

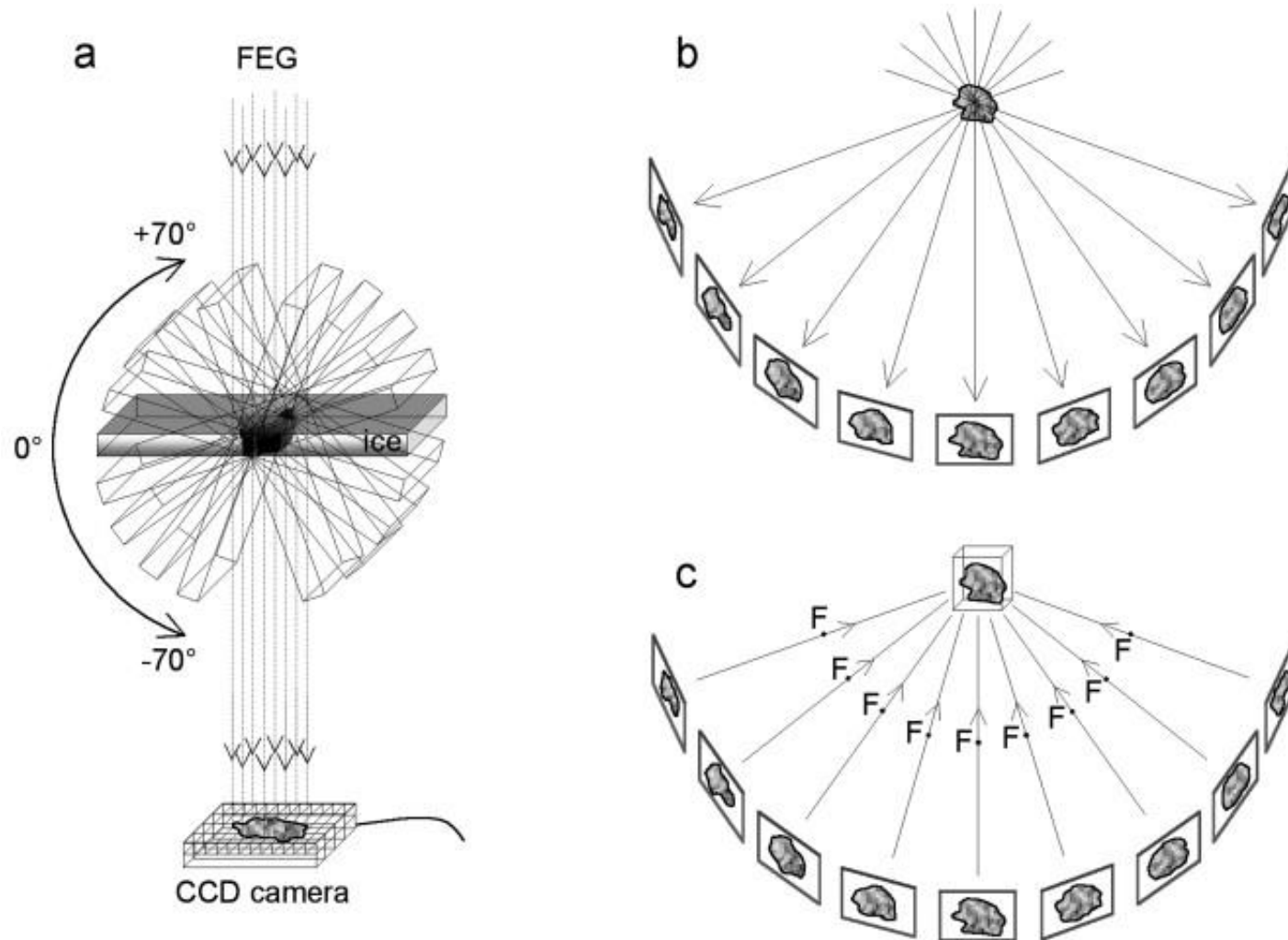
Cryo-Electron Tomography: Image Processing & Interpretation

Nadav Elad

26 Nov 2020

IMpaCT online tomography lecture course

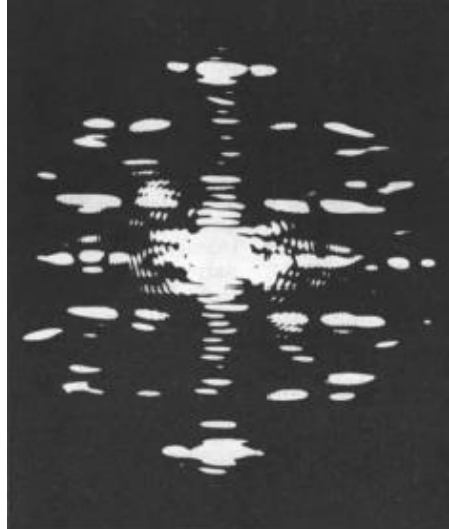
Tomography



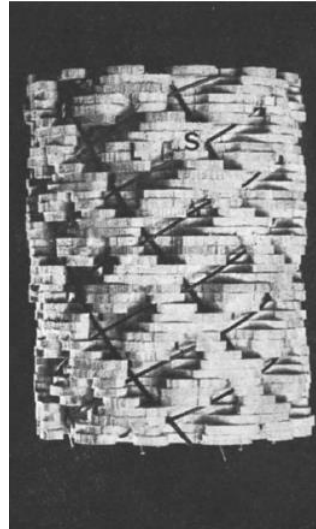
Principle of 3D reconstruction from EM micrographs



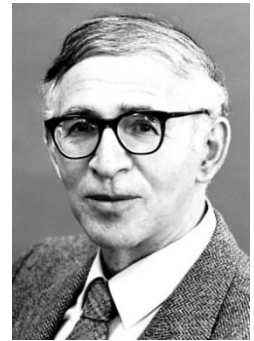
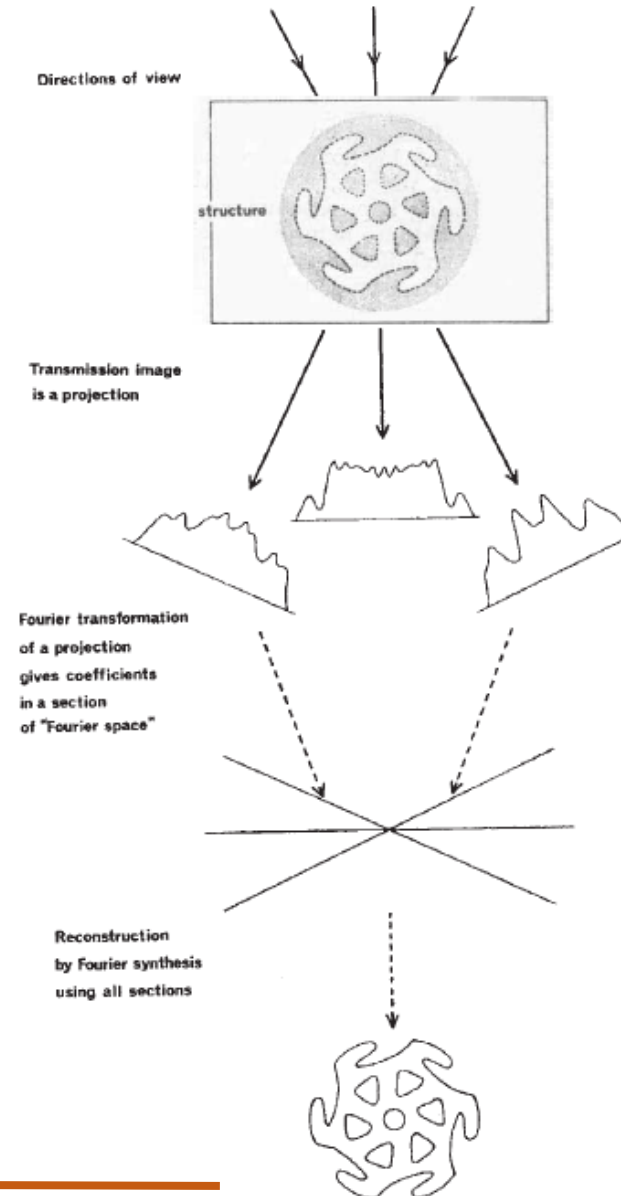
TEM projection



Fourier transform



3D map



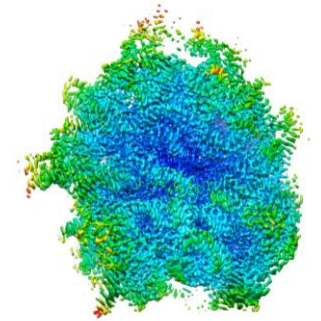
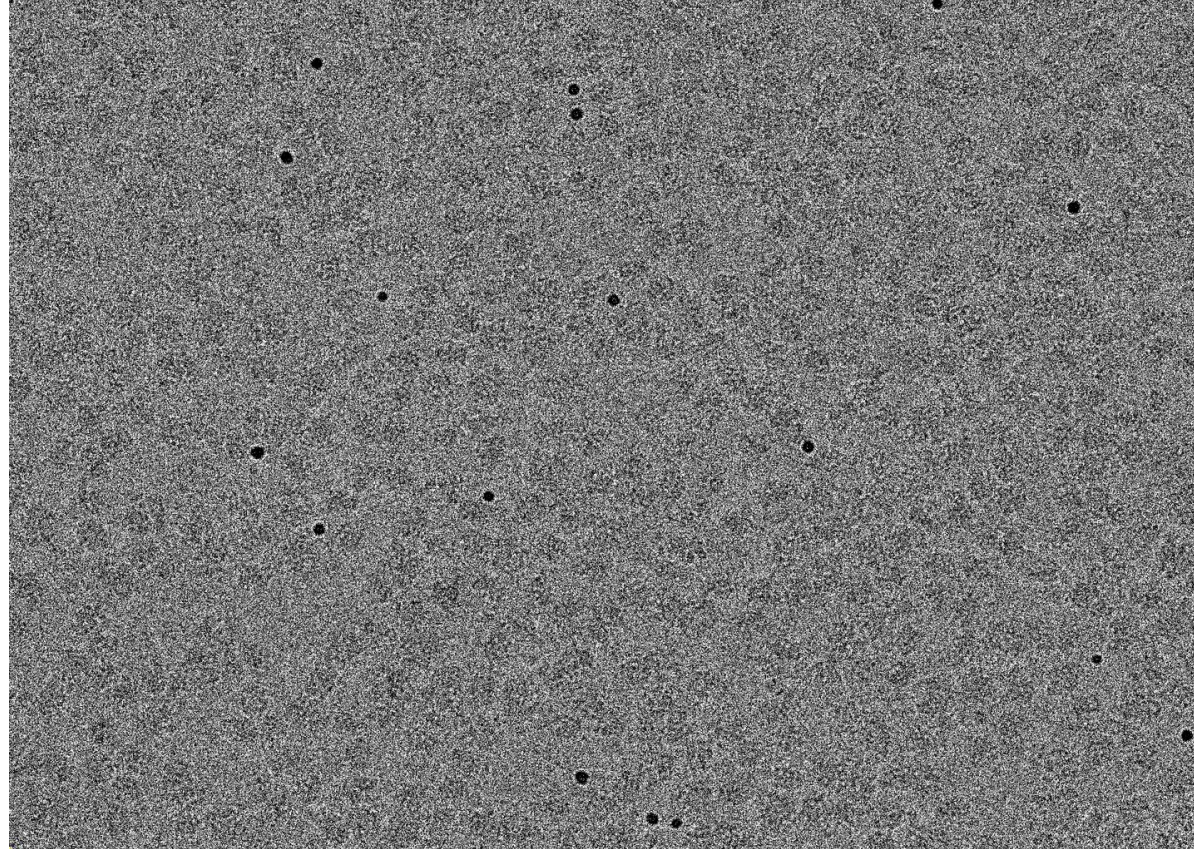
DeRosier and Klug (1968) Nature

