## An introduction to cryoEM and national cryoEM center resources Christina Zimanyi, PhD New York Structural Biology Center Friday, May 9, 2025 NYSBC SEMC

### Workshop has three components

#### Friday May 9, 2025. Introduction to cryoEM.

Goal: Introduce cryoEM for biomolecules. Introduce National Center & local resources.

10:00 – 11:00 Talk: CryoEM and the national centers. Brown Laboratory Rm 219

- 12:30 3:00 Office Hours: Small group discussions (by appointment check your email)
- 4:00 5:00 Seminar: Recent advances in cryoEM. Brown Laboratory Rm 219

#### Monday May 19, 2025. Hands-on grid preparation workshop. 12 participants. Goal: Demystify the grid making process.

9:30 – 4:00 Hands-on: Grid handling, negative stain grid prep & room temperature screening, and cryo grid prep at the Biolmaging Center.

#### Friday May 30, 2025. Evaluation of cryoEM grids

Goal: Gain experience evaluating micrographs and see outcomes of the grid making session.

- 10:00 12:00 Live demo of cryoEM screening remotely on NCCAT's Glacios
- 12:00 1:00 Break
- 1:00 3:00 Review of cryoEM images from the workshop samples

### The teams who made this workshop possible





BIO MAGING CENTER

University of Delaware **CryoEM** champions







Mahira

Eugene Chua



Aragon







Ed Eng



Jeff Alex de Kieft Marco



Jeffrey Caplan



Shannon Modla



Fabio Gonzalez

Sharon Rozovsky



Yujue Liu

Henry Nwaora



Sadik Sattar

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### National Center for CryoEM Access and Training: NCCAT







NIH Aim: broaden access to high-resolution cryoelectron microscopy for biomedical researchers, and cultivate a skilled workforce through the development and implementation of cryoEM training material

+ very cool people

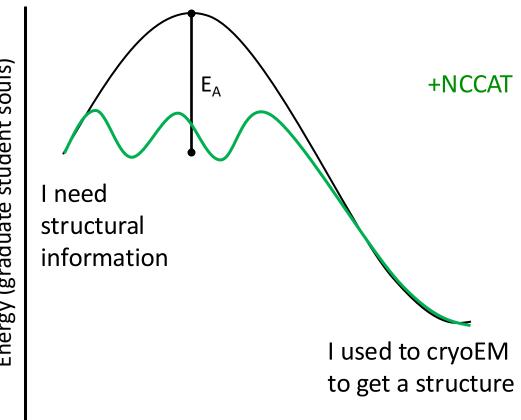








### NCCAT's mission is to lower barriers for cryoEM use



Structure determination coordinate

 $E_A$  = Samples + Instrumentation + Expertise + \$\$

E<sub>A</sub> = Samples + Instrumentation + Expertise + \$

#### Workshops

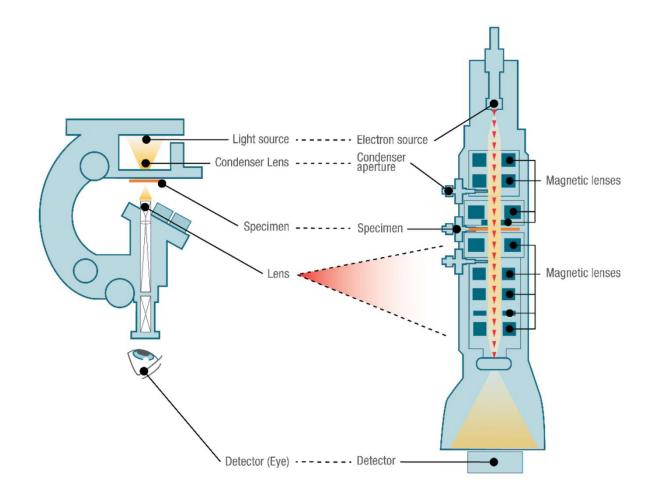
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### Roadmap for the talk: a practical guide to cryoEM samples

- CryoTEM basics and challenges for imaging biomolecules
- Single Particle Analysis (SPA) workflow
- SPA practical sample preparation tips
- How the National Centers can help

### Transmission electron microscopy in one slide



$$d = \frac{\lambda}{2NA}$$

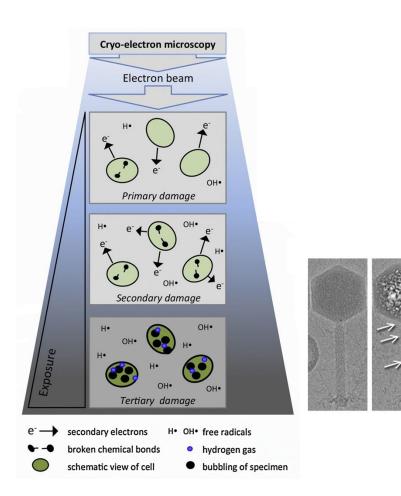
 $e^-$  @ 80-300 keV  $\rightarrow \lambda = 2-4 \text{ pm}$ 

Theoretical resolution limit ~ Å

Sample requirements:

- Thin (~100 nm)
- Stable under vacuum

### Electron microscopy on biological samples has unique challenge



- Radiation sensitivity requires low dose
- Objects are low contrast
- Low signal-to-noise

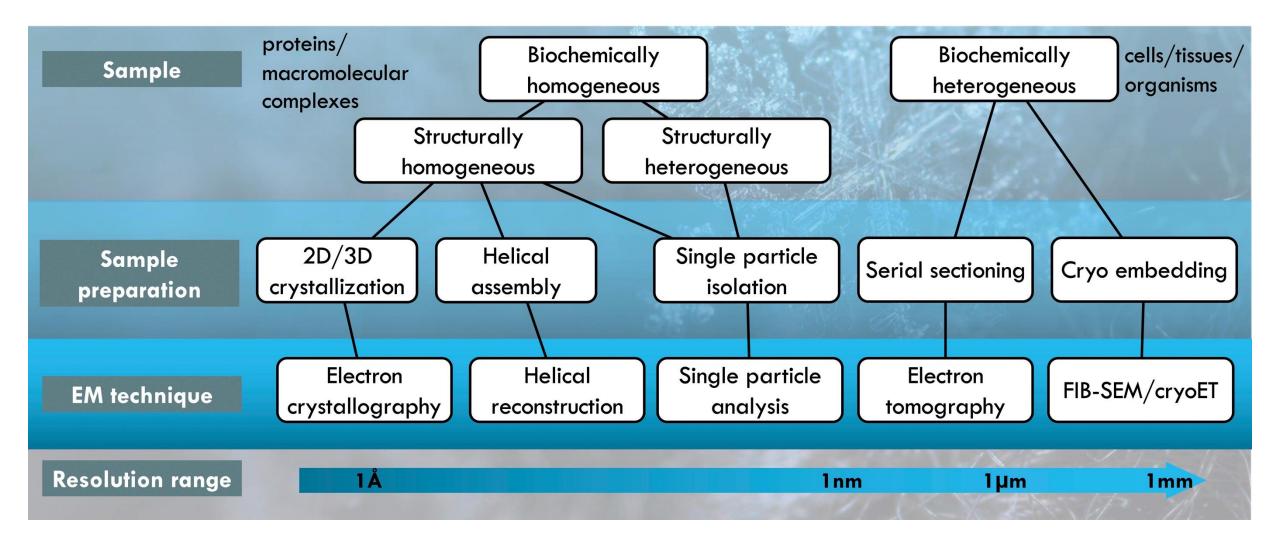
But we can get high-resolution reconstructions!

