





The Winter-Spring 2022 EM Course January 12, 2022

Journal club articles in detail:

1. A comparison of original and modern plunge freezing techniques

Adrian et al. 1984 & Razinknov et al. 2016

These papers are focused on sample preparation methodology.

2. The best voltage for biological cryo-EM

Peet et al. 2019 & Naydenova et al. 2019

These papers deal with the microscopes and cover details of optics and information loss in EM.

3. The beginning of the resolution revolution

Liao et al. 2013

Seminal work on TRPV1 by Yifan Cheng's lab. Widely considered to be the "beginning" of routine high resolution cryo-EM. The discussion should focus on t technological and scientific advancements that made this work possible. There are far too many to explicitly assign, so it is left more open-ended.

4. HIV trimer controversy and Einstein from noise

Mao et al. 2013 & Henderson 2013 & van Heel 2013

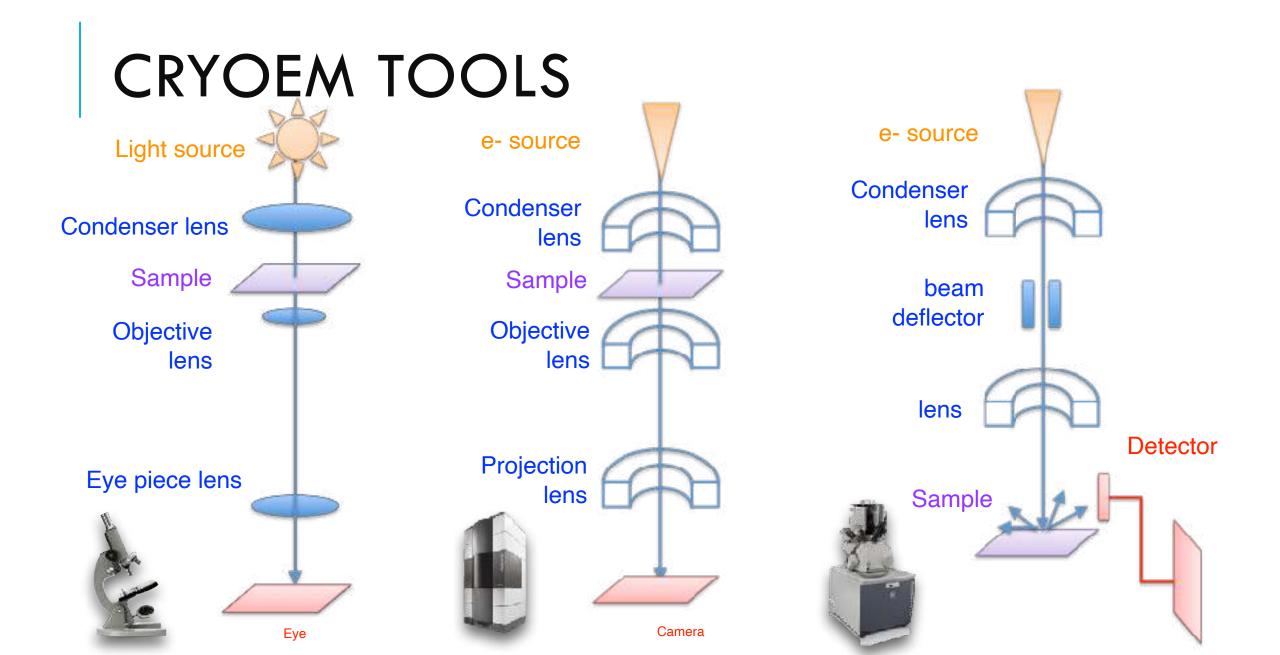
The first paper is a cryo-EM structure of the HIV trimer, and the second two are criticisms of that paper's EM data processing. It is a significant case study in what can go wrong in EM.