Tomogram reconstruction from tilt series

- Alignment by cross correlation
- Fiducial model
- Accounting for distortions
- Weighted back projection
- The projection theorem
- SIRT

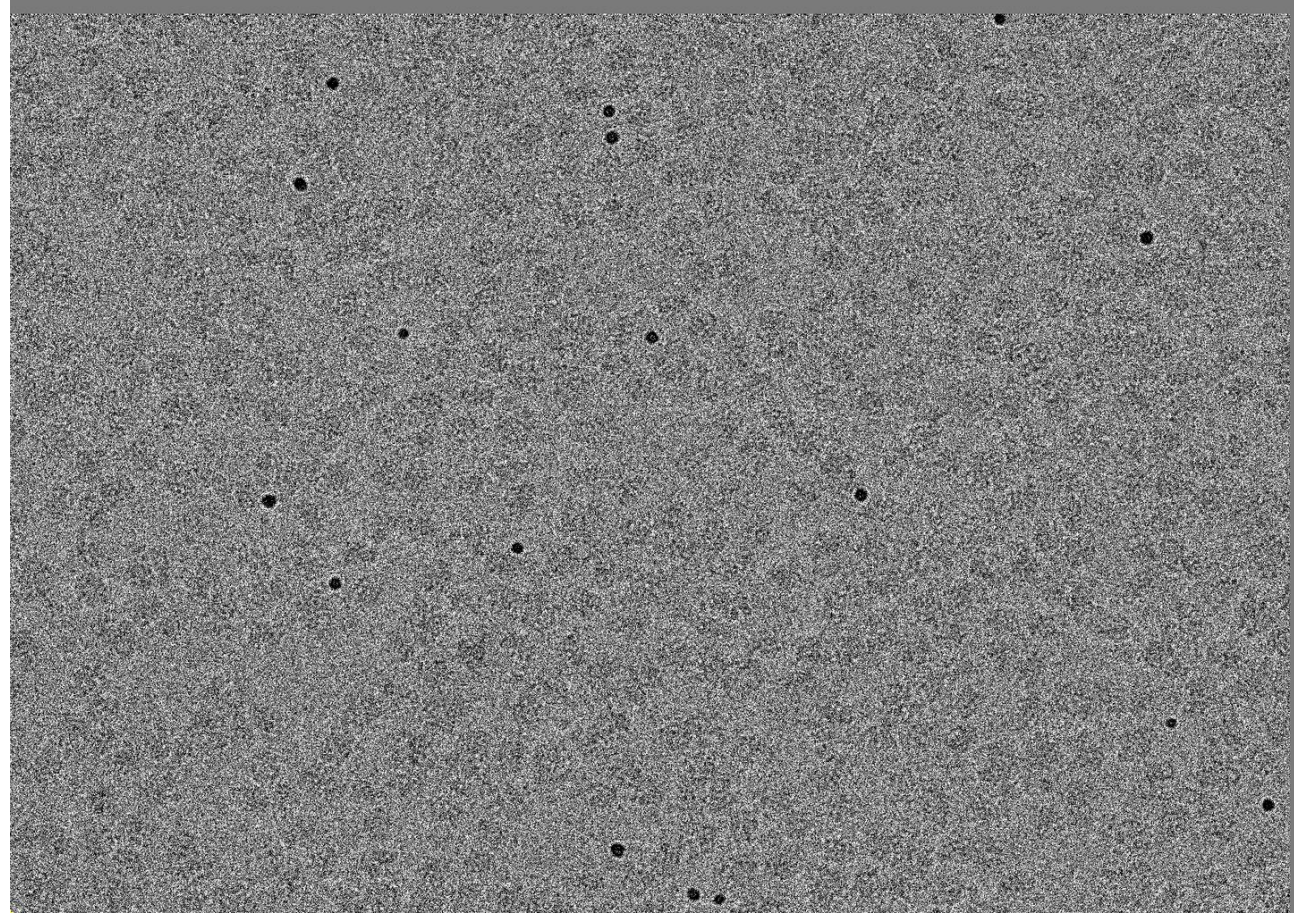
Raw tilt series

- Titan Krios @WIS
- 300 kV
- K3 direct detector
- Energy filter with 20eV slit
- SerialEM
- +60° to -60°, 2° increment
- Dose symmetric tilt scheme
- 81k magnification, 1.1 Å/pixel
- Dose/tilt: 2.46 e/Å
- Total dose: 150 e/Å
- 1.8 μm defocus