- Better detectors
- Better processing

Mishyna et al. (2017) Micron 96: 57-64

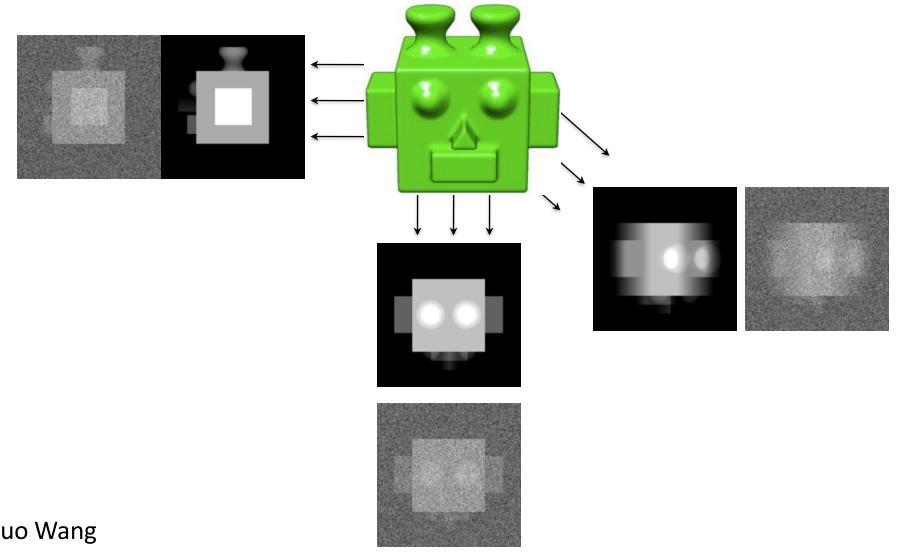
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### Sample preparation depends on the system of interest



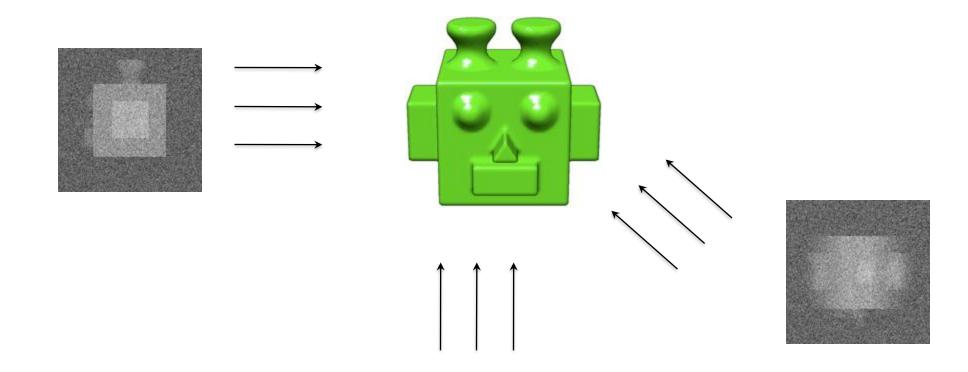
Slide credit: Ed Eng

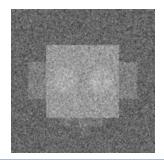
### **Image formation and 3D reconstruction**



Slide credit: Liguo Wang

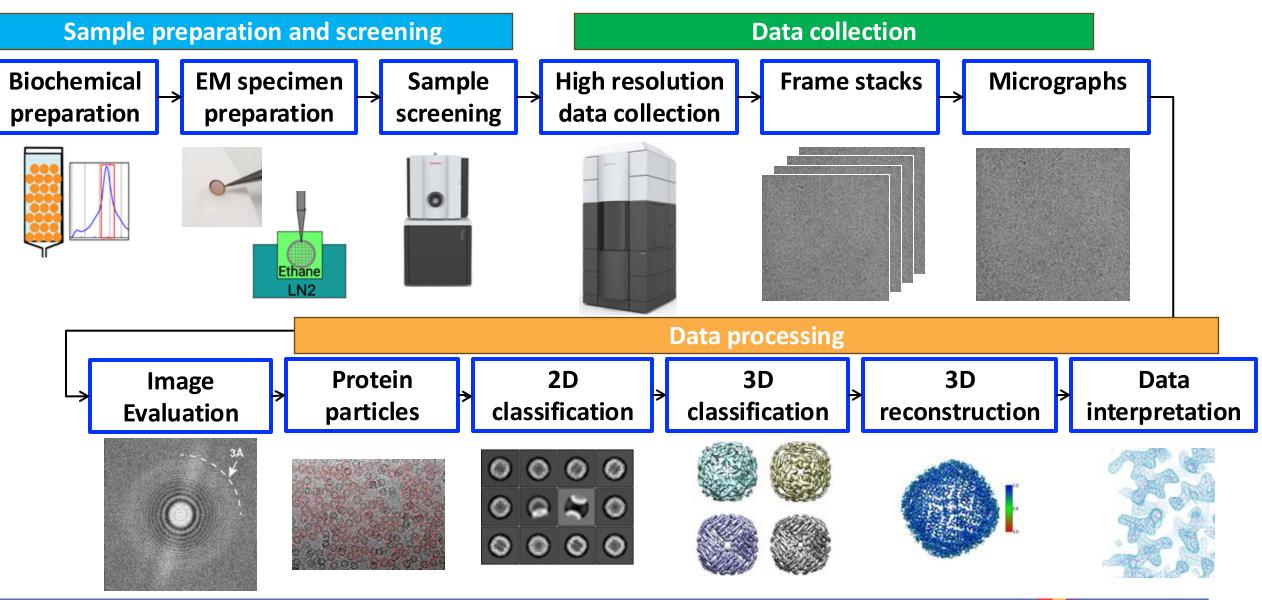
### **Image formation and 3D reconstruction**





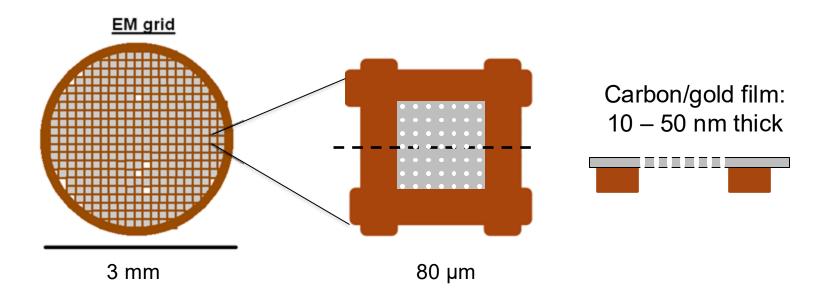
Slide credit: Liguo Wang

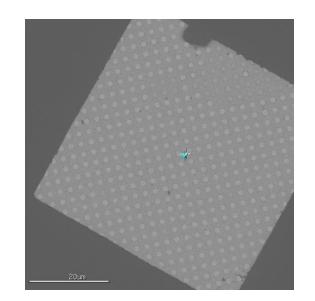
### The typical SPA workflow has many steps



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### Holey TEM grids are used for SPA cryoEM





- An EM grid: a circular metal mesh (Cu or Au).
- A thin film sits across the mesh.
- The thin film has holes (0.6-2 µM diameter) where an aqueous sample is suspended.

Mainly purchased from companies.

