle mask in Angstrom.
mol_mass         1500.0        ! Molecular mass in kDa of particle or helical segment.
Symmetry         I             ! Symmetry of particle.
pix_size         3.11          ! Pixel size of particle in Angstrom.
dstep            14.0          ! Pixel size of detector in micrometer.
Aberration       2.0           ! Spherical aberration coefficient in millimeter.
Voltage          120.0         ! Beam acceleration voltage in kilovolt.
Amp_contrast     0.07          ! Amplitude contrast.
```

Import particle stack to Relion

```
[user1@fulab frealign_recon1]$ ls
```

```
all_particles.star  initmodel0001.mrc  params.000.par      start.mrc  thread000.log  
files_to_remote_host  note                prepRefineFrealign.log  start.mrcs  thread001.log  
[user1@fulab frealign_recon1]$
```

```
data_  
loop_  
_rlnImageName  
_rlnMicrographName  
_rlnDefocusU  
_rlnDefocusV  
_rlnDefocusAngle  
_rlnVoltage  
_rlnSphericalAberration  
_rlnAmplitudeContrast  
1@/usr1/cyfu/demo/start.mrcs 1 34109.6 34384.8 29.41 300 2 0.07  
2@/usr1/cyfu/demo/start.mrcs 1 34109.6 34384.8 29.41 300 2 0.07  
3@/usr1/cyfu/demo/start.mrcs 1 34109.6 34384.8 29.41 300 2 0.07  
4@/usr1/cyfu/demo/start.mrcs 1 34109.6 34384.8 29.41 300 2 0.07  
5@/usr1/cyfu/demo/start.mrcs 1 34109.6 34384.8 29.41 300 2 0.07  
6@/usr1/cyfu/demo/start.mrcs 1 34109.6 34384.8 29.41 300 2 0.07  
7@/usr1/cyfu/demo/start.mrcs 1 34109.6 34384.8 29.41 300 2 0.07  
8@/usr1/cyfu/demo/start.mrcs 1 34109.6 34384.8 29.41 300 2 0.07  
9@/usr1/cyfu/demo/start.mrcs 1 34109.6 34384.8 29.41 300 2 0.07  
10@/usr1/cyfu/demo/start.mrcs 1 34109.6 34384.8 29.41 300 2 0.07  
11@/usr1/cyfu/demo/start.mrcs 1 34109.6 34384.8 29.41 300 2 0.07  
12@/usr1/cyfu/demo/start.mrcs 1 34109.6 34384.8 29.41 300 2 0.07
```

Import particle coordinates to Relion

Run name
stack4

Output directory
/myamiimages/17feb16z/stacks

Description

Preset: upload
 Wait for more images after finishing

Show Advanced Options

Density modifications:
 Invert image density
Show Advanced Stack Options

Particles: dogrun2 (4,040 parts)

Stacks: None

96 Box Size (Unbinned, in pixels)
 (override boxsize)

1 Binning

Fast Insert

Ctf Correct Particle Images

CTF Confidence Cutoff
Use Values Above: 0.8 (between 0.0 - 1.0)

Show Advanced CTF Options

Hide Advanced Stack Options_2

No Mask Assessed for this Session

Raw frame processing if available:
start frame: start frame total frame: total frames

Filter Values:
 Low Pass (in Angstroms)
 High Pass (in Angstroms)
 Pixel Limit (in Standard Deviations; 0 = off)
 Particle Correlation Cutoff

Remove particles with CCC below: 0.5

Remove particles with CCC above: 1.0

Defocal pairs:
 Use defocal pairs

Limit # of particles to:

Only create EMAN boxfiles

Helical Alignment:
 Apply rough helical rotation angles
 Apply fine helical rotation angles

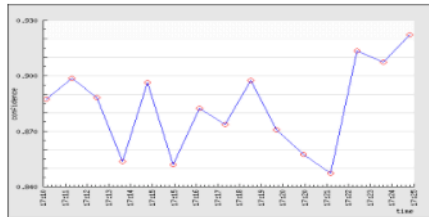
Just Show Command