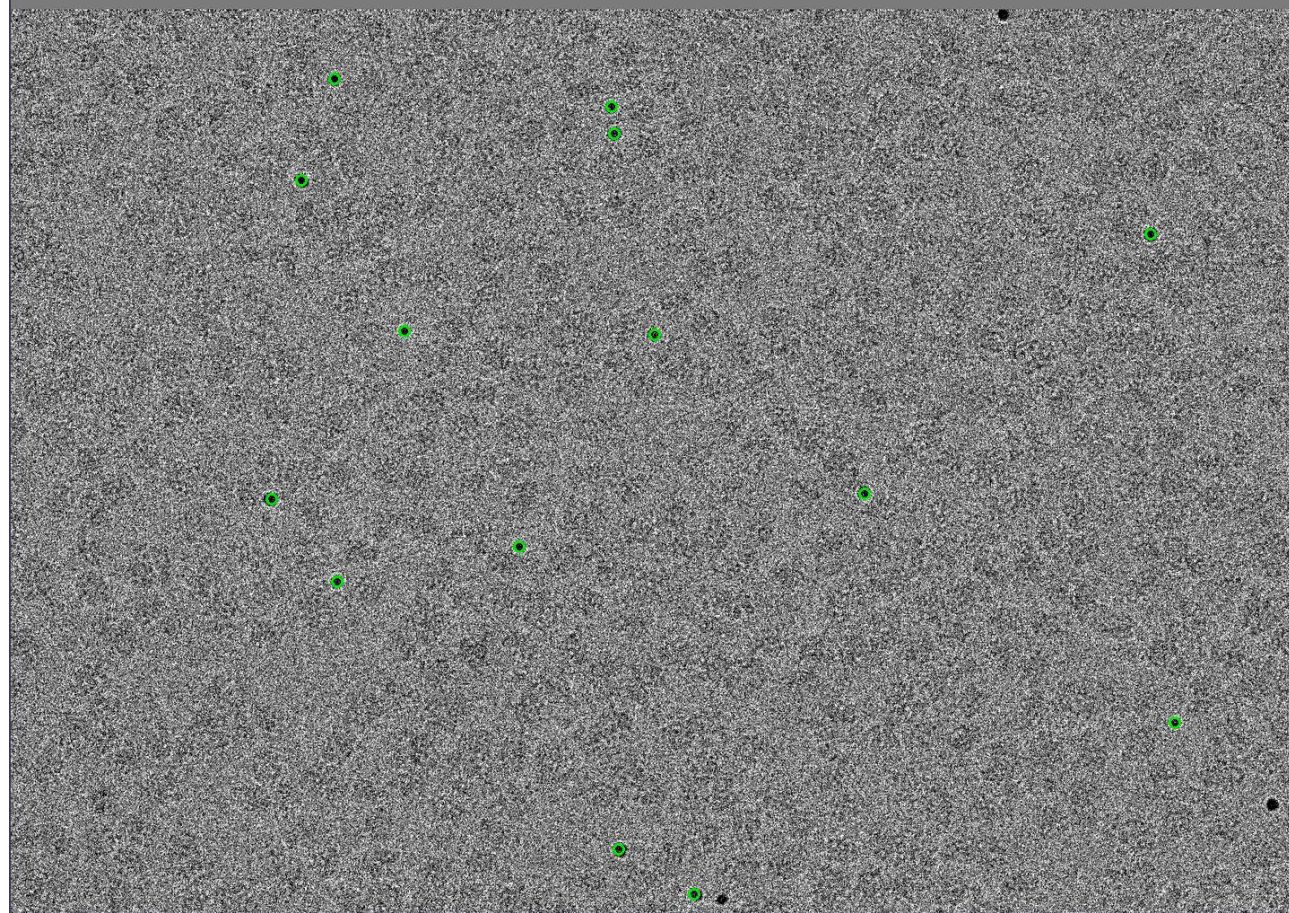


S. Aureus 70S ribosome
from
Elinor Breiner-Goldstein
Yonath group

Alignment of tilt series by cross correlation

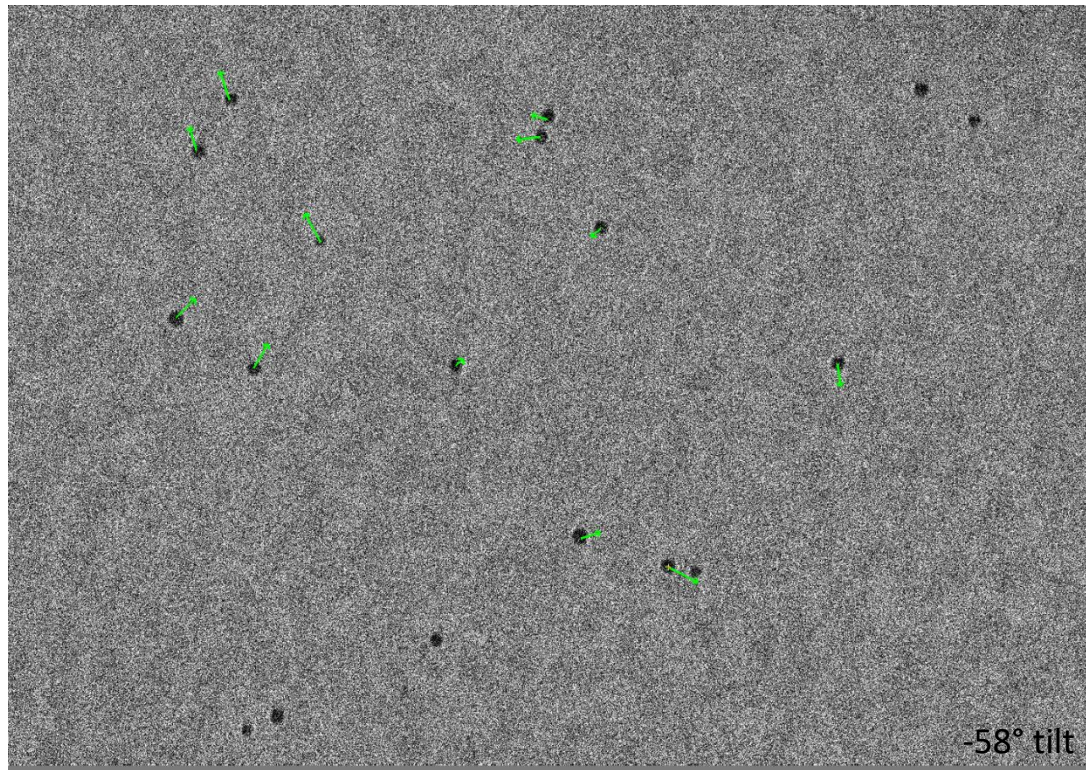


Alignment of tilt series with fiducial markers



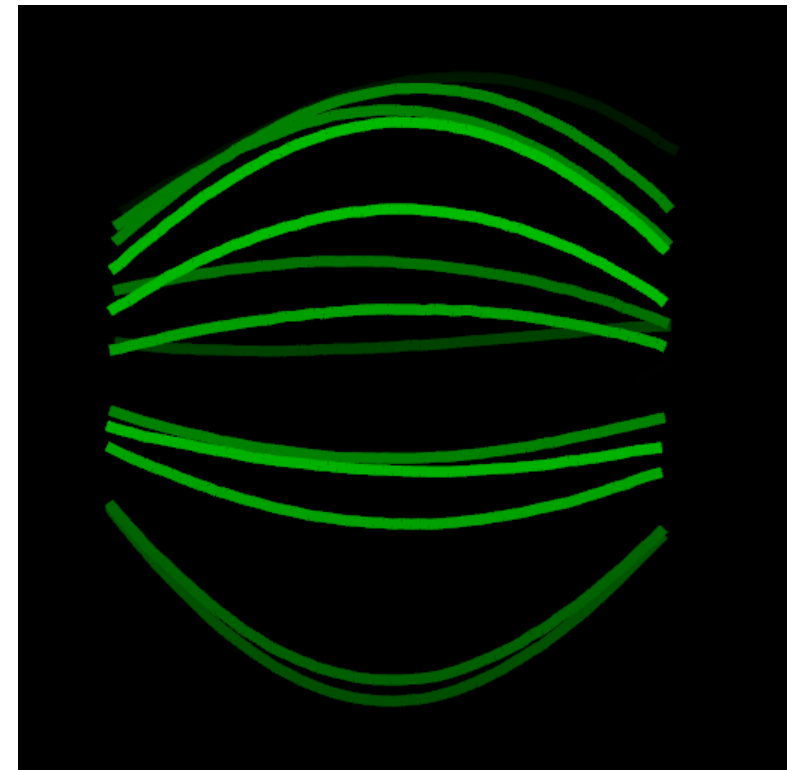
Fiducial model

Residual vectors



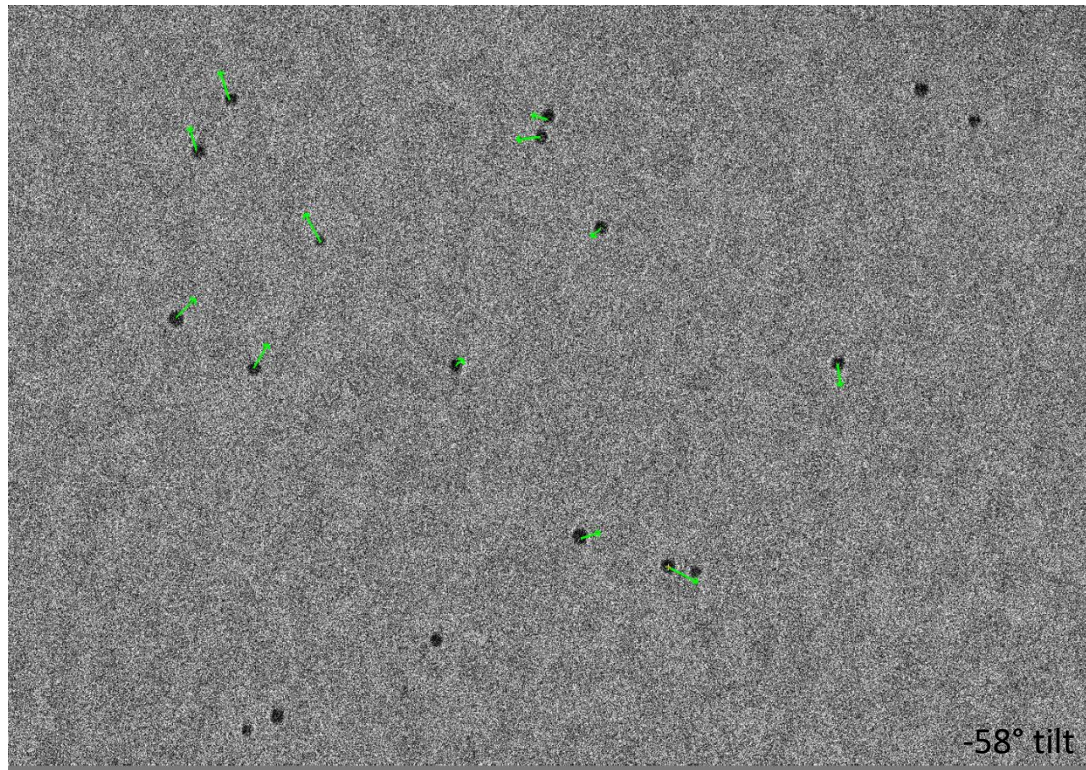
mean residual error 0.479, sd 0.324 nm

Fiducial model



Fiducial model - accounting for distortions

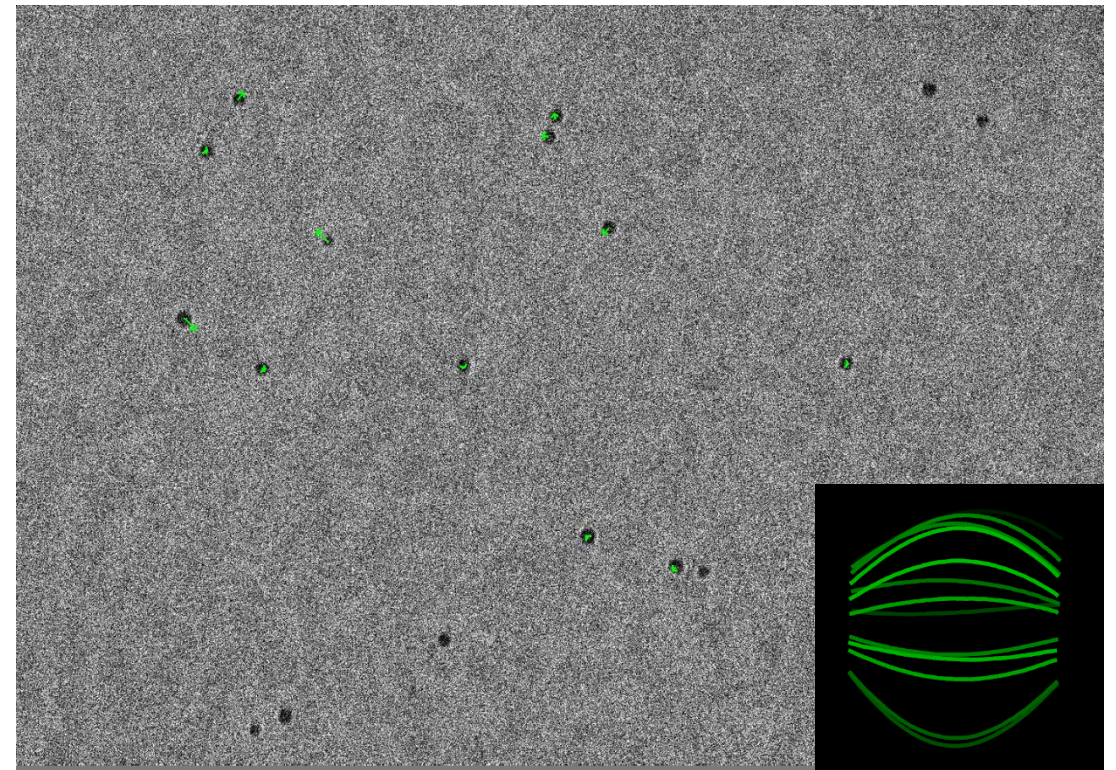
No corrections



Mean residual error 0.479, sd 0.324 nm

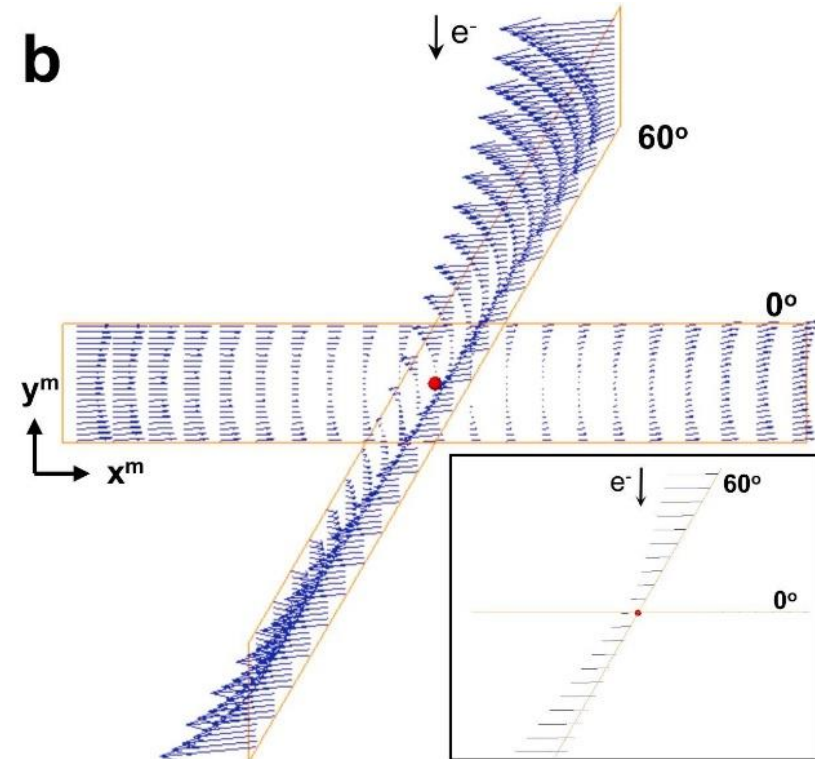
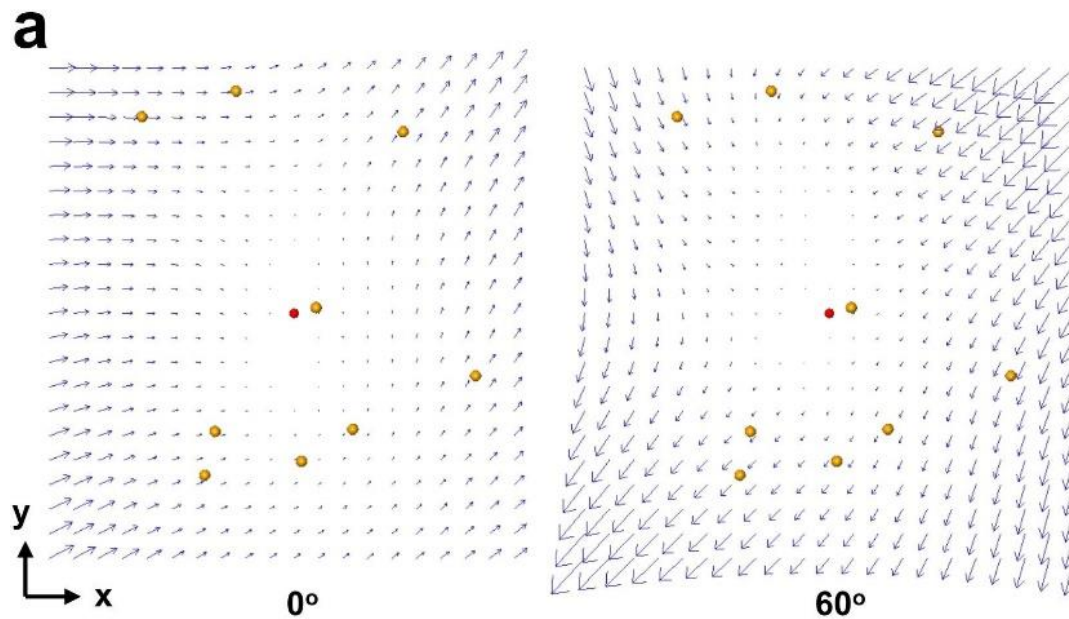
With correction:

