

Cryo-ET Basics

Lu Gan

National University of Singapore
Centre for Bioluminescence Sciences
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Lecture outline

1. What is tomography?
2. Sample preparation (what kind?)
3. Principles of reconstruction
4. Beware of artifacts
5. Example studies

What is tomography?

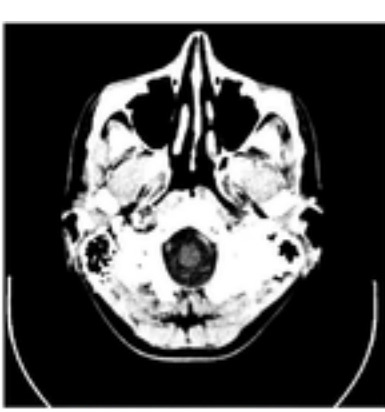
τέμνειν: to cut (Greek)

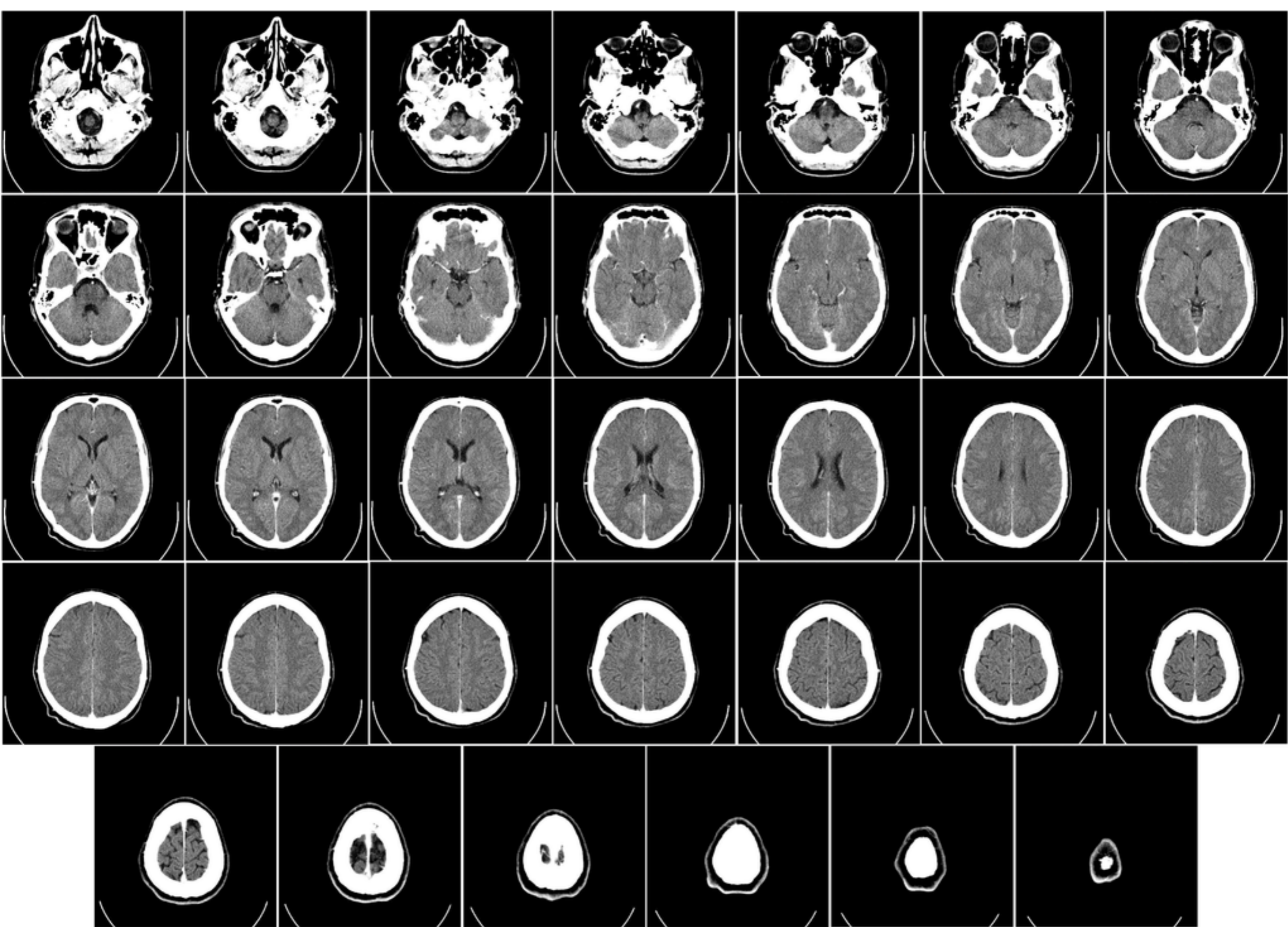
Cut, in the virtual sense

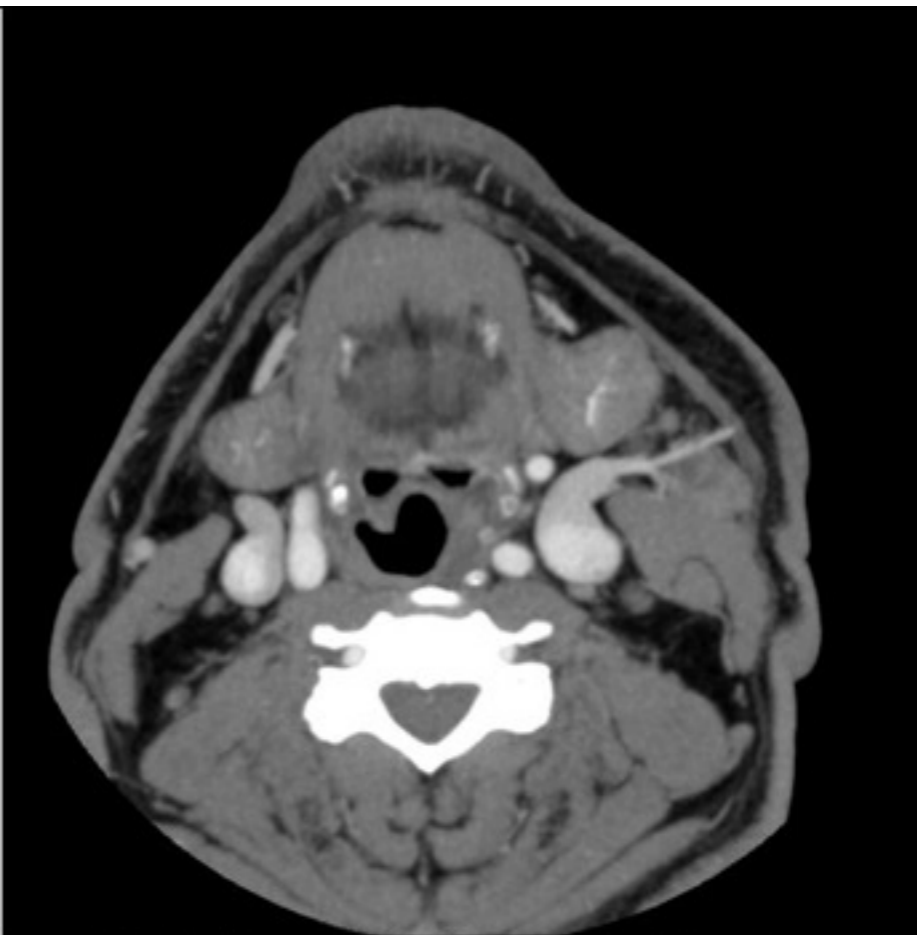
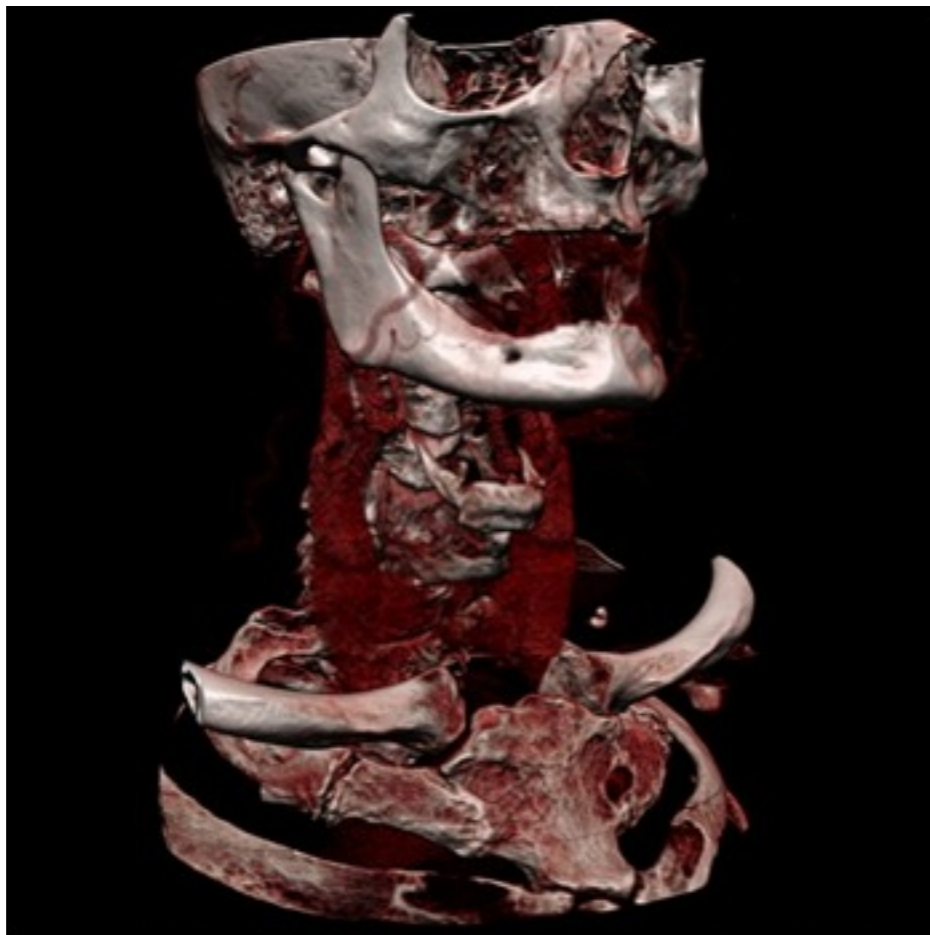
CAT Scan



Computed Axial Tomography







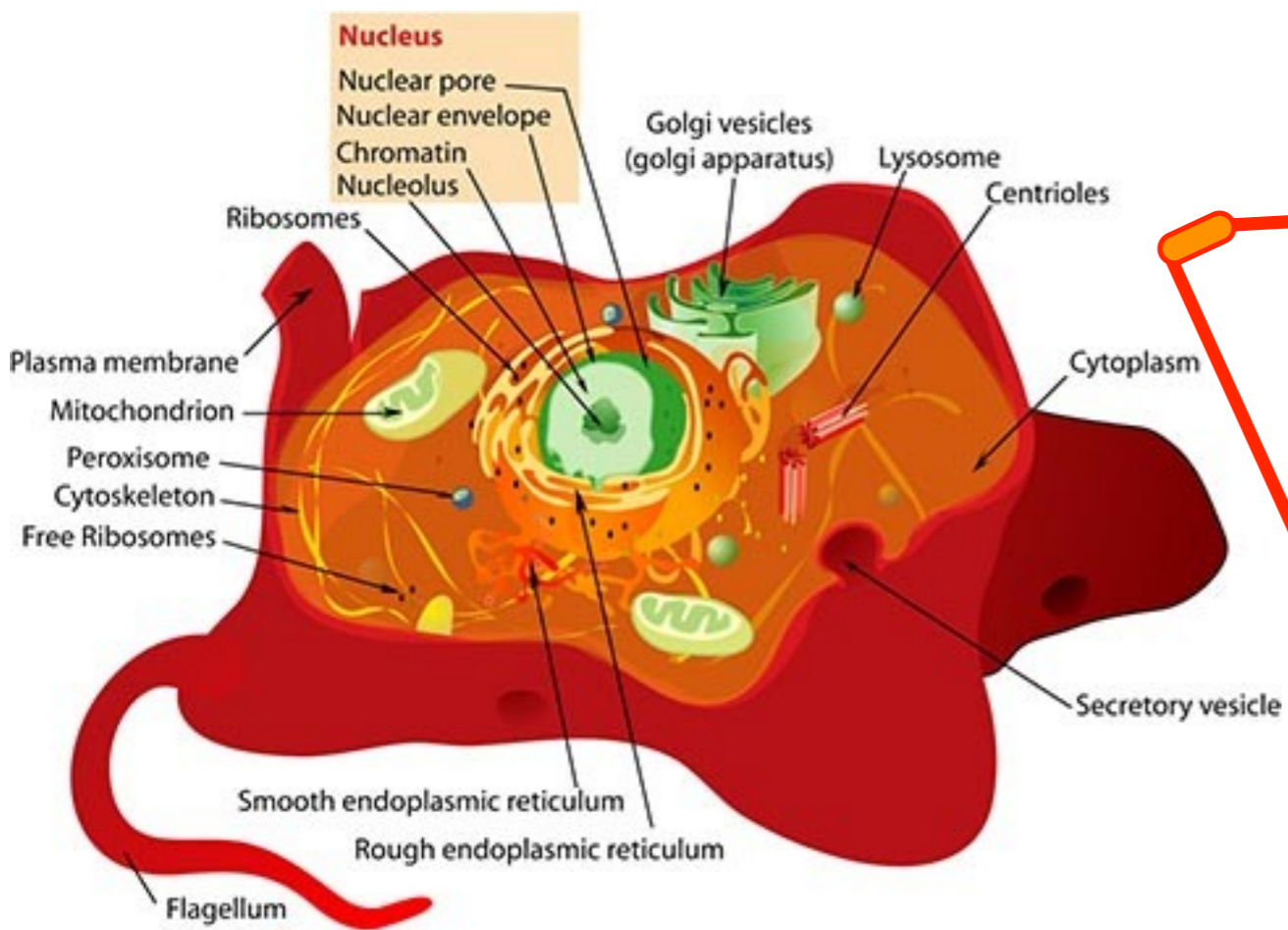
1. What is tomography?

2. Sample preparation (what kind?)

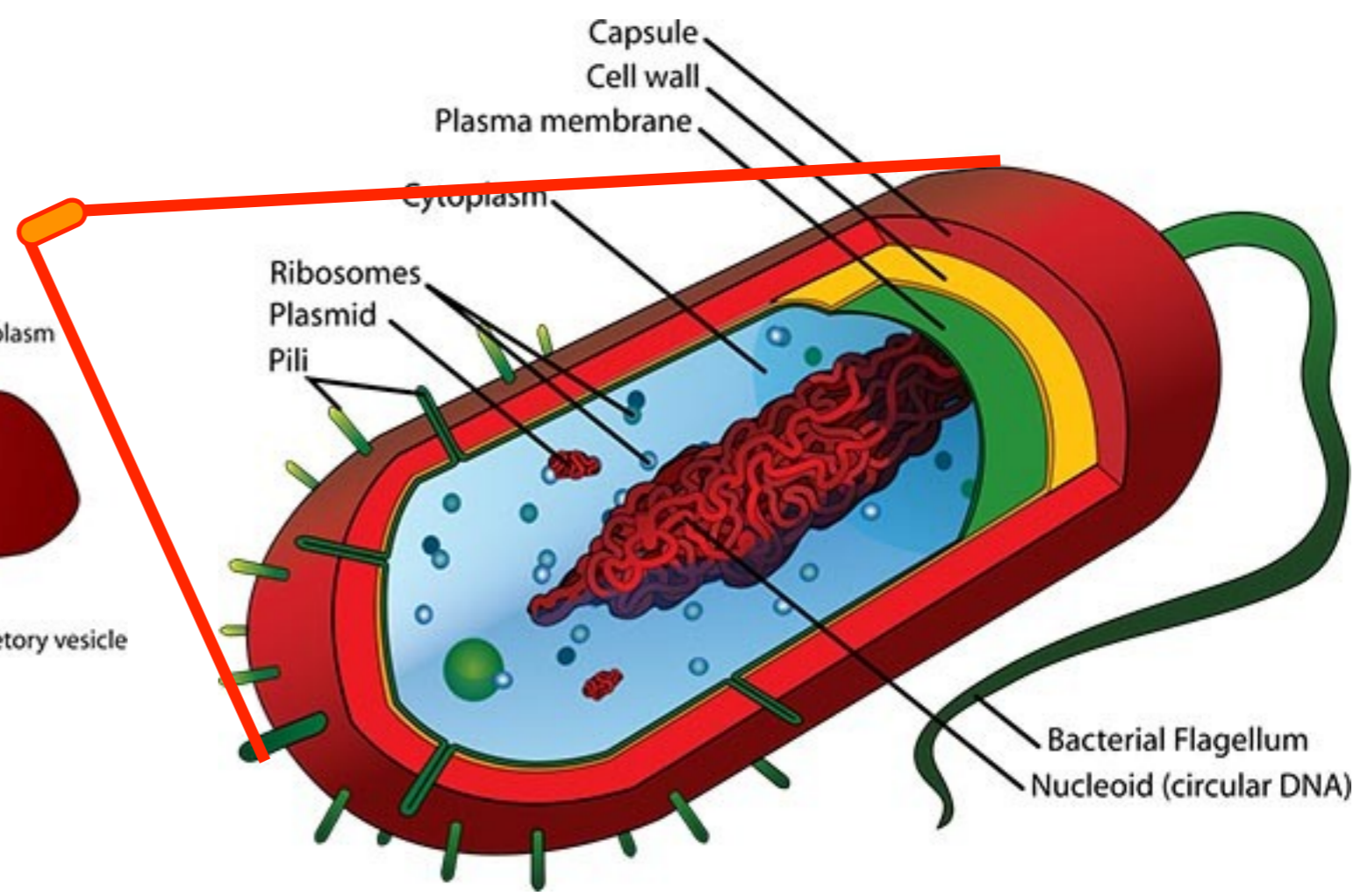
3. Principles of reconstruction

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5. Example studies

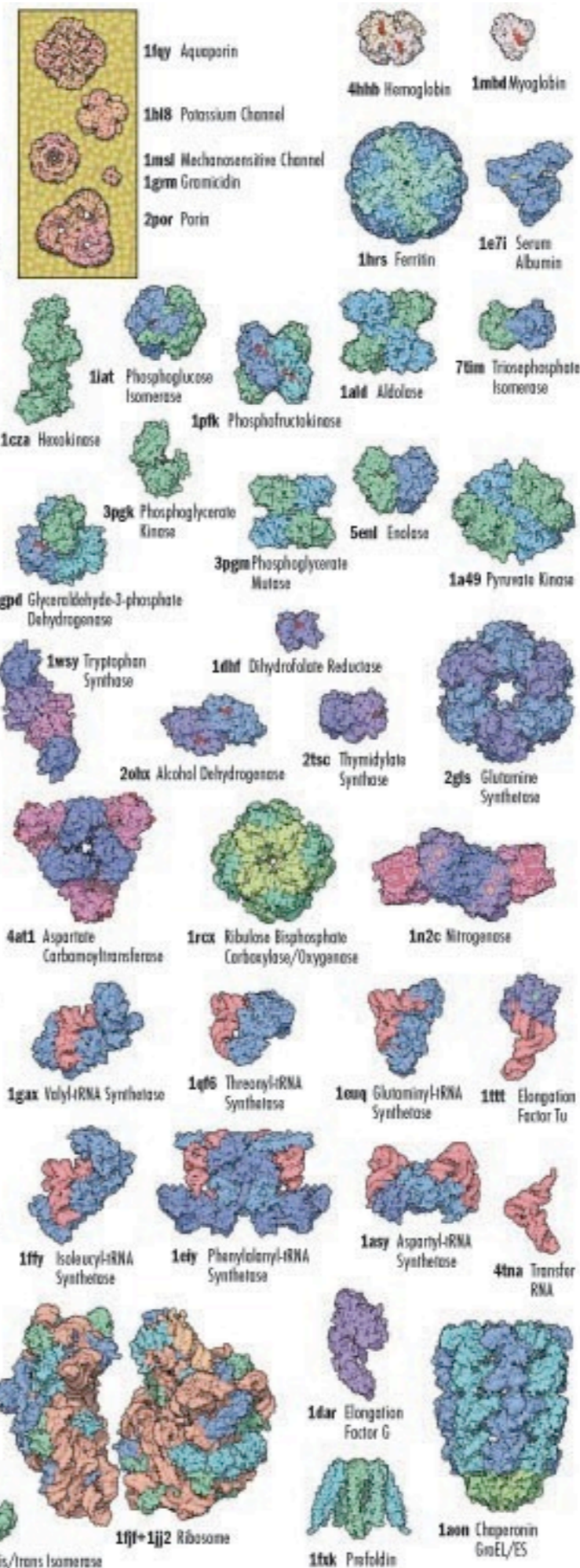
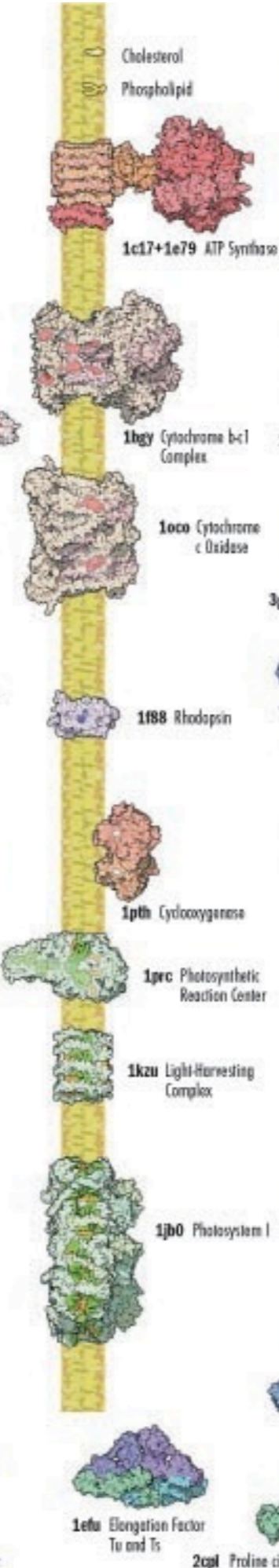
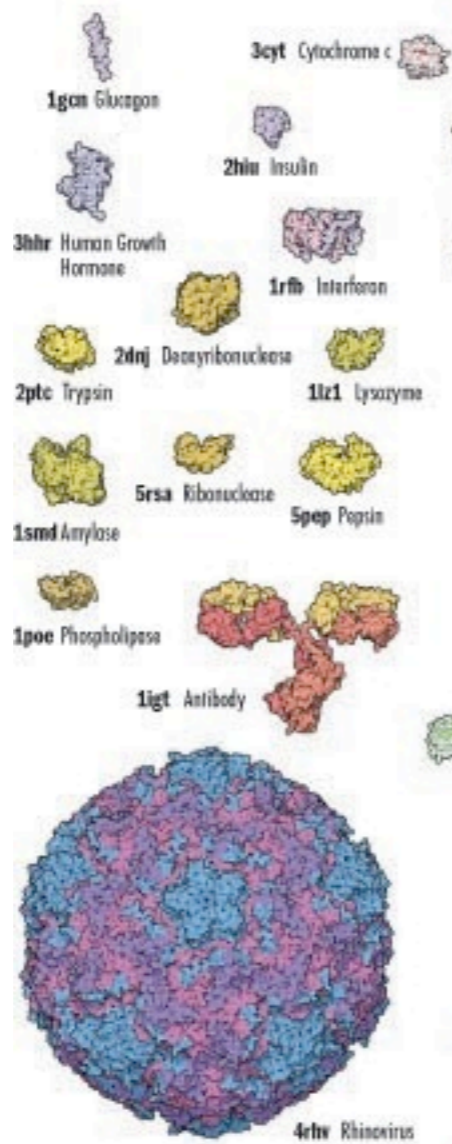


$\geq 10\mu\text{m}$

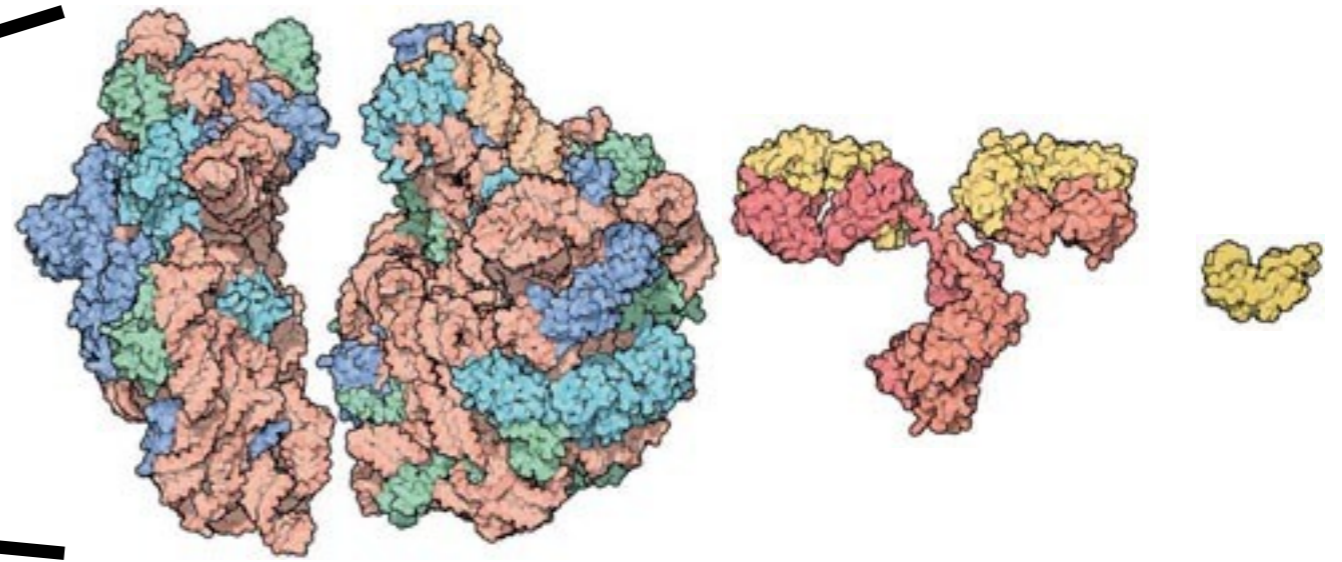
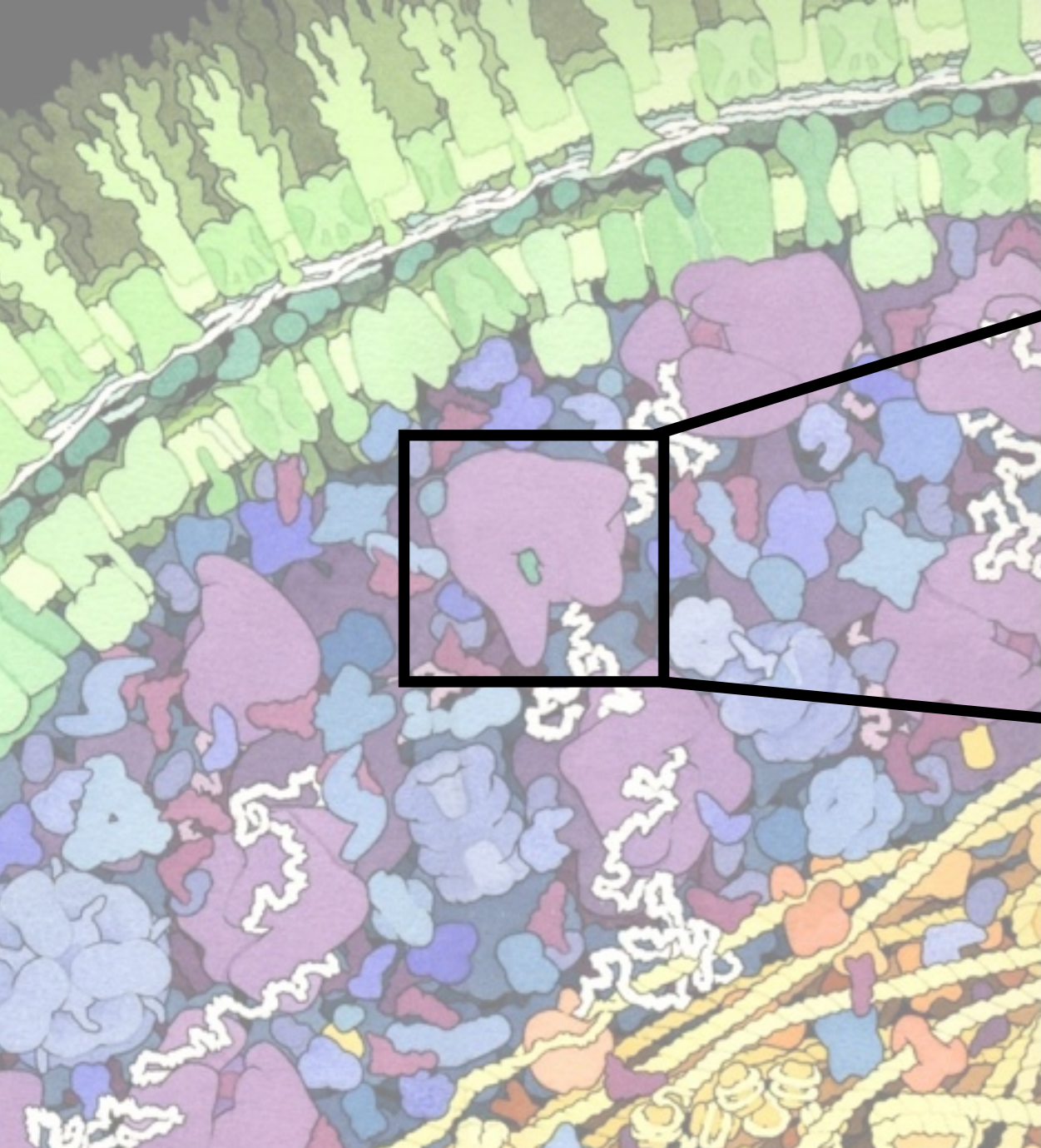


$\sim 1\mu\text{m}$

MOLECULAR MACHINERY: A Tour of the Protein Data Bank



PROTEIN DATA BANK
<http://www.pdb.org/> • info@rcsb.org
 RESEARCH COLLABORATORY FOR
 STRUCTURAL BIOINFORMATICS
 RUTGERS, THE STATE UNIVERSITY OF NEW JERSEY
 SAN DIEGO SUPERCOMPUTER CENTER
 NATIONAL INSTITUTE OF STANDARDS AND TECHNOLOGY

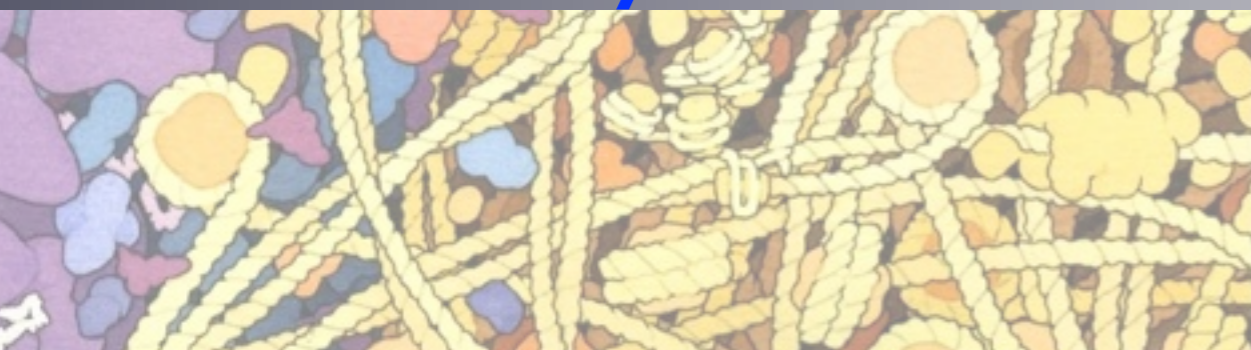


Crystallography

Single-particle EM

Tomography

Hybrid methods (Mike Schmid)



Why it's not easy to get to near-atomic resolution

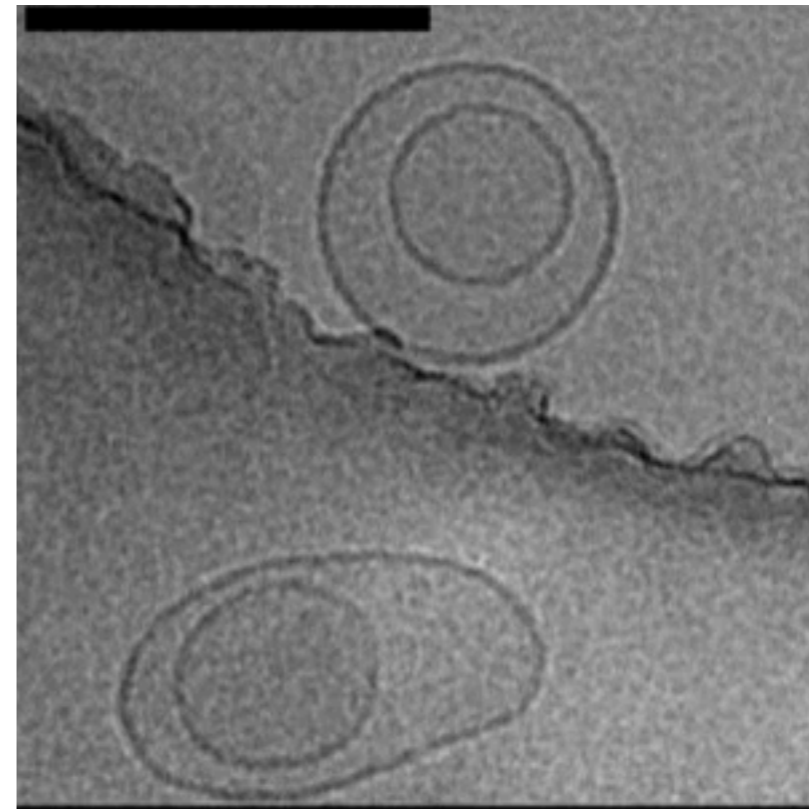
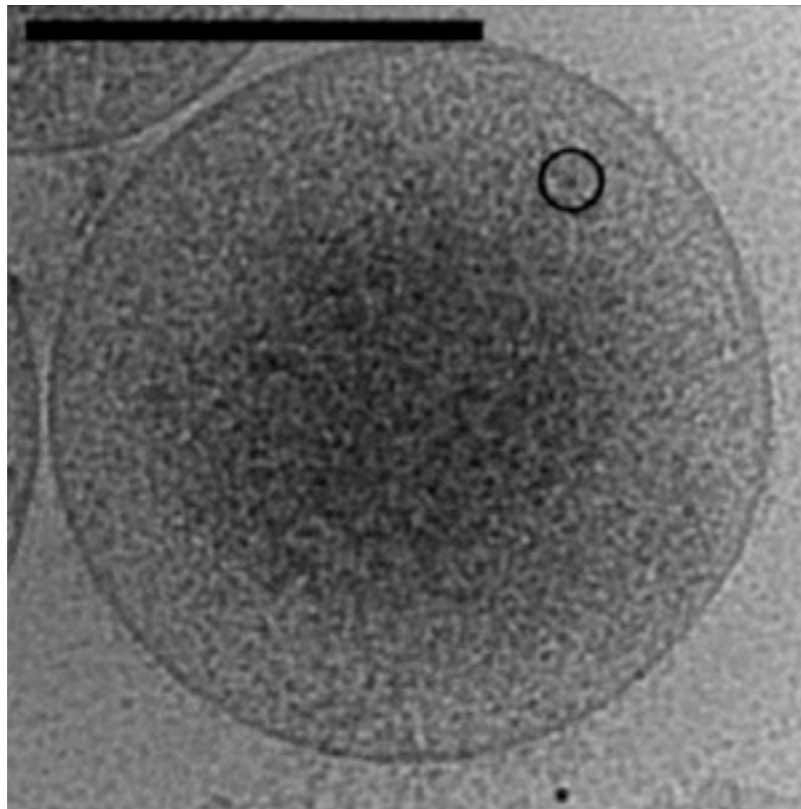
	Biological	Graphene	“Materials”
flux	10 pA/cm ²	1 A/cm ²	>> 10 pA/cm ²
dose	10 e ⁻ /Å ²	> 10 ¹⁷ e ⁻ /Å ²	>> 10 e ⁻ /Å ²