5. Challenges in and recommendations for validating cryo-EM data

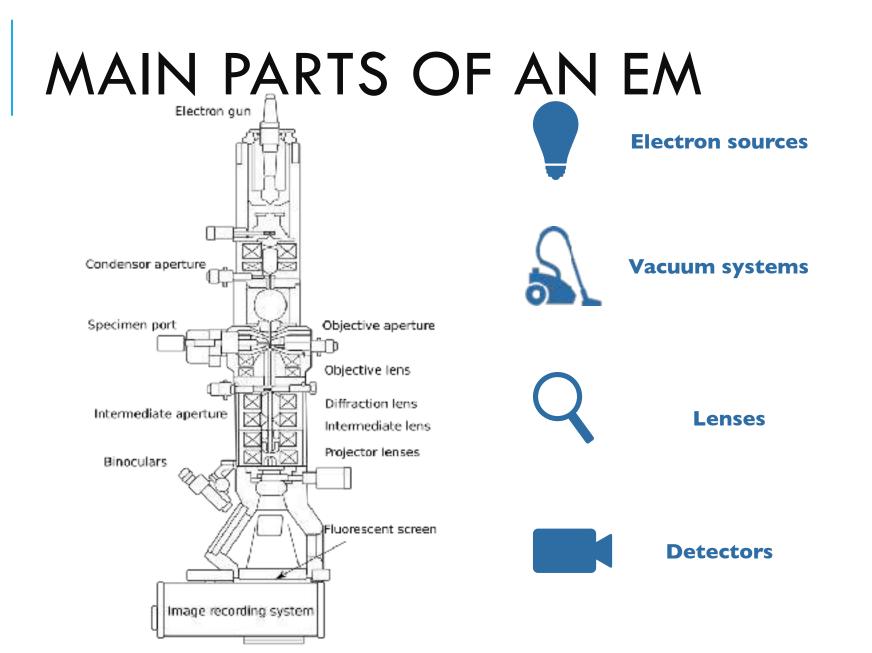
Henderson et al. 2012 & Neumann et al. 2018

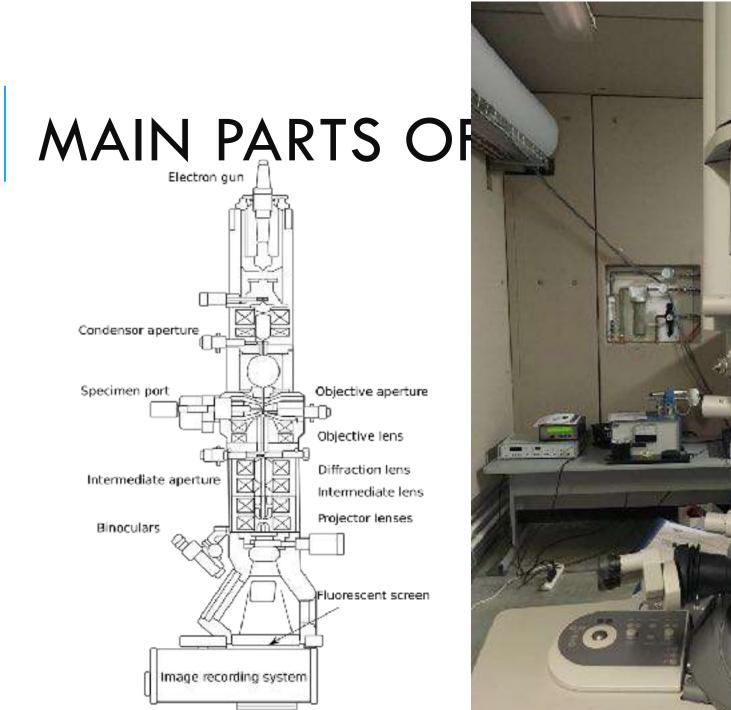
The first paper is the set of recommendations from the first Electron Microscopy Task Force Meeting, and the second is a more recent approach to validatio light of the resolution revolution.