Rotation, magnification, tilt angle, image distortions



Mean residual error 0.294, sd 0.164 nm

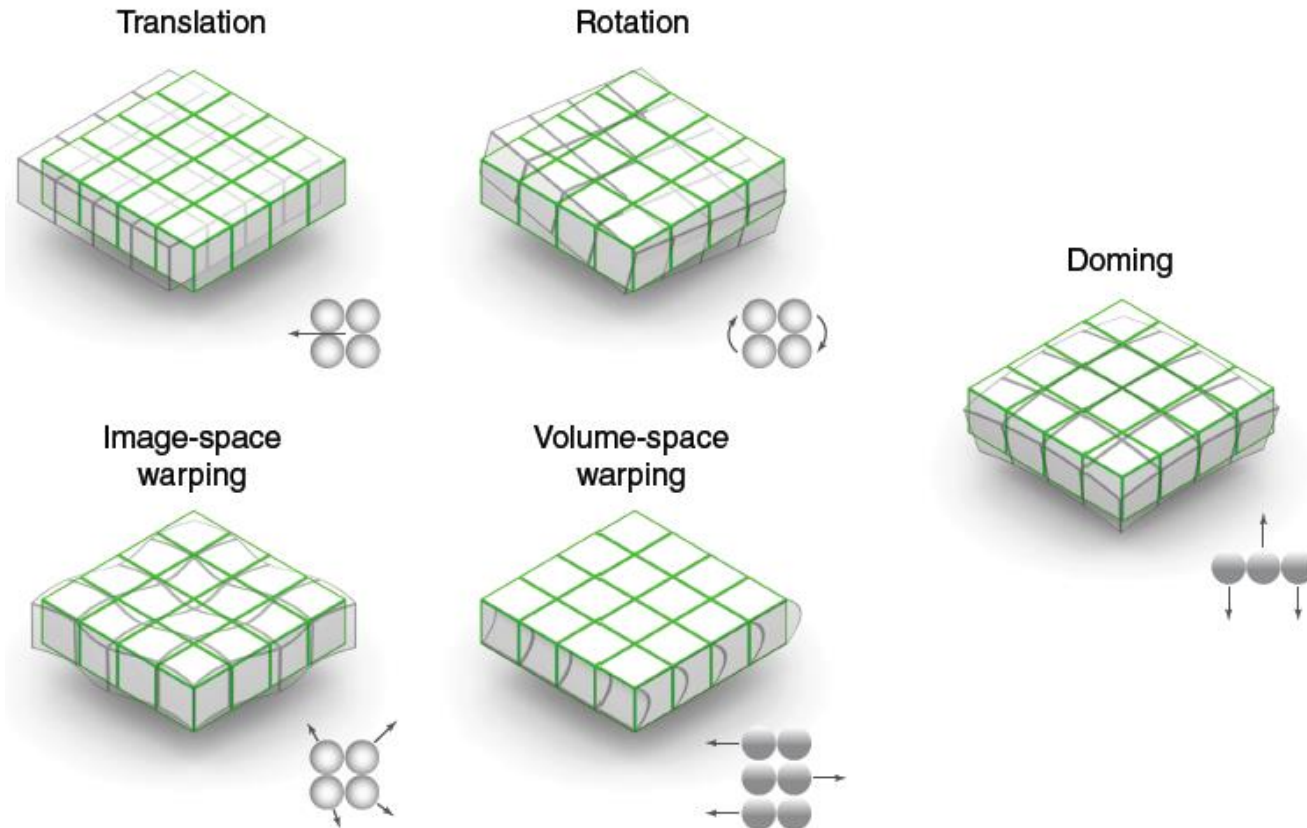
Accounting for distortions



TomoAlign software

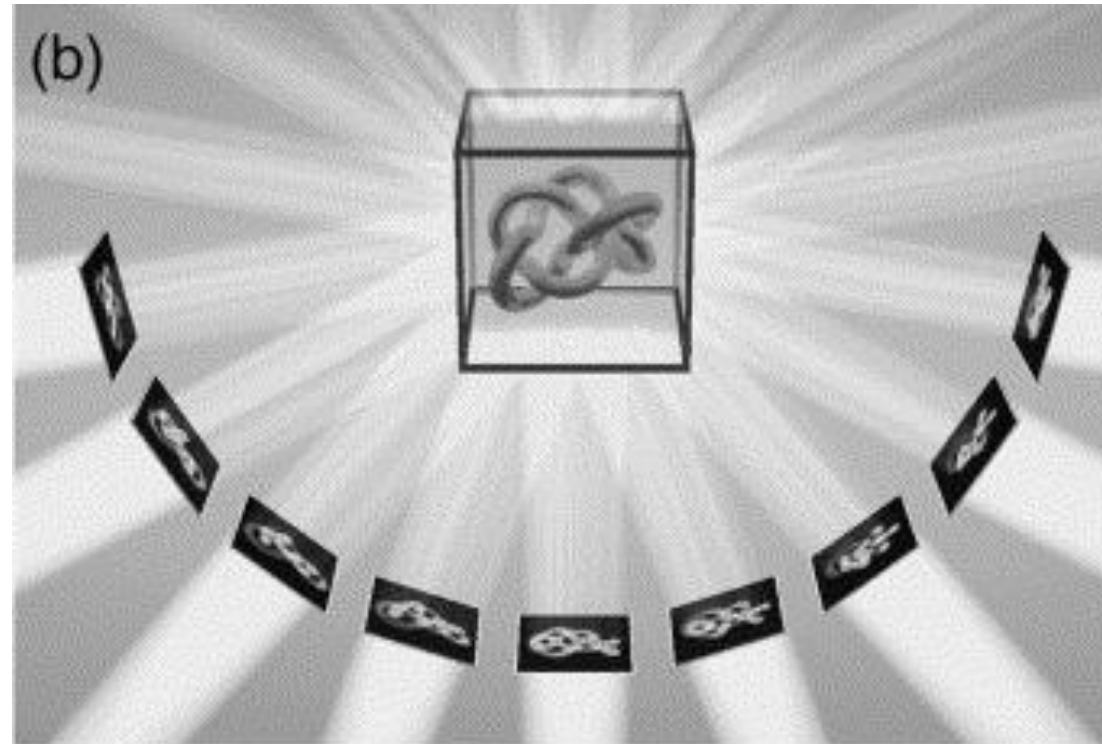
Fernandez et al (2018) *JSB*. Cryo-tomography tilt-series alignment with consideration of the beam-induced sample motion

Accounting for distortions

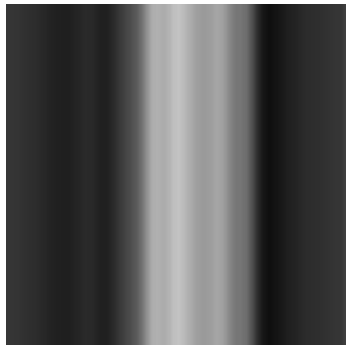
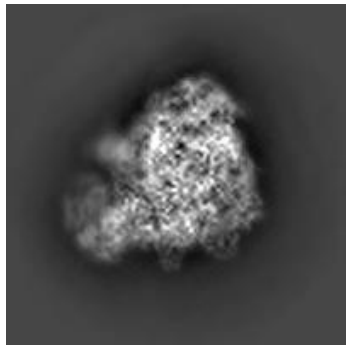


Tegunov et al (2020) *BioRxiv*. Multi-particle cryo-EM refinement with M visualizes ribosome-antibiotic complex at 3.7 Å inside cells

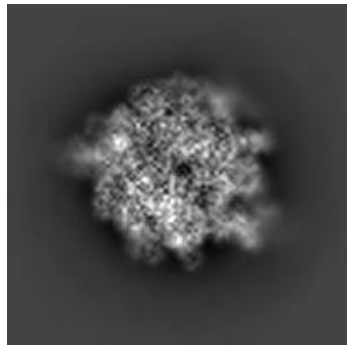
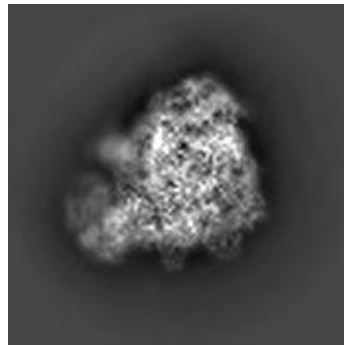
Back-projection