Why it's not easy to get to near-atomic resolution

	Biological	Graphene	“Materials”
atom	$Z < 8$	$Z = 6$	$Z > 8$
contrast	Phase	Phase	Amplitude
defocus	1 - 10 μm	$\sim 100\text{nm}$	$\ll 1\mu\text{m}$

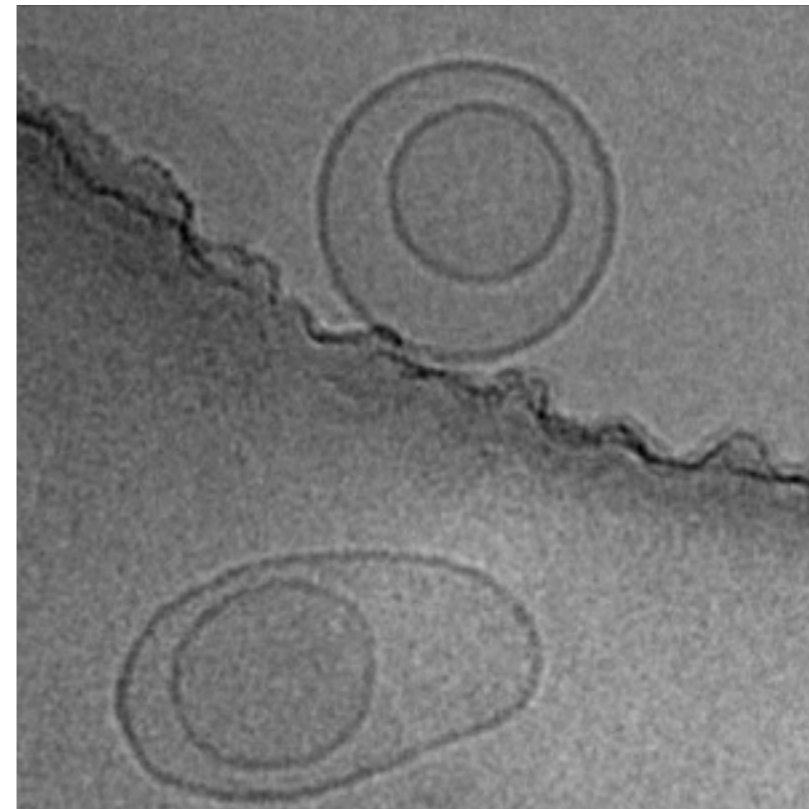
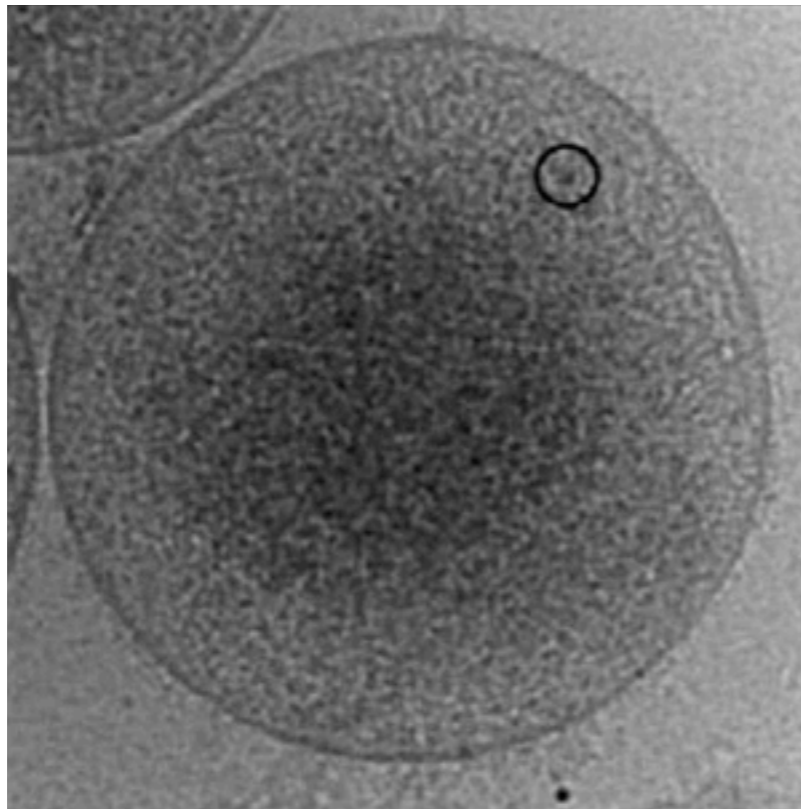
What does this mean for your sample?

$10 \text{ e}^-/\text{\AA}^2$



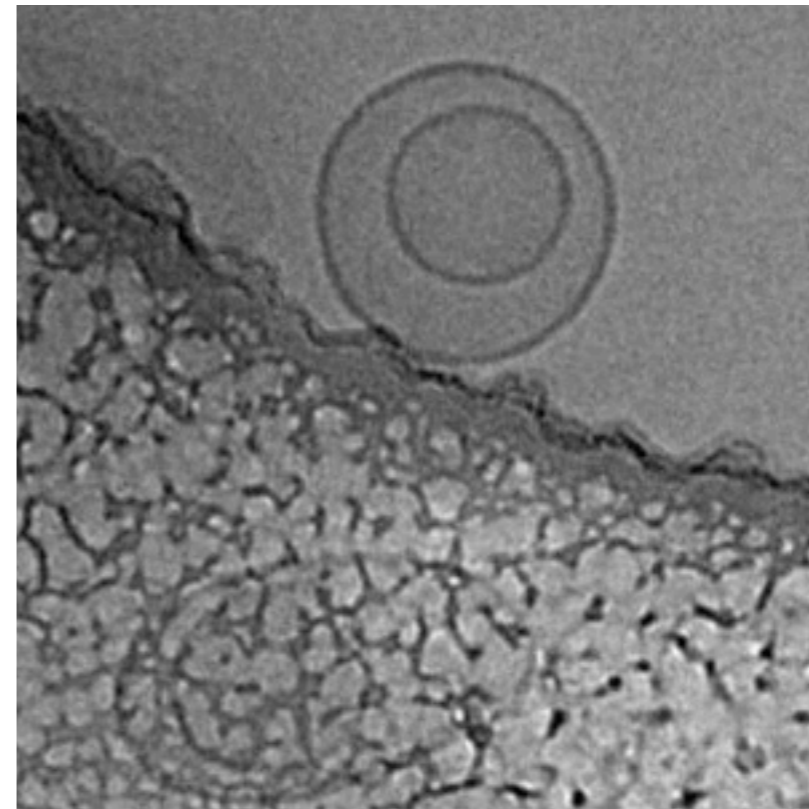
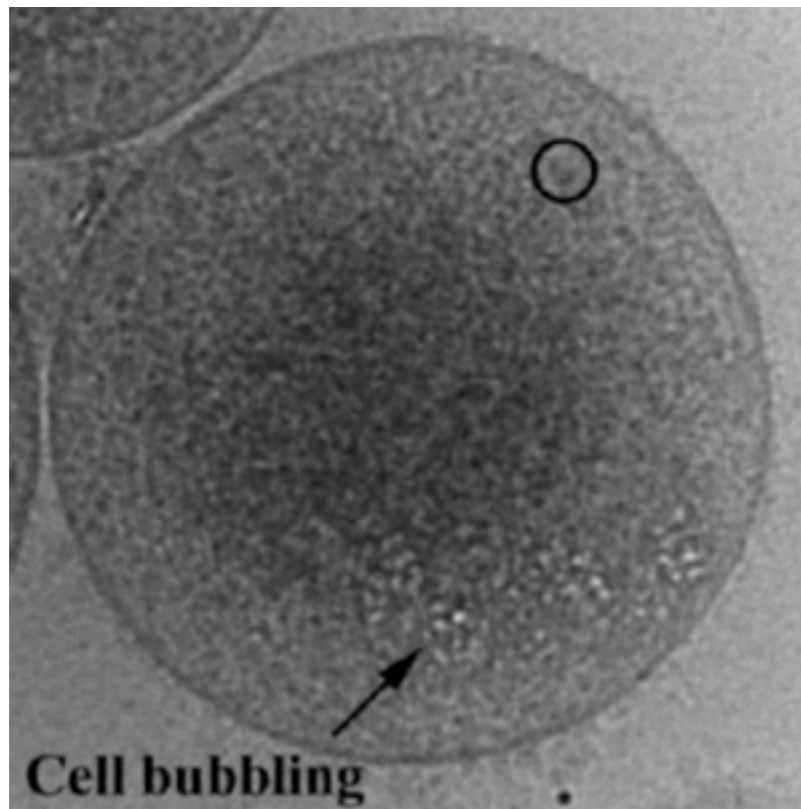
What does this mean for your sample?

40 e⁻/Å²



What does this mean for your sample?

140 e⁻/Å²



When starting with a new type of sample, do a dose series to find out the acceptable dose.

Single particle

Tomography

Sample	Protein complexes, viruses	viruses, small cells
max thickness	500 nm	500 nm
preparation	plunge freeze, neg. stain	plunge freeze, high- pressure freeze, embedding, sectioning (plastic + cryo)
fiducials (alignment)	n/a	colloidal gold

Single particle

Tomography

# of images	10 to 10,000	40 - 120
# of particles	1,000 to 1,000,000	ONE
dose / image	$\sim 20 \text{ e}^-/\text{\AA}^2$	$1 \text{ e}^-/\text{\AA}^2$
final product	“reconstruction” / density map	“tomogram” / density map

Single particle

Tomography

resolution

3.5 - 10 Å

40 - 80 Å

imaging /
reconstruction

1 - 100 days

0.5 - 2 hours

reconstruction

1 - 365 days

10 minutes *

recs / paper

1 - 10

10 - 100

Your time and TEM time are valuable resources. Plan your experiments carefully.

* Post-tomographic image processing can take weeks to months.

What quantities are measurable in a cell?

Quantity

Example

Distances

Diameter of an E.R. tubule

Volumes

Enlargement of lipid body

Counts

Envelope spikes on a virion

Positions

Distribution of ribosomes in stressed cells

If the structure is not resolvable, you must use subtomogram averaging (Mike Schmid's lecture).

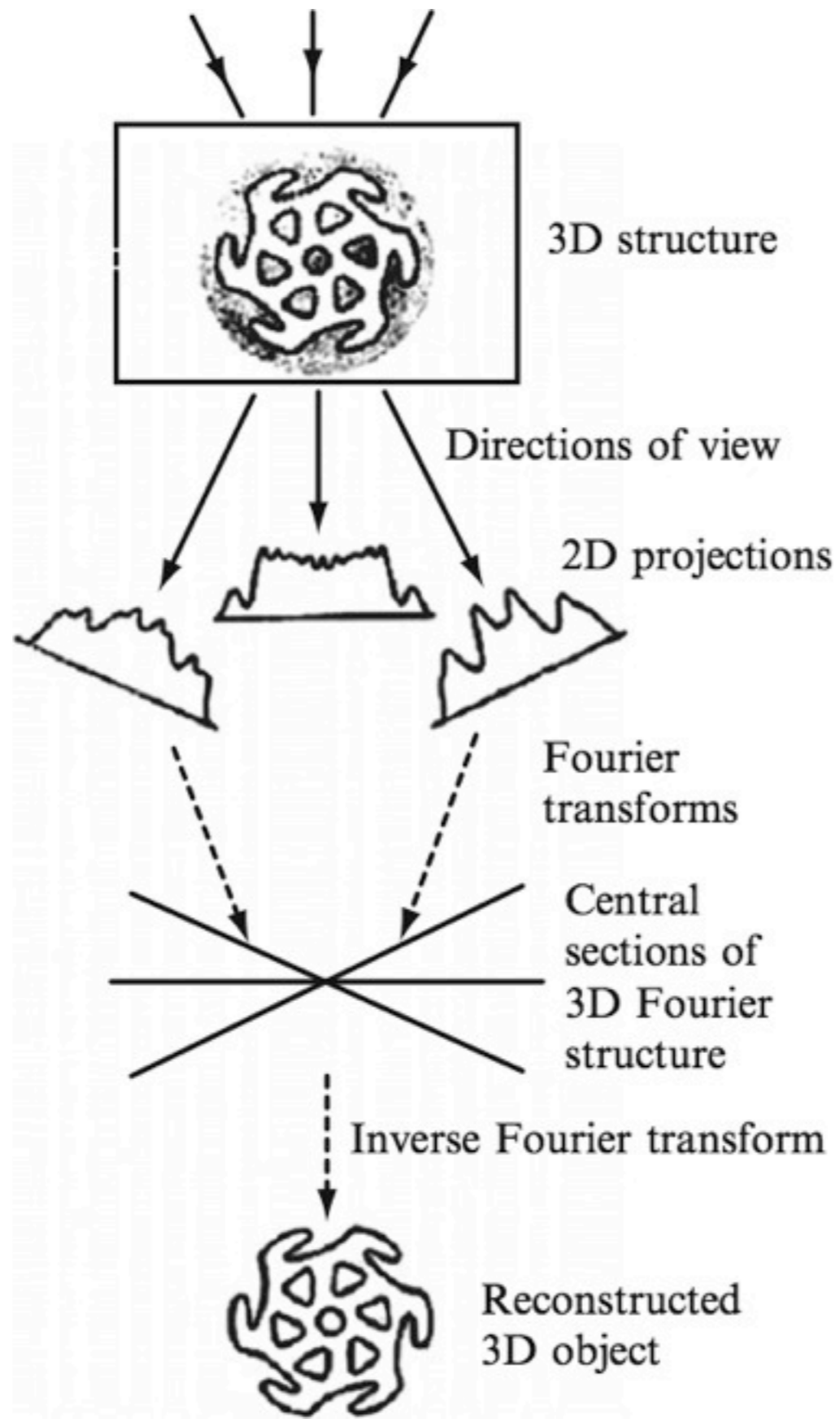
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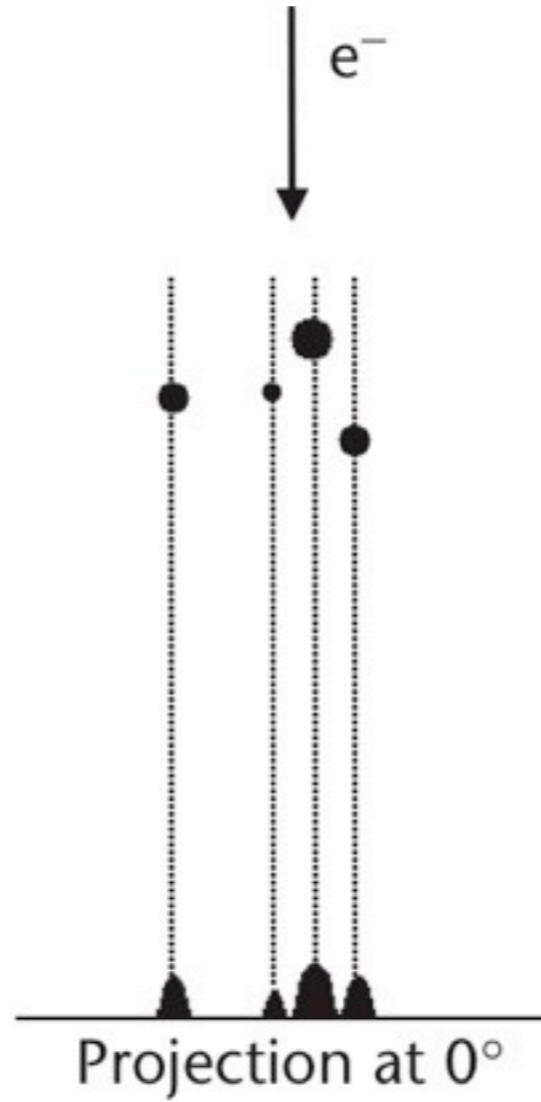
3. Principles of reconstruction

4. Beware of artifacts

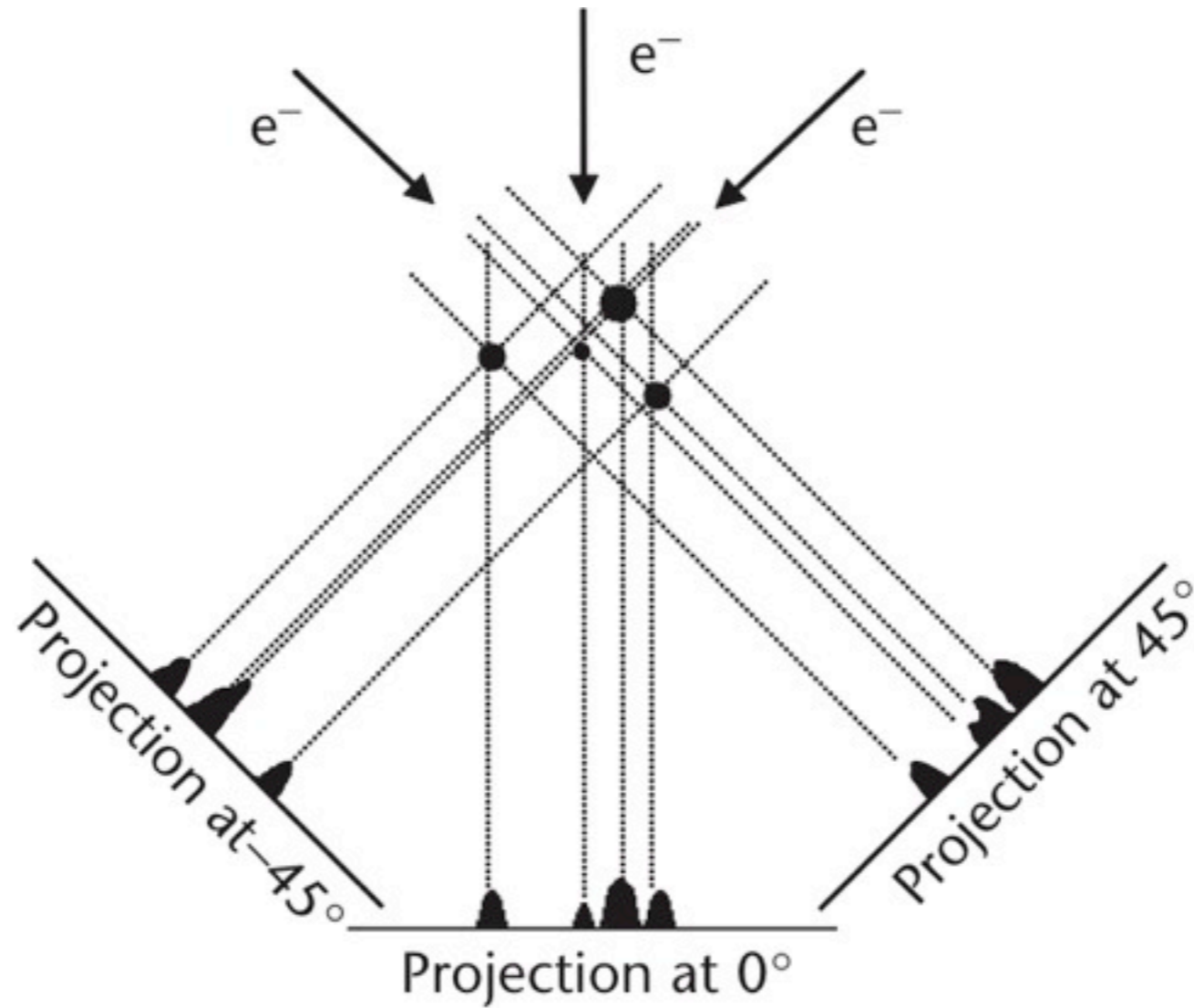
5. Example studies



A cryo-EM image is a “projection”



Tilt series: a set of projections from one object

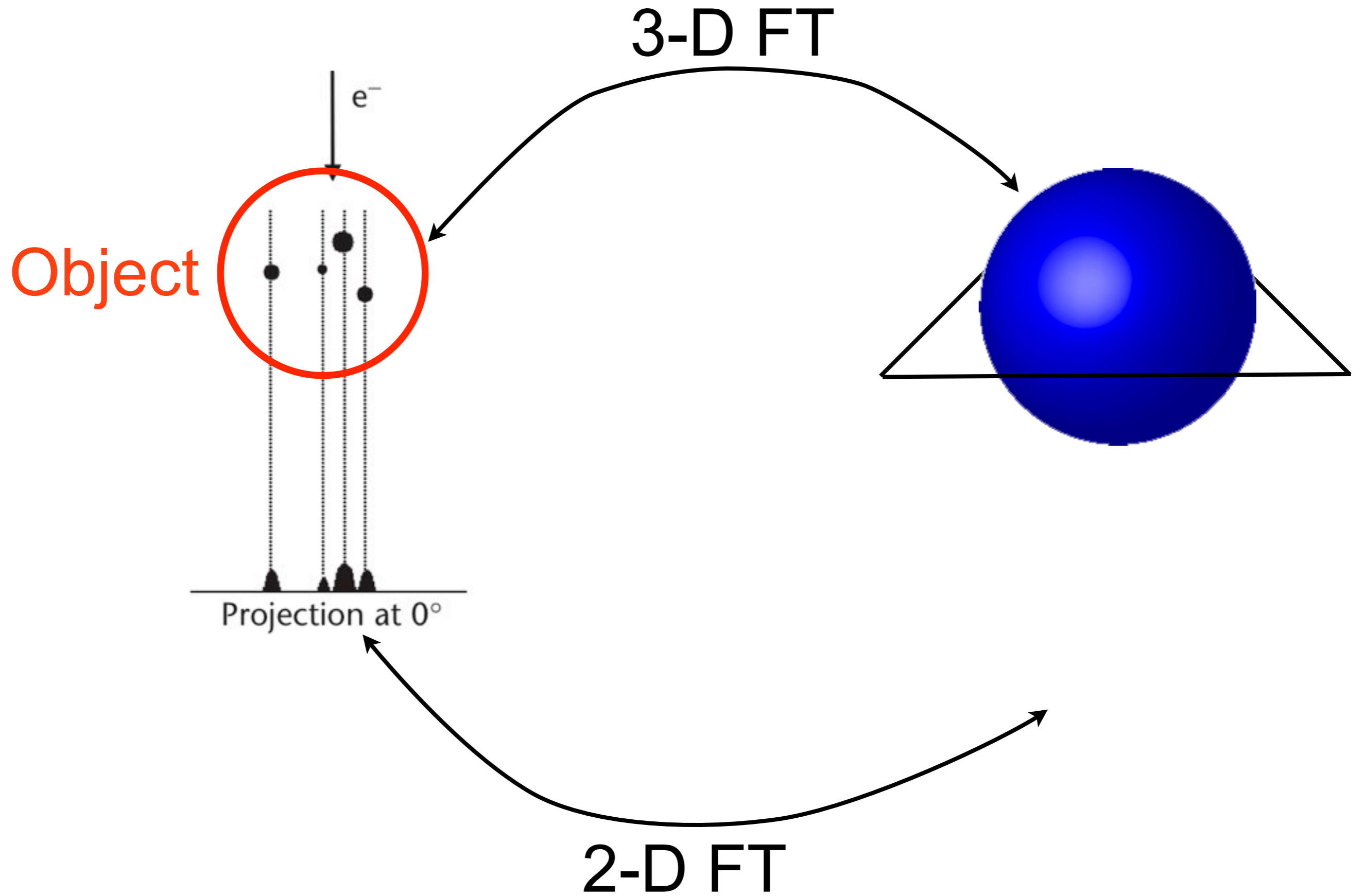


How can we understand (use) projections?

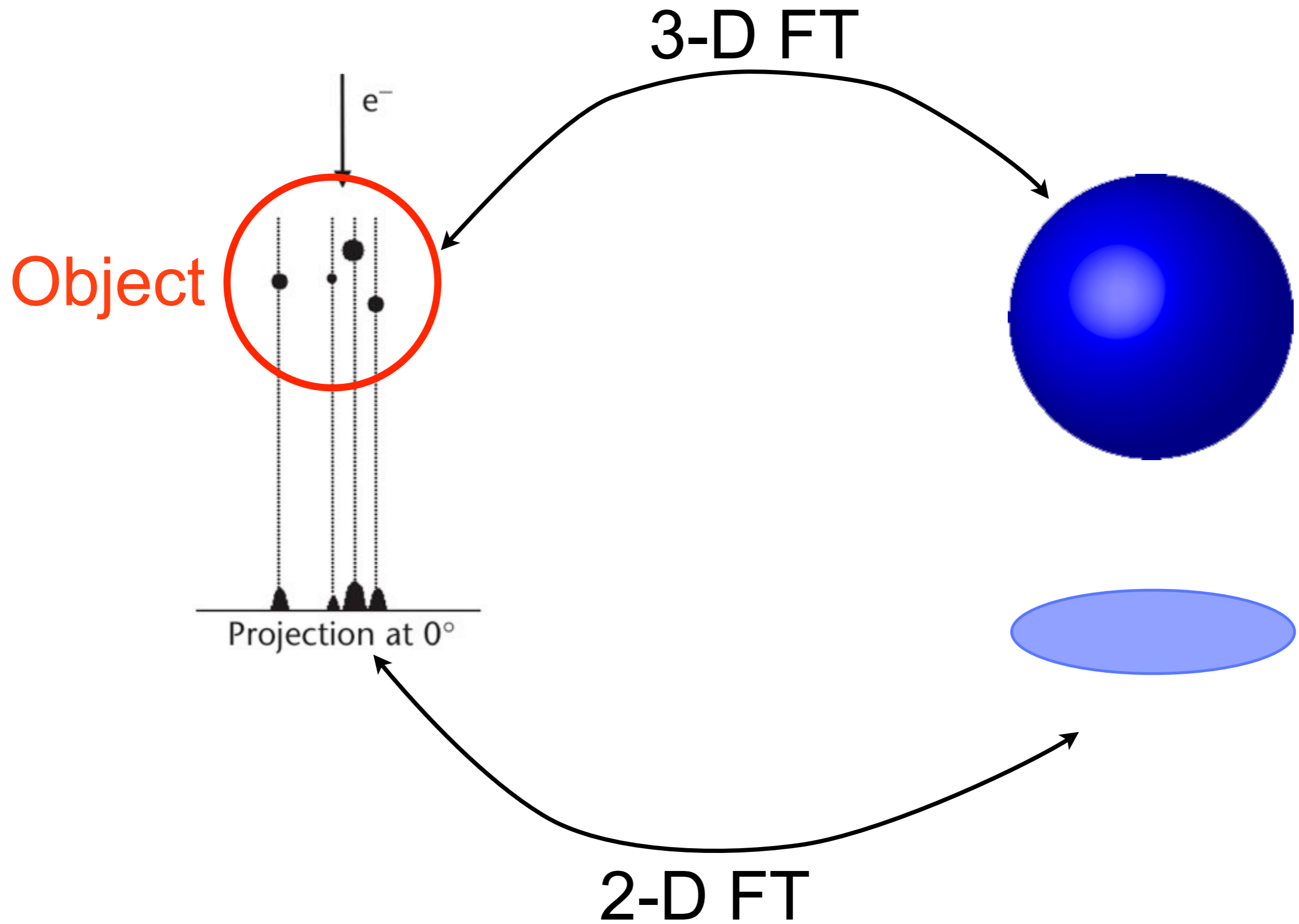
The projection theorem:

A projection (2-D) in real space corresponds to a central section (2-D) perpendicular to the projection direction in Fourier space (3-D).

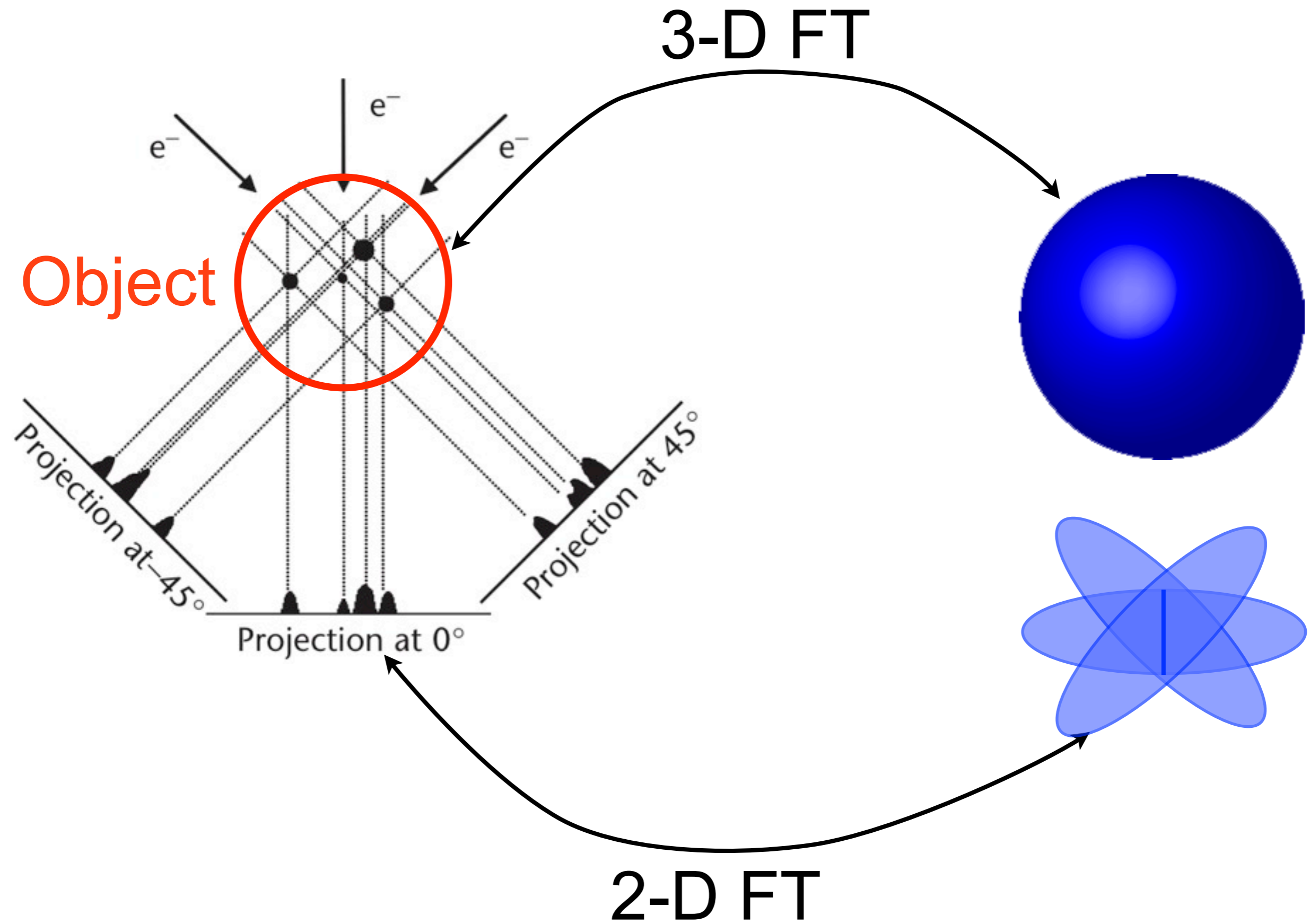
Tilt series: a set of projections from one object



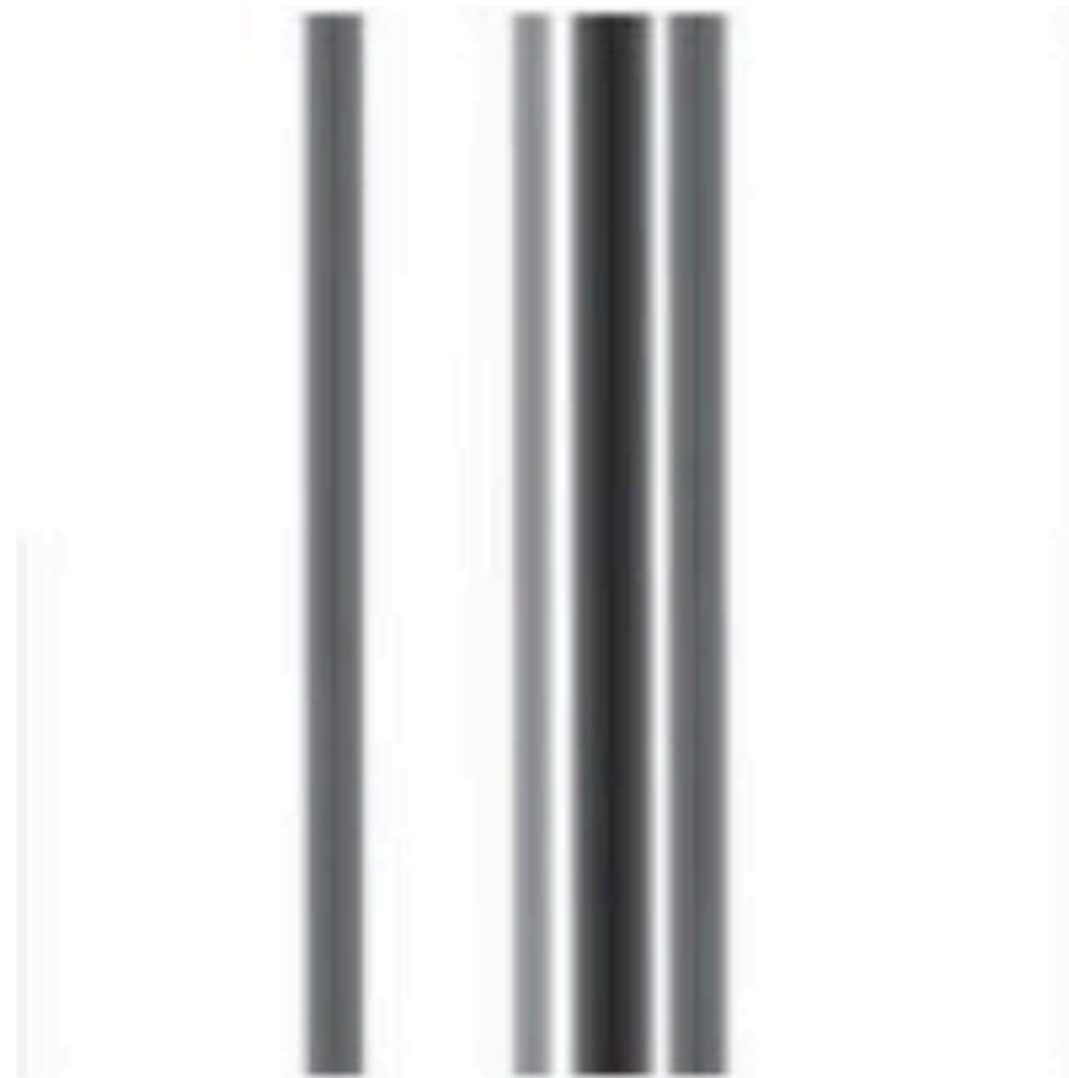
Tilt series: a set of projections from one object



Tilt series: a set of projections from one object



3-D image from 2-D images: back projection



1 Projection

How many images are needed?