```
[user1@fulab stack2]$ pwd
/myamiImages/appion/17feb16z/stacks/stack2
[user1@fulab stack2]$ ls
17feb16z_Falcon_2012_06_12-14_33_35_0.box
17feb16z_Falcon_2012_06_12-14_57_34_0.box
17feb16z_Falcon_2012_06_12-15_14_01_0.box
17feb16z_Falcon_2012_06_12-15_41_22_0.box
17feb16z_Falcon_2012_06_12-15_53_09_0.box
17feb16z_Falcon_2012_06_12-15_56_10_0.box
17feb16z_Falcon_2012_06_12-16_26_22_0.box
17feb16z_Falcon_2012_06_12-16_44_07_0.box
17feb16z_Falcon_2012_06_12-16_55_40_0.box
17feb16z_Falcon_2012_06_12-16_59_12_0.box
```

1803	672	96	96	-3
868	1639	96	96	-3
1570	1550	96	96	-3
1050	26	96	96	-3
1633	315	96	96	-3
1742	722	96	96	-3
1412	439	96	96	-3
397	671	96	96	-3
1380	220	96	96	-3
1248	768	96	96	-3
1089	814	96	96	-3
1530	516	96	96	-3
1584	1092	96	96	-3
412	724	96	96	-3
169	930	96	96	-3
888	179	96	96	-3

Import CTF star file to Relion

Confidence values during run



Difference fr



Generate defocus histogram with applied cutoff

Cutoff method:

Cutoff value (0-1):

[download star file for RELION](#)

[download best ctf data](#)

[download best ctf EMX file](#)

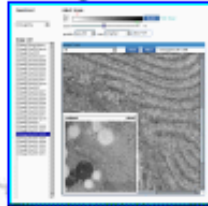
Ctf Run: 1 ctfindrun1 hide delete download ctf data					
Time:	2017-02-16 17:52:10				
Path:	/myamiImages/appion/17feb16z/ctfctfindrun1				
	nb	min	max	avg	stddev
defocus1	15	2.02 µm	3.41 µm	2.73 µm	0.43 µm
defocus2	15	2.03 µm	3.44 µm	2.77 µm	0.44 µm
angle_astigmatism	15	-87.290	85.000	27.654	43.560
amplitude_contrast	15	7.000x10 ⁻²	7.000x10 ⁻²	7.000x10 ⁻²	0
confidence_30_10	15	0.823	0.913	0.872	2.626x10 ⁻²
confidence_5_peak	15	0.767	0.922	0.872	3.774x10 ⁻²
resolution_80_percent	15	8.674	13.737	11.261	1.393
resolution_50_percent	15	7.198	9.457	8.024	0.784

```

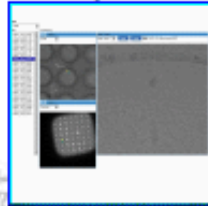
1 |
2 data_
3
4 loop_
5 _rlnMicrographName #1
6 _rlnCtfImage #2
7 _rlnDefocusU #3
8 _rlnDefocusV #4
9 _rlnDefocusAngle #5
10 _rlnVoltage #6
11 _rlnSphericalAberration #7
12 _rlnAmplitudeContrast #8
13 _rlnMagnification #9
14 _rlnDetectorPixelSize #10
15 _rlnCtfFigureOfMerit #11
16 micrographs/17jan09y_20170107b_1_00023gr_00004sq_v02_00004hl_v01_00002en.mrc micrograph
s/17jan09y_20170107b_1_00023gr_00004sq_v02_00004hl_v01_00002en.ctf:mrc 19969.210000 209
25.760000 86.640000 200.000000 2.000000 0.070000 10000.000000 1.080000 0.716469
17 micrographs/17jan09y_20170107b_1_00023gr_00004sq_v02_00004hl_v01_00003en.mrc micrograph
s/17jan09y_20170107b_1_00023gr_00004sq_v02_00004hl_v01_00003en.ctf:mrc 16739.590000 175
16.950000 -85.340000 200.000000 2.000000 0.070000 10000.000000 1.080000 0.695531
18 micrographs/17jan09y_20170107b_1_00023gr_00004sq_v02_00005hl_v02_00003en.mrc micrograph
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95.960000 -79.540000 200.000000 2.000000 0.070000 10000.000000 1.080000 0.515900
19 micrographs/17jan09y_20170107b_1_00023gr_00004sq_v02_00007hl_v01_00004en.mrc micrograph
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09.240000 -74.580000 200.000000 2.000000 0.070000 10000.000000 1.080000 0.574156
20 micrographs/17jan09y_20170107b_1_00023gr_00004sq_v02_00008hl_v01_00002en.mrc micrograph
s/17jan09y_20170107b_1_00023gr_00004sq_v02_00008hl_v01_00002en.ctf:mrc 22308.230000 239
53.470000 -60.000000 200.000000 2.000000 0.070000 10000.000000 1.080000 0.691933
    
```

Appion and Leginon DB Tools

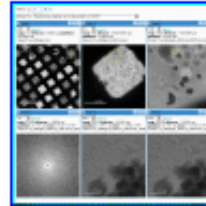
Image Viewer



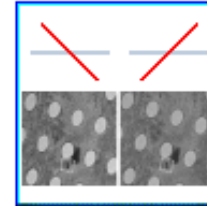
3 Way Viewer



LOI



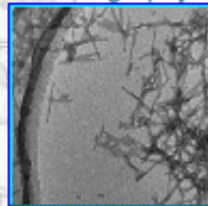
RCT



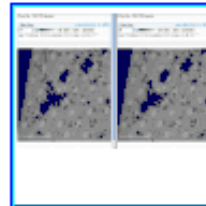
2 Way Viewer



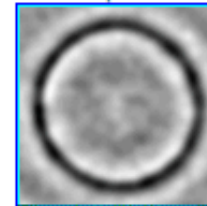
Tomography



Dual Viewer



Hole Template viewer



Administration



Project DB