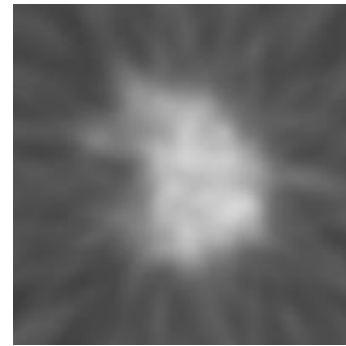
Back-projection



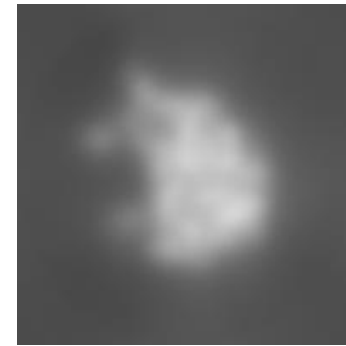
1 angle



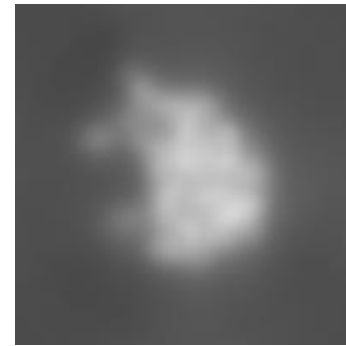
2 angles



9 angles



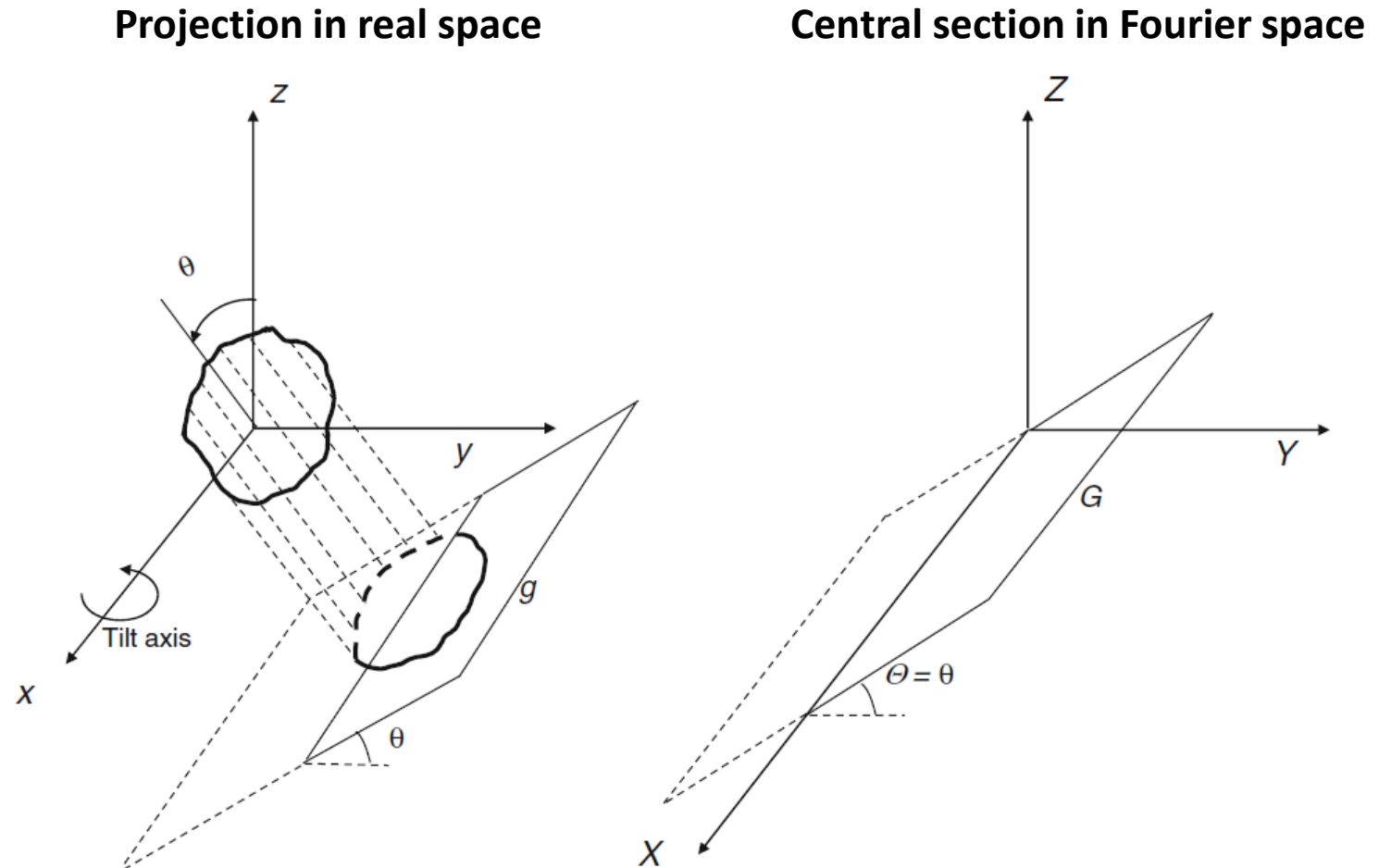
36 angles



180 angles

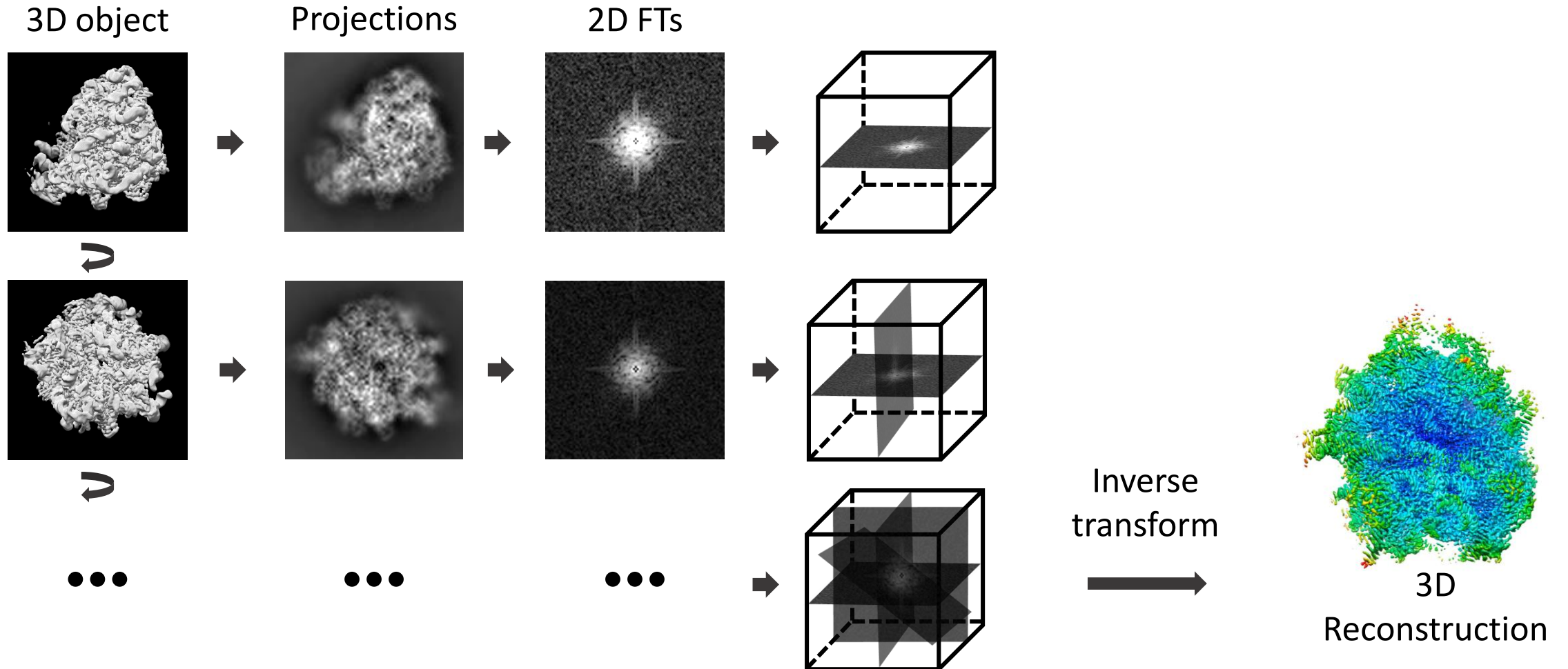
The central section theorem

The 2D FT of an object's projection forms a central plane through the 3D FT of the object

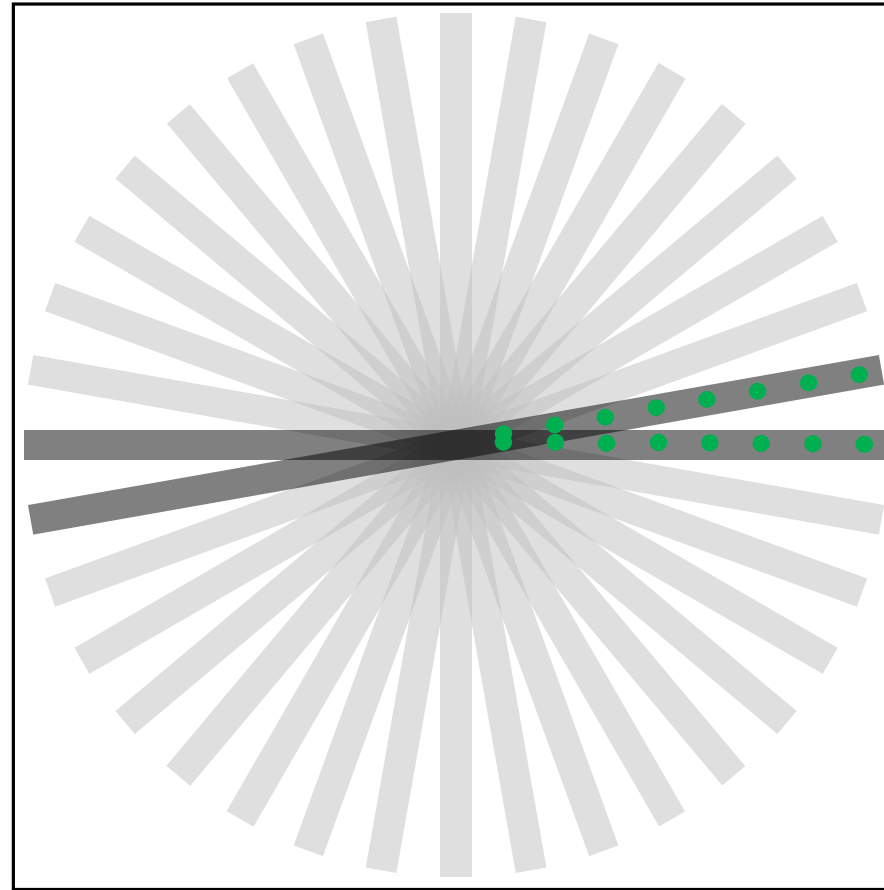
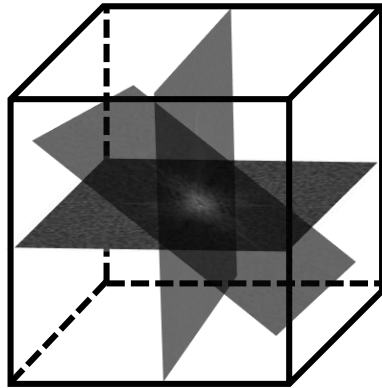