The Crowther criterion:

$$m \sim \pi * D / d$$

m = number of images

D = diameter of object

d = resolution

How to use the Crowther criterion

A bacterial cell is ~ 500 nm thick

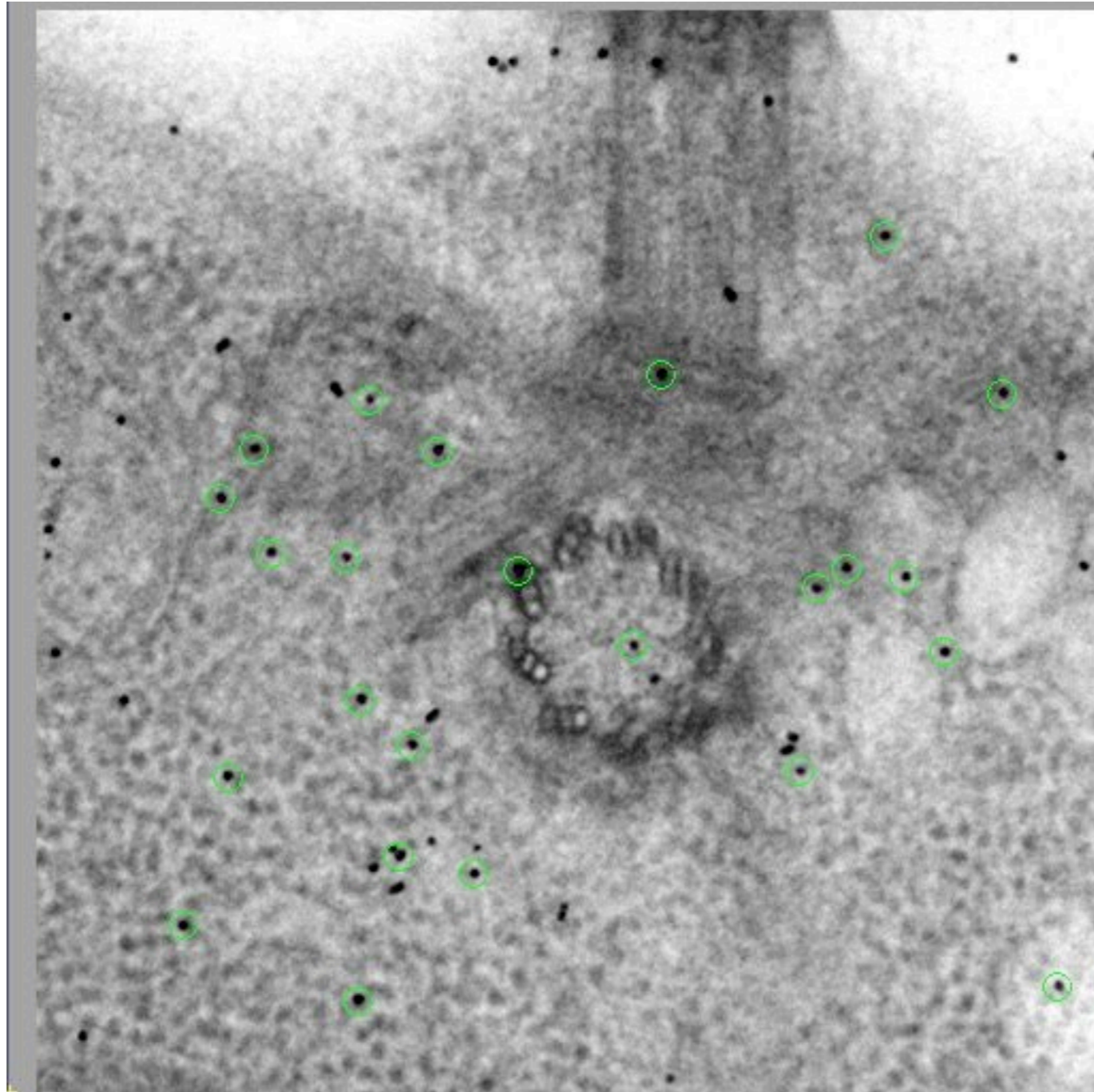
Desired (realistic resolution) ~ 10nm

m ~ 157 images, **distributed over 180°**

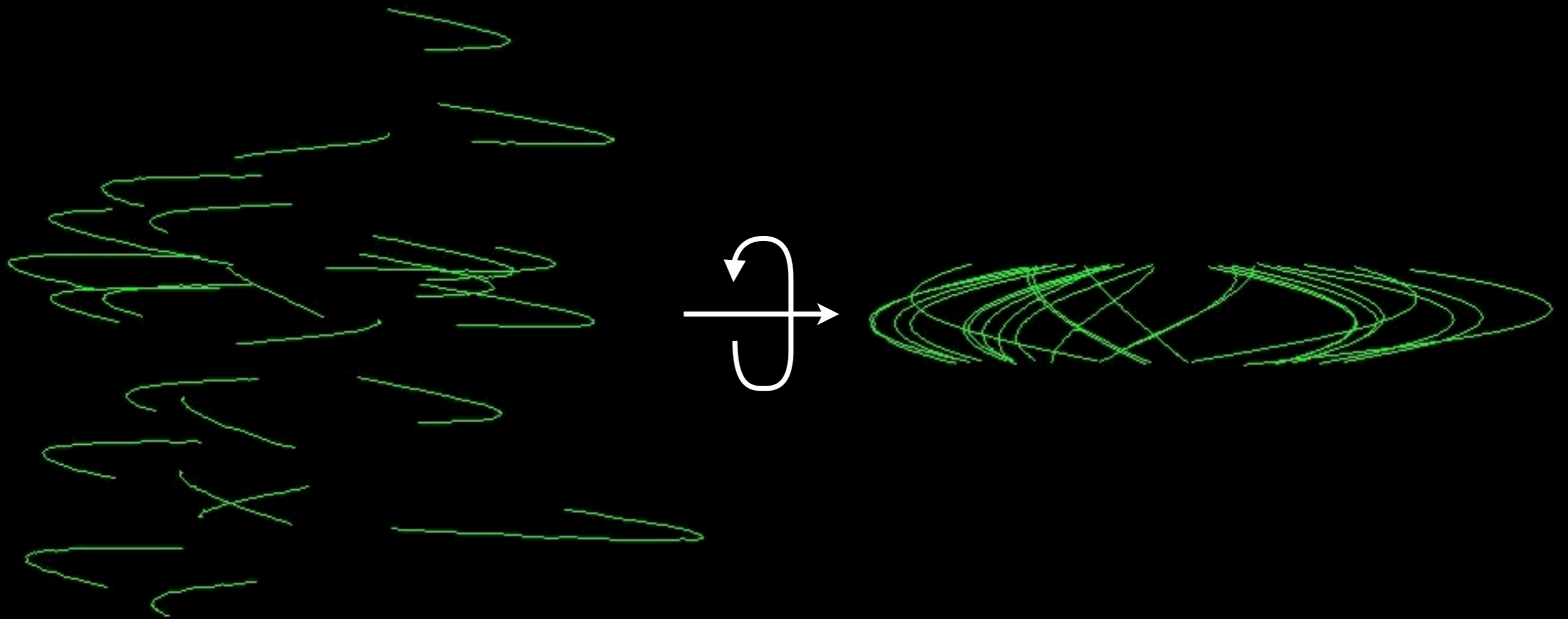
∴ the tilt *increment* should be ~ 0.9°

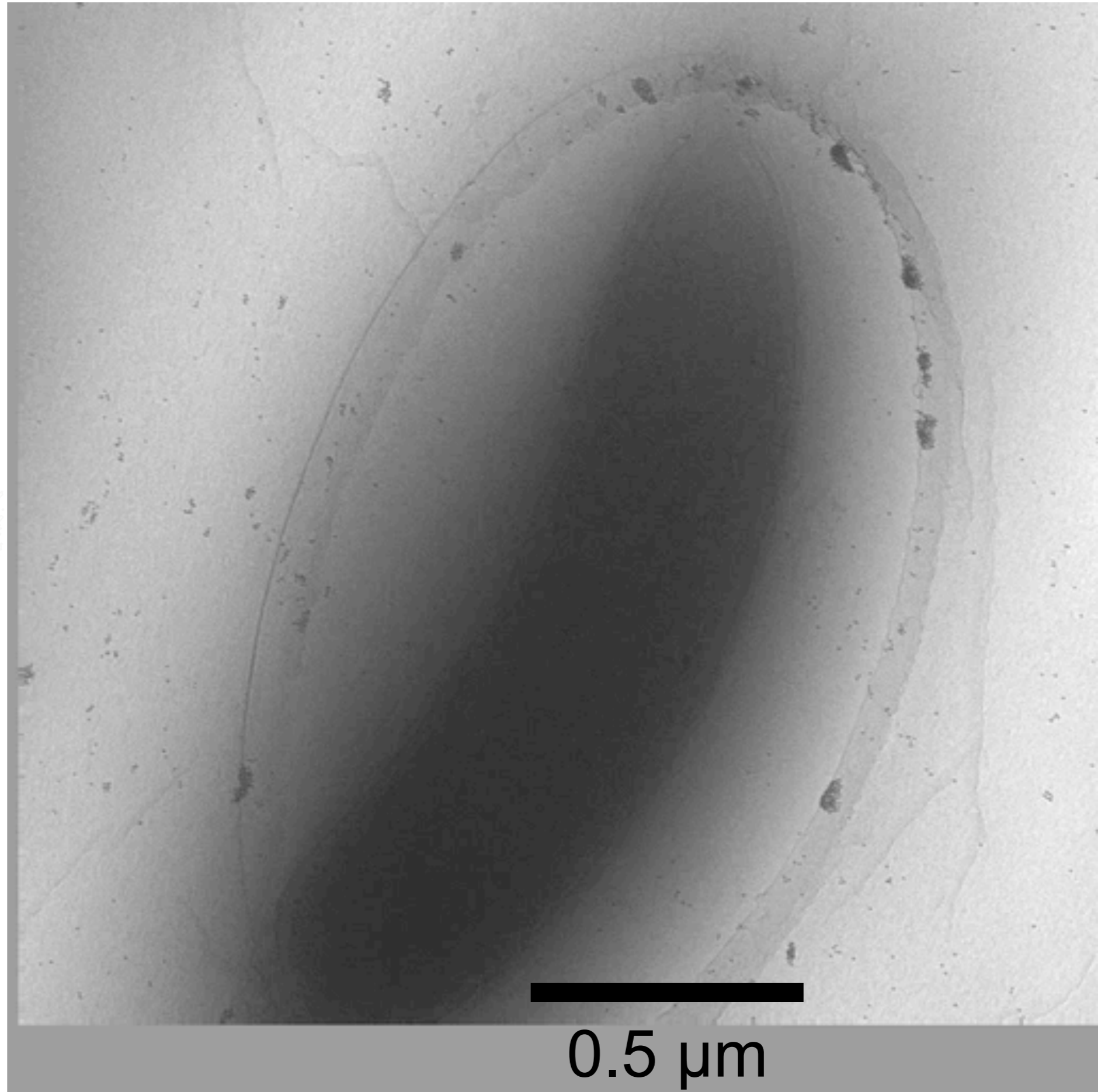
In practice, microscopists don't follow this rule exactly. They determine imaging parameters empirically for each sample.

Image alignment is assisted using gold fiducials



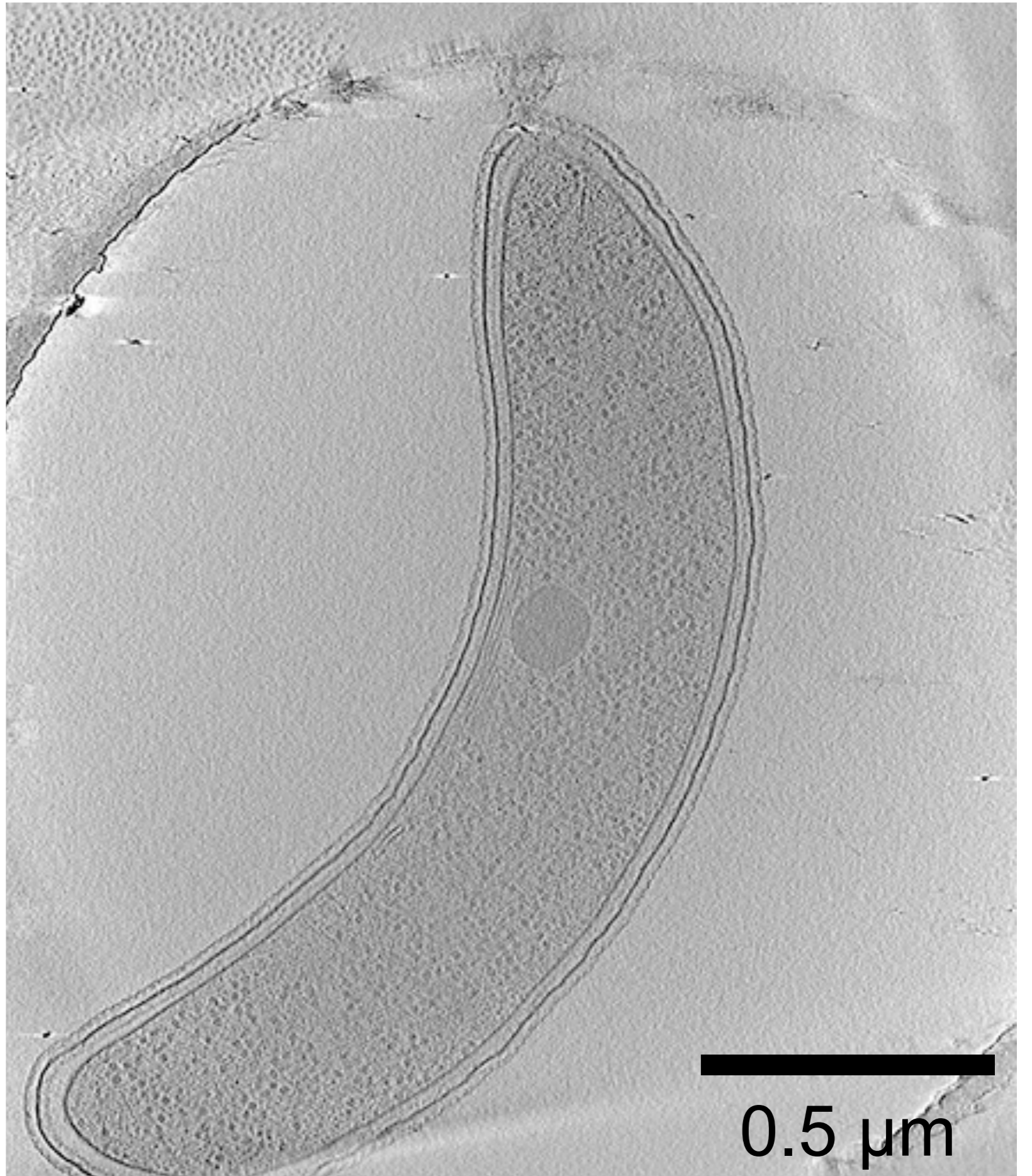
Aligned fiducials have a smooth “trajectory”





Briegel, 2006

Tuesday, July 10, 12



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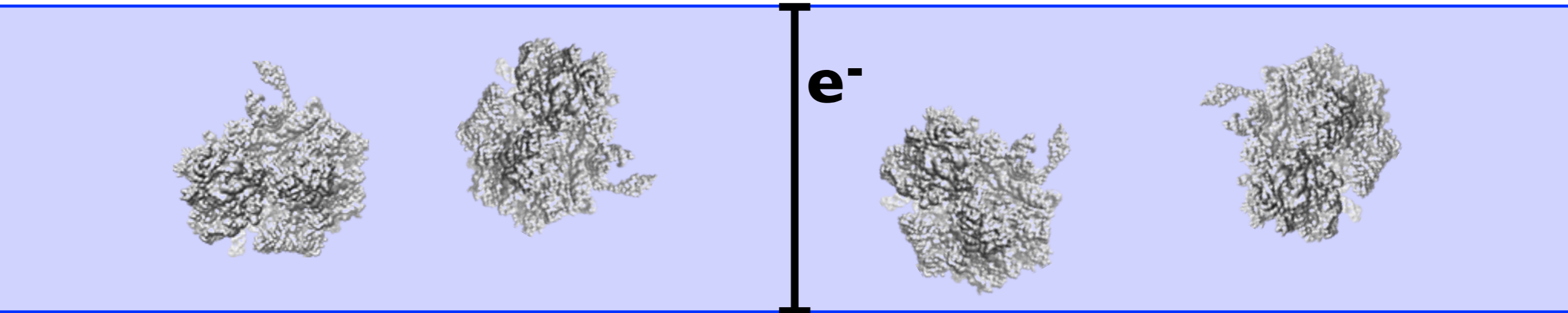
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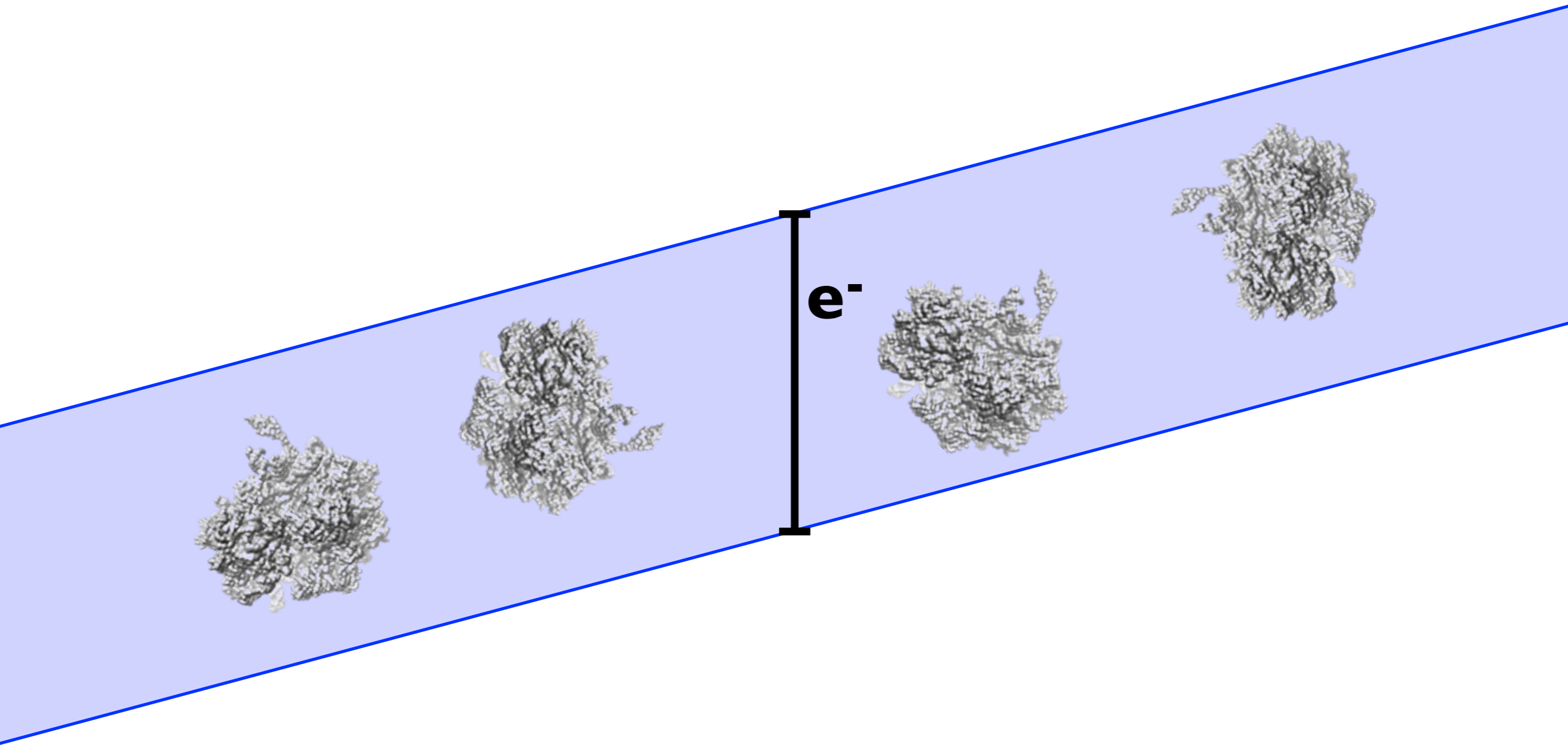
5. Example studies