6. TBD

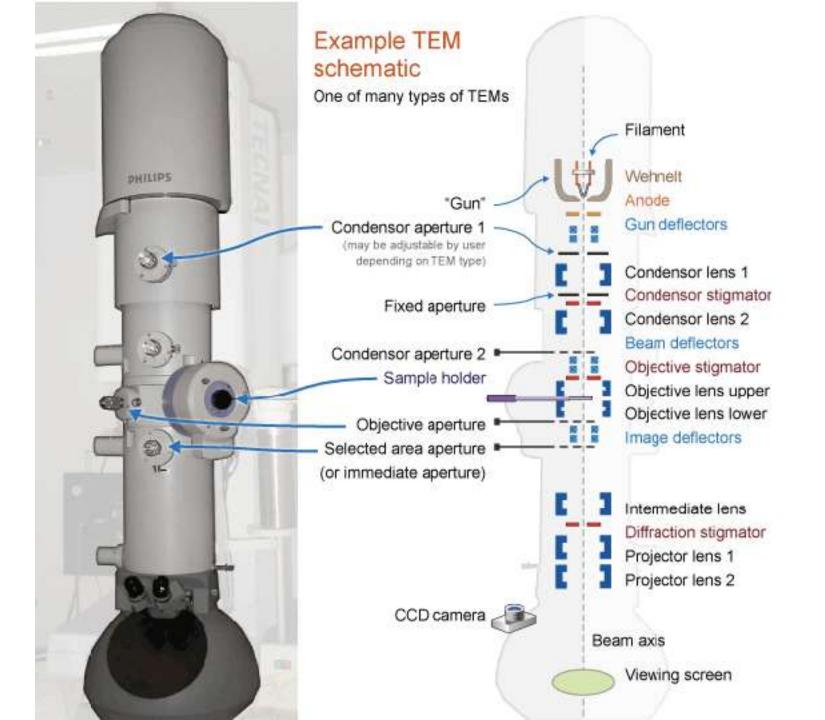




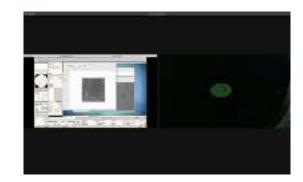


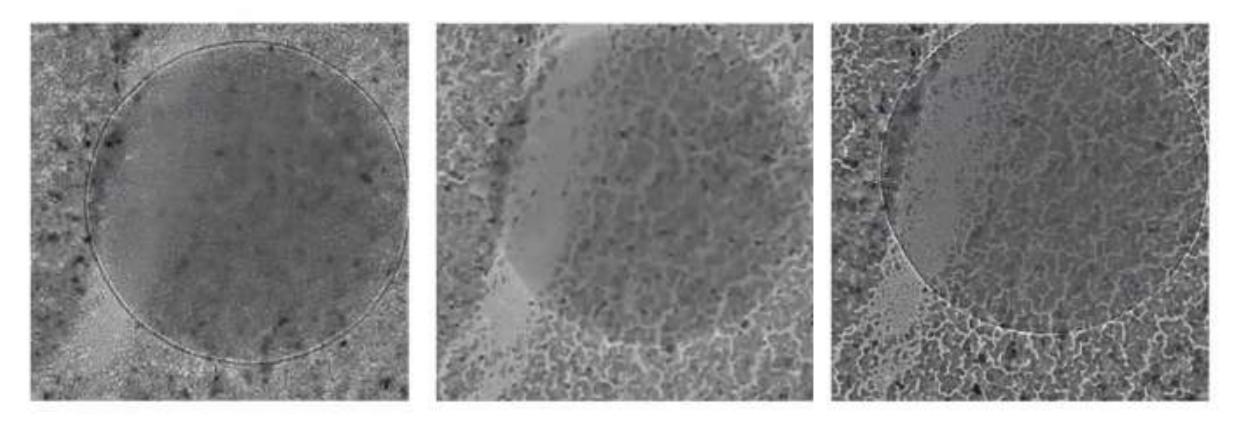






FOCUS





K3 specs



https://www.gatan.com/K3

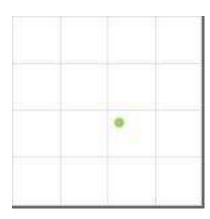
Specifications

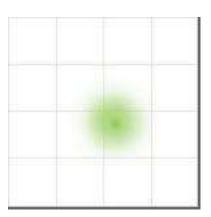
	K3	K3 Base					
TEM operating voltage (kV)	200/300						
Sensor size (pixels)	5,760 × 4,096	3,456 x 4,098					
Readout modes	Counting Super-resolution	Counting					
Max. image size (pixels)	11,520 x 8,184 Super-resolution	3,456 x 4.09					
Performance relative to physical Nyquist (DOE)							
Peak	>0.87 / >0.83	>0.8					
0.5	>0.53/>0.53	>0.5					
Sensor read-out (full fps)	>1500						
Transfer speed to computer (full fps)	>75	>25					
Mation correction	Inline						
Gatan Microscopy Suite [®] software	Includ	bei					
Automation support	Latitude and other third-party software						

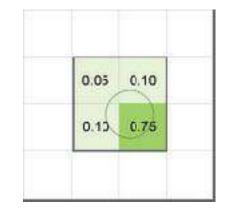
Specifications are subject to change without notice.