The central section theorem

The 2D FT of an object's projection forms a central plane through the 3D FT of the object

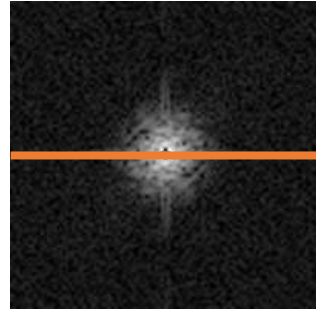


Over sampling of low frequencies in Fourier space

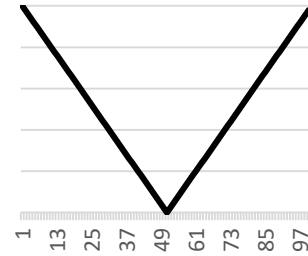


Weighted back-projection

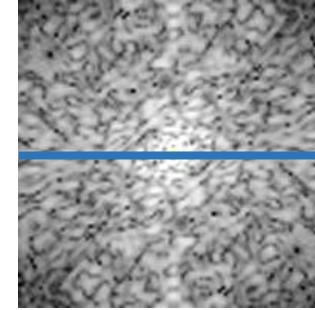
FT of tilt



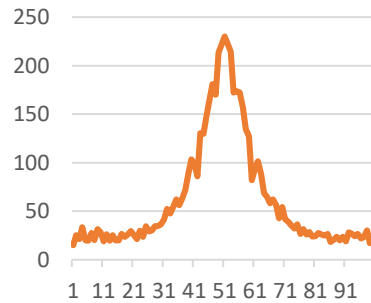
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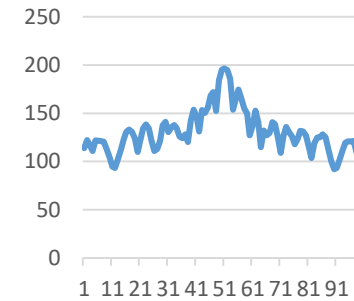
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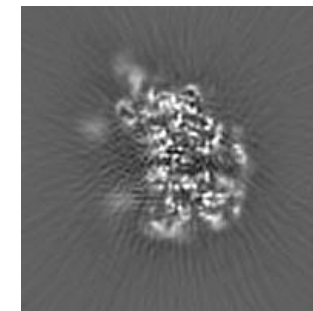
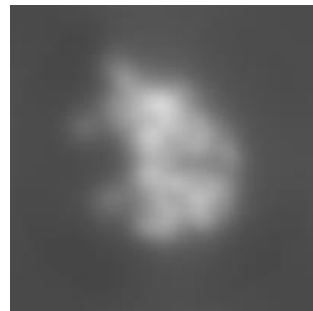
Cross section
of FT