0°

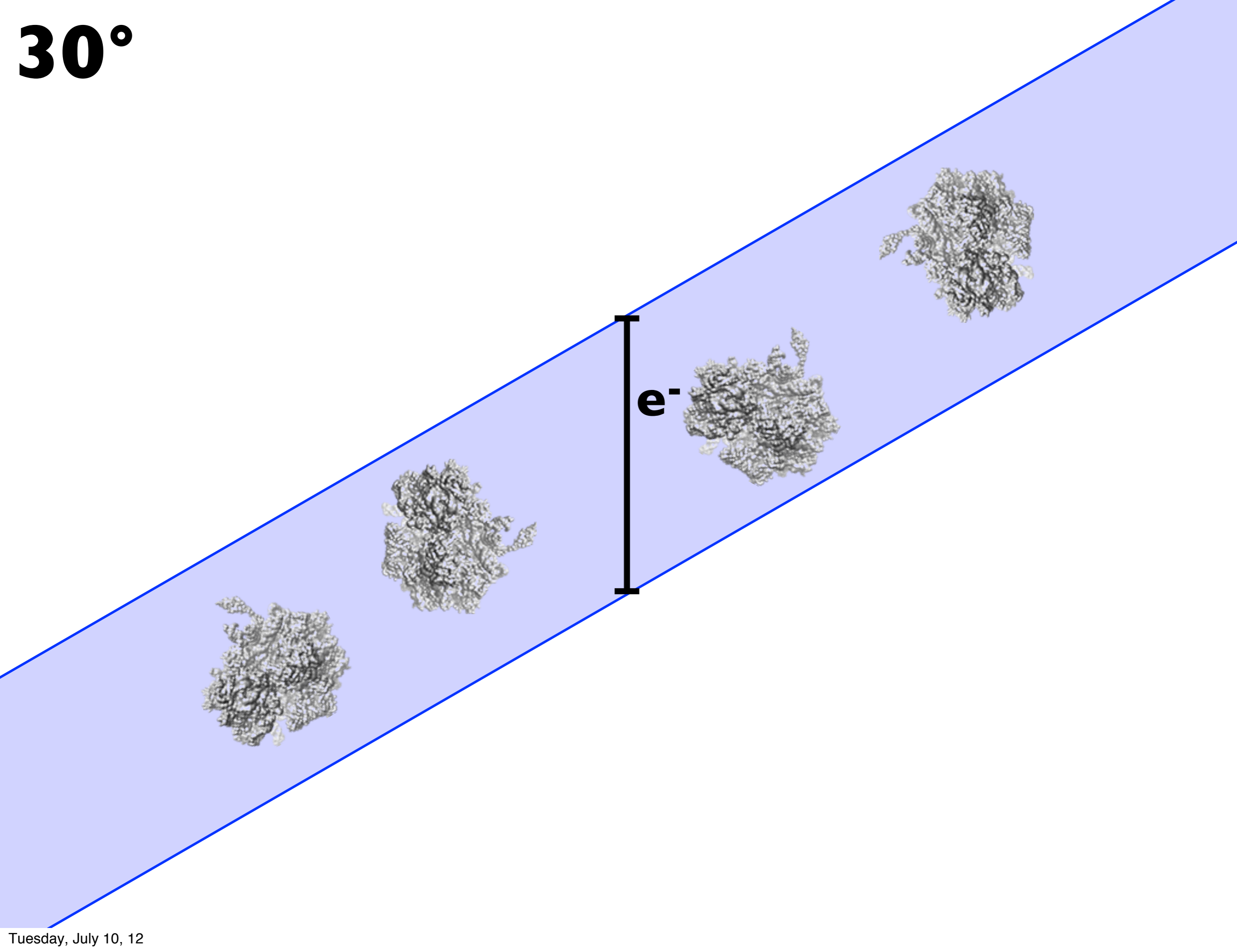
cryo-ET: missing wedge



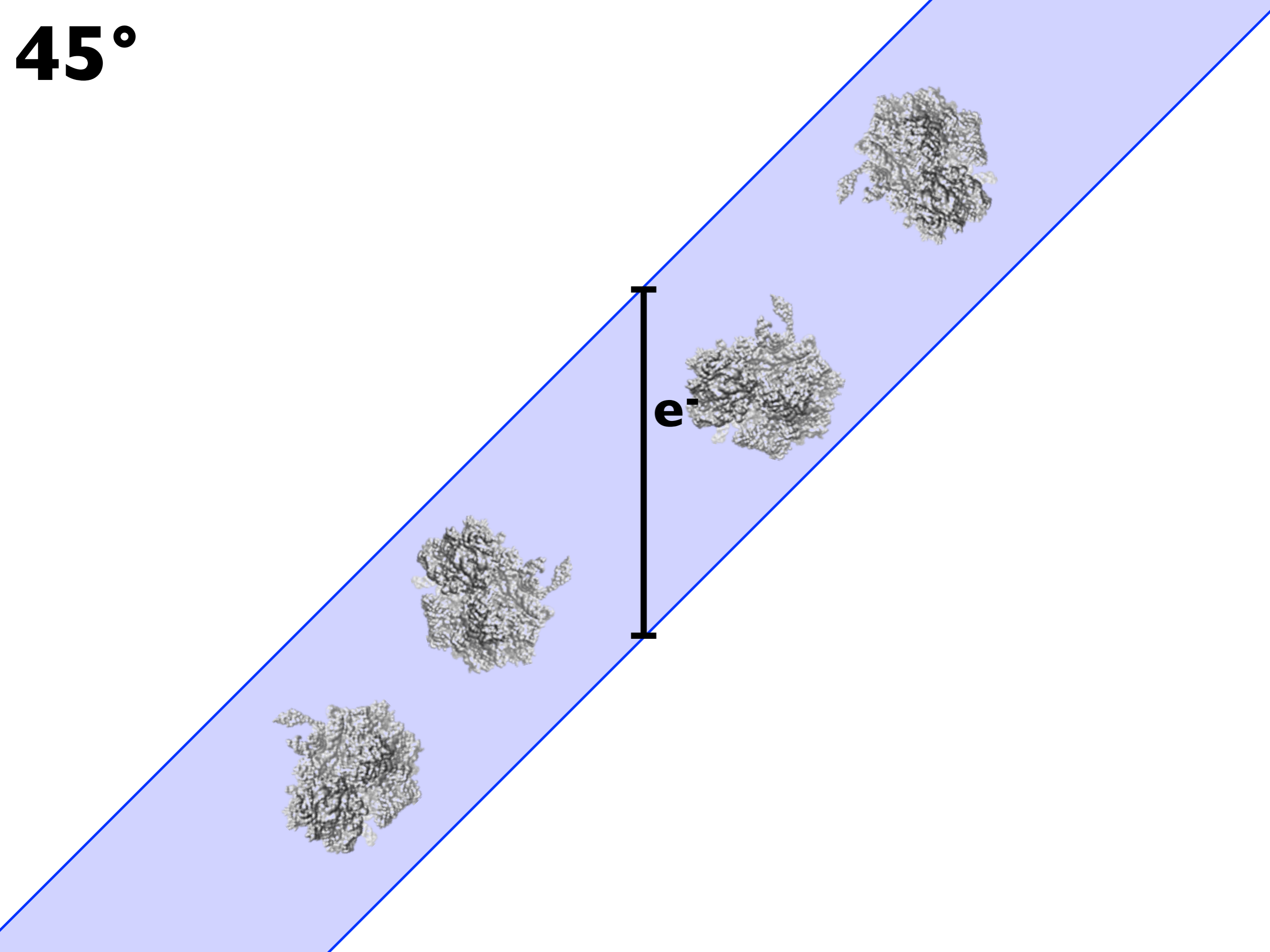
15°



30°

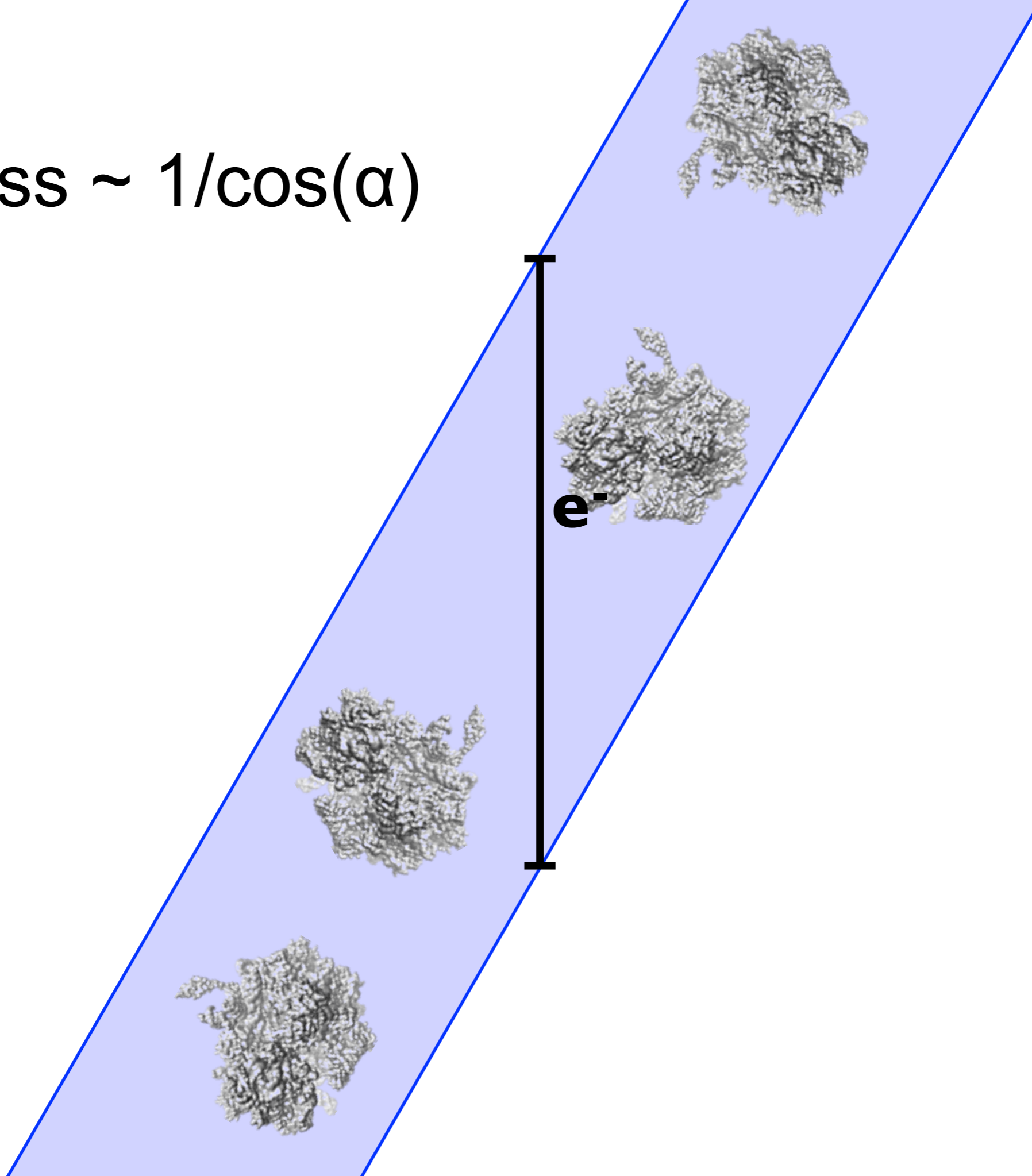


45°

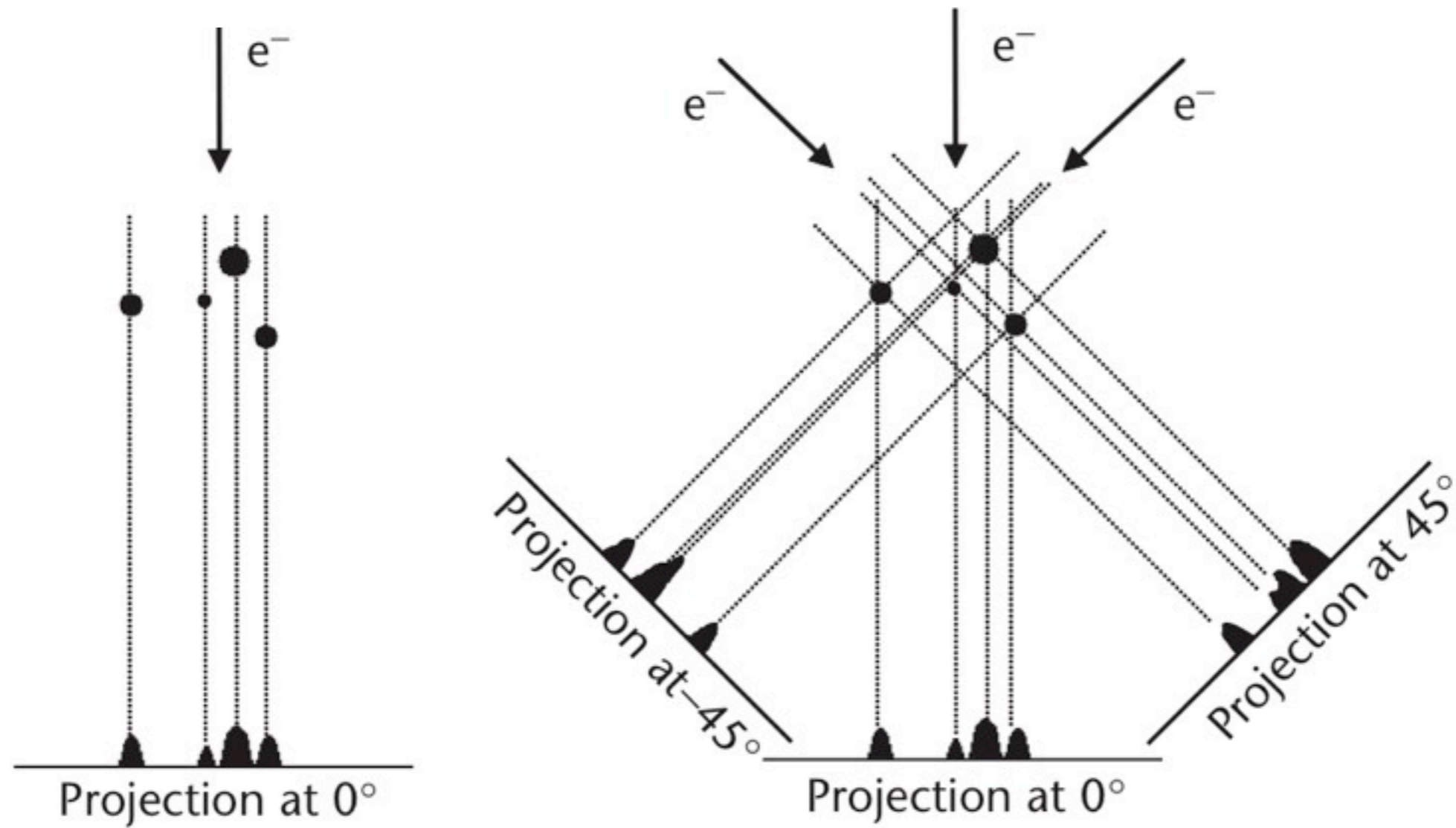


60°

thickness $\sim 1/\cos(\alpha)$



cryo-ET: missing wedge



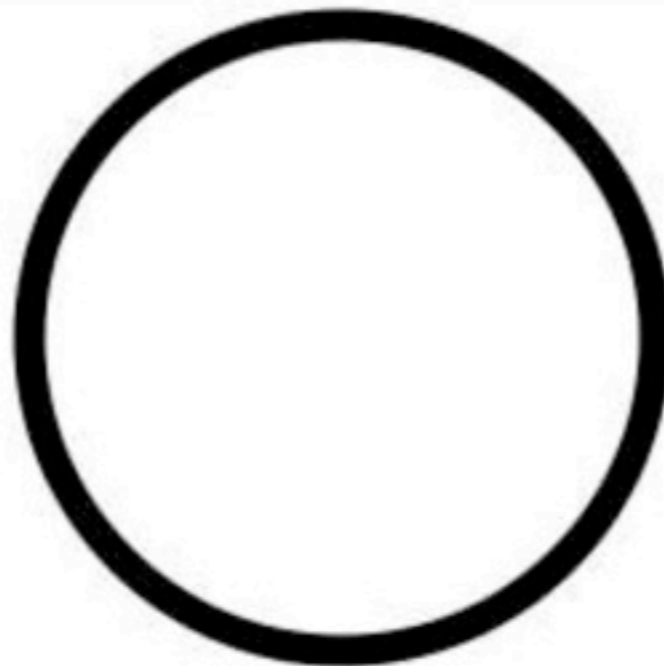
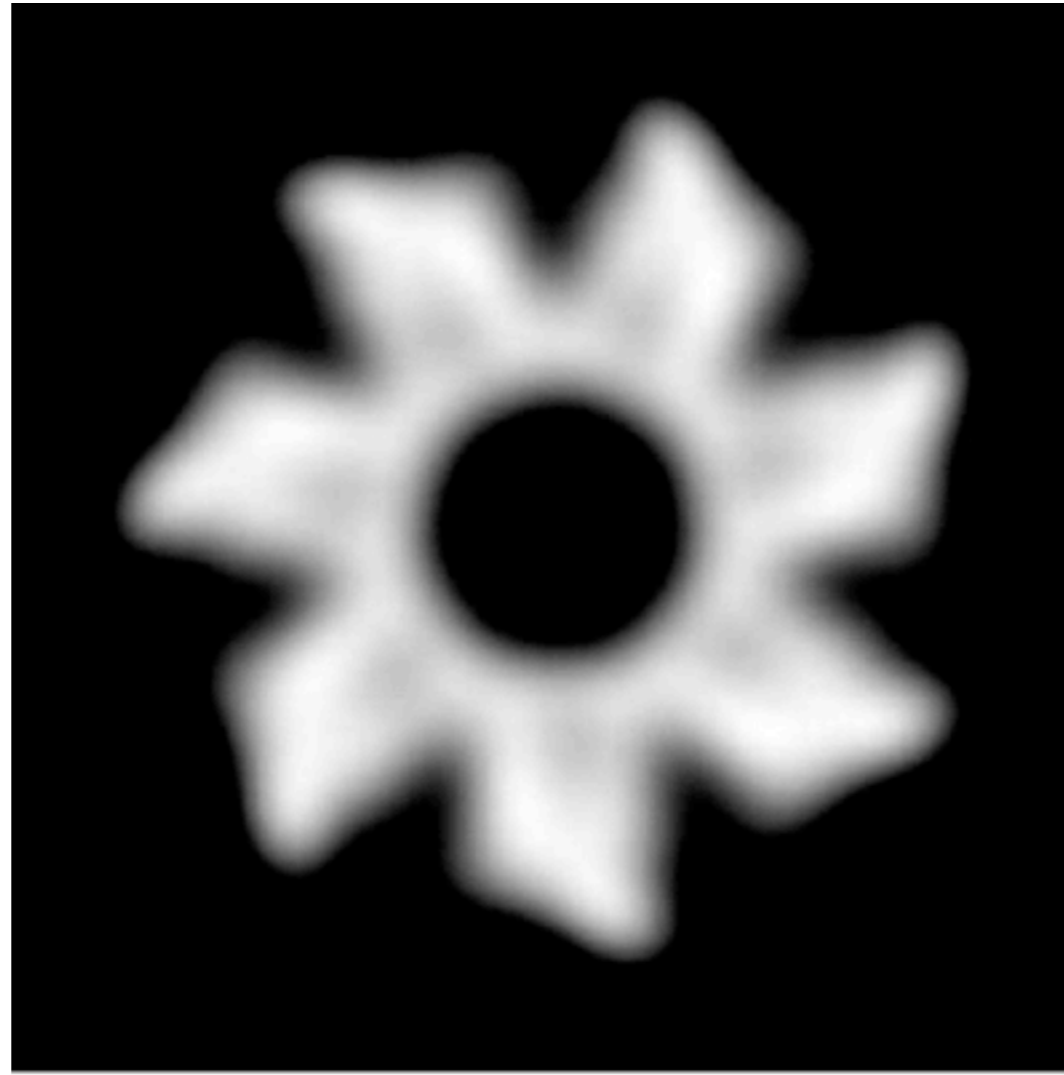
cryo-ET: missing wedge in reciprocal space



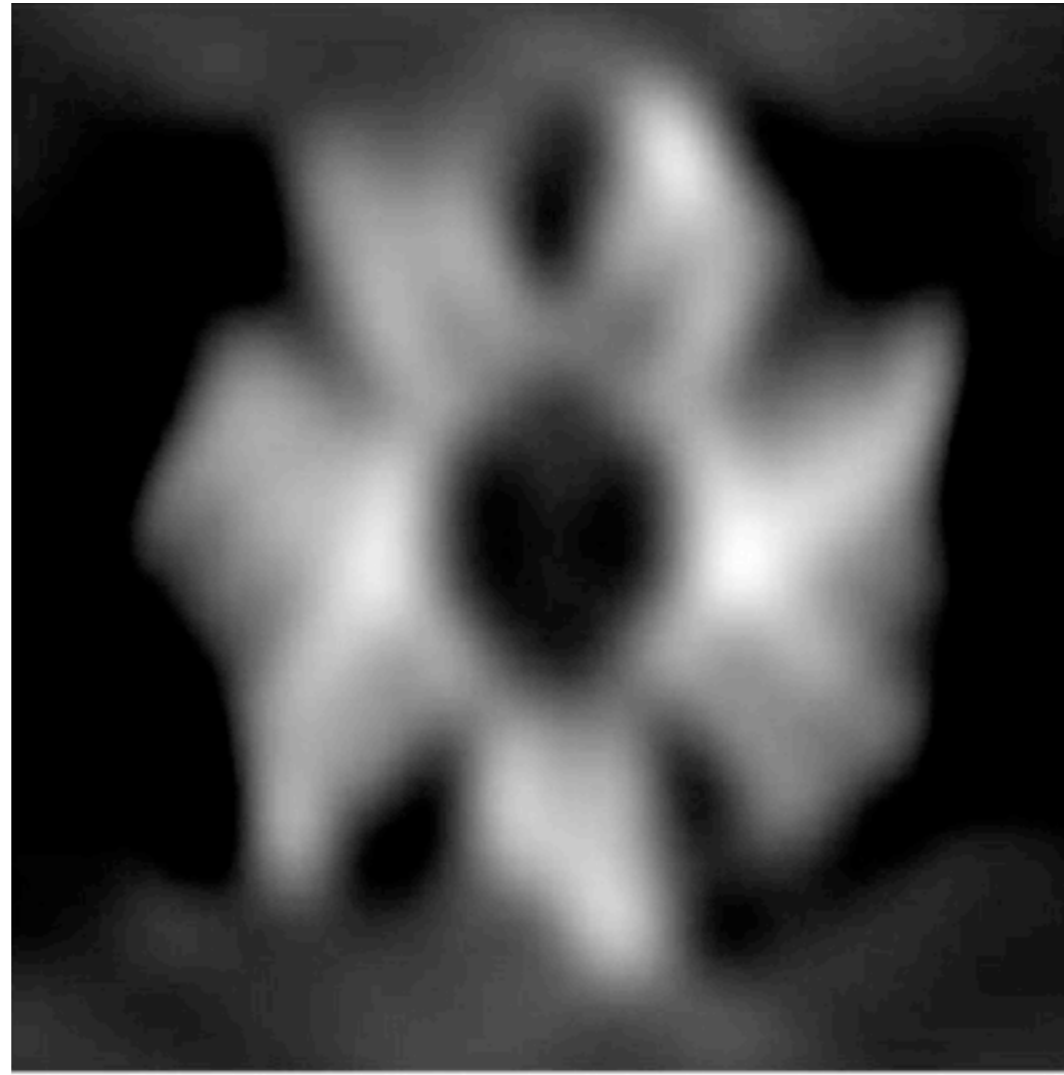
Angular range
[-50° , $+50^\circ$]



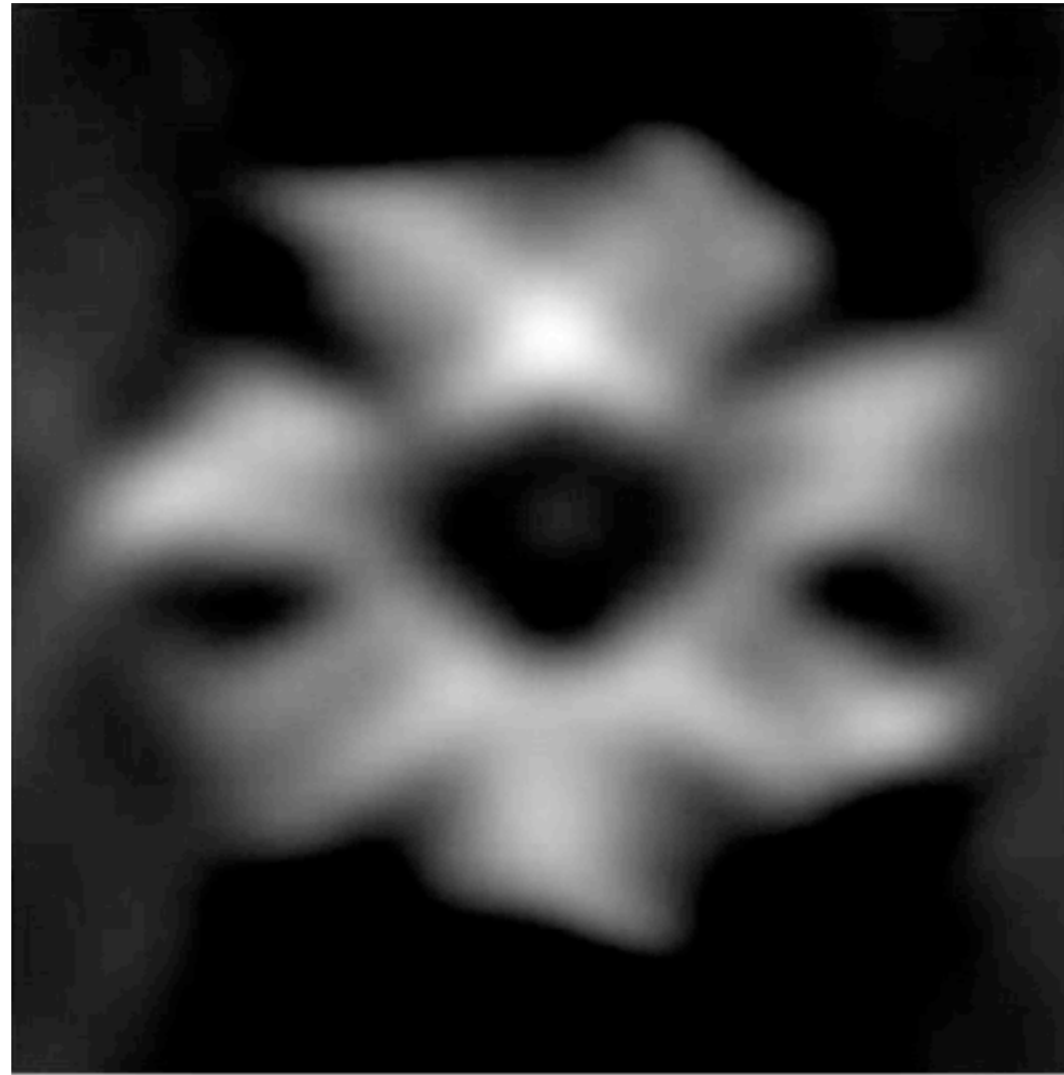
Cryo-ET: missing wedge effect in real space



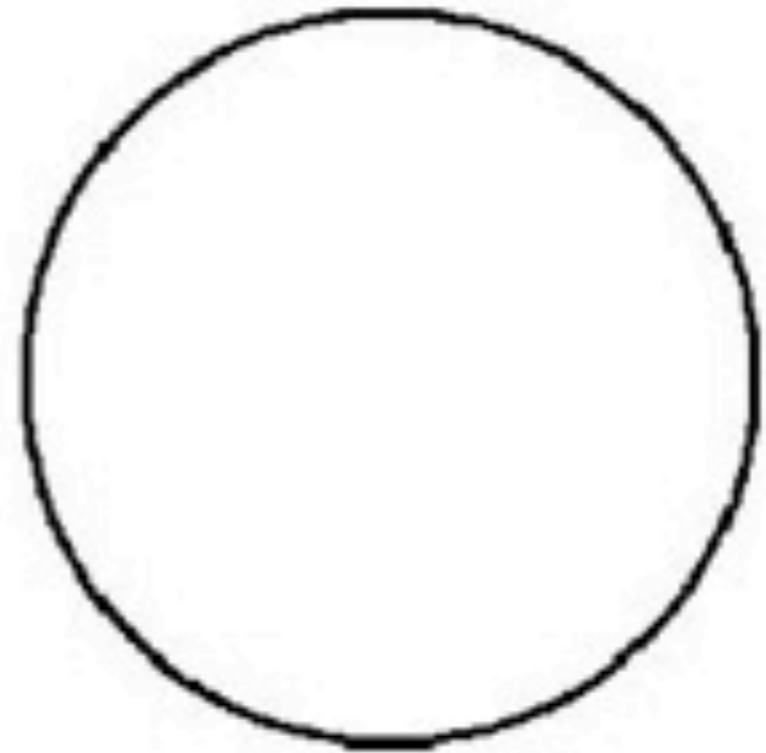
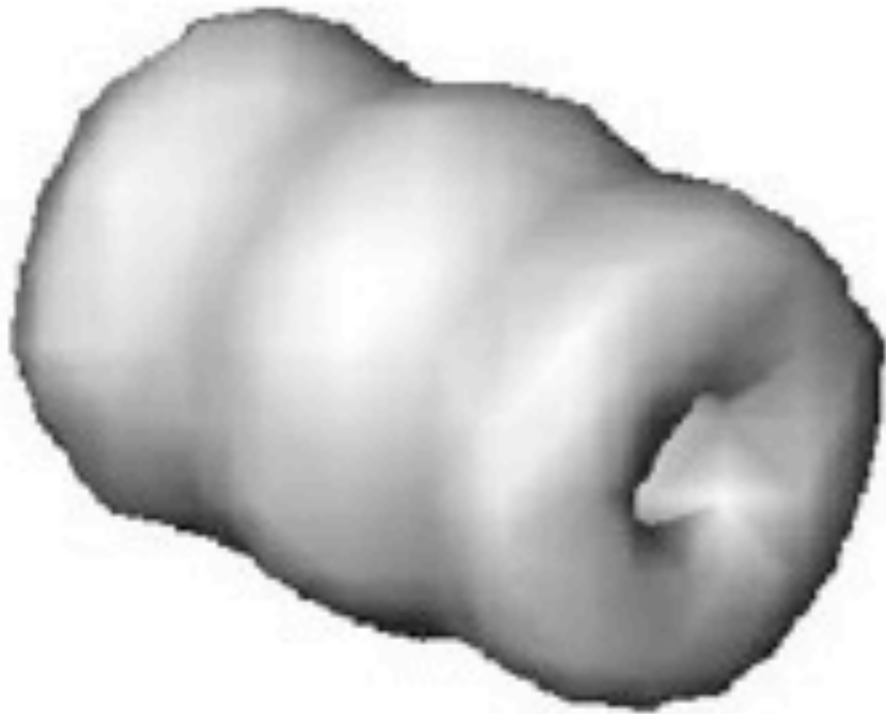
Cryo-ET: missing wedge effect in real space



Cryo-ET: missing wedge effect in real space



Cryo-ET: missing wedge effect in real space



Cryo-ET: missing wedge effect in real space



The contrast transfer function

$$\text{CTF}(s; \Delta f) \approx \sin(\gamma(s; \Delta f))$$


Phase perturbation function:

$$\gamma(s; \Delta f) = 2\pi(-\frac{1}{2} \Delta f \lambda s^2 + \frac{1}{4} C_s \lambda^3 s^4)$$

A = % amplitude contrast

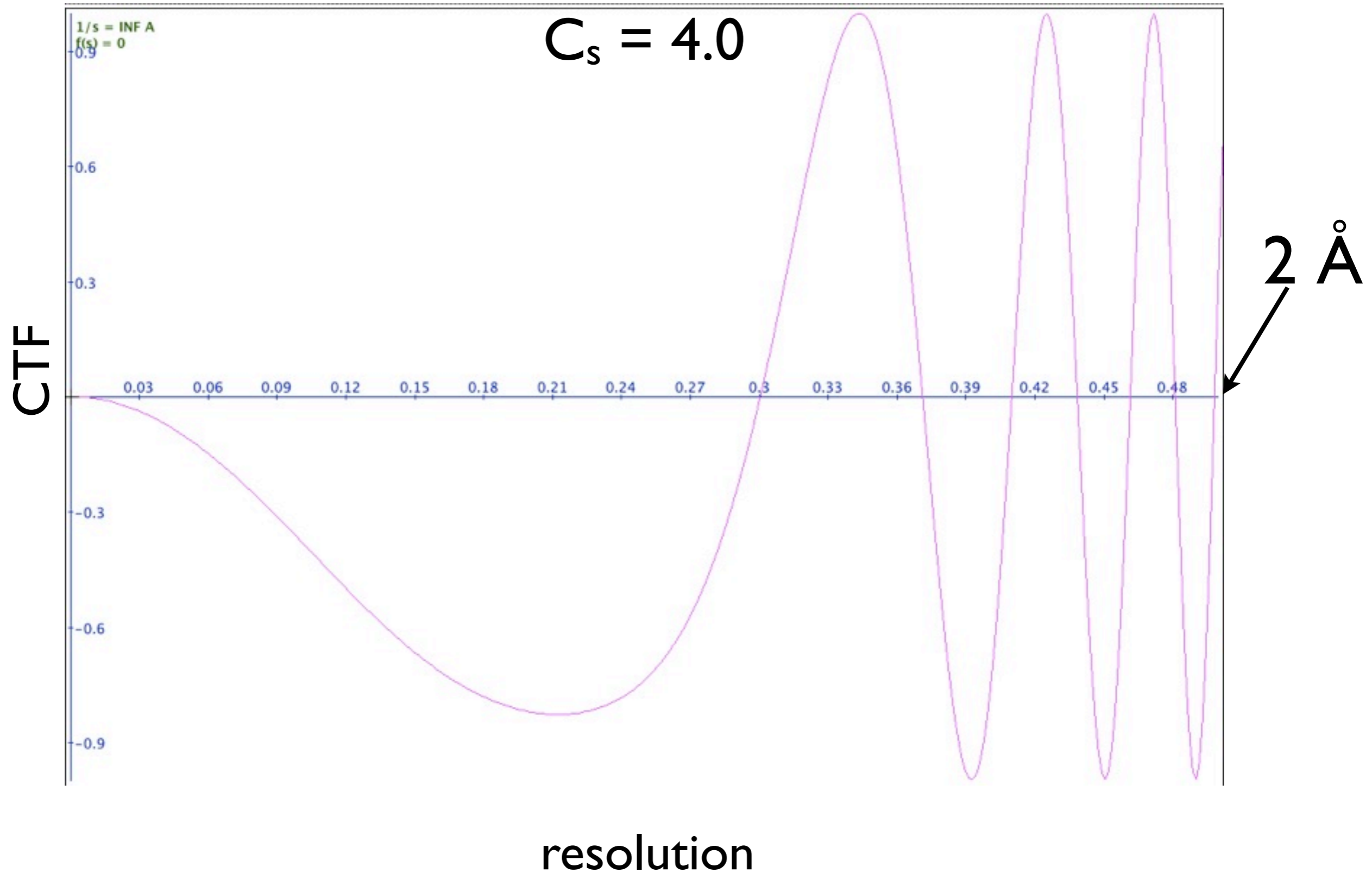
Δf = underfocus

λ = electron wavelength

C_s = sph. aberr. coefficient

s = spatial frequency (resolution)

cryo-ET: underfocus matters



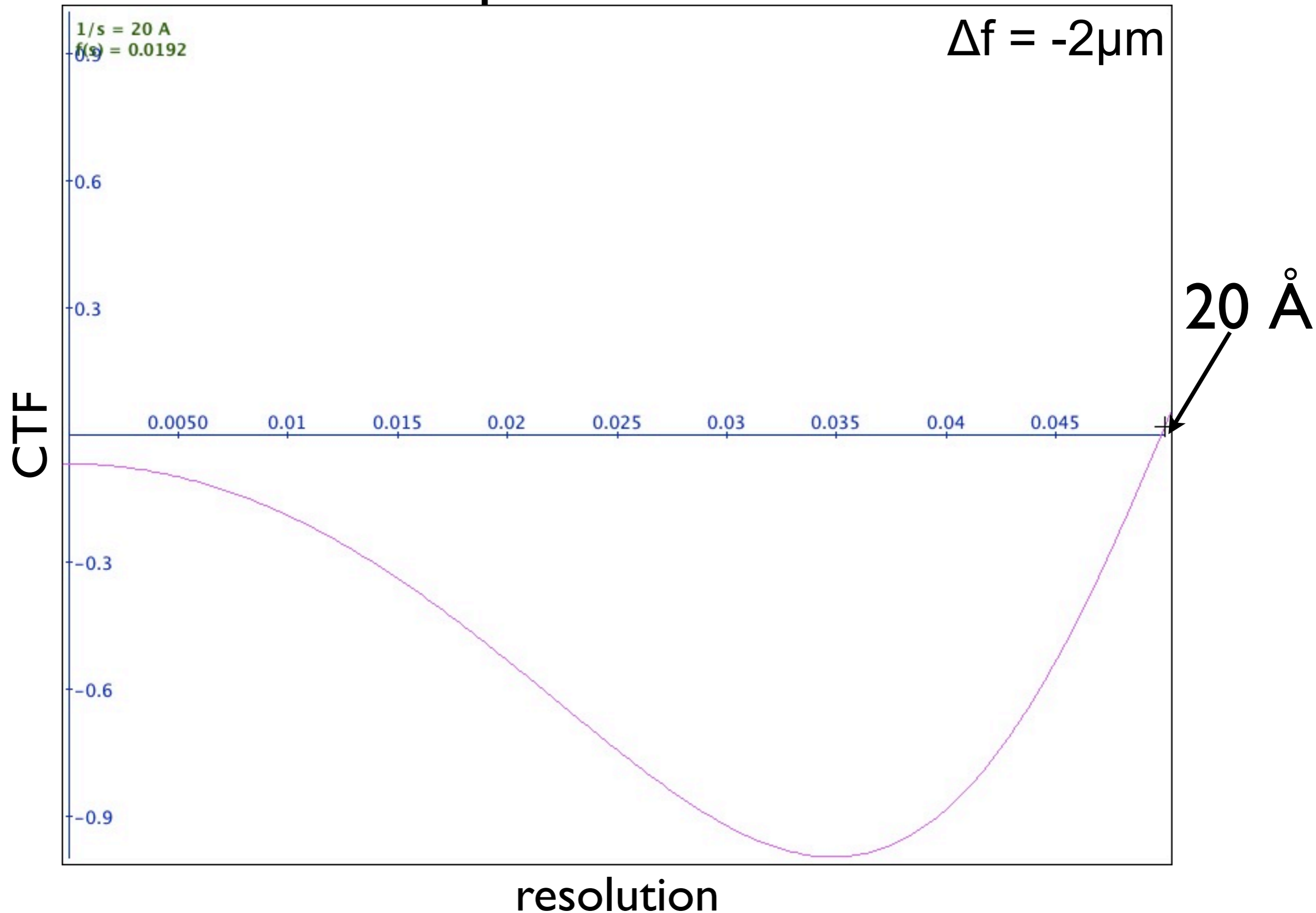
The contrast transfer function

$$\text{CTF}(s; \Delta f) \approx -\sin(\pi \Delta f \lambda s^2)$$

Phase perturbation function:

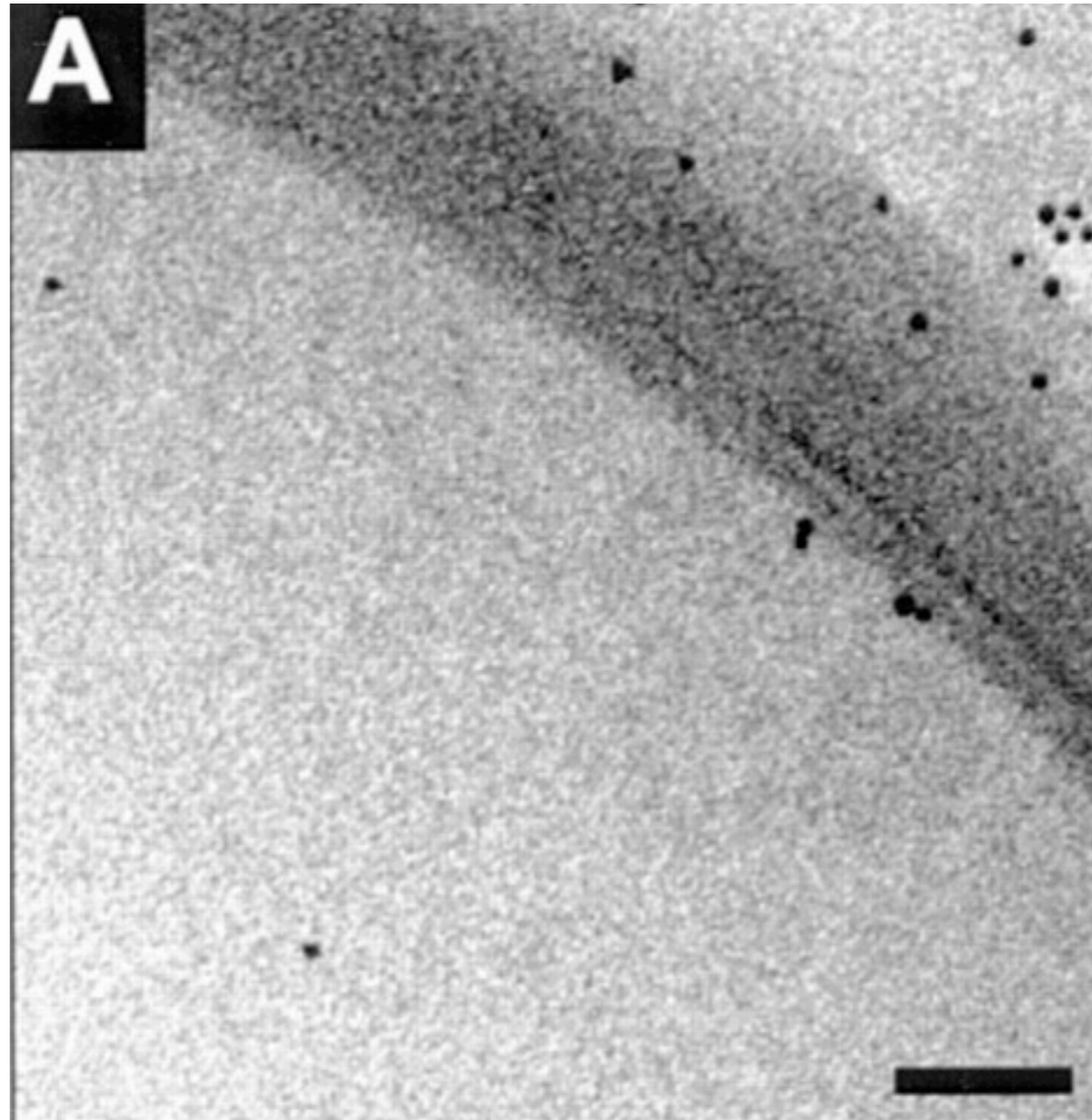
$$\gamma(s; \Delta f) = 2\pi(-\frac{1}{2} \Delta f \lambda s^2)$$

“close to focus” = poor low-resolution contrast

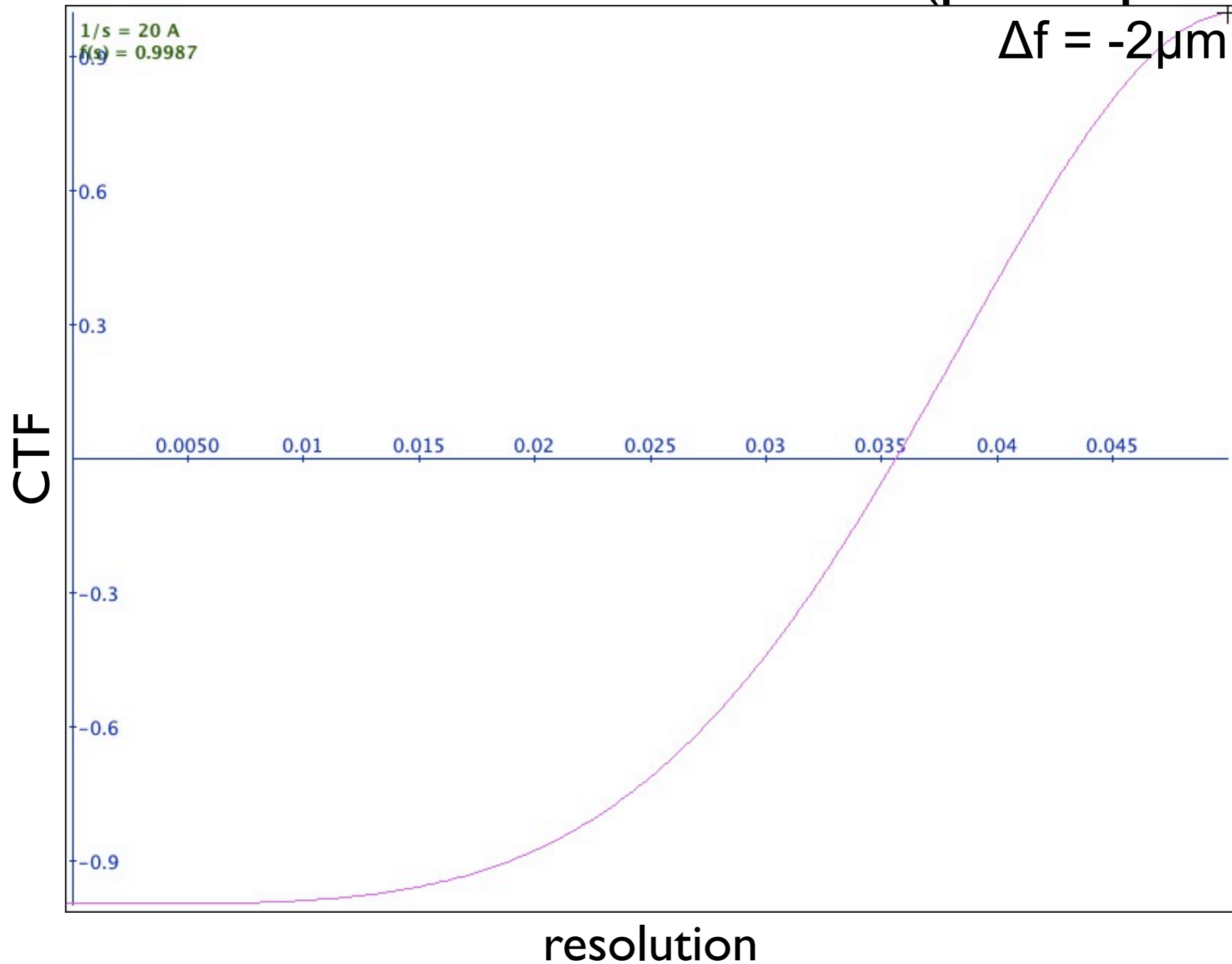


hard to detect molecules; worse in cells

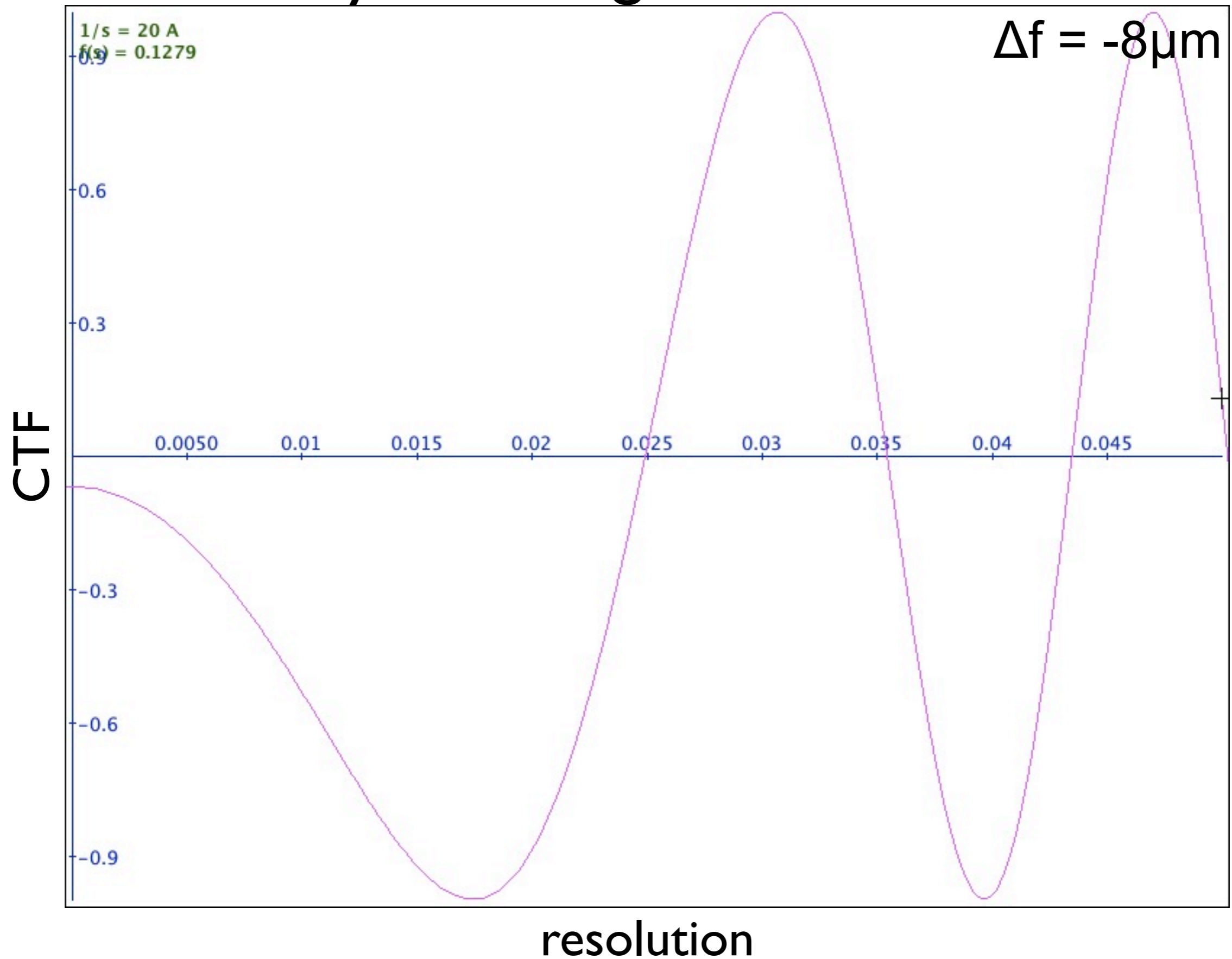
$$\Delta f = -0.5\mu\text{m}$$



ideal contrast transfer function (phase plate)