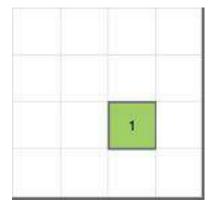
Counting mode

5,760 x 4,096 px 11,520 x 8,184 px









Electron enters detector.

Electron signal is scattered.

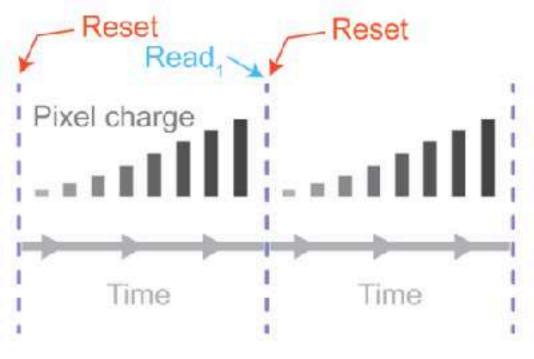
Charge collects in each pixel.

Events reduced to highest charge pixels.

https://www.gatan.com/improving-dqe-counting-and-super-resolution

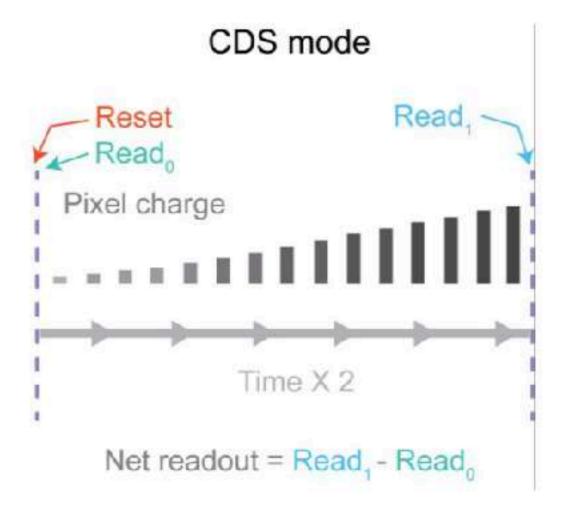
K3 lowers Read Noise with Correlated Double Sampling (CDS)