### Single particle cryoEM specimens are prepared on grids



CryoEM 101 (cryoem101.org)

## There are two major hurdles for practical cryoEM sample preparation

Optimizing the sample before it goes onto a grid.

For averaging, particles must be homogeneous (conformational and compositional) or if not, then well characterized.

• Getting the sample nicely frozen in a thin film on a grid.



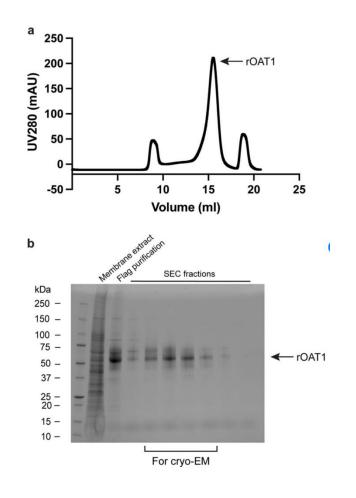
### Assessing sample quality before freezing is vital

Assess **purity**: SDS-PAGE, mass spectrometry

Assess **homogeneity:** size exclusion, SEC-MALS, mass photometry, SAXS, <u>negative stain EM</u>

Don't start vitrification until you know you have a good sample.

Garbage in -----> Garbage out



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Dou et al. Nat Struct Mol Biol (2023) **30:** 1794–1805

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## Negative stain EM is a useful tool for lower resolution sample characterization

#### Negative Stain EM:

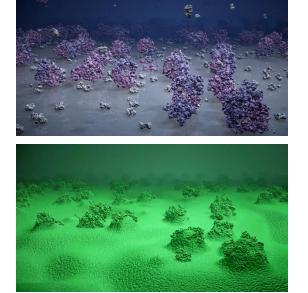
- Sample adsorbed to thin support
- Contrast comes from stain
- Resolution limited by size of stain grains (10s of Å)
- Lower sample concentration (µg/mL)
- Room temp imaging

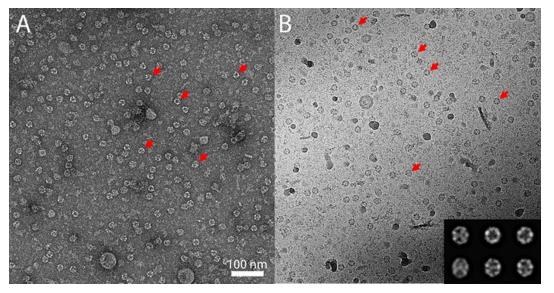
#### Cryo-EM:

- Sample suspended in liquid and frozen
- Contrast comes from sample itself
- Resolution limited by sample/data processing (1s of Å)

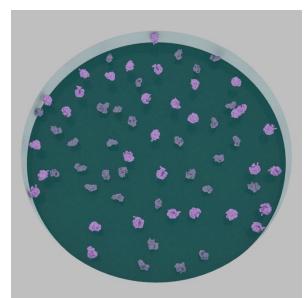
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- Higher sample concentration (mg/mL)
- Requires cryo



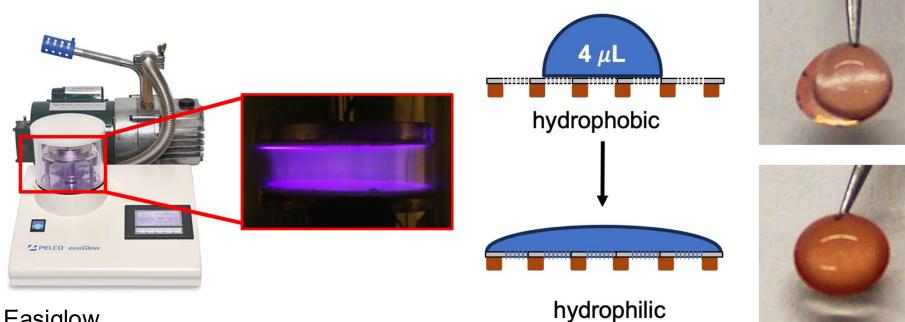


Baron S, et al. (2018) PLOS ONE 13(9): e0204457.



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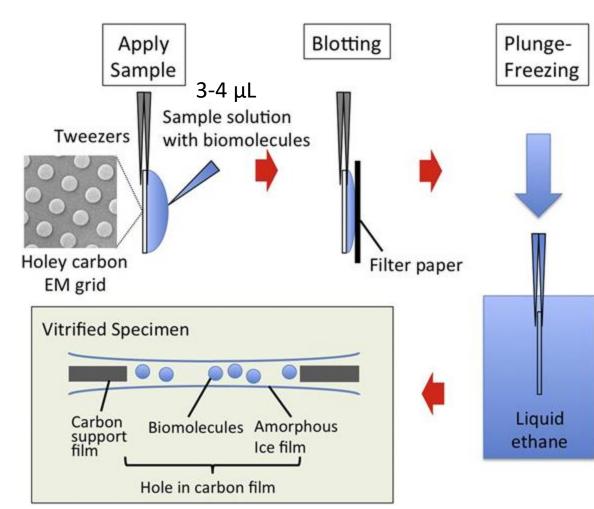
### Grids are glow discharged to change surface hydrophobicity



Pelco Easiglow Glow Discharge Cleaning System

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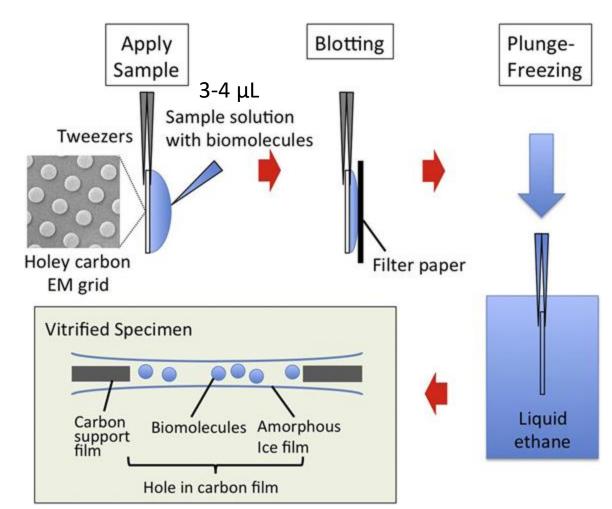
## The most common method for making frozen thin films is plunge freezing