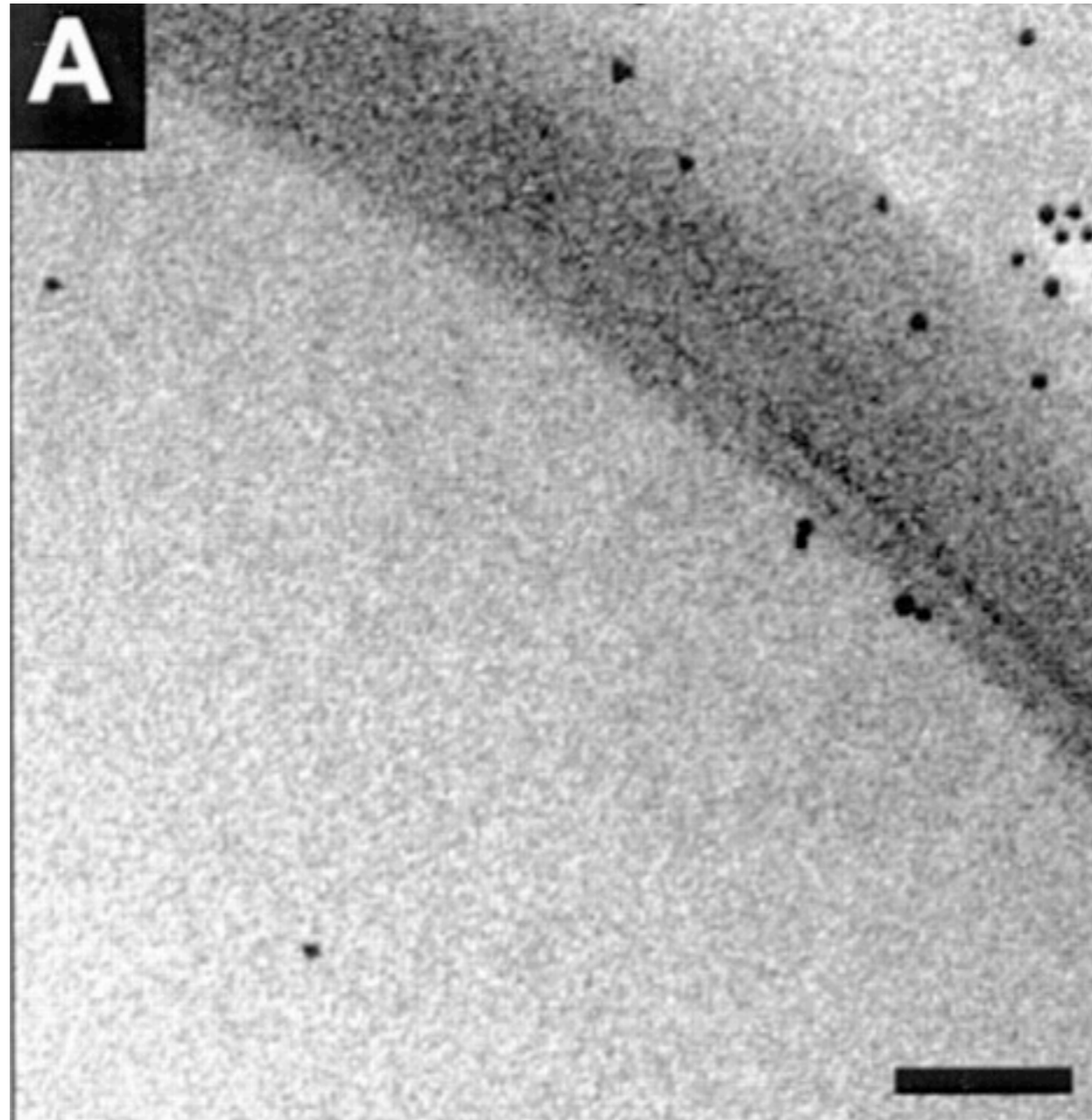


cryo-ET: large underfocus



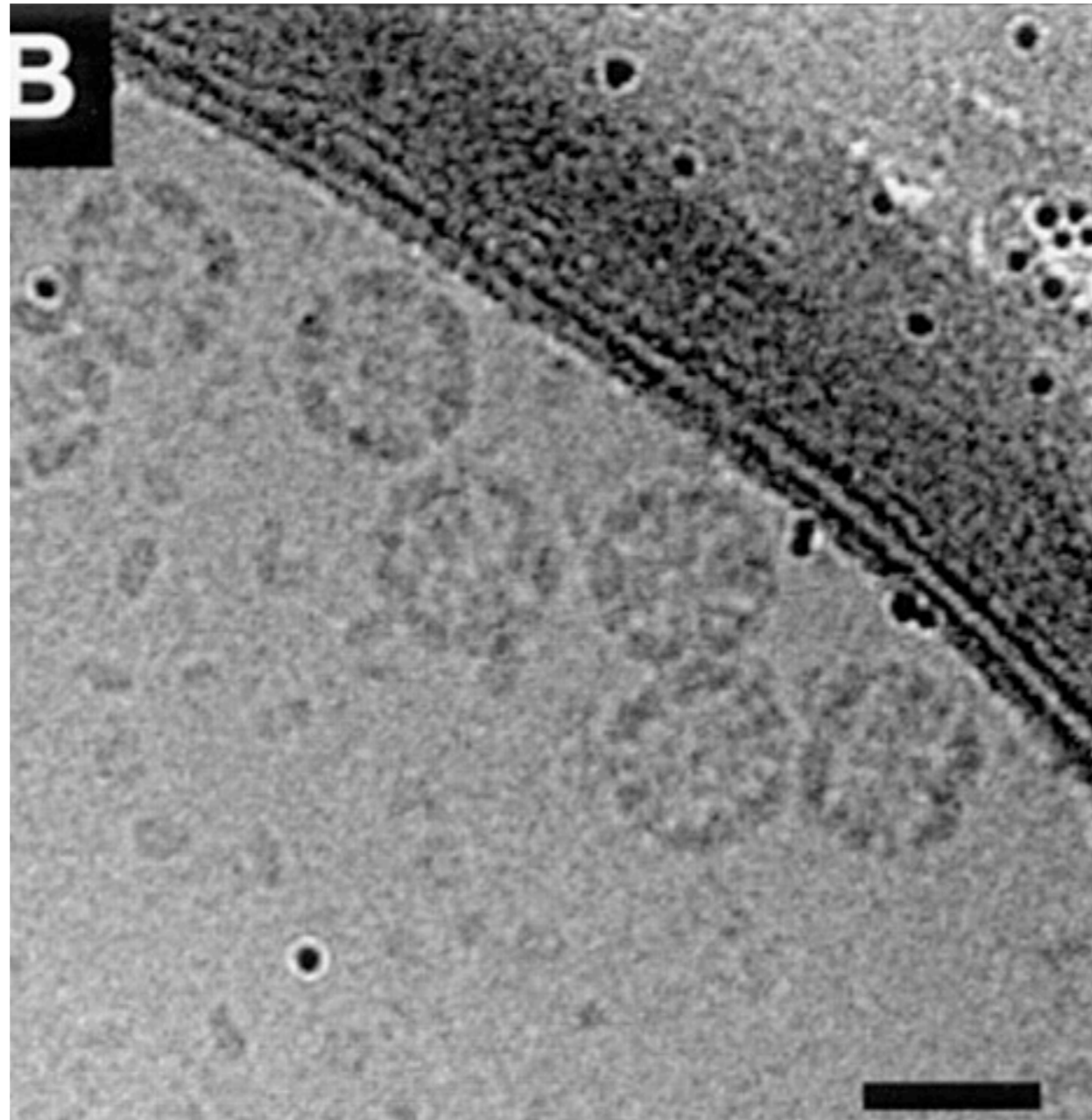
hard to detect molecules; worse in cells

$$\Delta f = -0.5\mu\text{m}$$



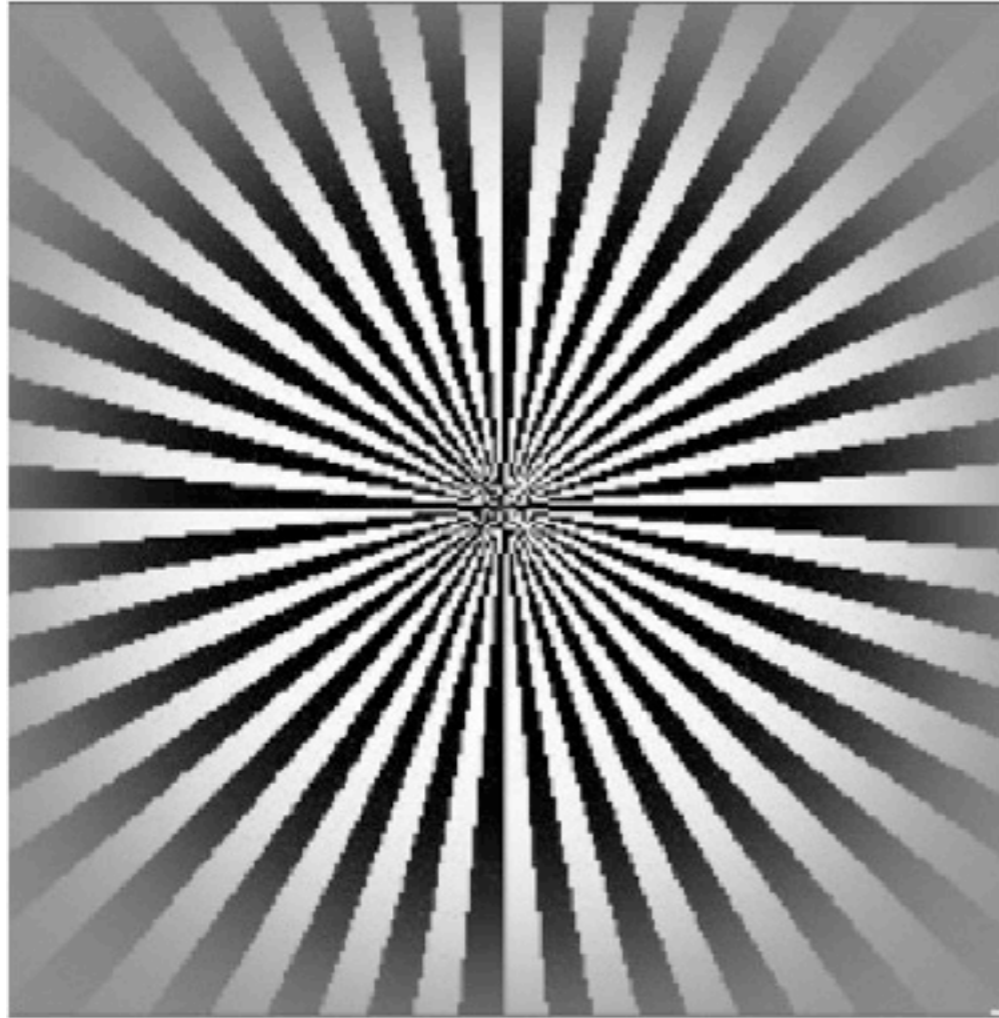
without phase plate: need large underfocus

$$\Delta f = -5.0\mu\text{m}$$



cryo-ET: large defocus

original

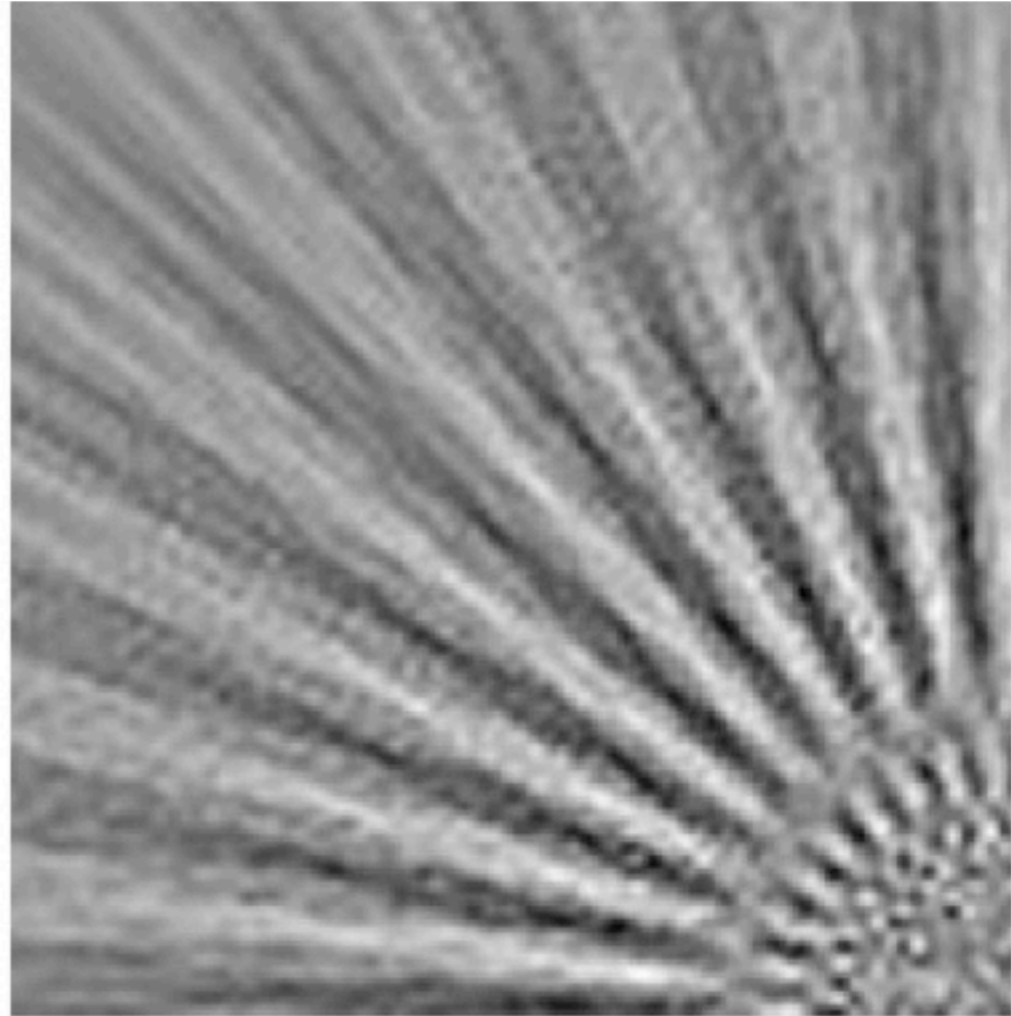
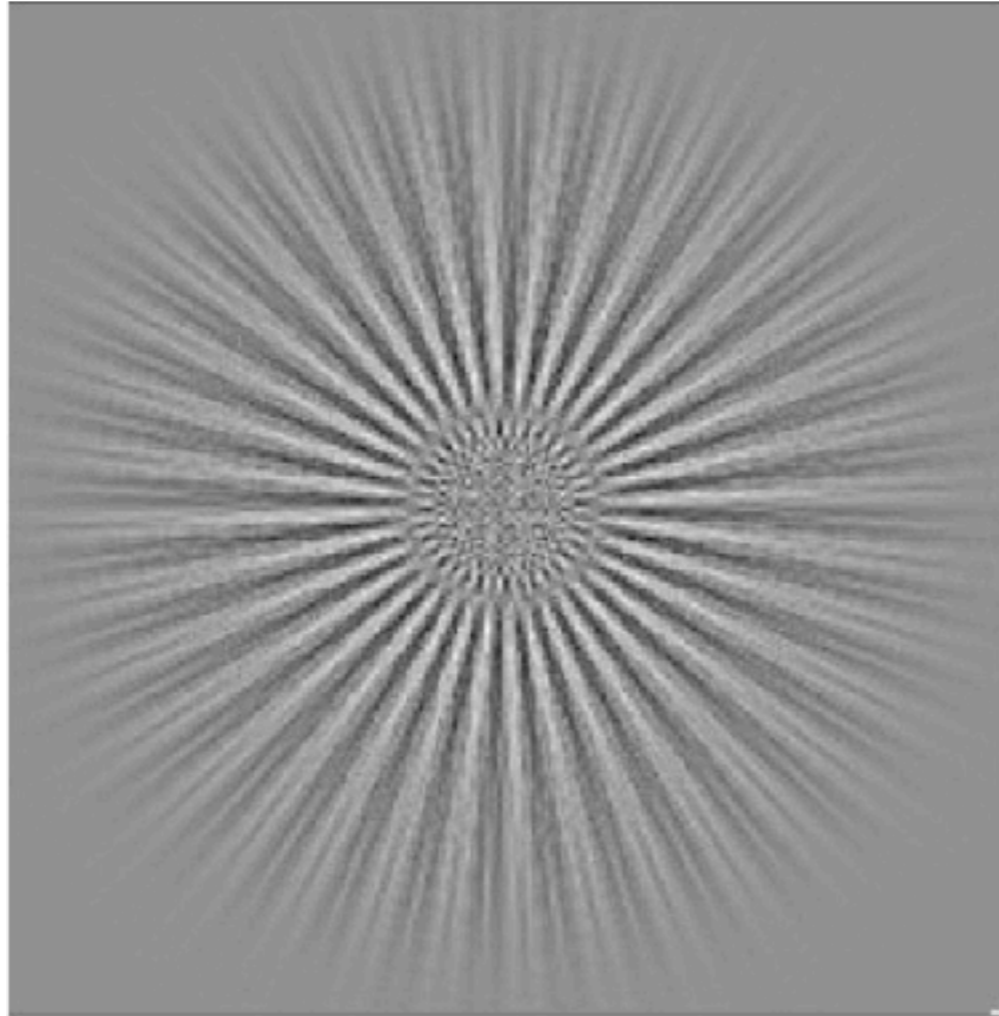


small spacing =
higher resolution



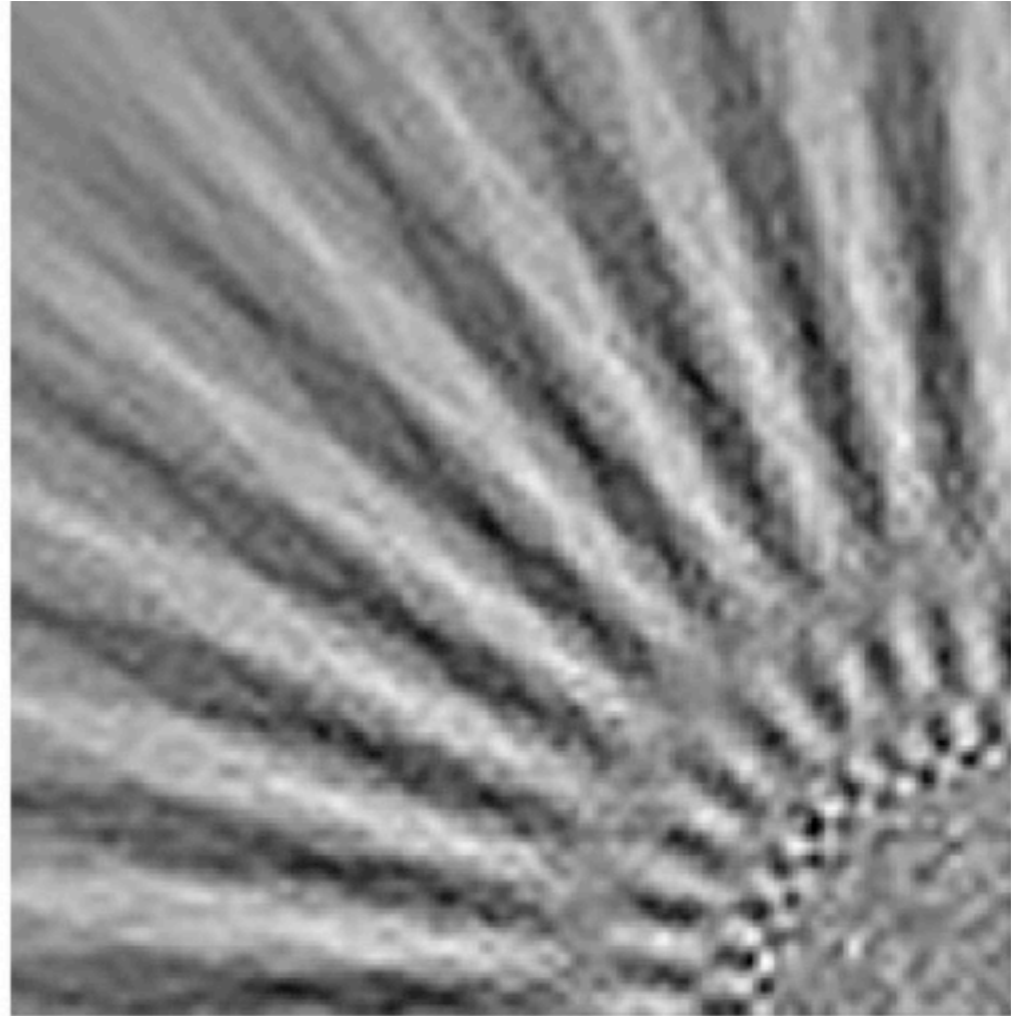
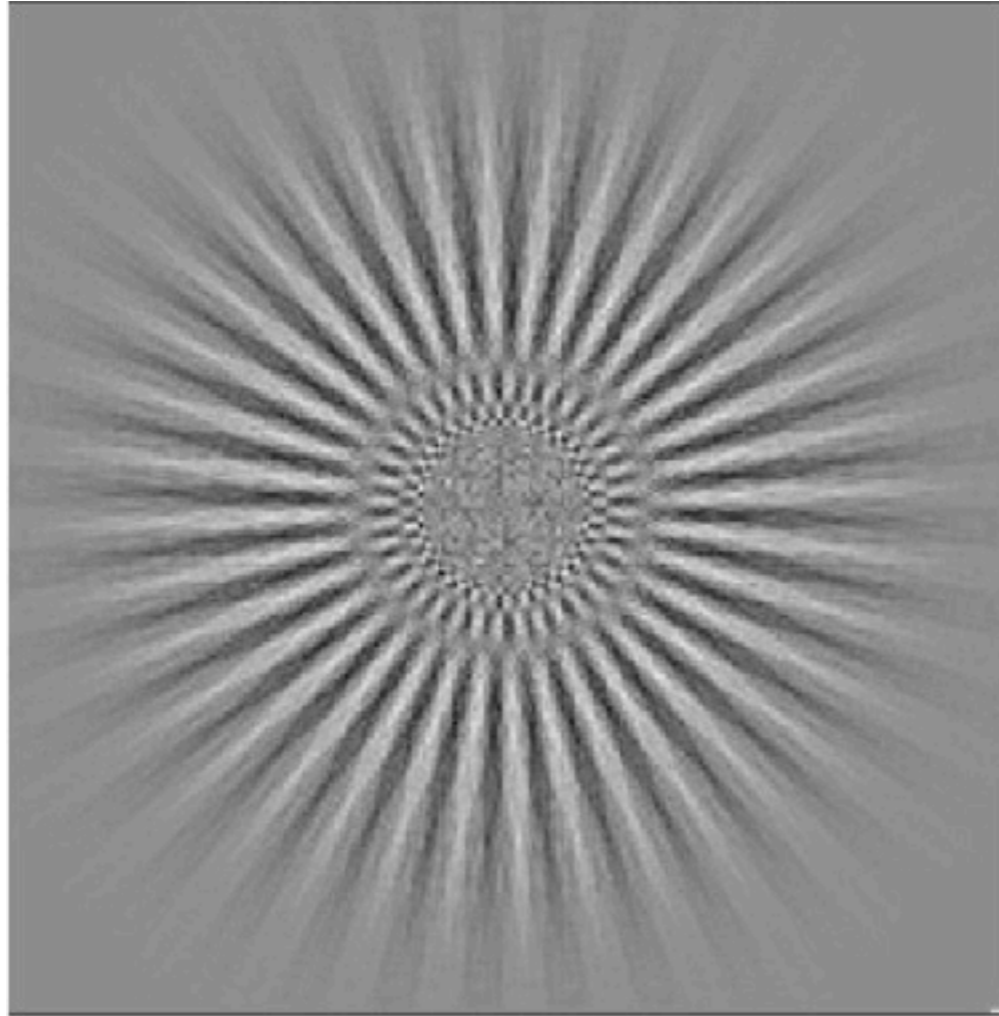
cryo-ET: large defocus

$$\Delta f = -2\mu\text{m}$$



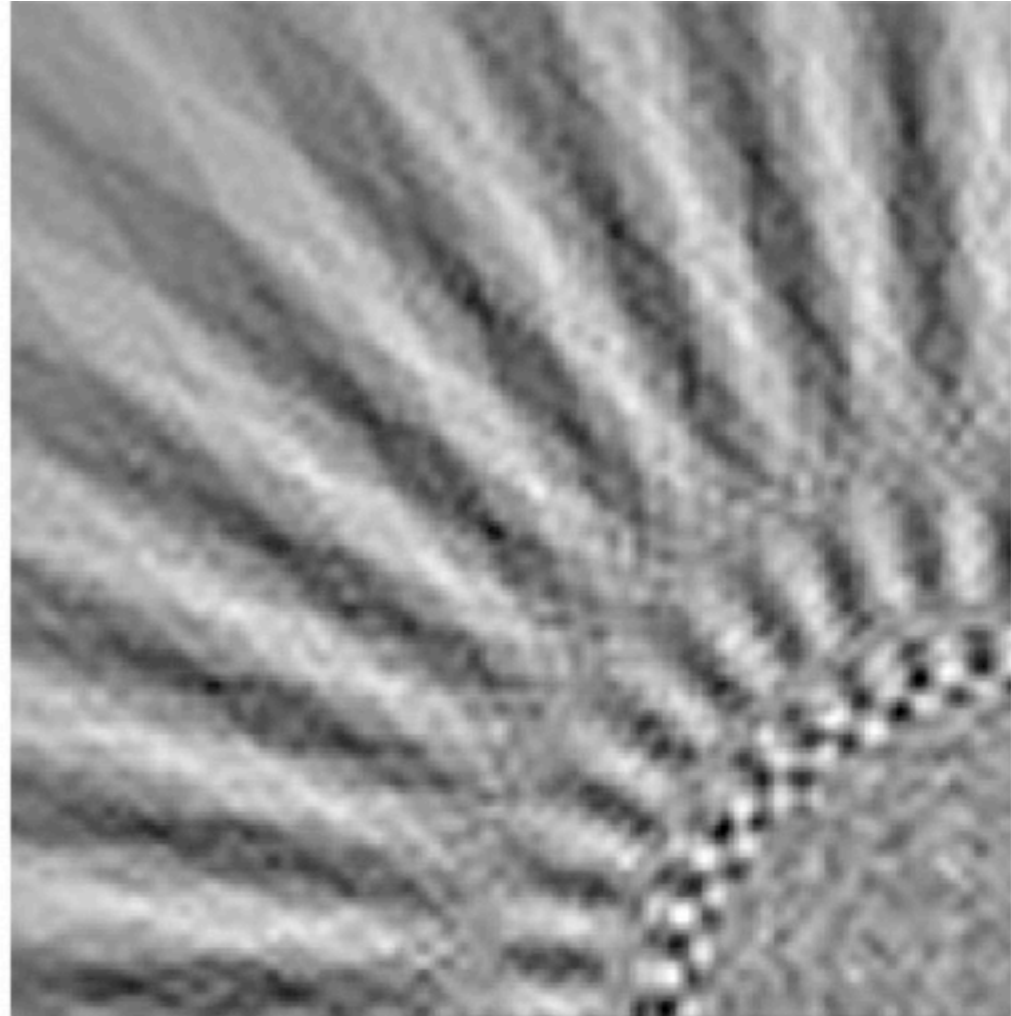
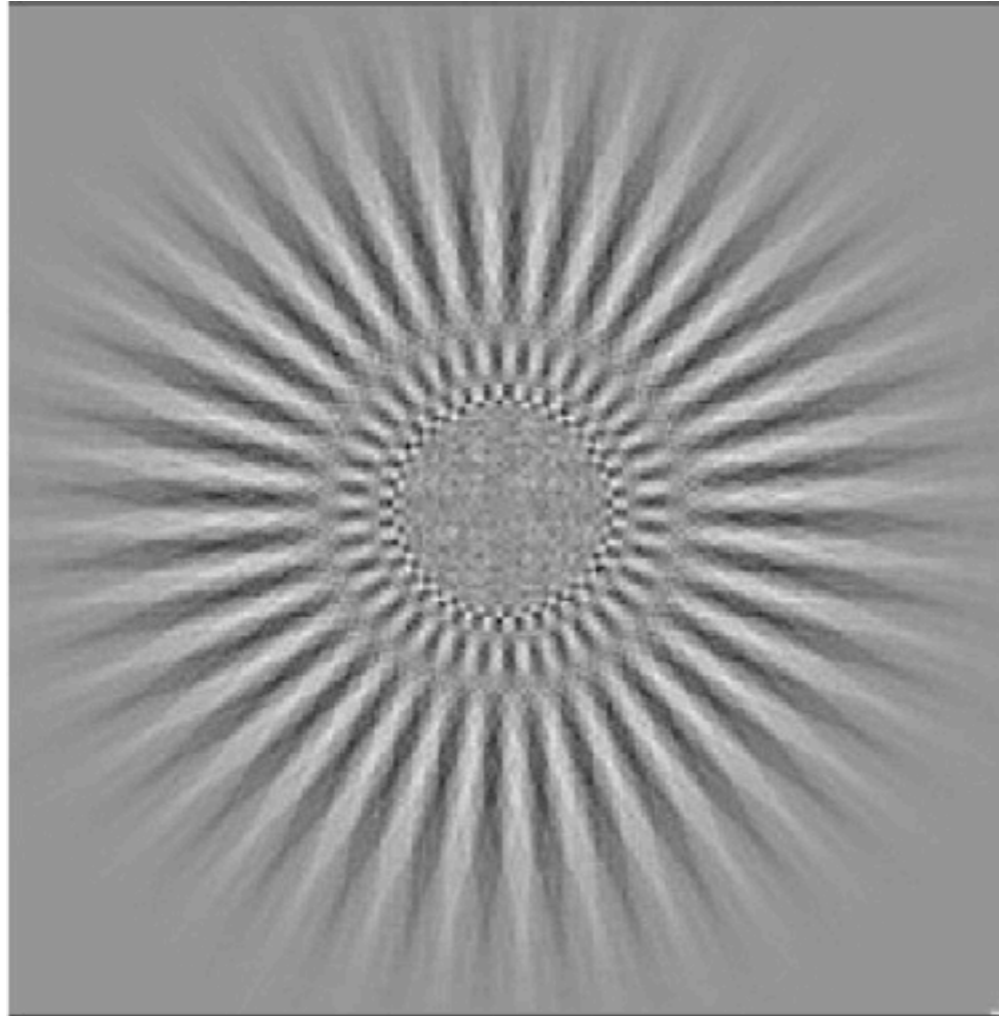
cryo-ET: large defocus