Standard mode

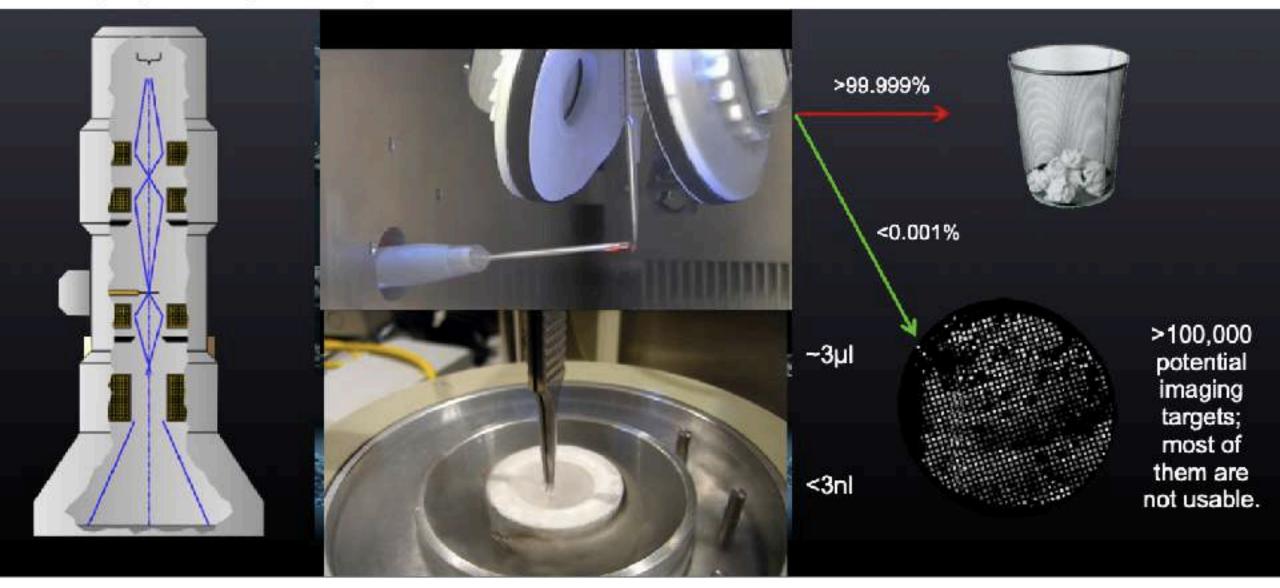


Net readout = Read

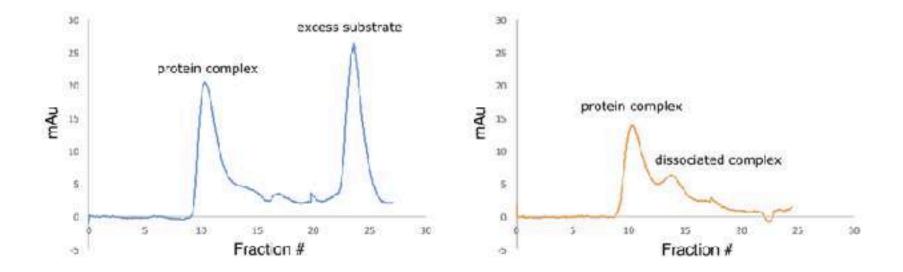
https://www.gatan.com/



Vitrifying a biological sample

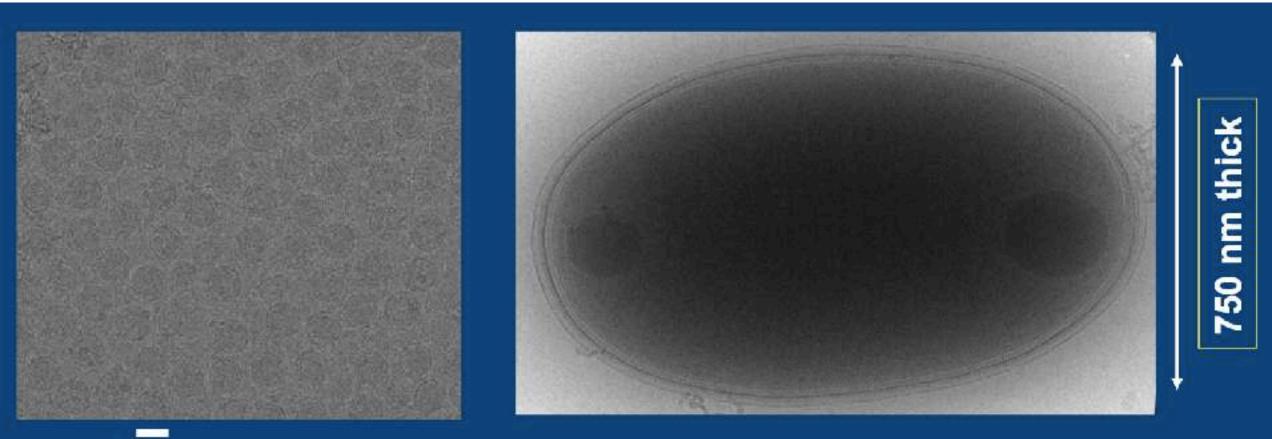


cryoem101.org



An example of an optimal gel filtration profile is shown on the left. The protein complex is enriched and abundant, and well separated from other peaks (e.g., excess substrate). On the right, a less optimal gel filtration profile for the same protein complex is shown (prepared in the absence of its substrate). Note that there are multiple peaks that are not well resolved, and the major complex species is less abundant.

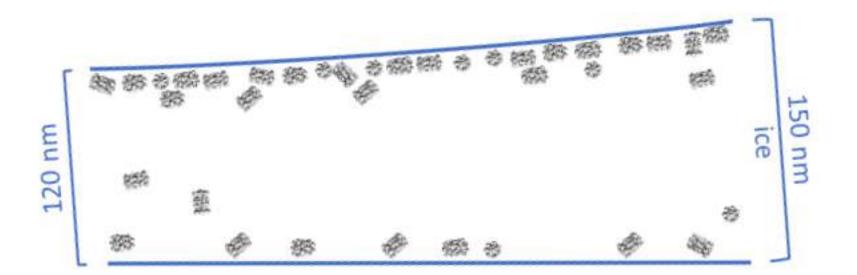
How thin do I need my sample?