Murata & Wolf, 2018

## The most common method for making frozen thin films is plunge freezing

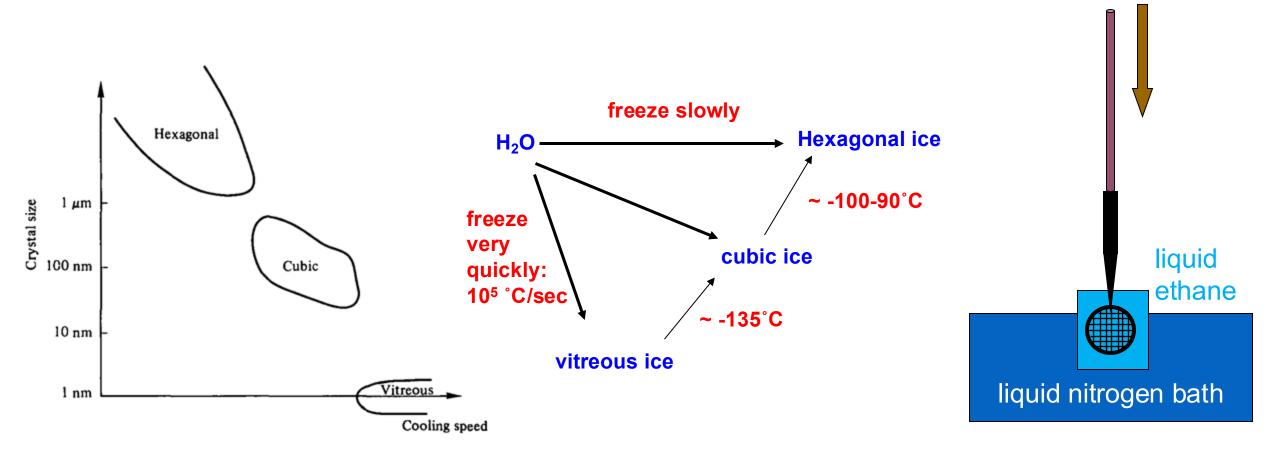




Murata & Wolf, 2018

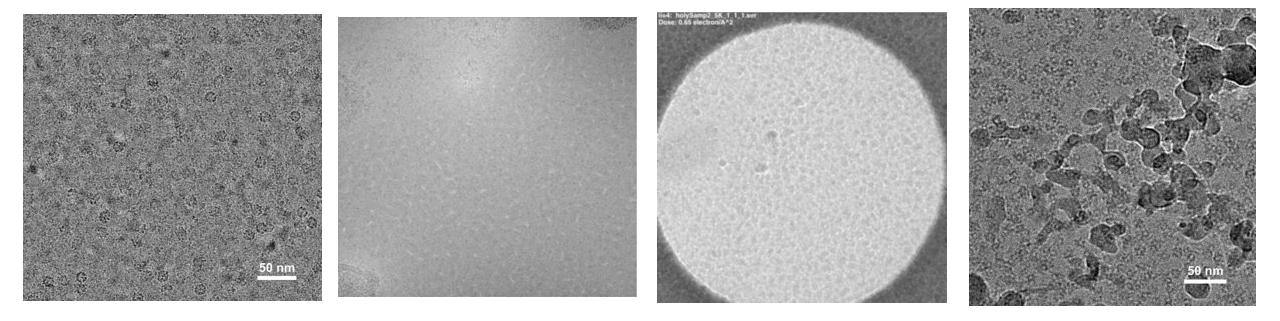
### Fast freezing allows for the vitrification of water

Vitreous ice: An amorphous solid state in which water is frozen without adopting a crystalline structure



Dubochet, et. al. (1988). Quarterly Reviews of Biophysics, 21(2), 129-228

### **CryoEM practitioners have seen many kinds of "bad ice"**



Crystaline ice

Potential sources:

- Freezing not fast enough
- Ice is too thick

"Leopard skin" usually from a grid warming up and refreezing

Potential sources:

- Grid comes out of cryogen during transfer
- Grid warms on microscope stage

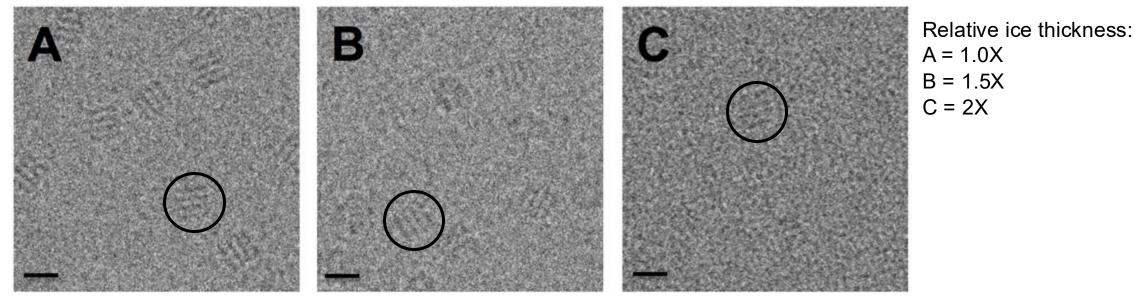
Surface contaminating ice

Potential sources:

Dirty nitrogen

### Ice thickness affects image contrast significantly

#### Cryo-EM images of GroEL



- Goal: as thin as possible
- How to control it: Blot parameters, grid type, buffer additives

http://nramm.scripps.edu/data/05may19a

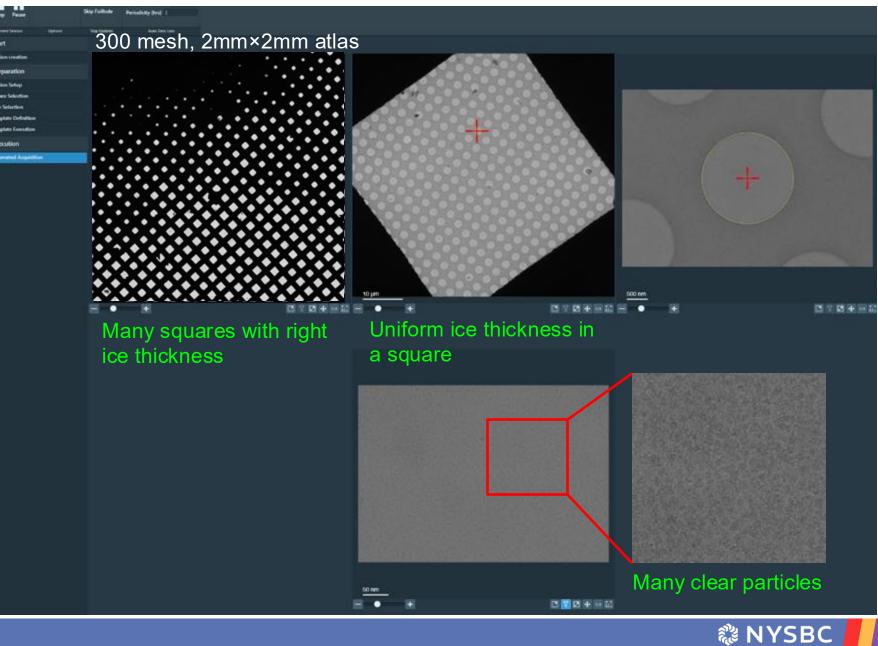
## Commercial plunge freezers provide environmental and timing control. Reproducability is still hard.



### There are two levels of quality control for a "good" grid

- 1. A sufficient area of uniformly distributed vitreous ice
- 2. Well distributed particles randomly oriented in the vitreous ice

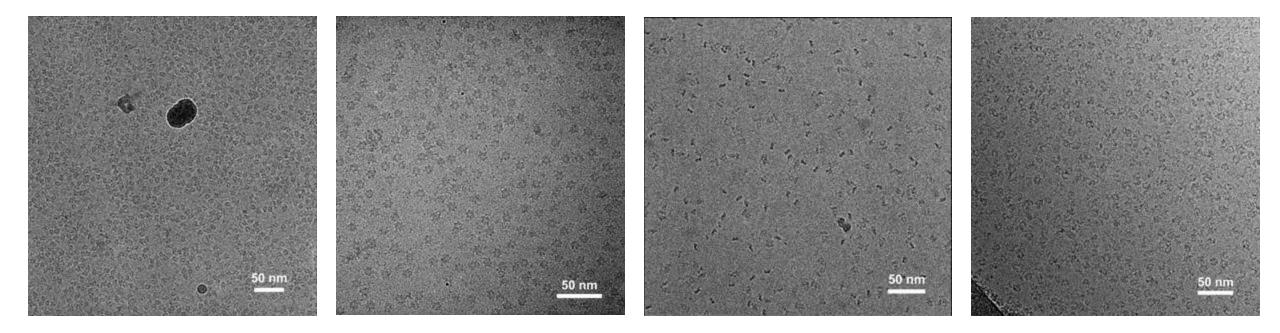
### Ideal example: Nice distribution of ice and sample