$$\Delta f = -5\mu\text{m}$$

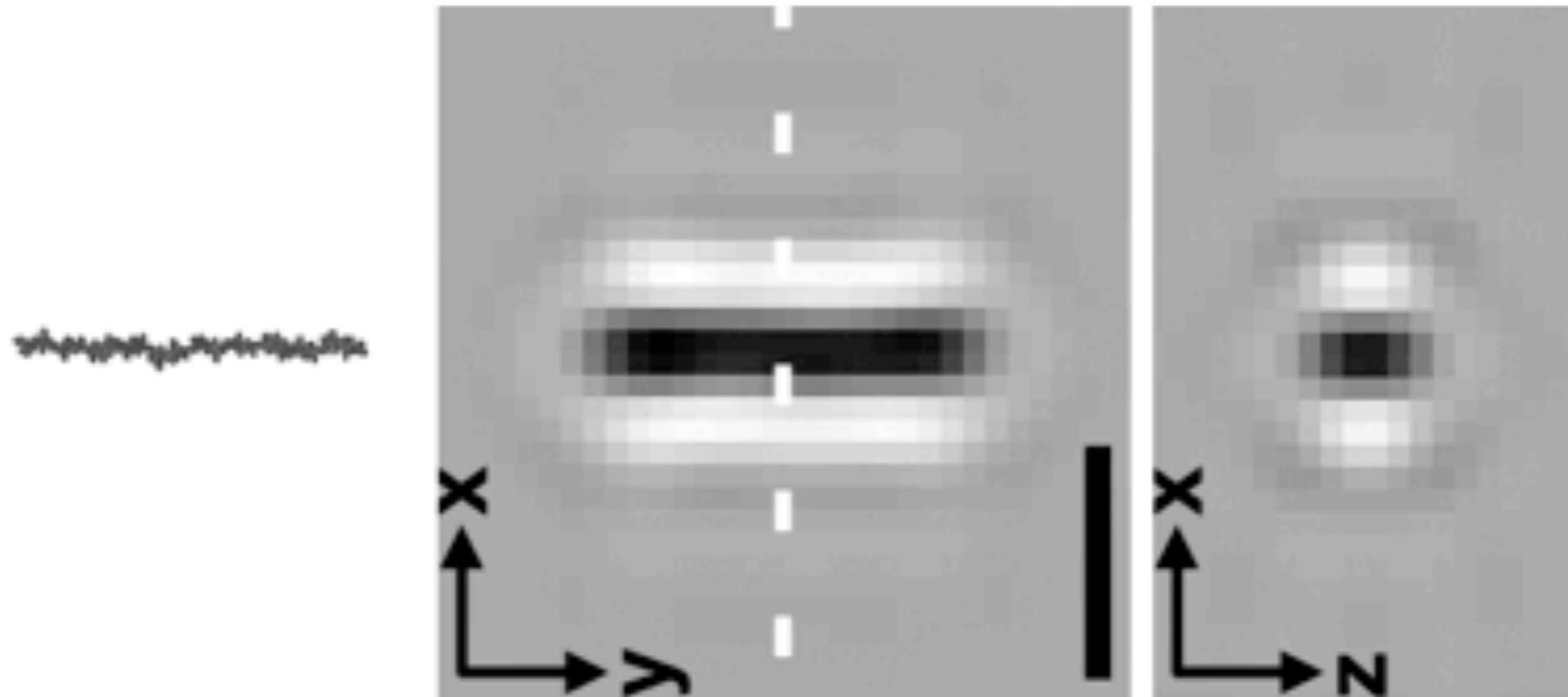


cryo-ET: large defocus

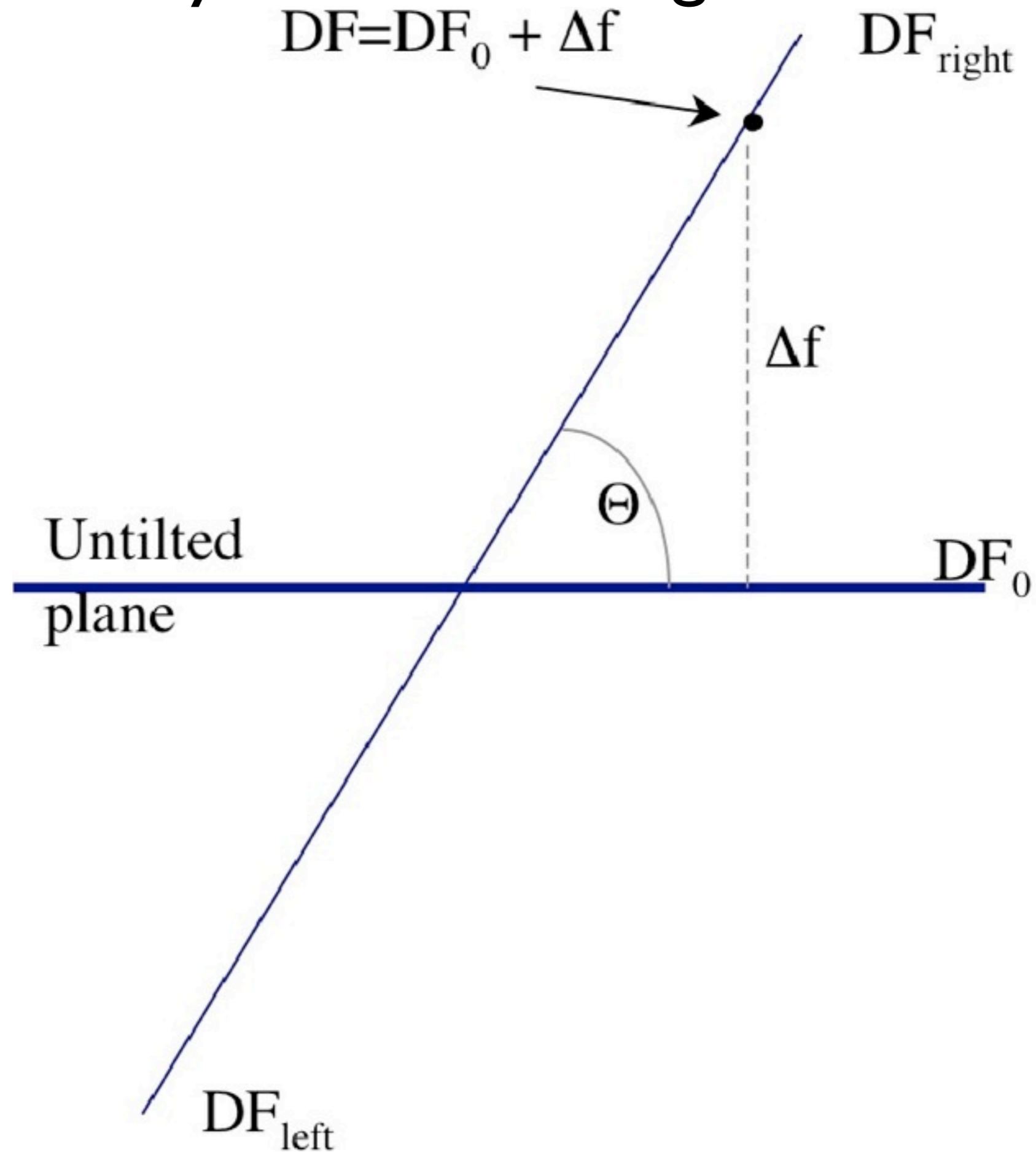
$$\Delta f = -8\mu\text{m}$$



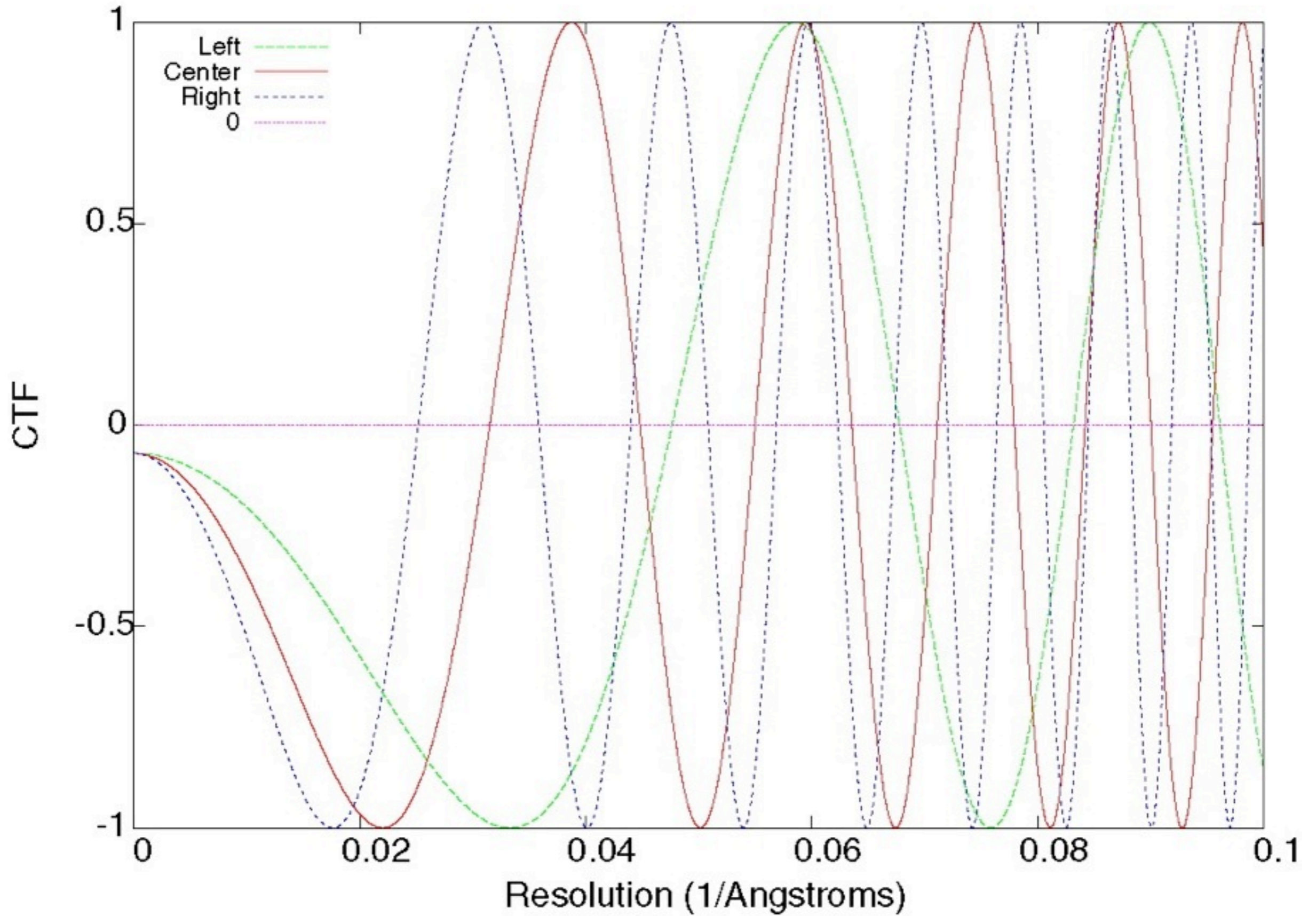
cryo-ET: large defocus



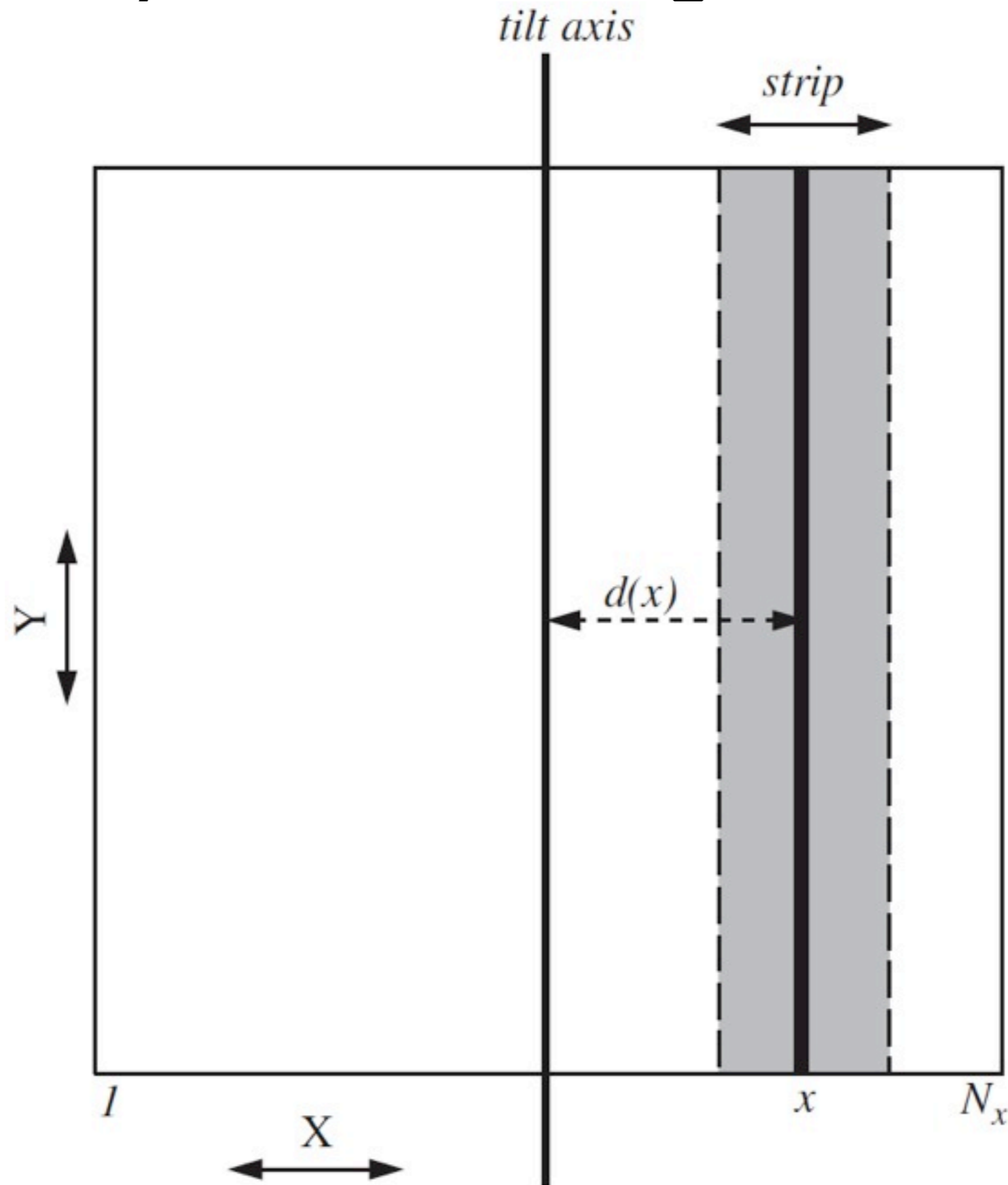
cryo-ET: defocus gradient



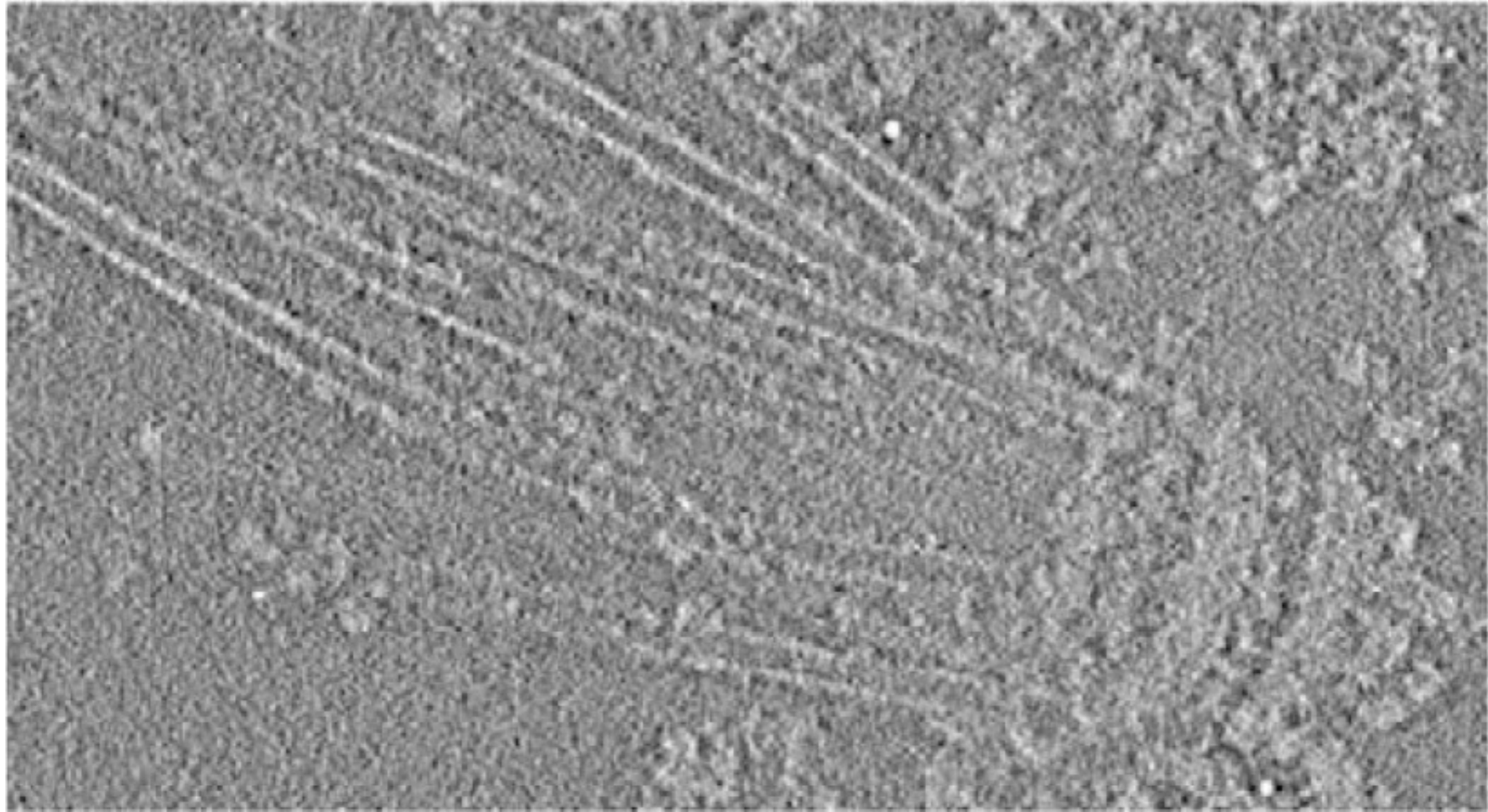
cryo-ET: defocus gradient



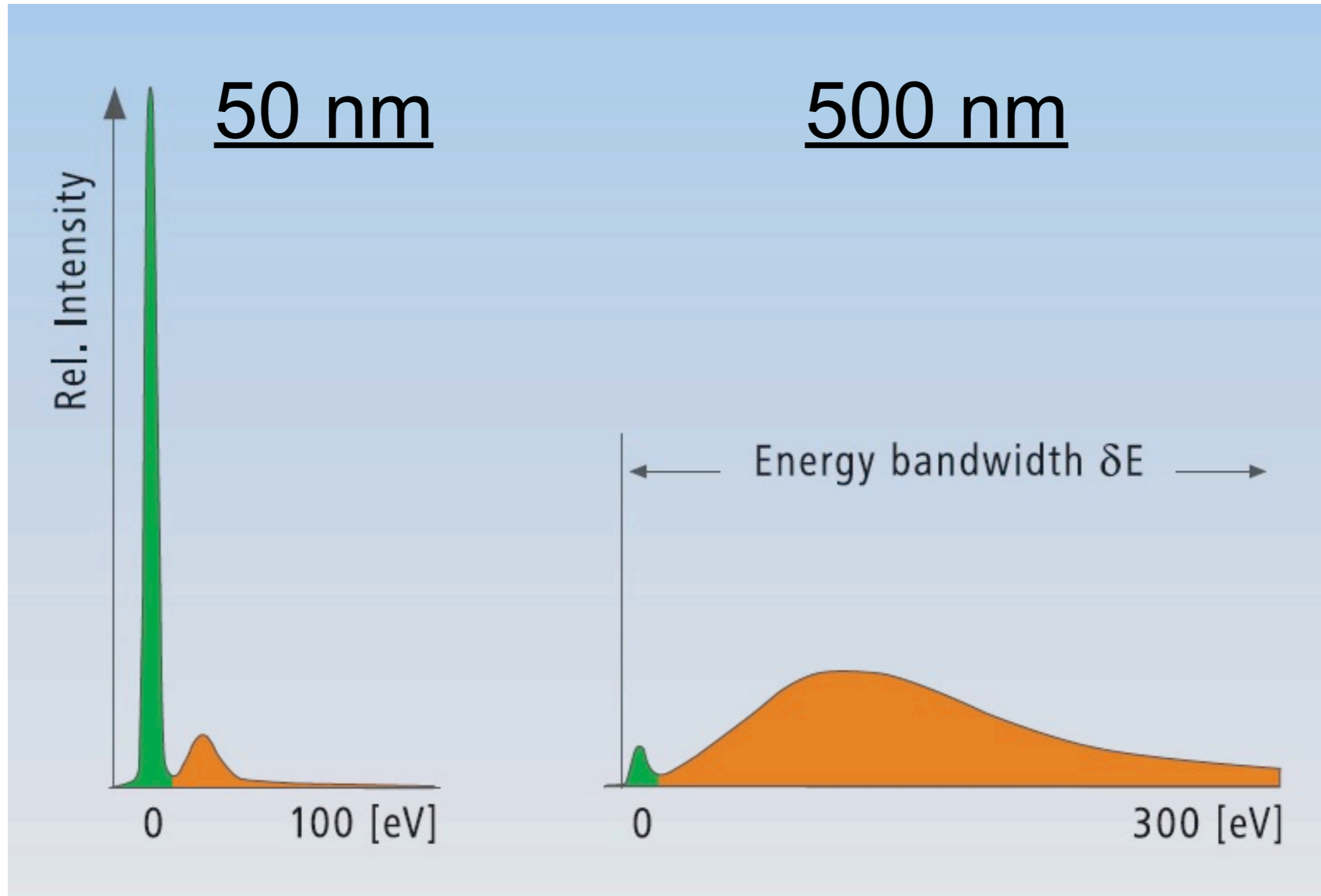
cryo-ET: defocus gradient

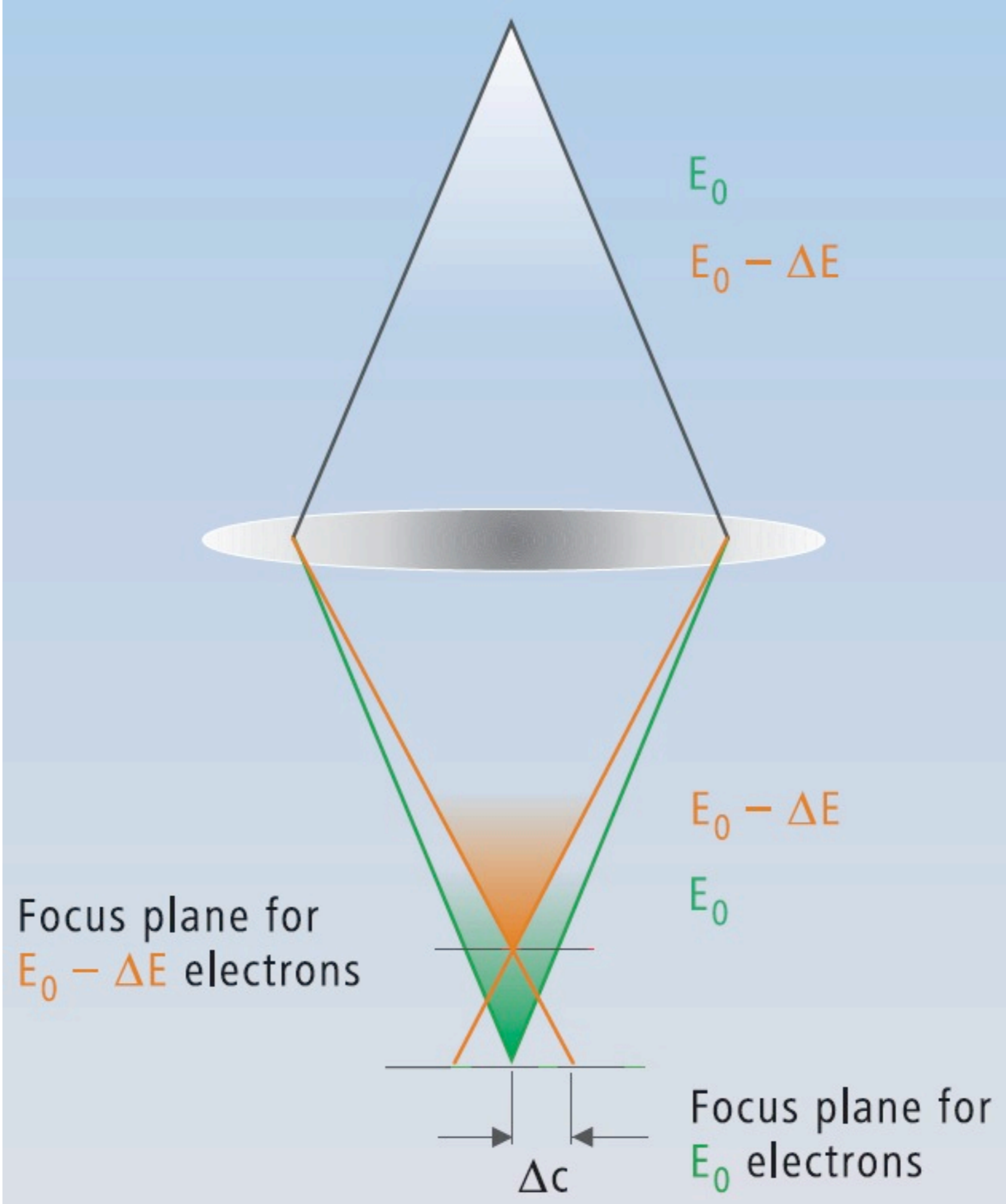


cryo-ET: defocus gradient



EELS Spectra, EPON sections





How to deal with samples that are too thick

\$\$\$\$ Make them thinner

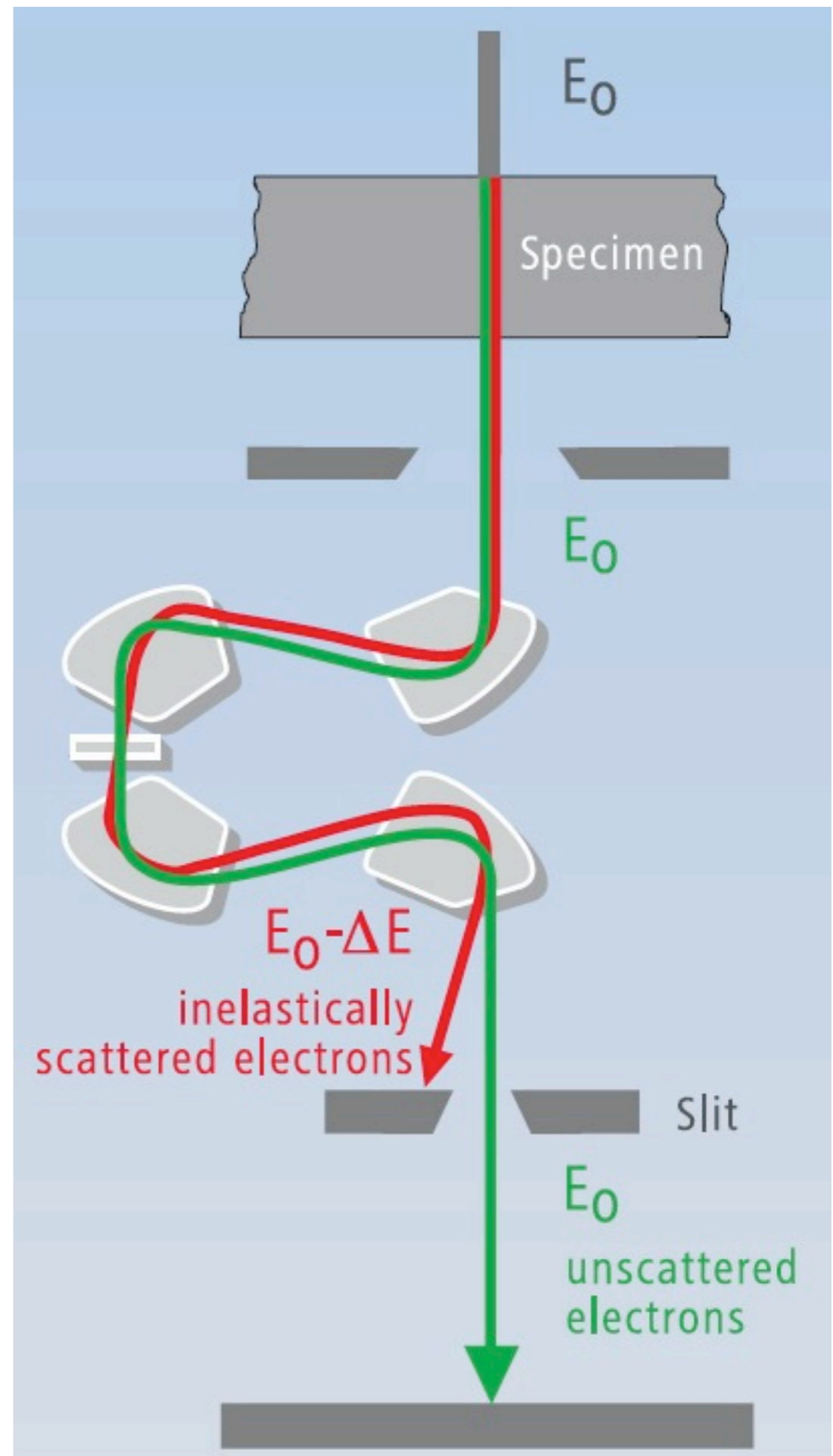
\$\$\$\$ Get rid of inelastically scattered electrons

\$\$\$\$\$\$\$\$\$\$\$\$ Correct chromatic aberration

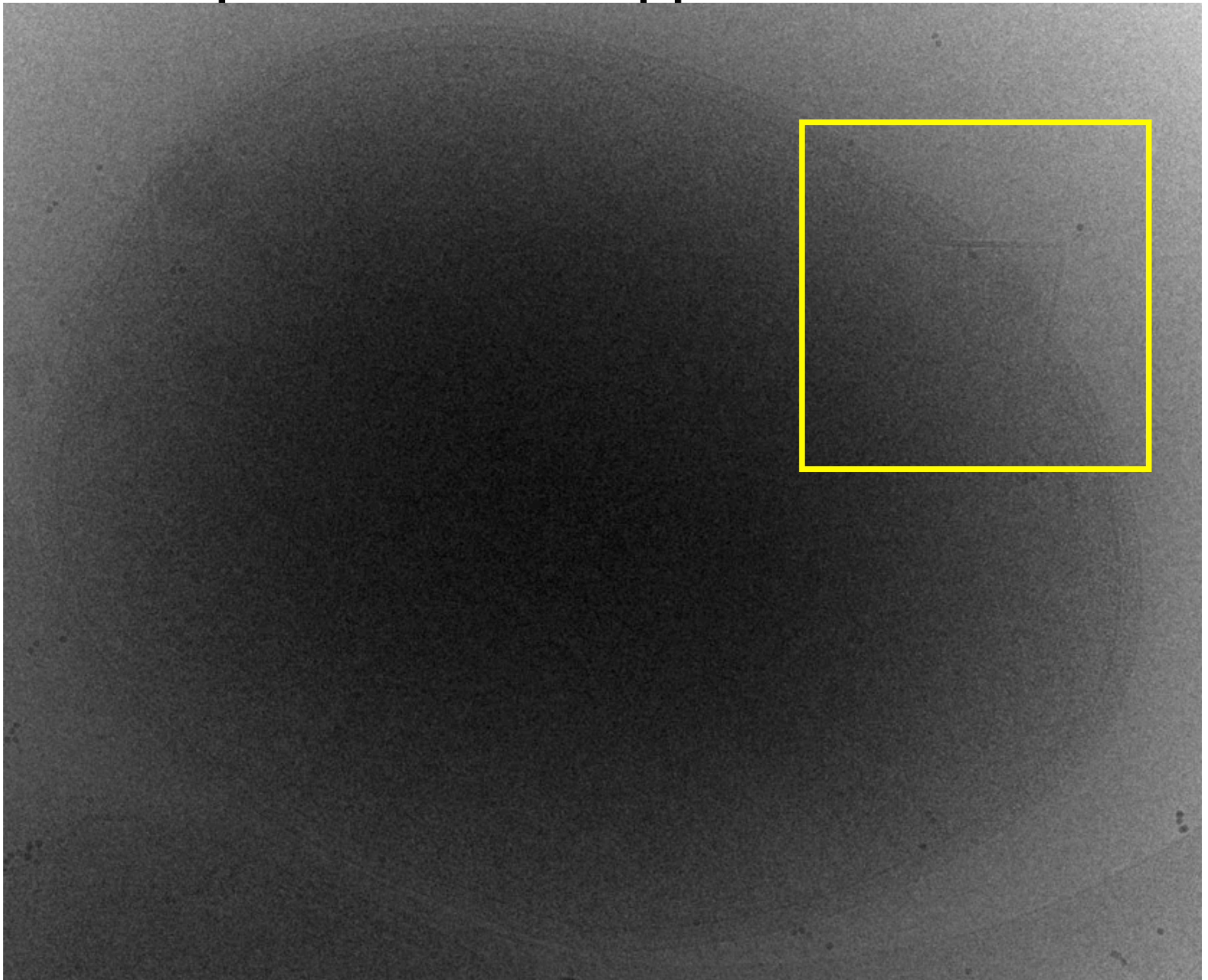
Energy filtered TEM (EF-TEM)

1. Disperse scattered electrons with an magnetic prism.
2. Remove inelastically scattered electrons with a selection slit.

When only the unscattered (E_0) electrons are selected, we call it “zero-loss” imaging mode.