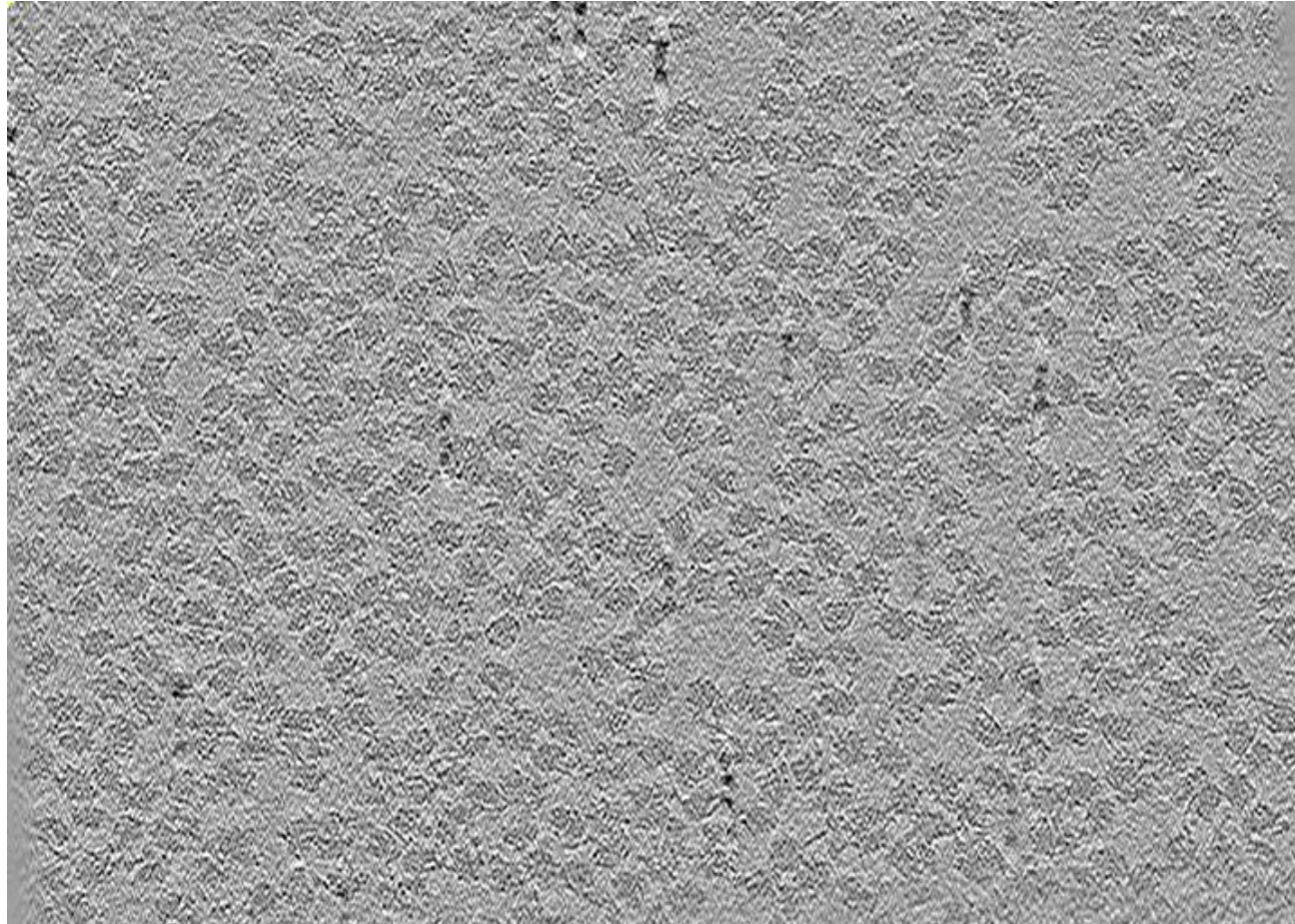
R-weighting of tilts



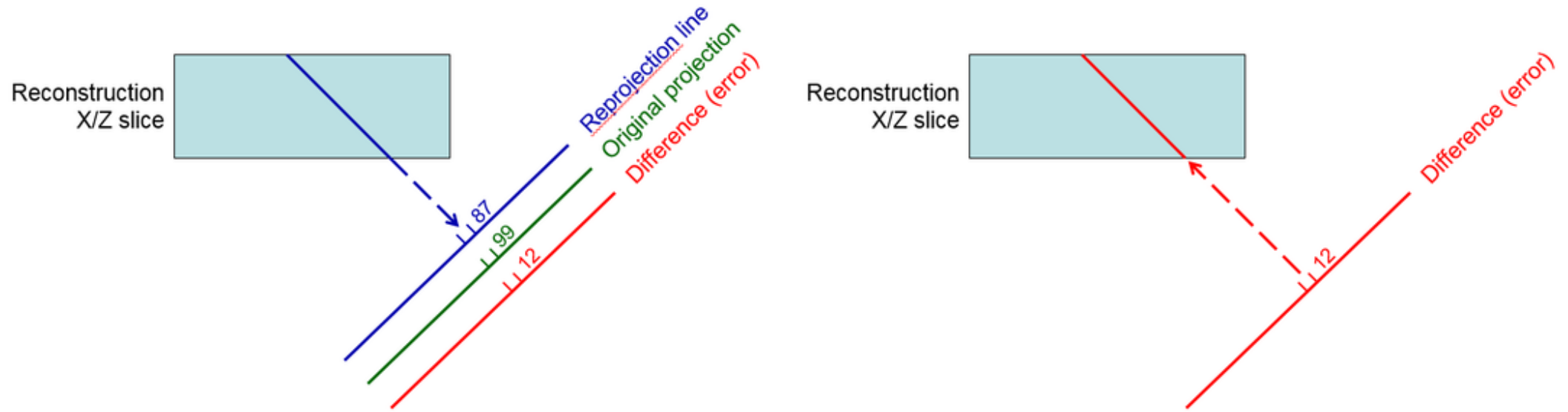
Slice through
reconstruction



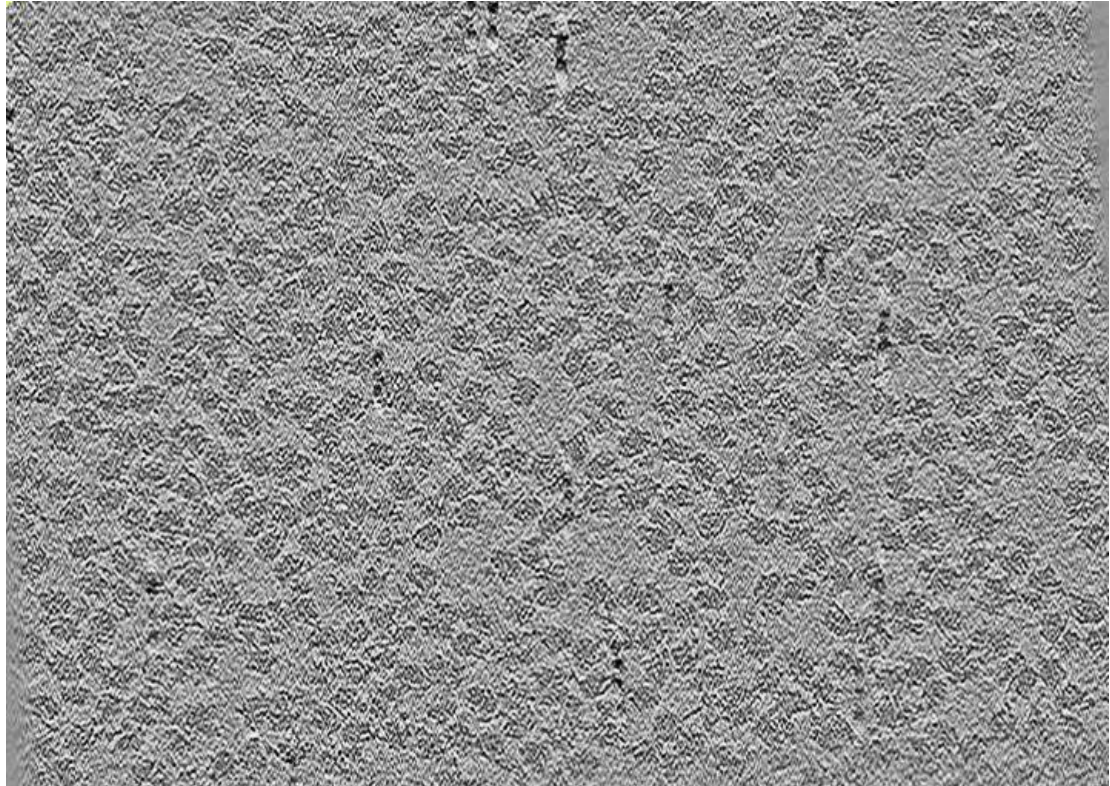
Reconstruction



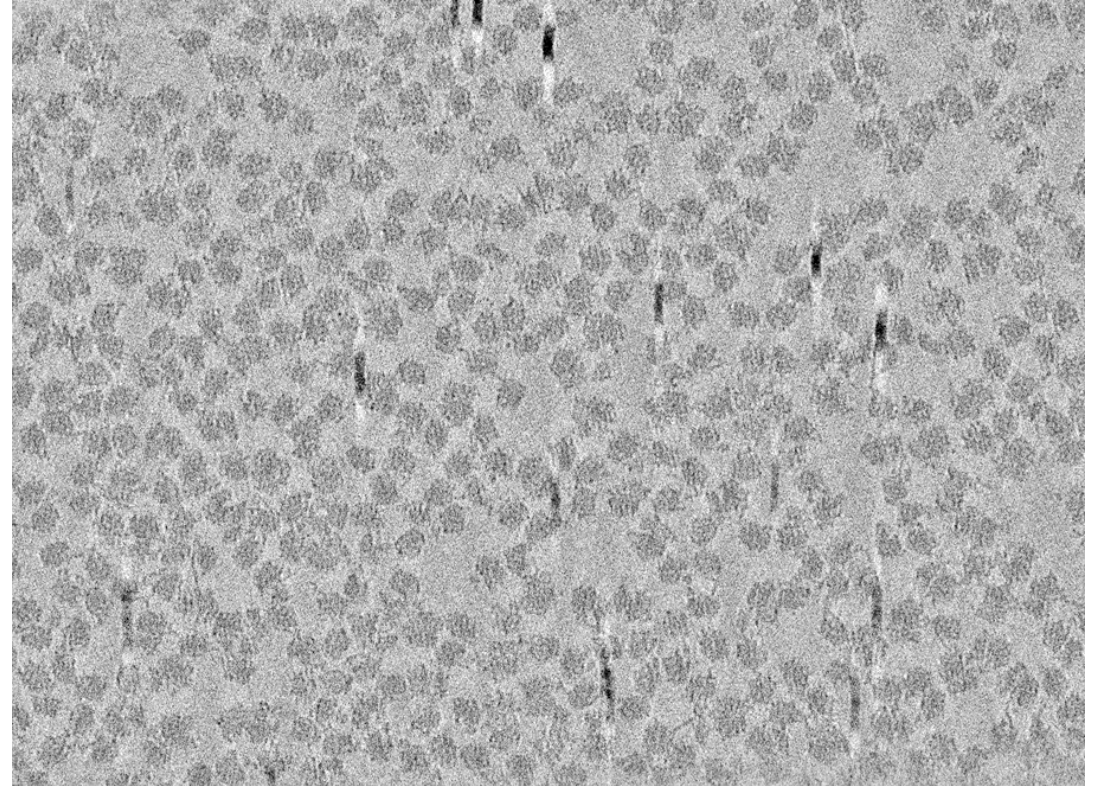
SIRT (Simultaneous Iterative Reconstruction Technique)



SIRT (Simultaneous Iterative Reconstruction Technique)



WBP

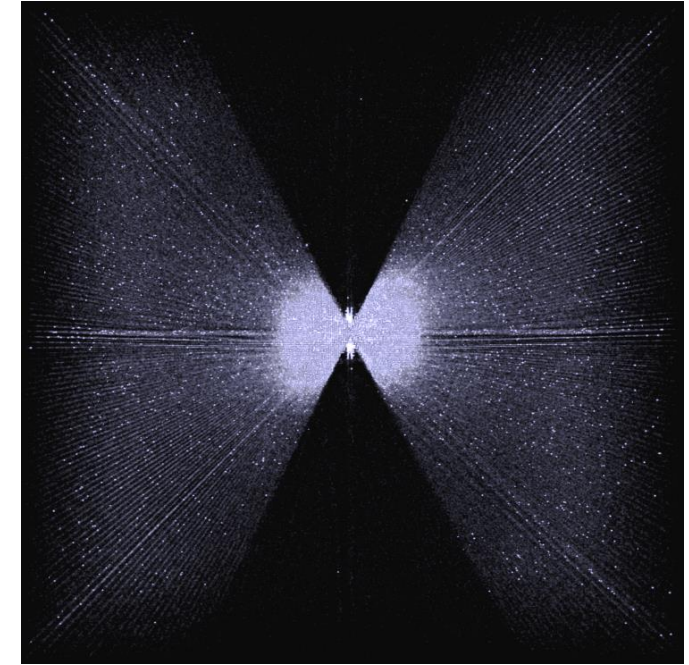
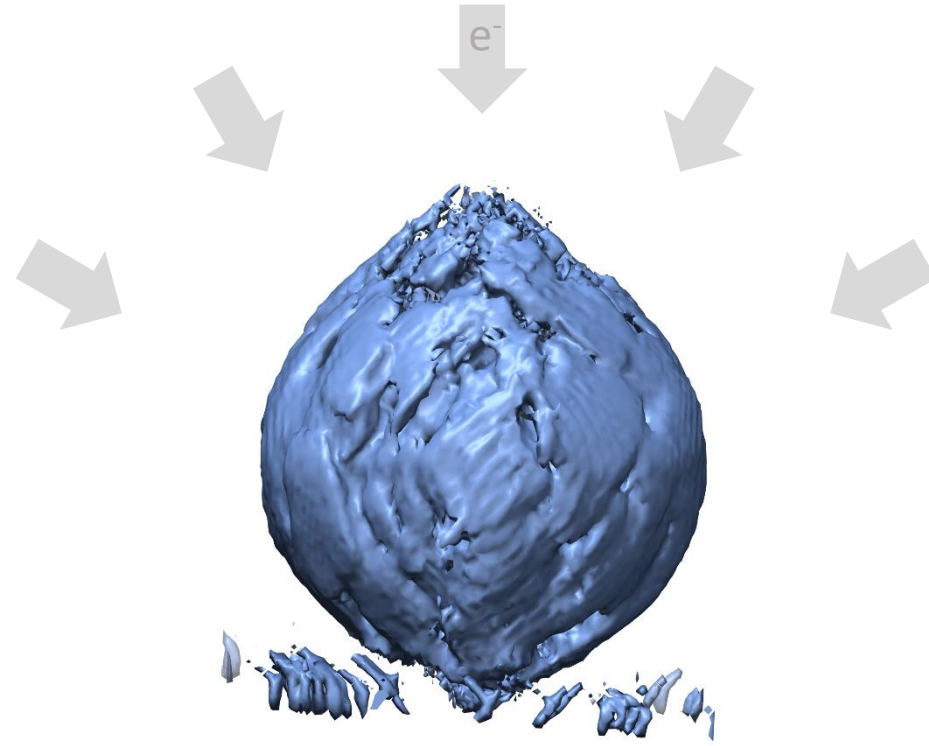
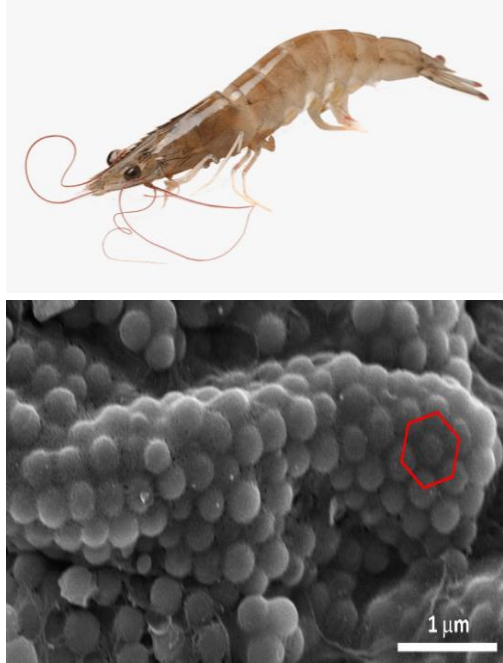


+ SIRT

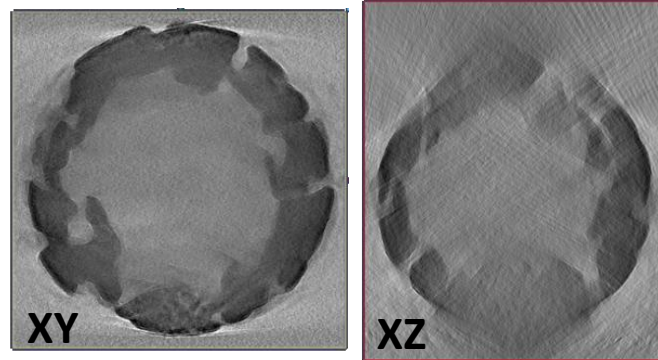
Missing information in cryo-ET

- Missing wedge
- Discrete sampling
- Electron dose
- Defocus gradient (CTF)