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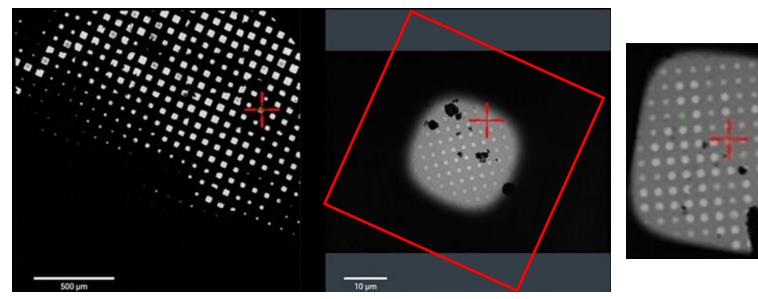
### **Good particle distribution is easy to spot**



cryoem101.org

### Not-ideal (and common) example: Poor ice quality

2mmx2mm atlas



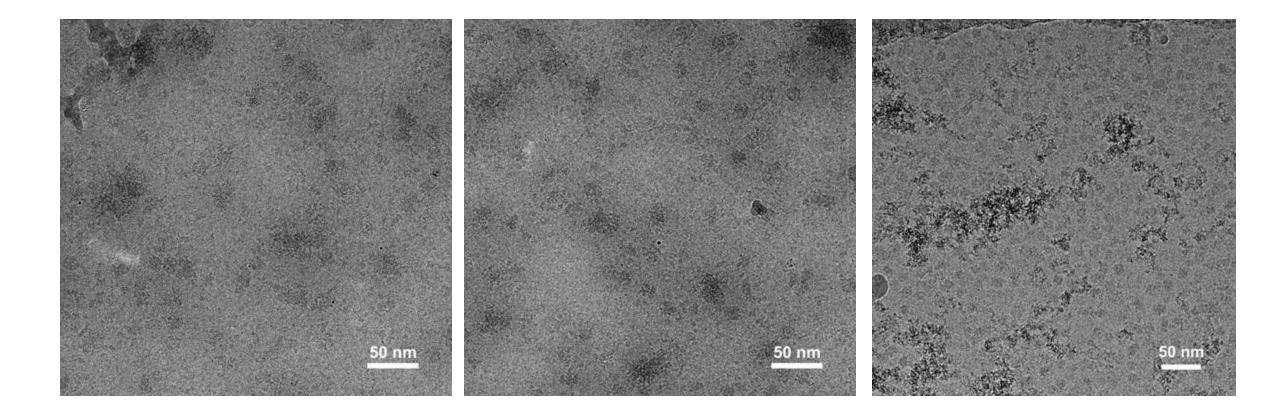
Too few squares with thin ice

Too thick ice around bars

Non-uniform ice thickness

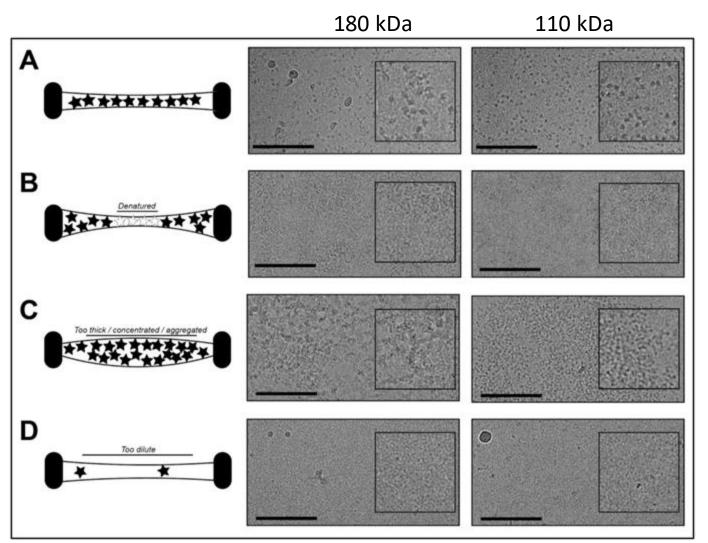


### Aggregation happens, even in good ice



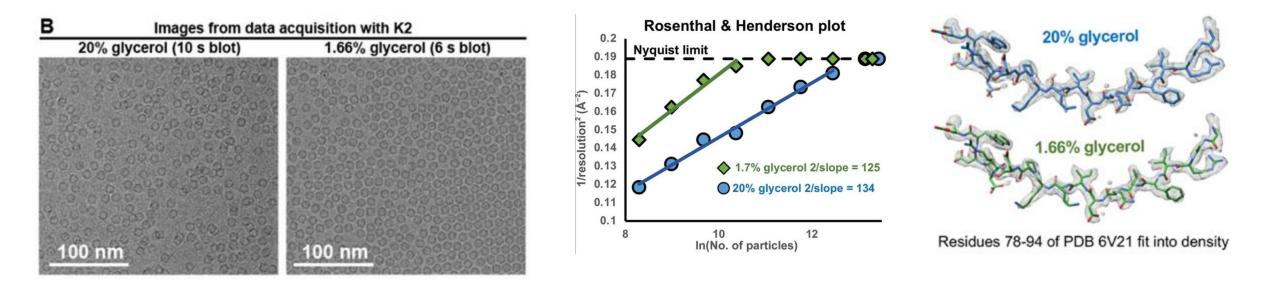
#### cryoem101.org

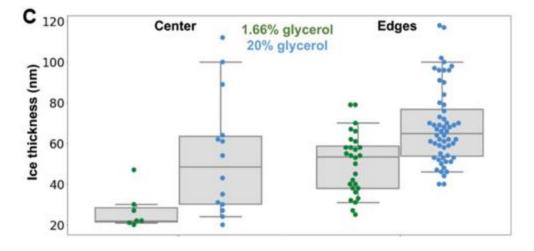
### **Biomolecules don't like to be in thin films**



Cianfrocco & Kellogg. J Chem Inf Model. 2020

### **Buffer also matters: What about glycerol?**





Balance between advice for "ideal" and what keeps your sample well behaved.