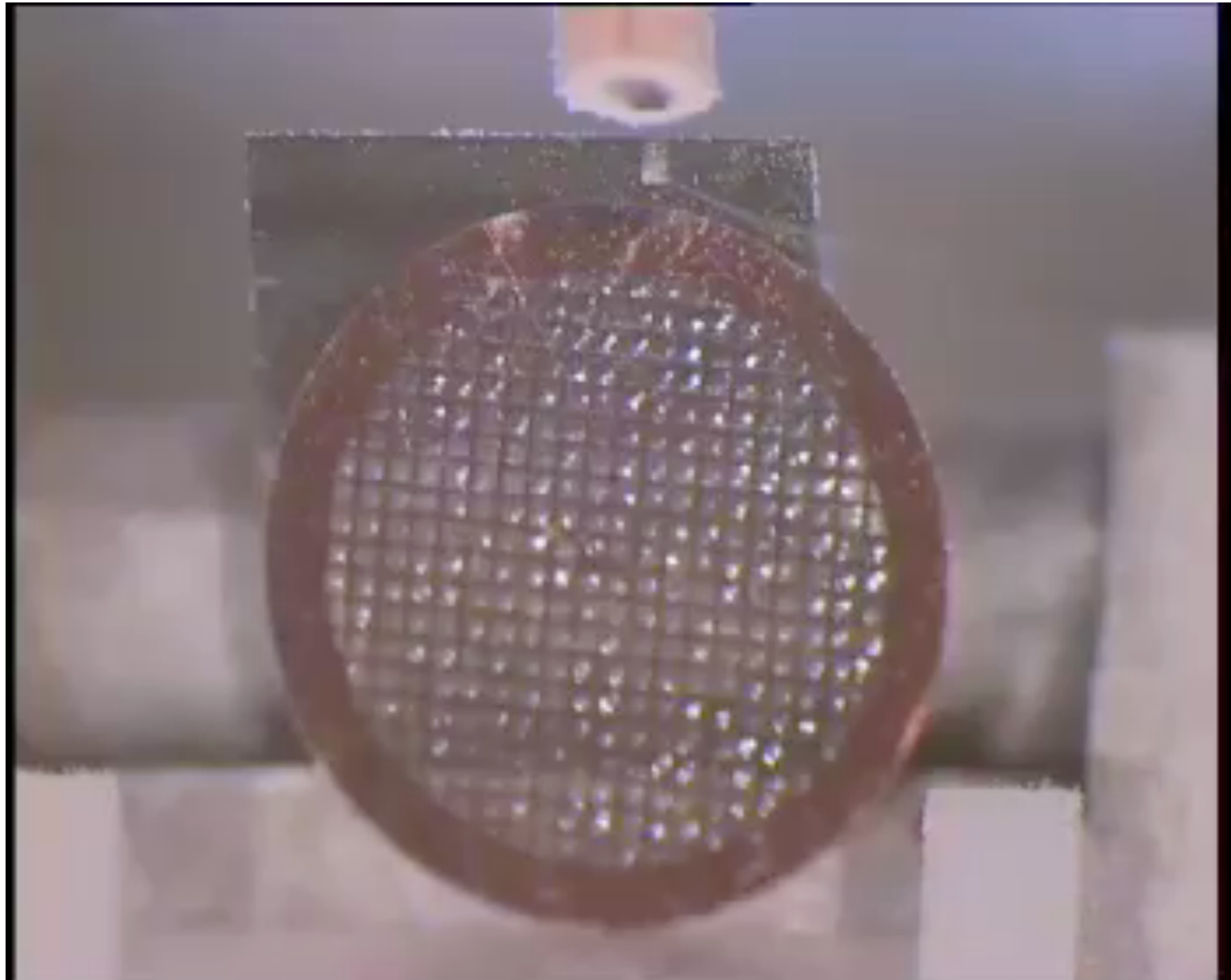
An example of EFTEM applied to archaeal cell

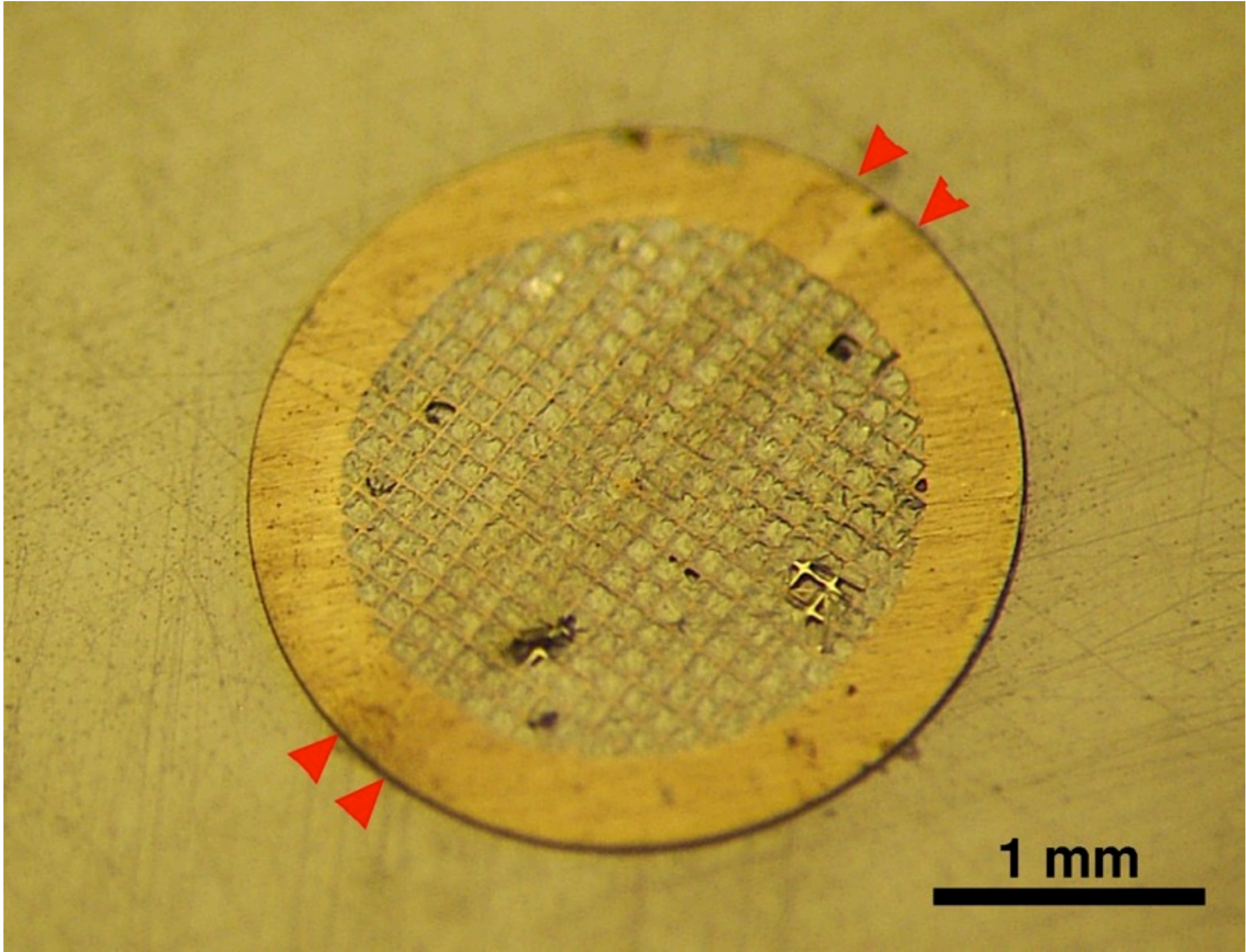


An example of EFTEM applied to archaeal cell



microtomy: making ultrathin samples





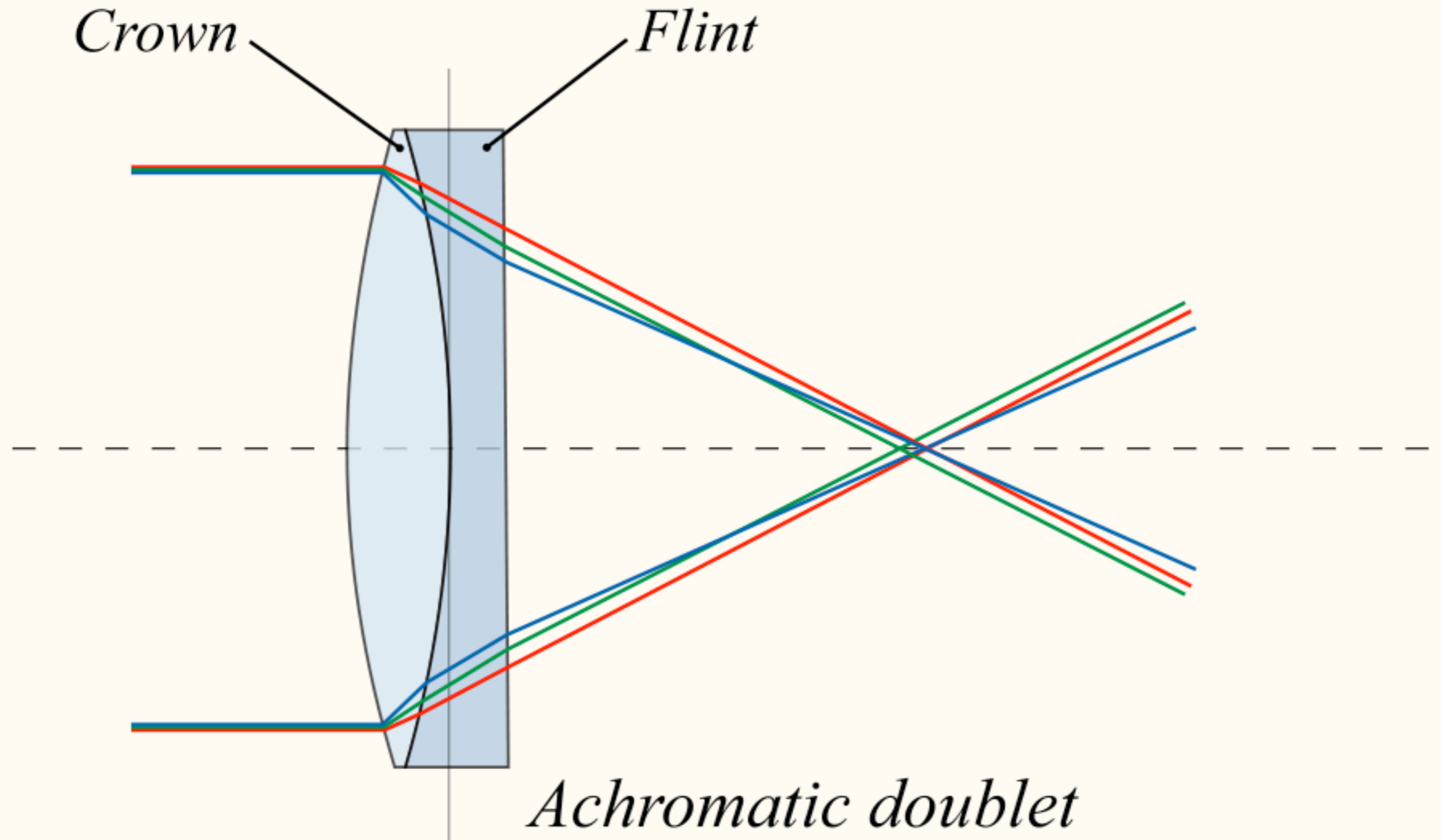
You can't beat physics

Table 3

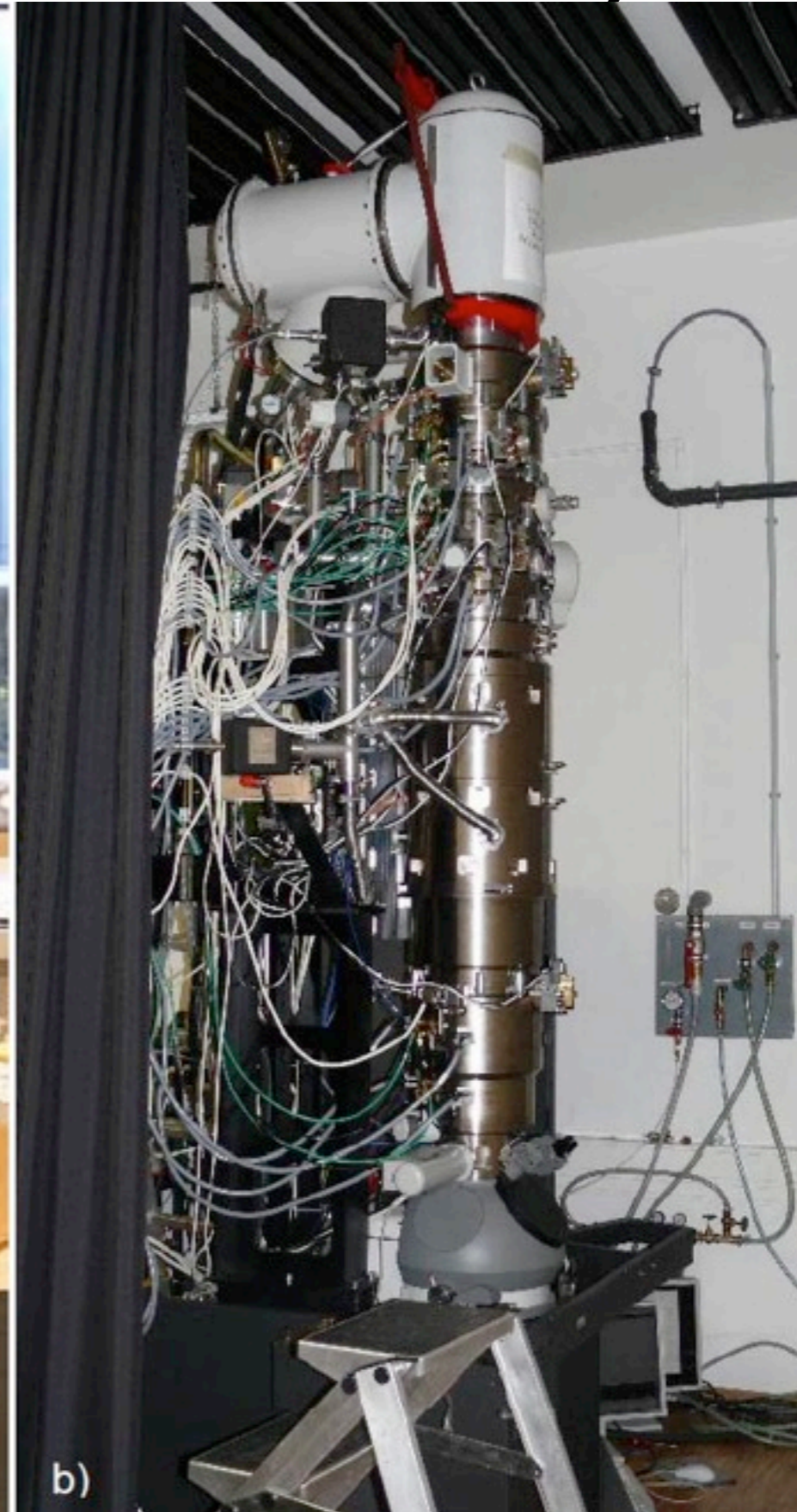
Experimental and theoretical elastic and inelastic scattering cross-sections and mean free path lengths for electrons in amorphous ice layers. The experimental errors of the cross-sections and mean free path lengths are about 10–15%, resulting in an error of 20–30% for μ

	exp.	CD and HR [9]
σ_{in} [10^{-4} nm ²]	3.82	3.06
Λ_{in} [nm]	84.8	106
σ_{el} [10^{-4} nm ²]	1.15	0.86
Λ_{el} [nm]	283.4	379
$\mu = \sigma_{in} / \sigma_{el}$	3.34	3.15
120 keV, $\rho_{ice} =$ 0.92 g/cm ³		

... or can you? Chromatic aberration correction



$C_s + C_c$ correction: the future of cryo-EM?



$C_s + C_c$ correction: the future of cryo-EM?



1. What is tomography?

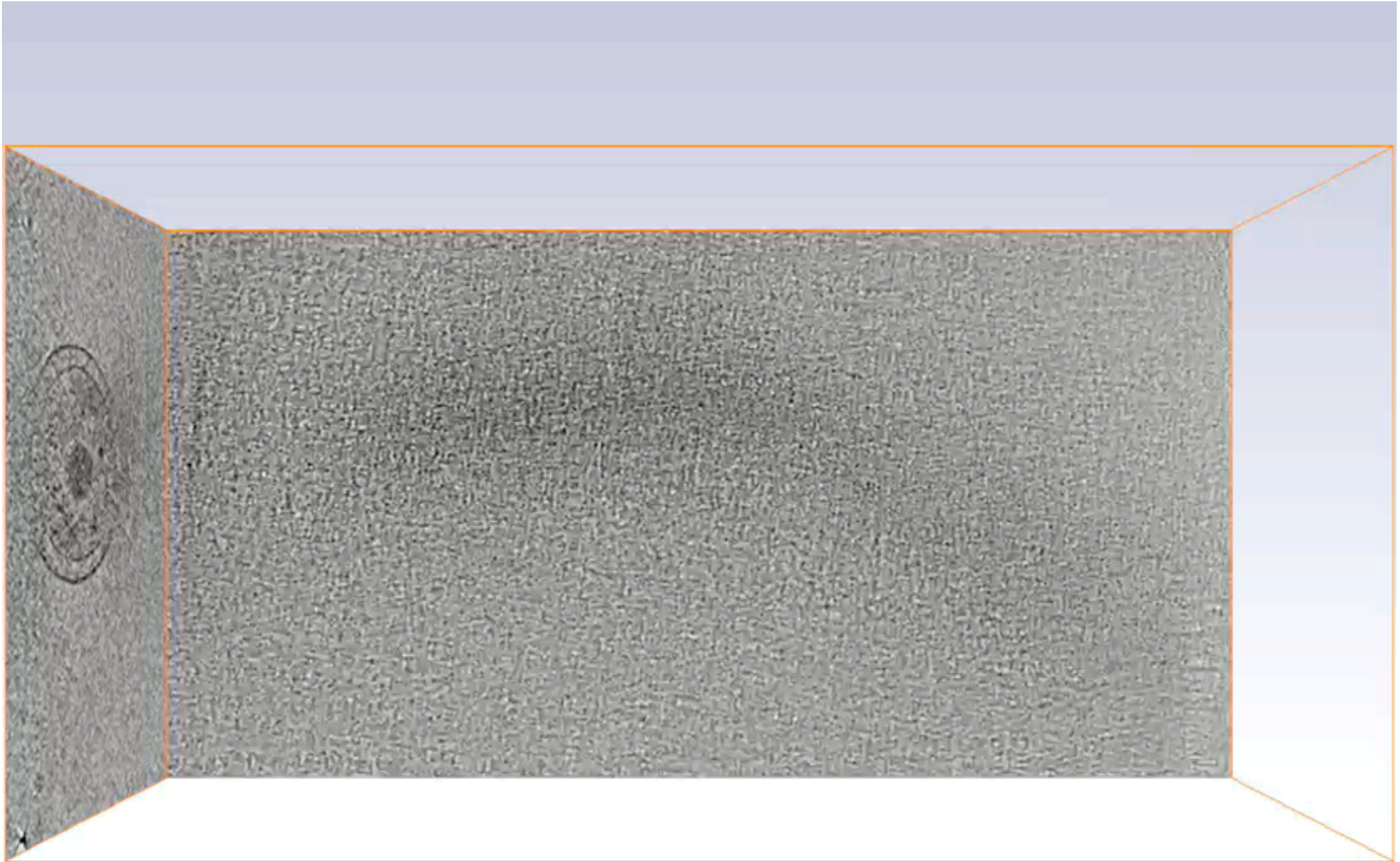
2. Sample preparation (what kind?)

3. Principles of reconstruction

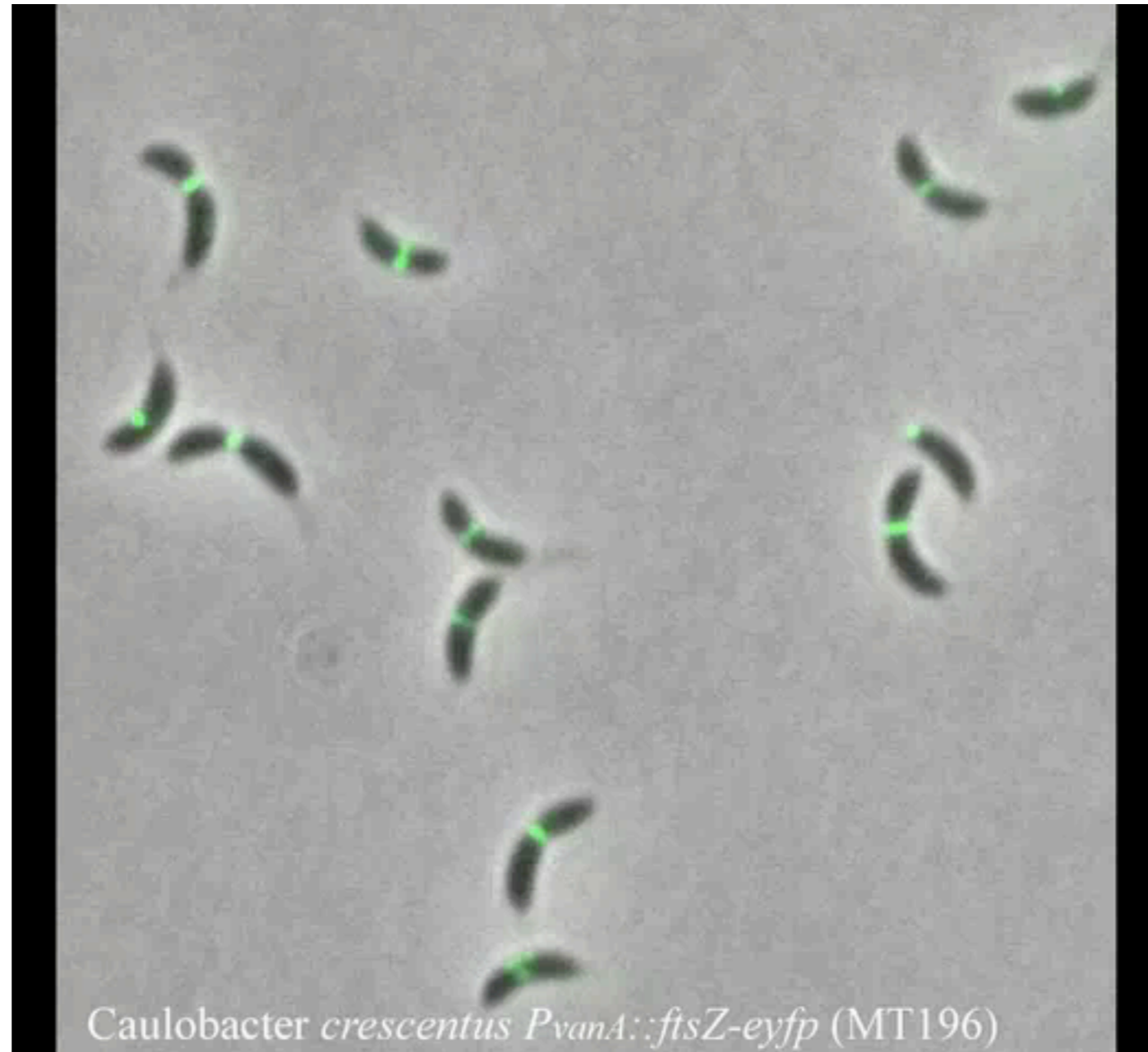
4. Beware of artifacts

5. Example studies

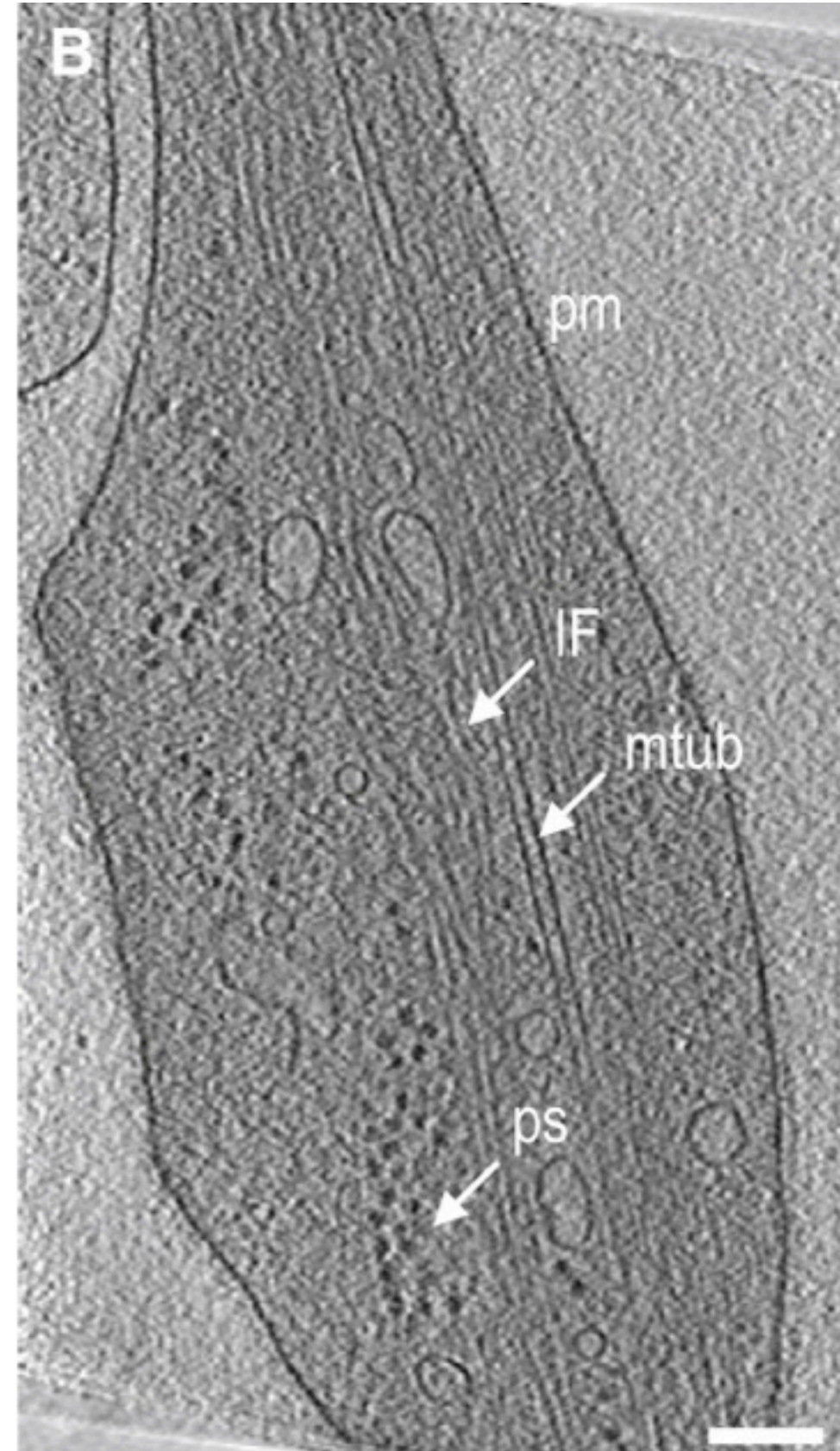
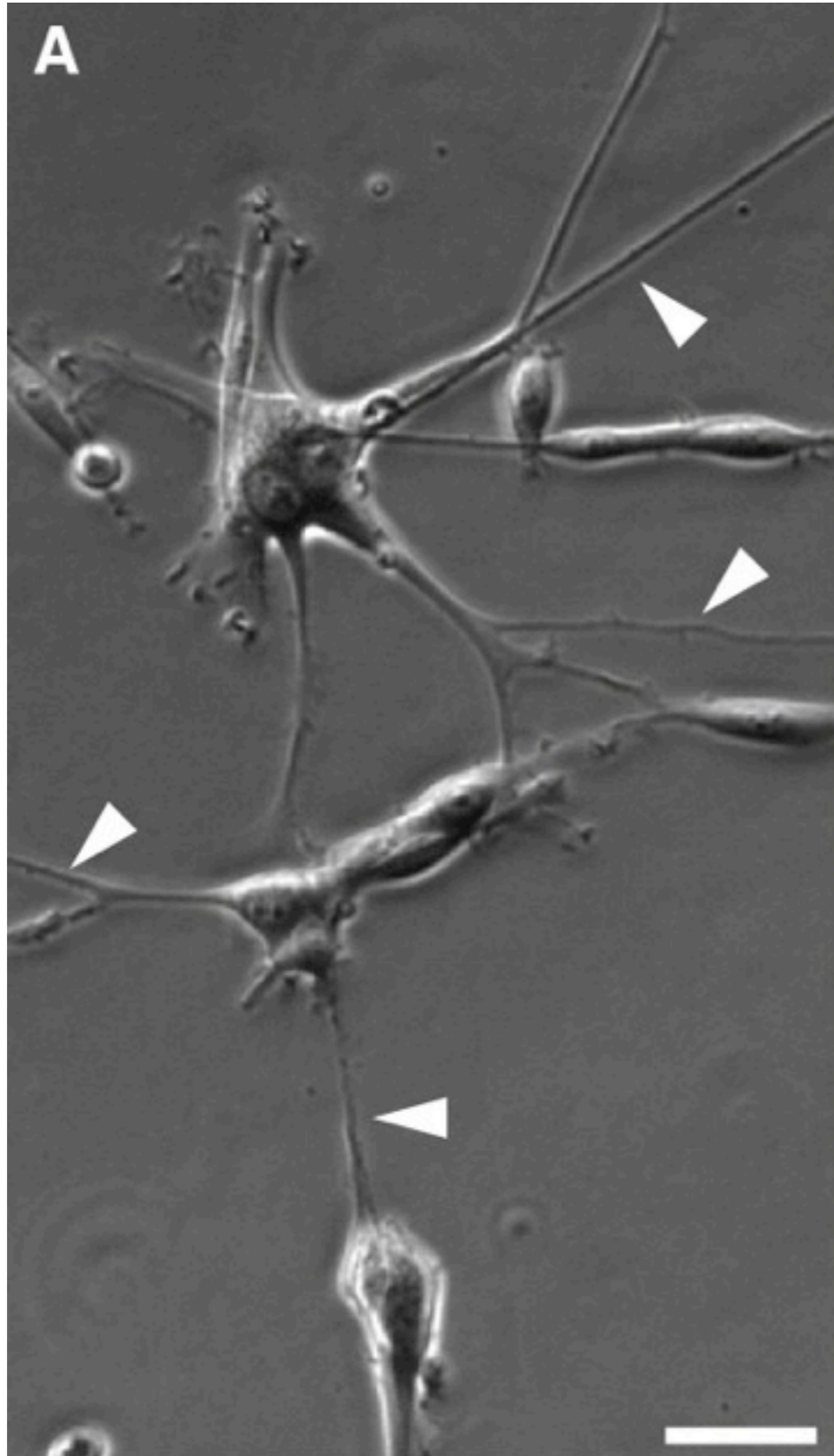
Examples



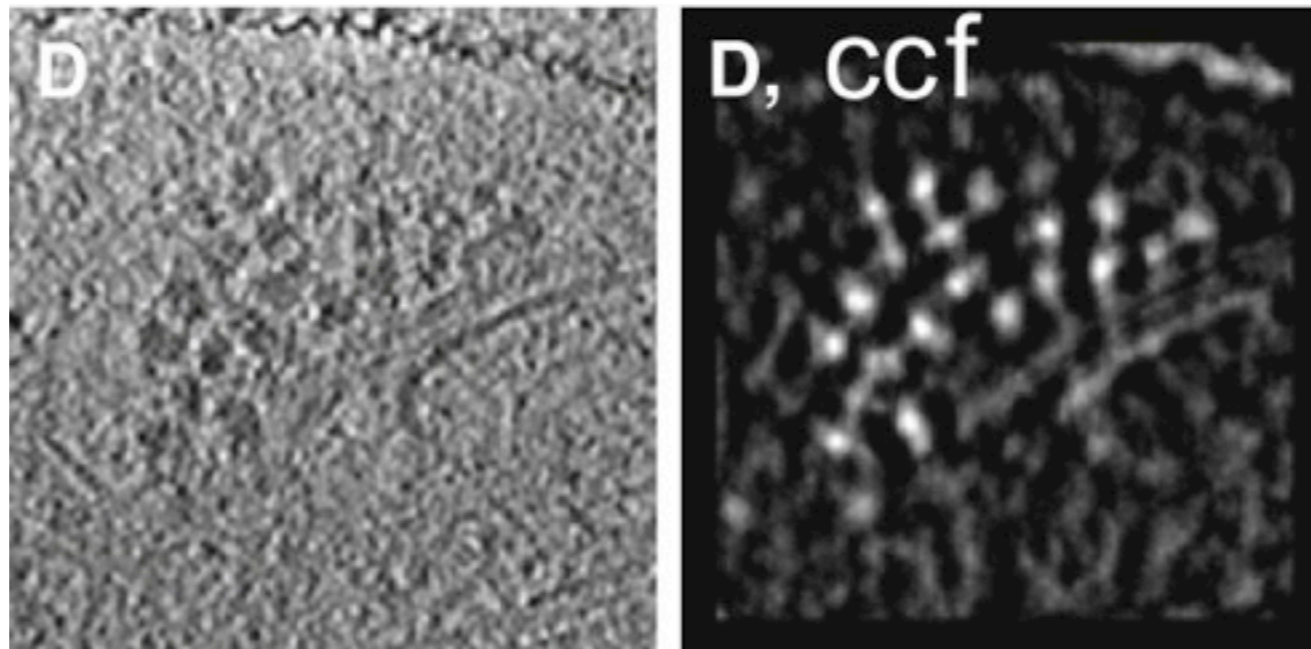
Examples



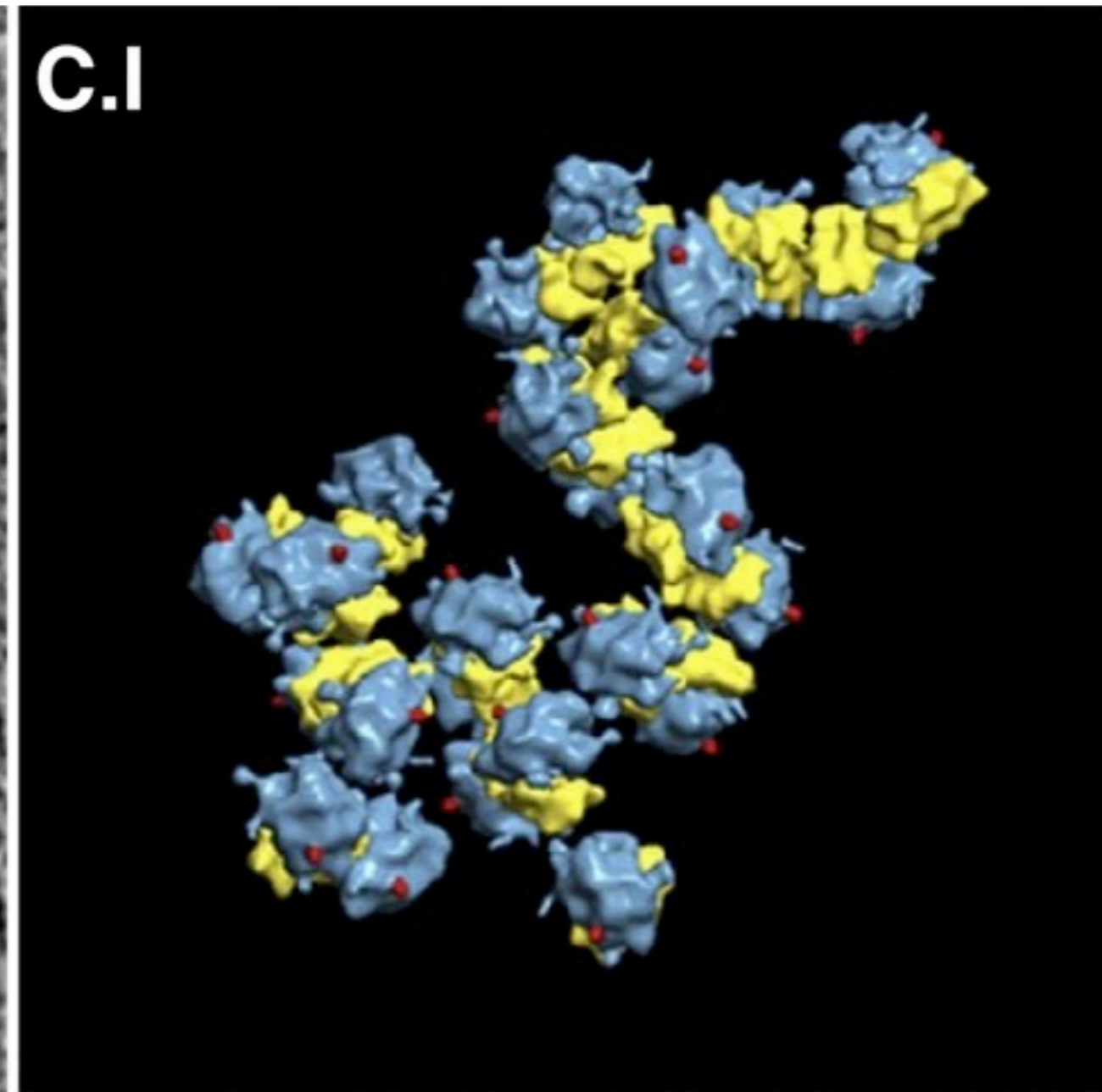
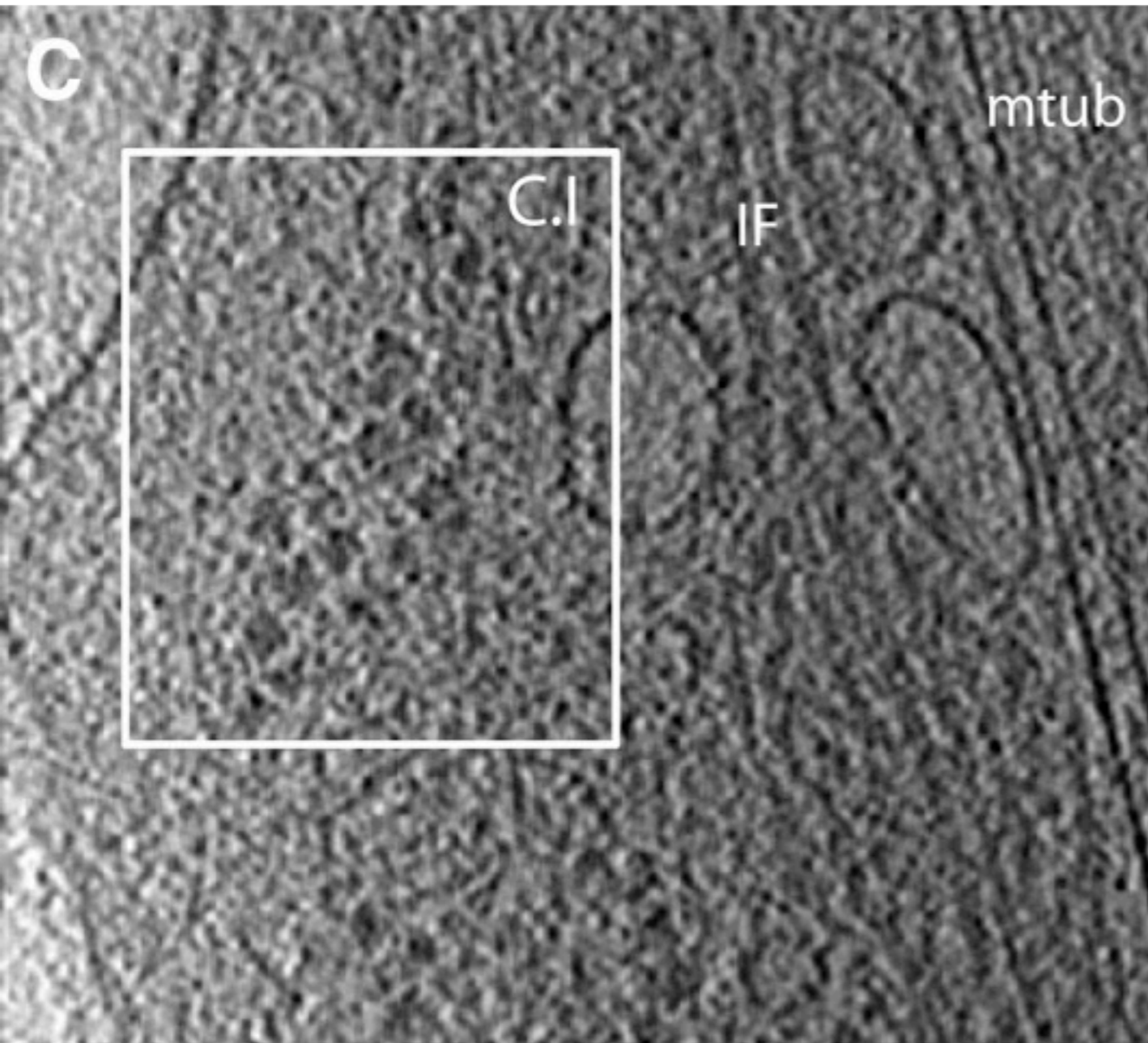
Examples