50 nm Bacteriophage (\u00f612)

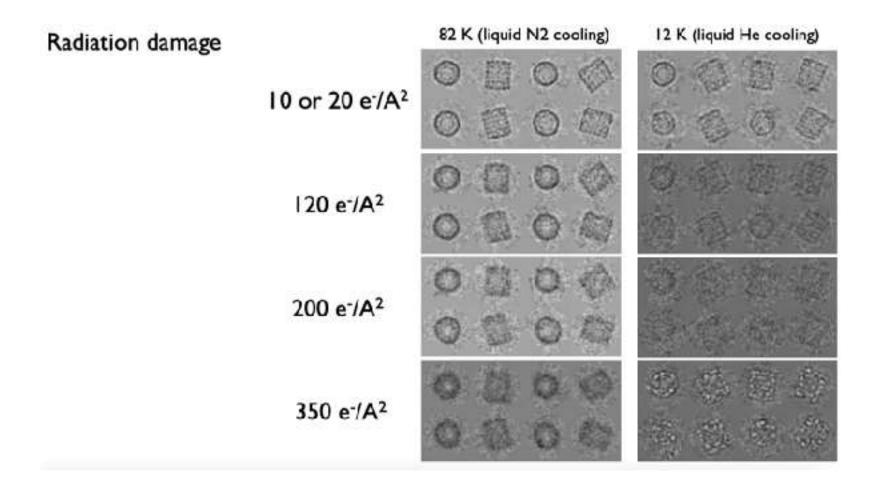
E. coli, Salmonella, Cyanobacteria

How thin do I need my sample?



Electron cryo-tomography analysis of single particles show that the overwhelming majority of particles adhere to the air-water interface and adopt a limited range of views. Image from <u>Noble et al. eLife 2018</u>.