Basanta et al. (2022). Acta Cryst. D78: 124-135

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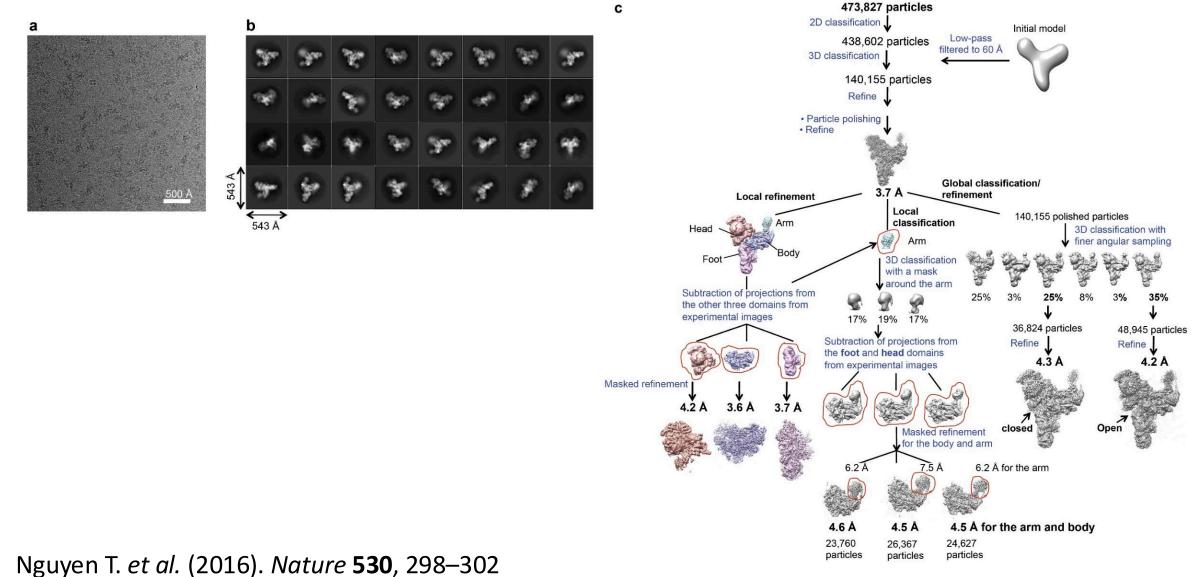
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## There are multiple ways to troubleshoot particle distribution/ice thickness on grids

- Check the literature for other samples similar to yours
- Grids: mesh size, foil type (carbon/Au/NiTi), additional support film (thin amorphous carbon, graphene, graphene oxide, streptavidin 2D crystals)
- Buffers: Detergents or additives (make sure your sample likes them)
- Ligands/binding partners: but validate your biochemistry
- Alternative instruments: Chameleon, VitroJet, home built solutions

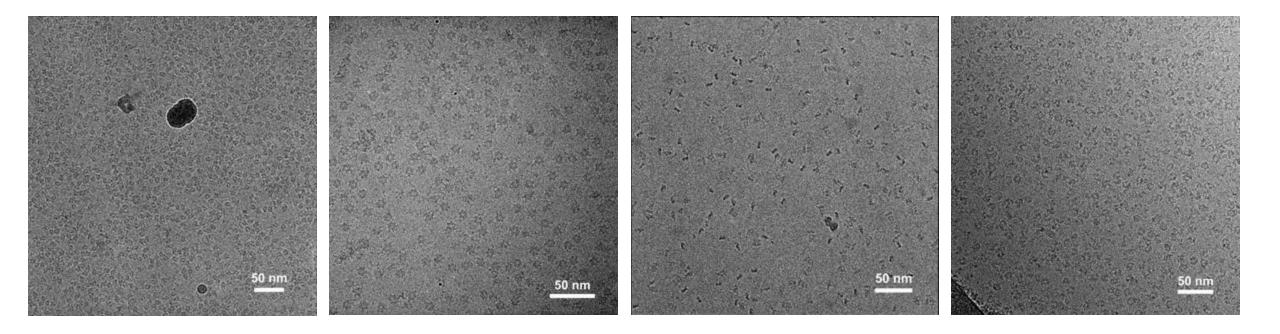
### Not every particle needs to be perfect



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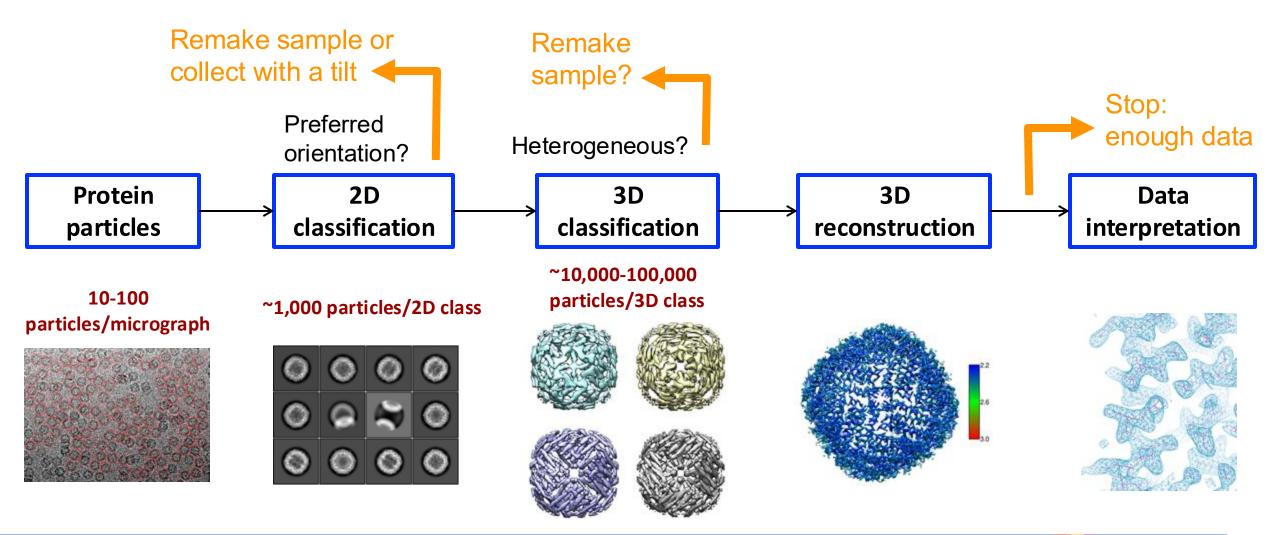
### **Good particle distribution is easy to spot!**



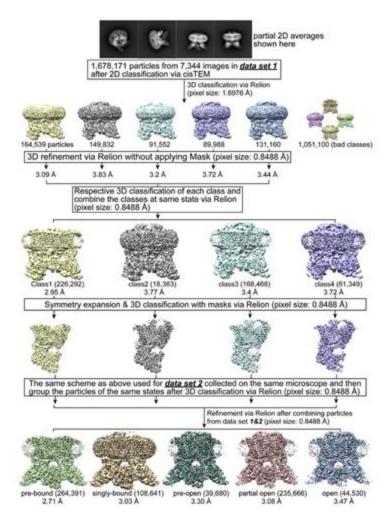
But other issues may become apparent later in processing:

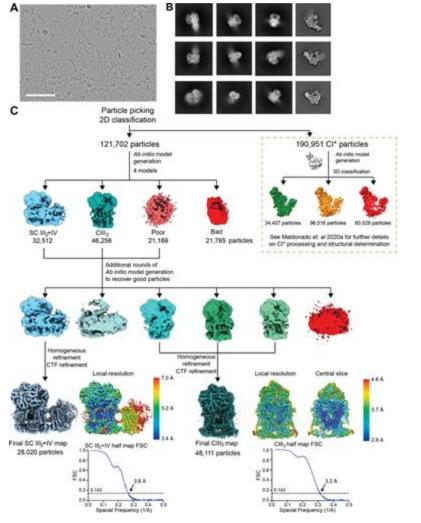
cryoem101.org

# Some issues that limit resolution are only apparent during downstream processing



## Heterogeneous samples can be characterized with advanced processing





Maldonado et. al. (2021) eLife. 10:e62047

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Zhang et. al. (2021) Cell. 184(20): 5138 - 5150