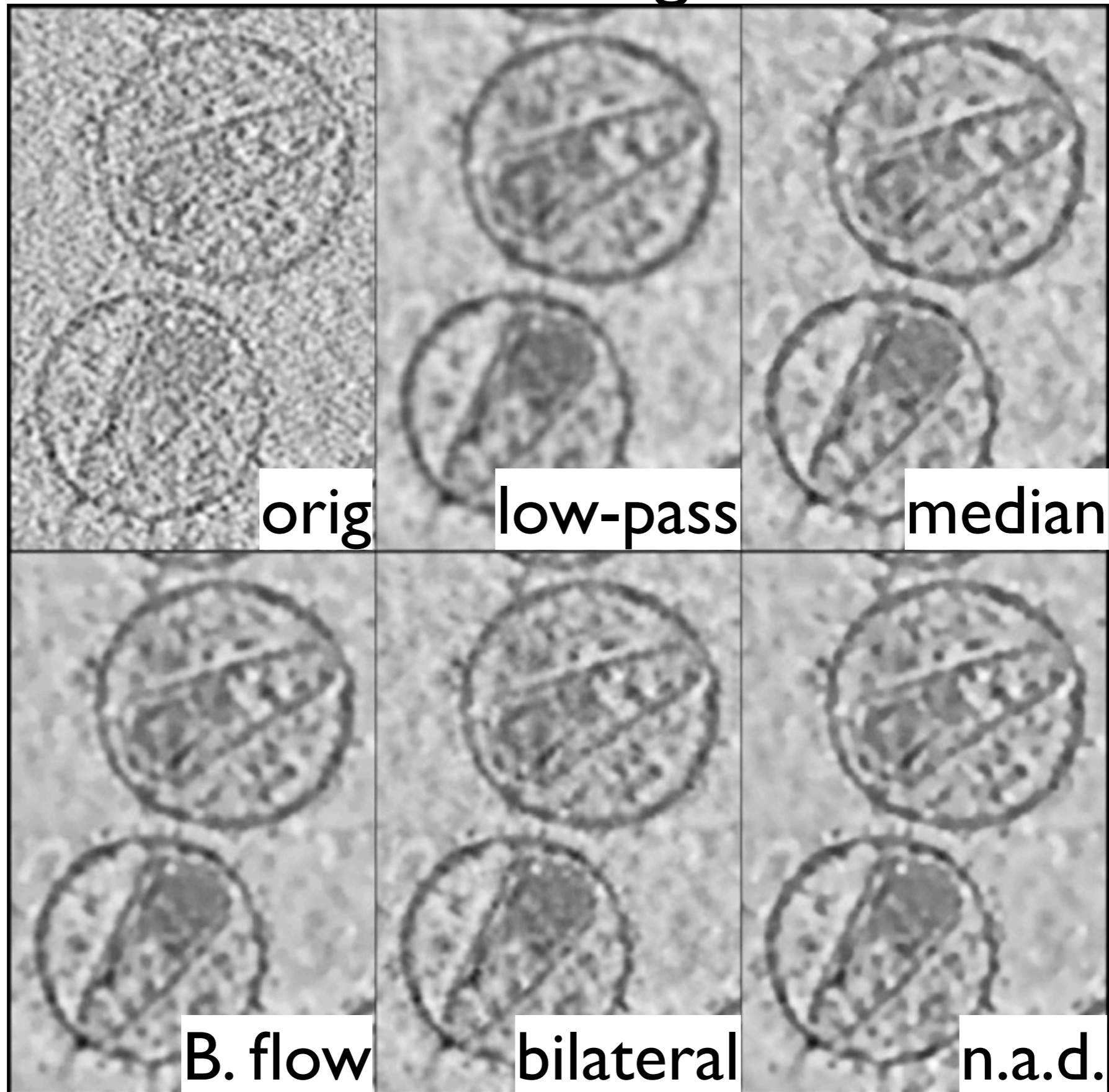
Examples



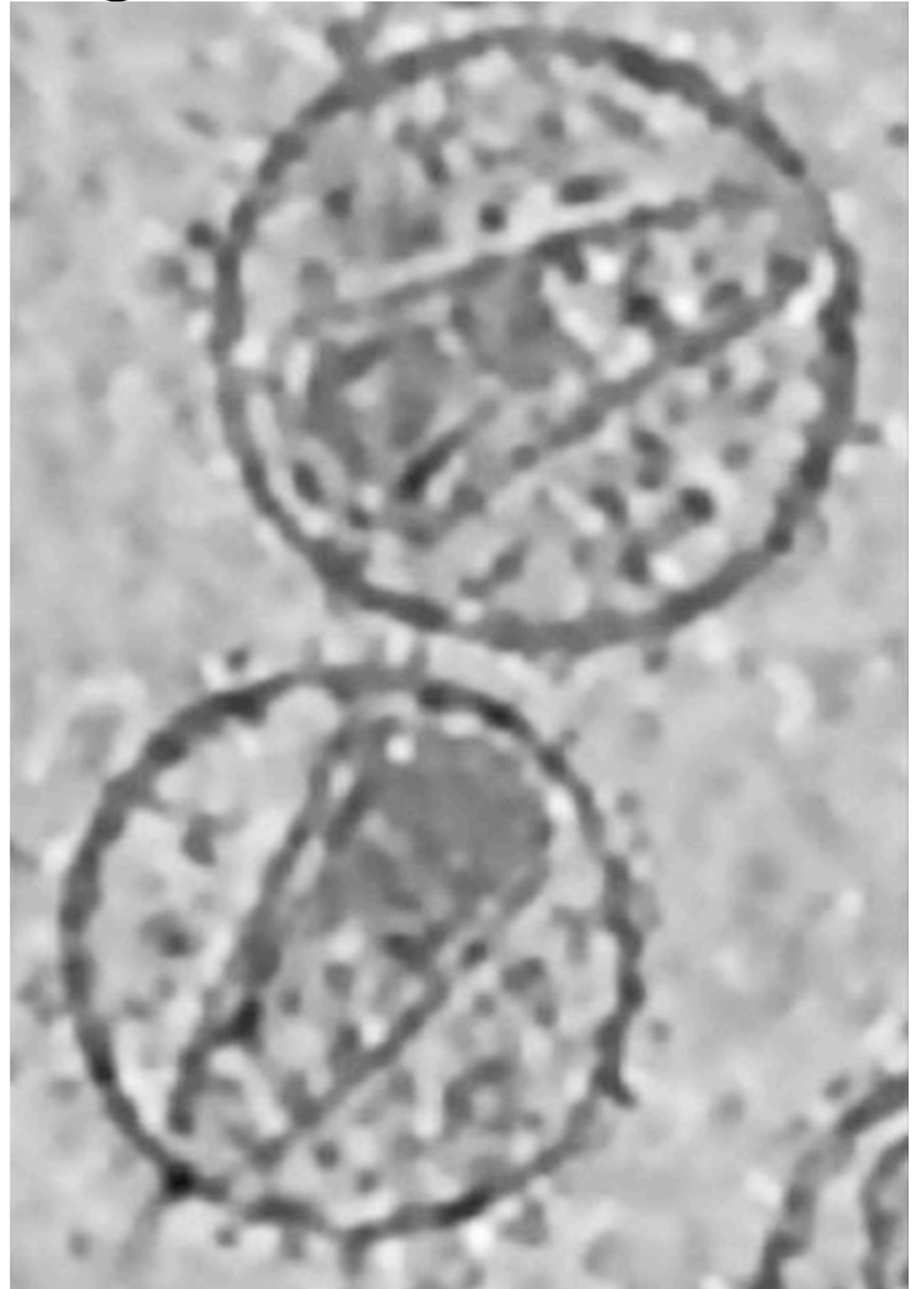
Examples



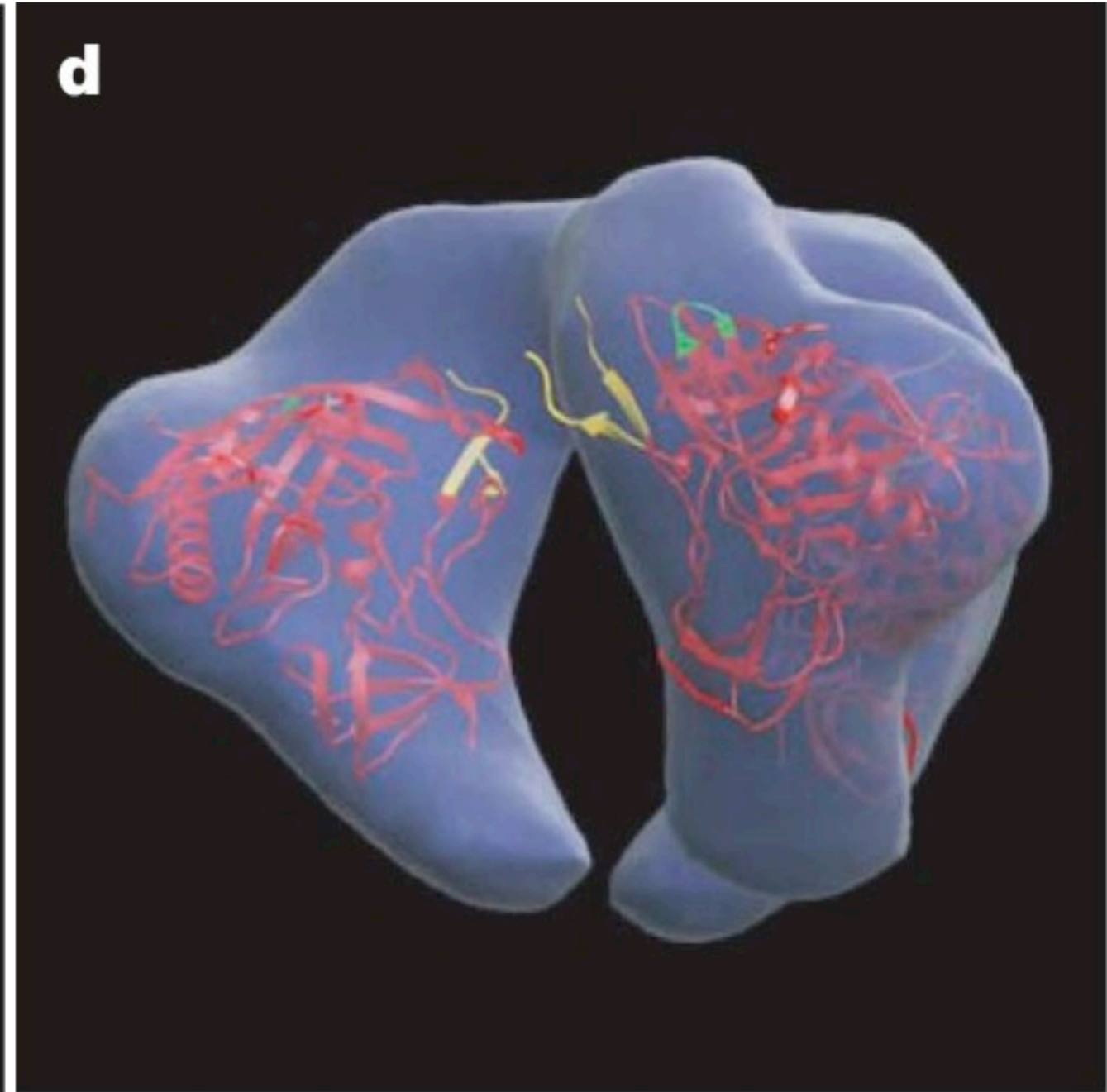
Filtering



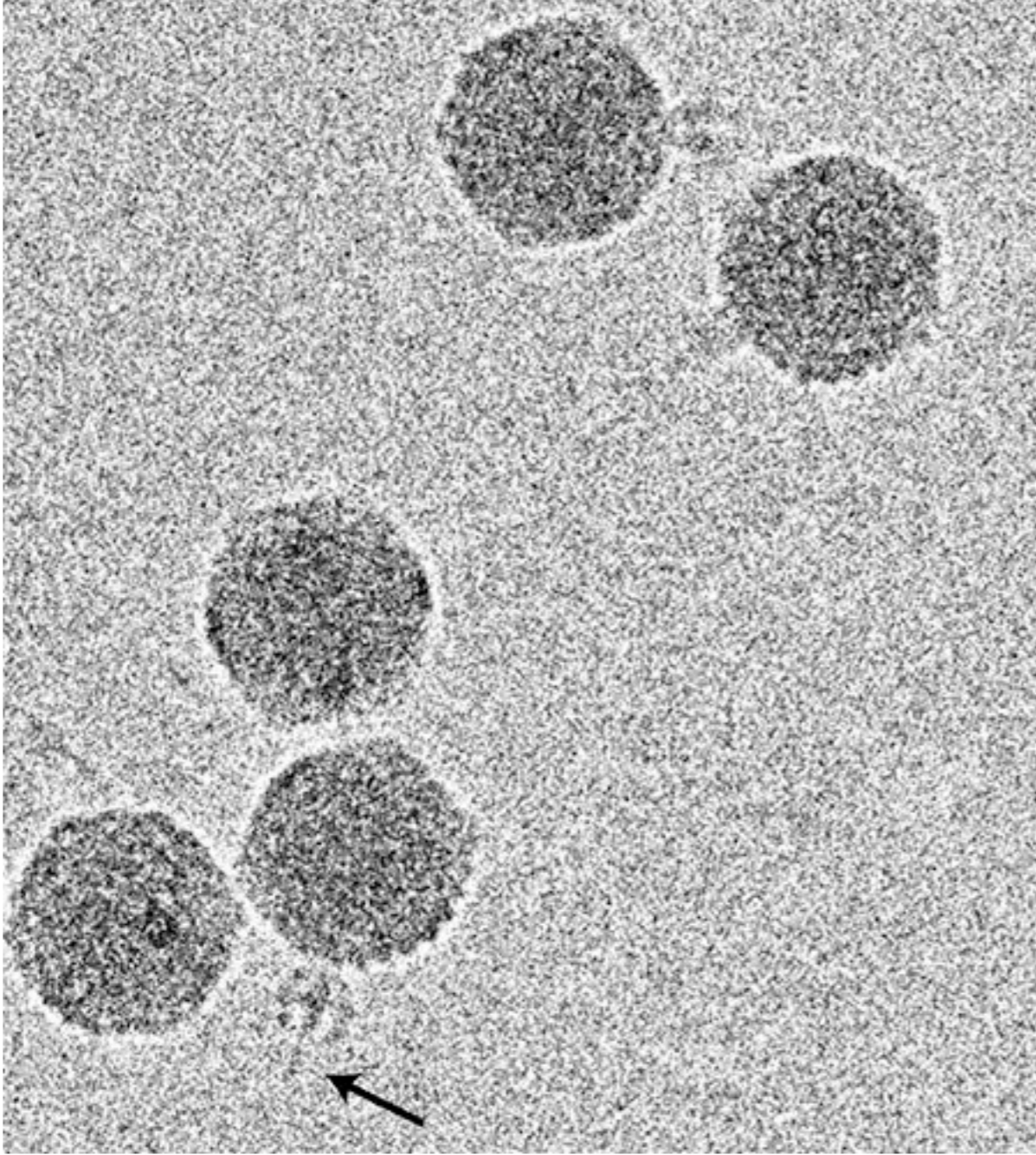
Filtering



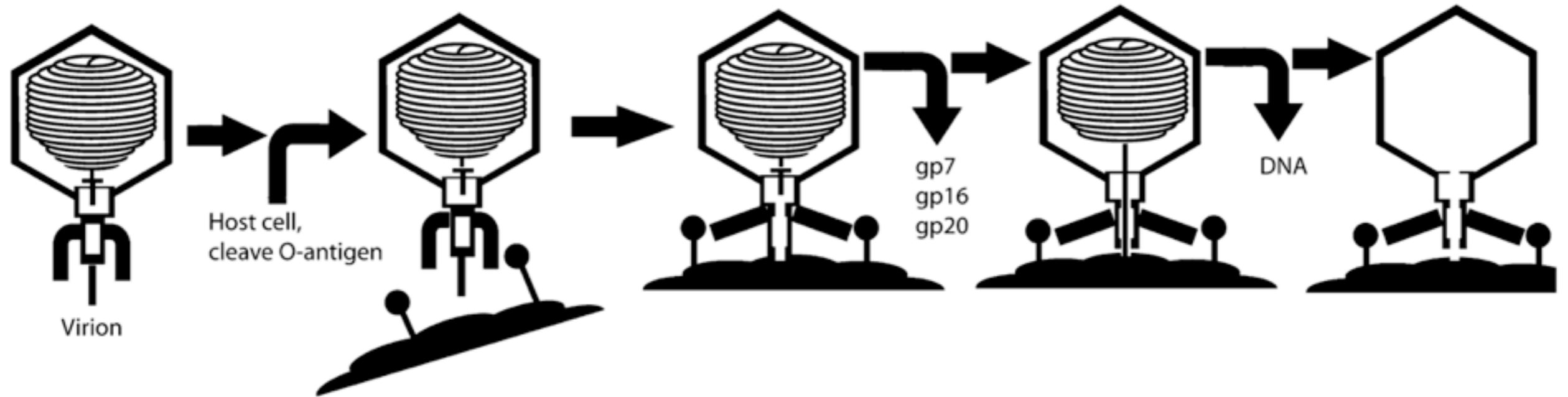
Subtomogram averaging (Mike Schmid)



Viruses + cells



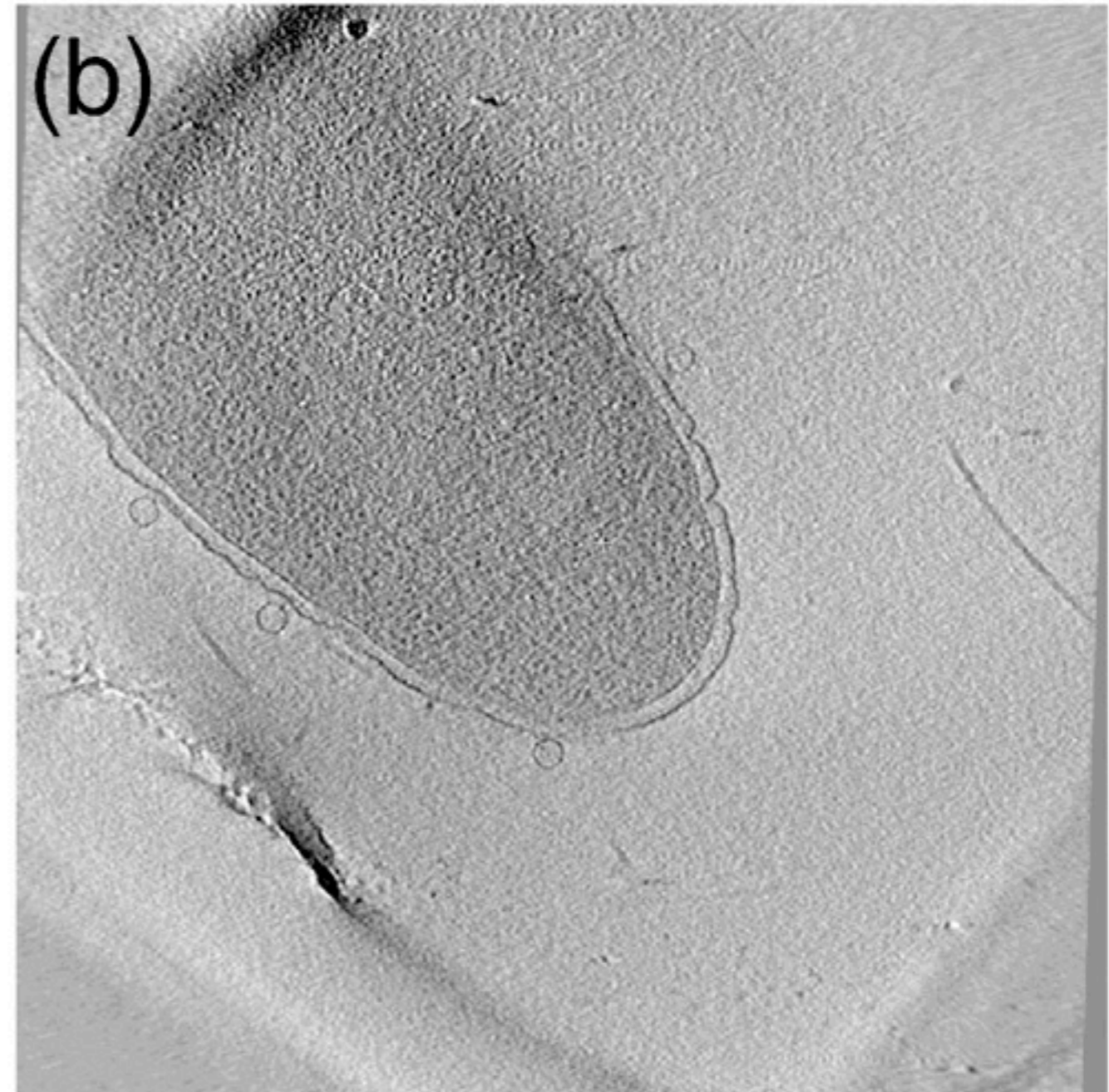
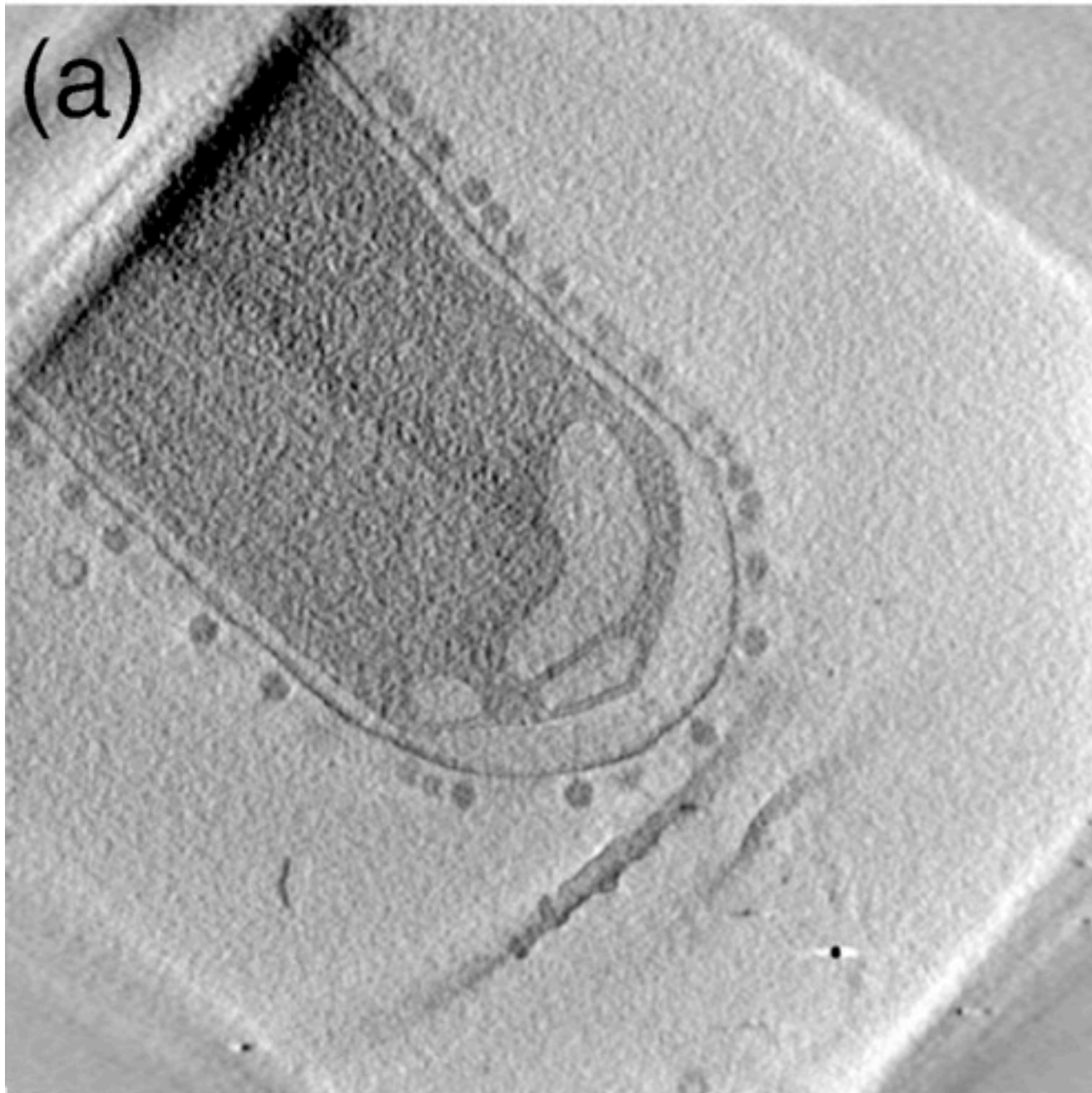
Viruses + cells



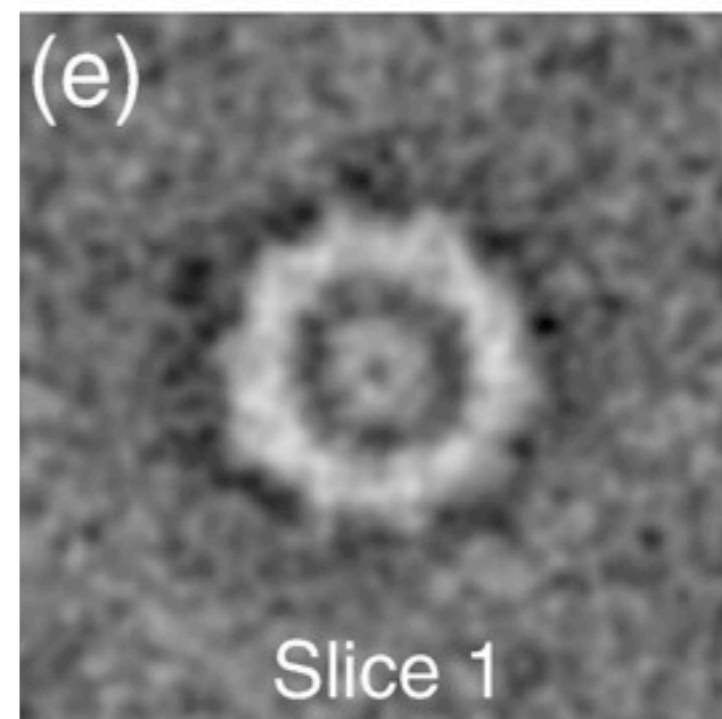
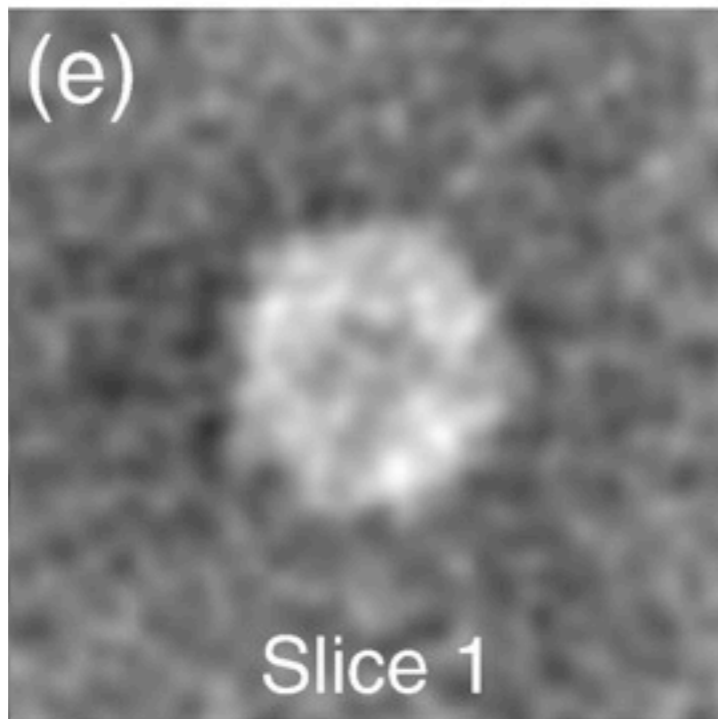
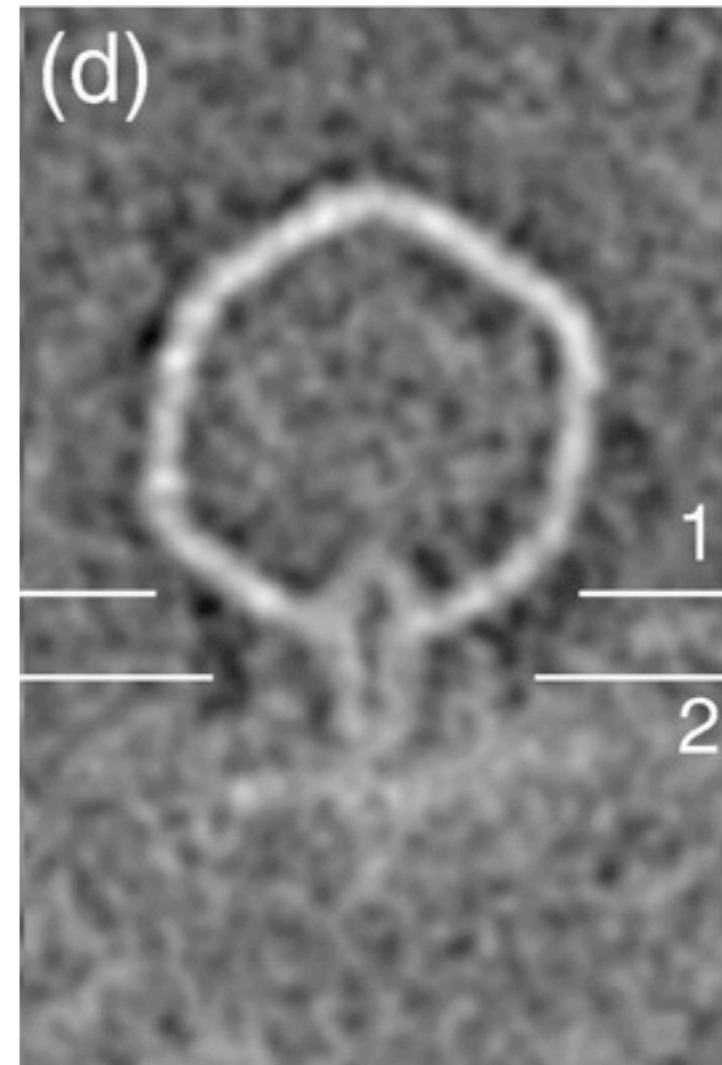
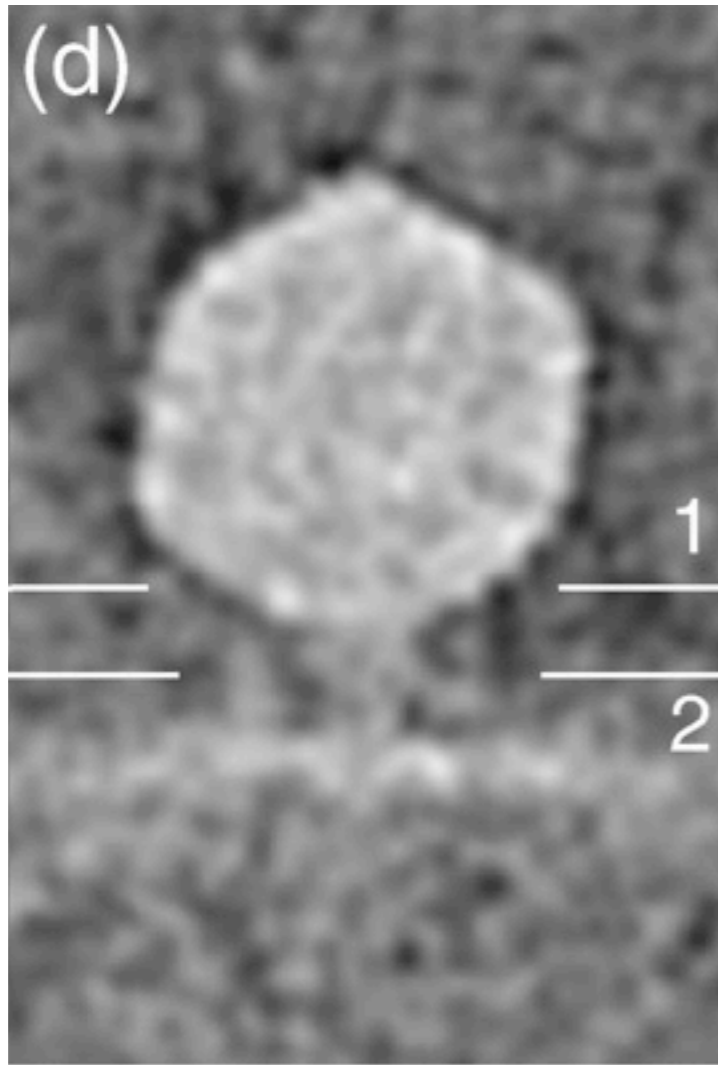
Viruses + cells

$\epsilon 15$ + Cell

$\epsilon 15$ + Cell



Viruses + cells



Recommended readings

Perspectives of Molecular and Cellular Electron Tomography

Koster (1997), J. Struct Biol 120, 276

The potential and limitations of neutrons, electrons and X-rays for atomic resolution microscopy of unstained biological molecules

Henderson (1995), Quart Rev Biophys 28, 171

Electron tomography of cells (recent examples highlighted)

Gan and Jensen (2012), Quart Rev Biophys 45, 27

Electron Tomography: Methods for Three-Dimensional Visualize of Structures in the Cell

Frank (2006), London, New York: Springer

Data collection:

- FEI Tomo
- JADAS
- Leginon
- TOM² Toolbox
- UCSF Tomo

Data processing:

- BSoft
- EMAN
- IMOD
- ProTomo
- SPIDER
- TOM² Toolbox

For a complete list:

en.wikibooks.org/wiki/Software_Tools_For_Molecular_Microscopy