https://cryo-em-course.caltech.edu/

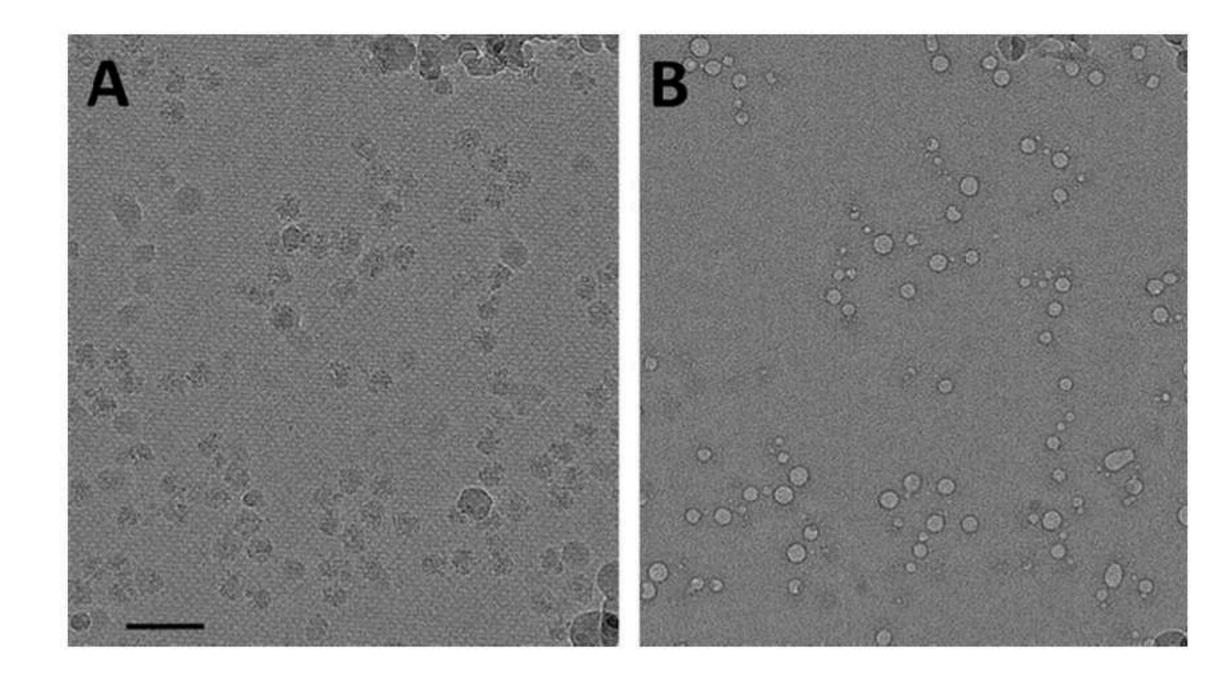


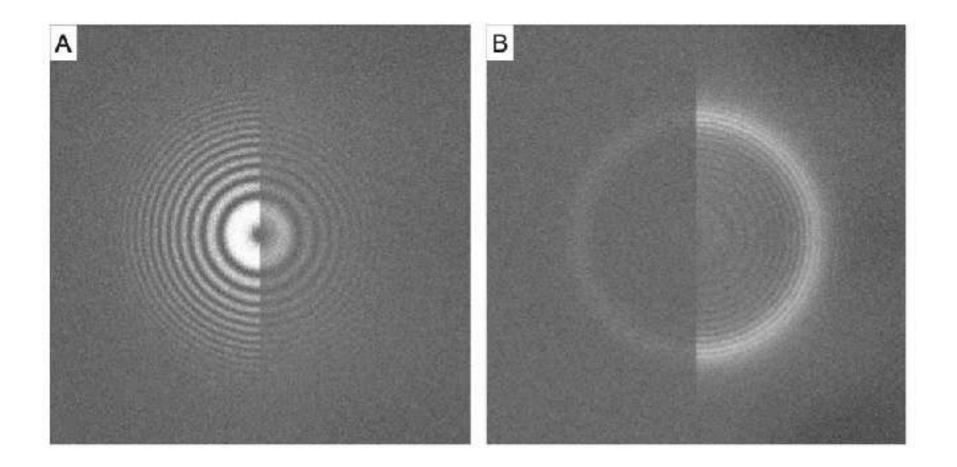
Specimen Behavior in the Electron Beam

R.M. Glaeser¹

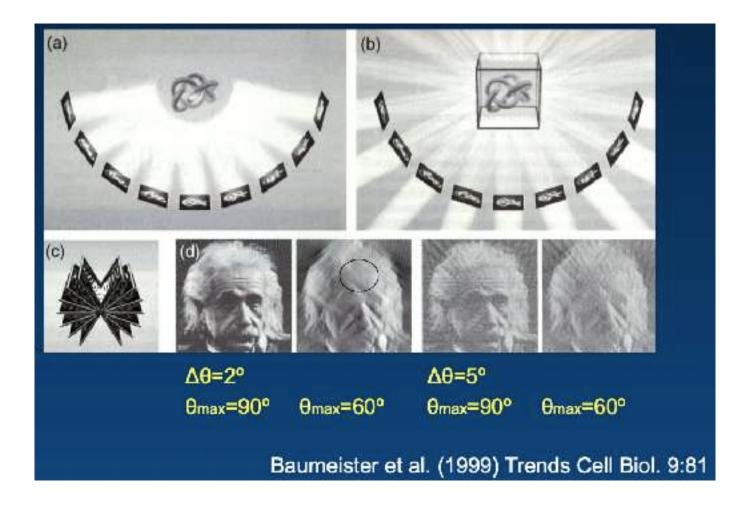
Lawrence Berkeley National Laboratory, University of California, Berkeley, CA, United States ¹Corresponding author: e-mail address: rmglaeser@lbl.gov

• The first notice- able bubbles appear after the accumulated exposure (for 300 keV electrons) is approximately 150 e/A. At this high exposure, high-resolution features would long since be destroyed, of course, but the macromolecular particles might still be visible.





Directional information loss



https://3dfsc.salk.edu

306

			0	-	0	-	0	۲	0		
	This is an application for remotely processing the SD Fourier she'l correlation of crycEM maps.	0	*	۲	*	۲	۲				
Instructions				-	130.	-	100	-	10		
1 Clok 'Register' or	the ravigation bar and follow the isstruc	tions to create an account.		1	100		100		14		
2 Novigate to the pro-	cessing form via the "Submit Job" link.		100	420	_	10		- 10			
O Enter your email so	ddisai and other required perameters is t	he form.				-		-	13		
You must uploait a jo appropriate pixel size	b rame, two haitmaps (mm format), a fu s. click "Submit (kb",	limao (also .mrc formati, and an	-	-	-	1	2	3.4	Ľ		
4 You should receive check your span fdo	an email to confirm your processing job. ters.	Il you do not receive ar email, please		-	-	赛		-	E		
5 When your lob is o	5 When your job is complete, you will receive another email with a link to view the results.	-	-	pee-g	-	Peril	-				
			1	-	-						