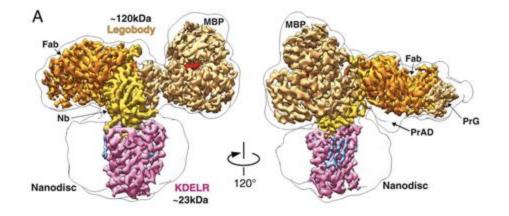
#### There are multiple strategies for stabilizing a sample

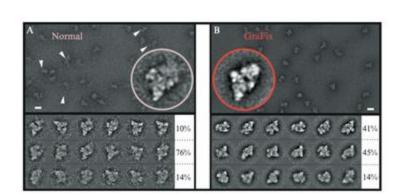
Particle	Resolution (Å)	Stabilization method	EMDB Accession No.
β-galactosidase	1.9	Small molecule inhibitor (PETG)	EMD-7770
Vps4	3.2	Non-hydrolyzable nucleotide analog (ADP·BeFx)	EMD-8887
Ribosome Quality Control Complex	8.2	Catalytic inactive mutant	EMD-6170
Insulin degrading enzyme	3.7	Fab antibody fragment	EMD-7062
ABCG2	3.1	Catalytic inactive mutant	EMD-0190
IGPD2	3.1	Small molecule inhibitor (C384)	EMD-3999

#### cryoem101.org

# A balance between size and heterogeneity can help you choose the best strategy

Fab, nanobodies, megabodies, DARPins, etc.





**Cross-linking** 

Purification tags: His<sub>10</sub>-Epitope Protein

To cleave or not to cleave...

Wu & Rapoport (2021) PNAS 118 (41): e2115001118

Stark (2010) Methods Enzymol. 481:109-26

What is the research question you are trying to address??

## **Every sample must be optimized but here's where you can start:**

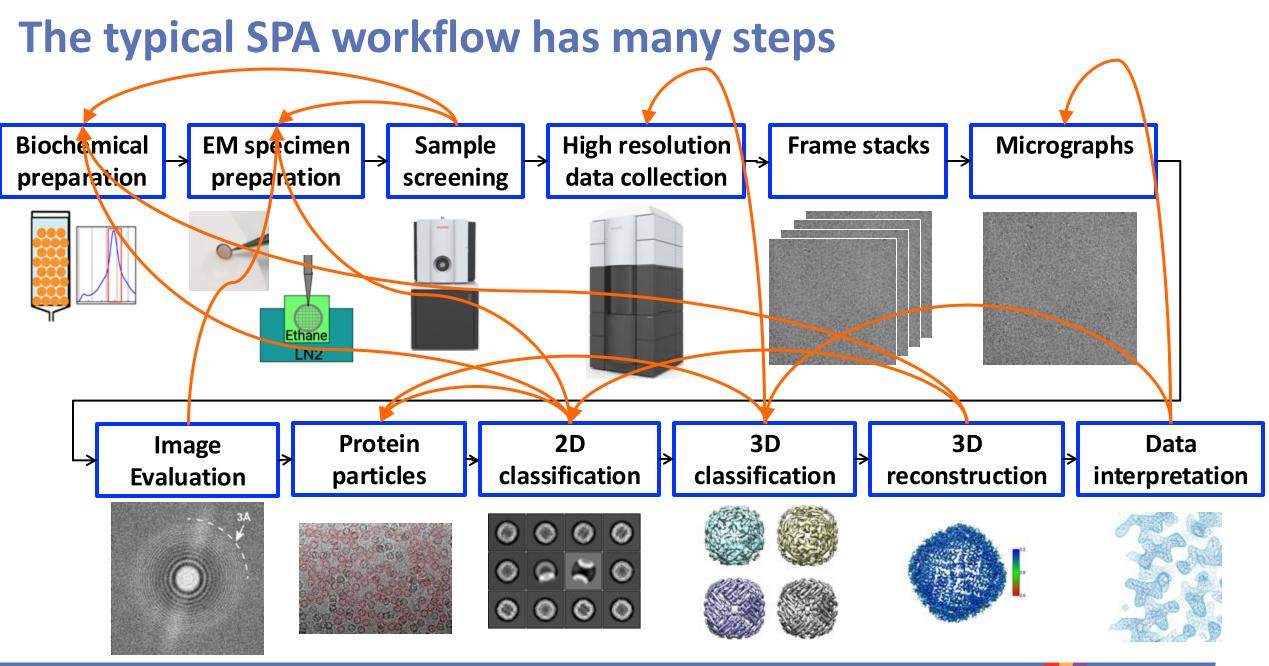
- For SPA cryoEM: ~1-5 mg/mL (or ~100x the concentration that looks good in negative stain).
- 3-4 μL per grid. Plan on needing ~a dozen grids to make progress (testing grid type/concentration/blot parameters/etc).
- As homogeneous as possible, measured by <u>non-EM</u> techniques!
- Proteins smaller than 100 kDa are challenging.

### **Cryo-sample preparation tips from the experts**

- Plan your freezing session in advance!
- Reduce contamination: Get everything ready before pouring LN<sub>2</sub>
- Check ethane level to ensure immersion of the grid be fast and careful during grid transfer steps
- Grids: 400 mesh grids for NS
  300 mesh grids for cryo-samples
- Glow discharge:
  20-30 mA, 20 s for carbon / 120 s for gold;
  10 mA, 5s for ultrathin carbon coated holey grids
- Reproducability is hand-to-hand dependent
- Working fast is helpful generally improves with experience

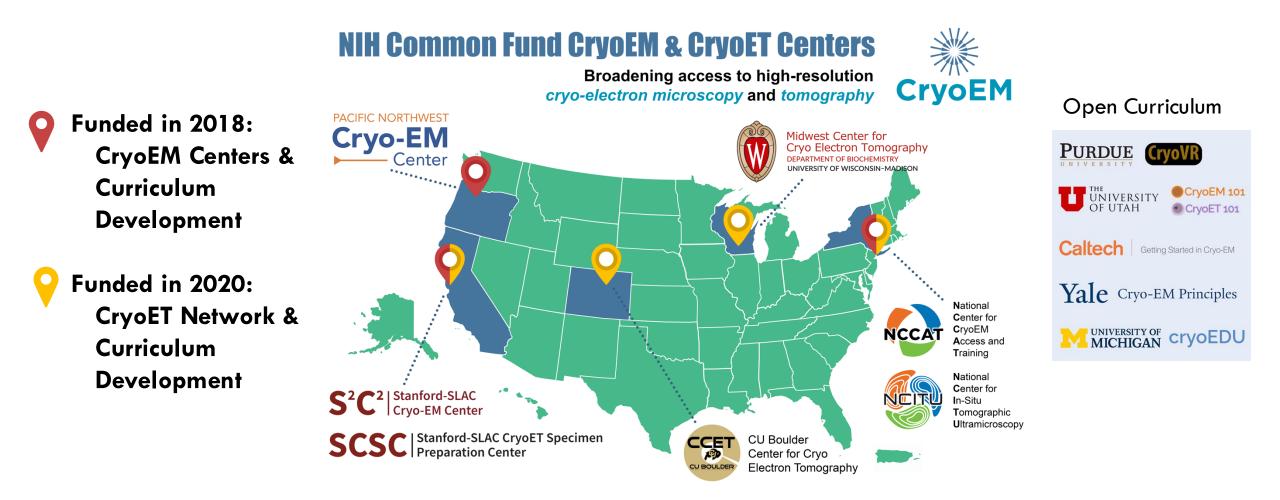
### **Cryo-sample preparation tips from the experts**

- Trial and error and a little bit of luck are all part of cryo-EM sample preparation.
- Ask advice of more experienced groups or instrumentation facility staff.
- Time spent doing biochemistry to make a sample as homogeneous as possible can save a significant amount of time during grid preparation and data processing.
- Time spent at the grid-preparation stage can make data collection on high-demand instruments more efficient.

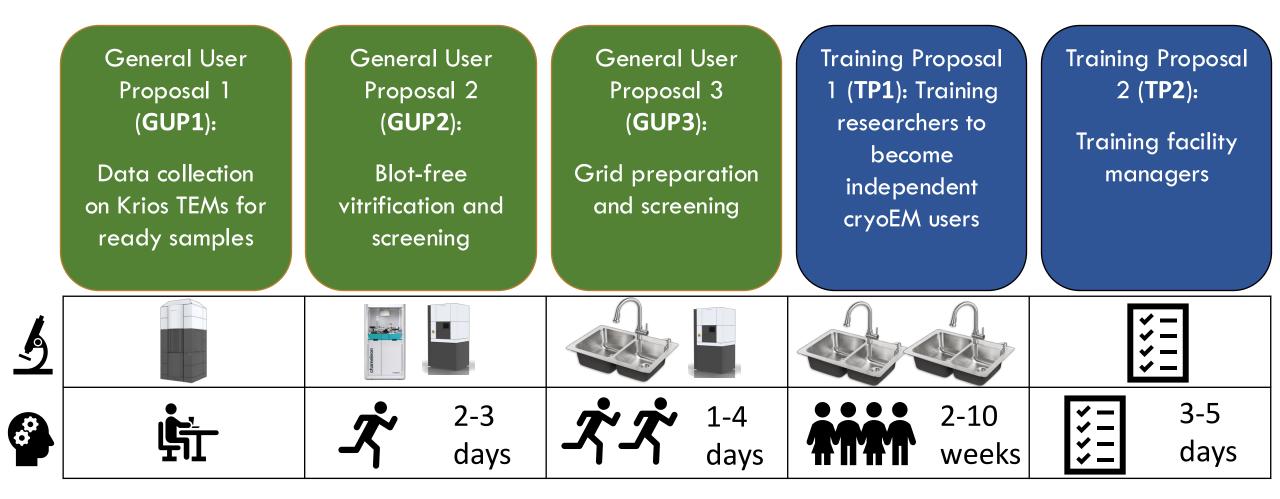


### Multiple centers share a mission make cryoEM accessible

https://cryoemcenters.org



#### NCCAT has five avenues of access

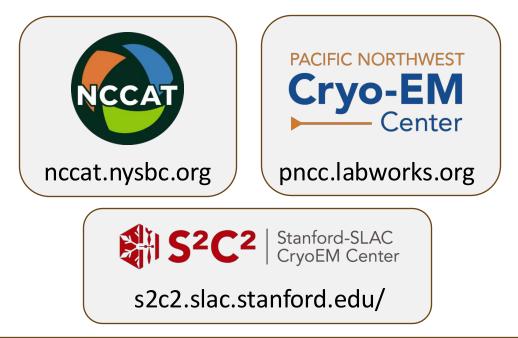


- All access categories require submission of a proposal that is scored by an external review committee to determine priority and duration of scheduling.
- Instrument & training time is at no-cost to the user.

### Accessing NIH-funded resources is the same but different

#### **Single particle focus**

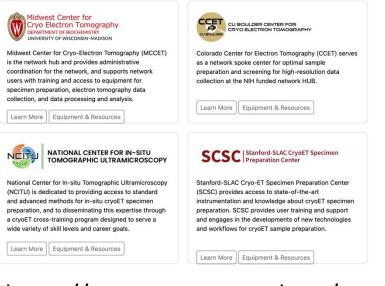
Multiple independent centers. Apply to each separately.



High-resolution data collection at the NCI National CryoEM Facility (NCEF) https://www.cancer.gov/research/resources/cryoem

#### **Cryo-electron tomography focus**

One stop shop. Proposals assigned by the hub.



#### https://www.cryoetportal.org/

## cryoemcenters.org

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## **Bio-Imaging Center**

Located in the Ammon Pinizzotto Biopharmaceutical Innovation Center:

590 Avenue 1743, Suite 141 Newark, DE 19713

https://bioimaging.dbi.udel.edu/

Need cryo-TEM help? Contact Us!



Shannon Modla, smodla@udel.edu Our center is equipped with a Thermo Talos L120 TEM with a Ceta 16M camera, a Thermo Vitrobot Mark IV, and a side-entry Gatan Elsa cryo-transfer holder.

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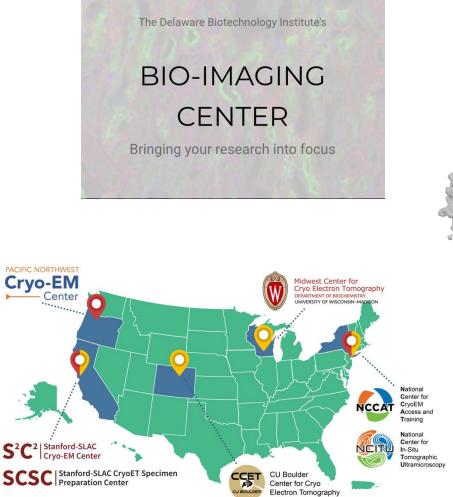
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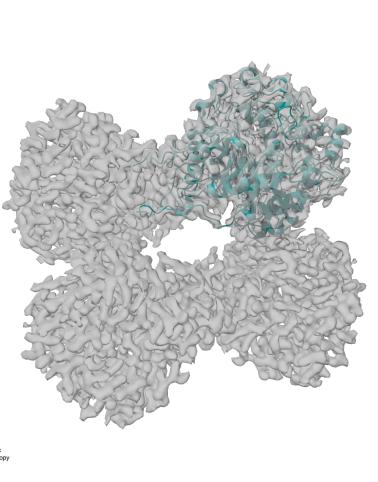
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We also have a Pelco easiGlow glow discharge system, a cryostorage dewar, and dry shipper with a Mitegen puck storage system.

#### **CryoEM** is easiest in a community





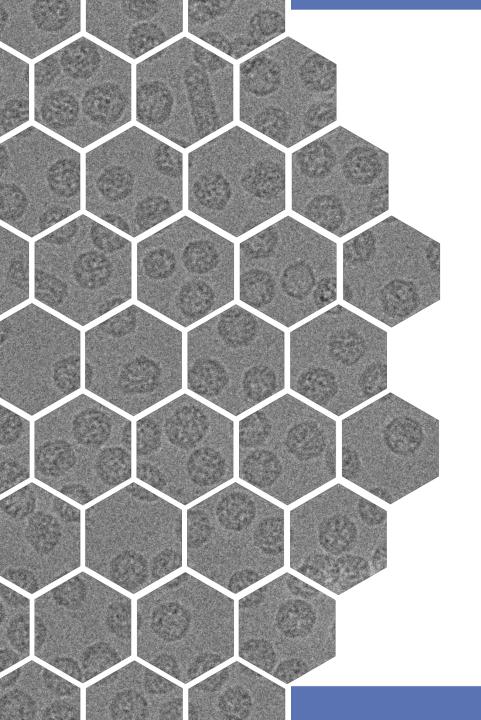






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## Let's make some grids!

Website: nccat.nysbc.org E-mail: nccatinfo@nysbc.org



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