Missing wedge



3D power spectrum

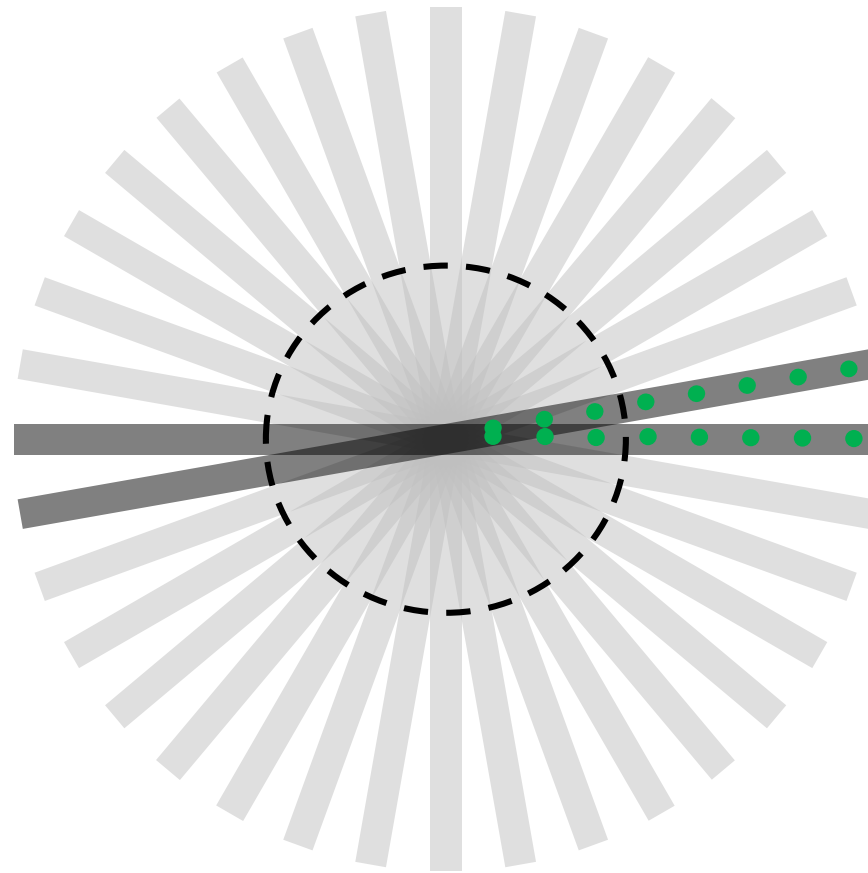


Missing information due to discrete sampling

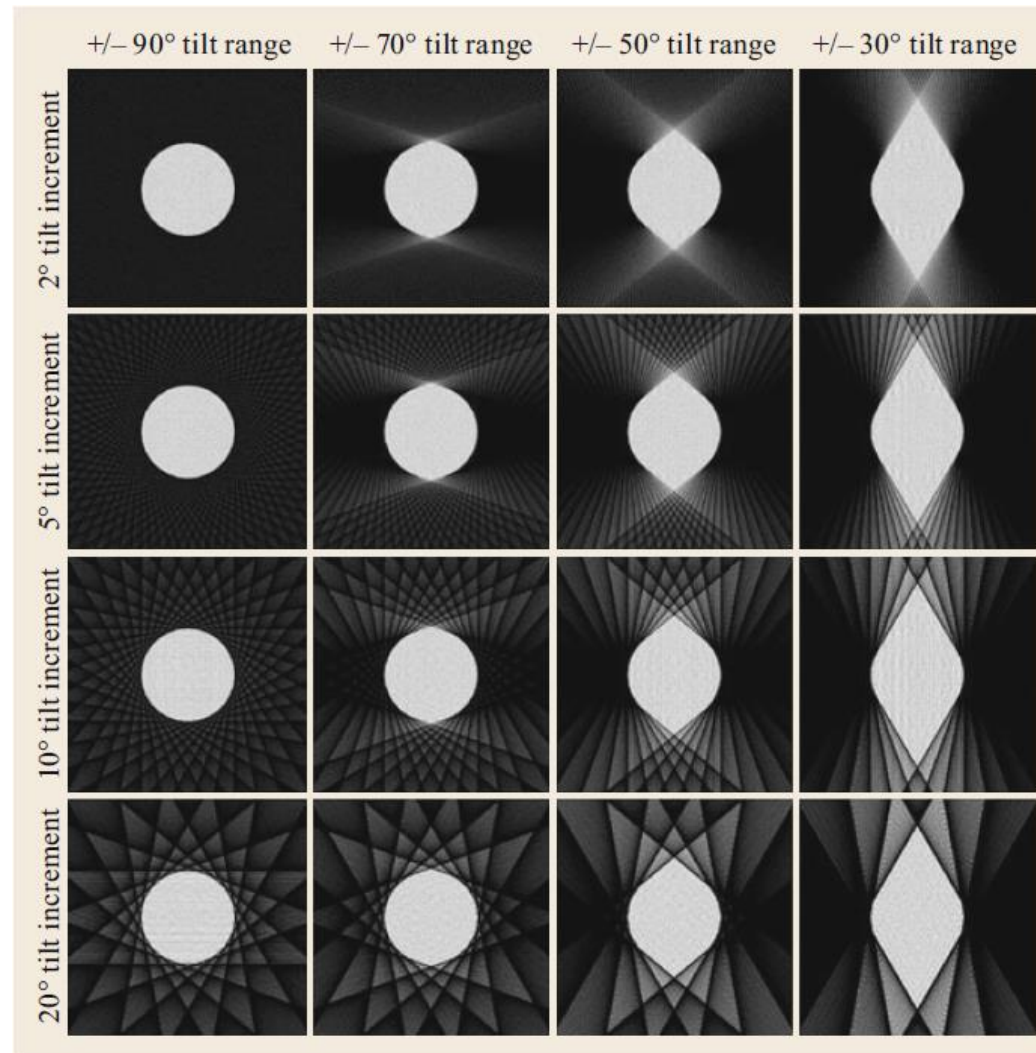
Crowther Criterion

The minimum number of views to reconstruct an object of diameter D to a resolution of r :

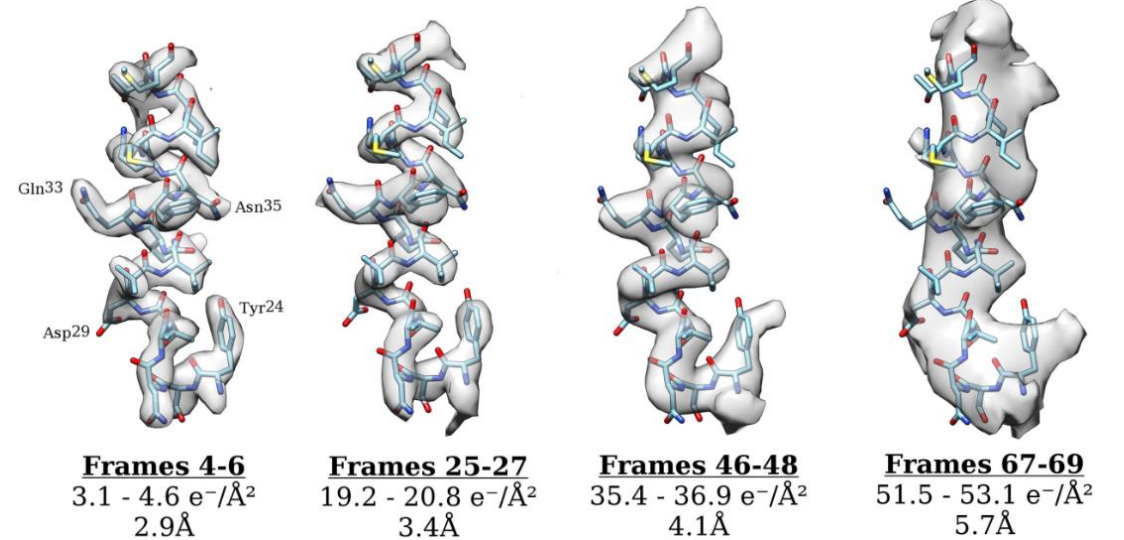
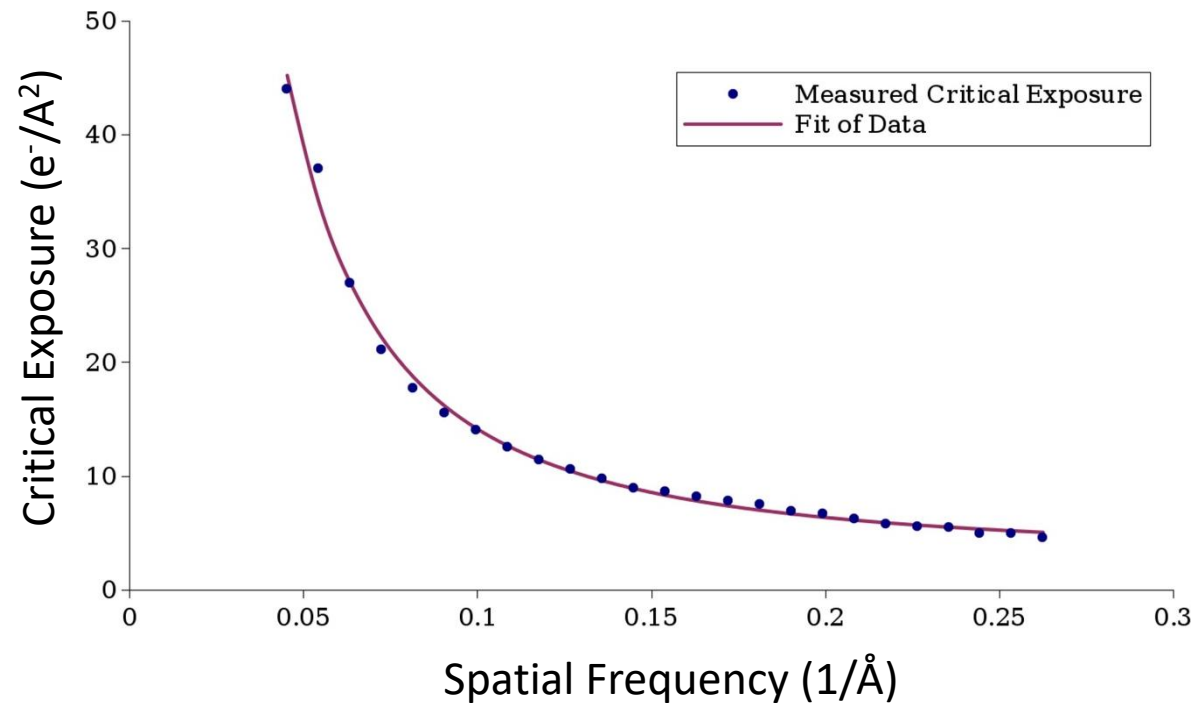
$$N = \pi D / r$$



Discrete sampling + missing wedge

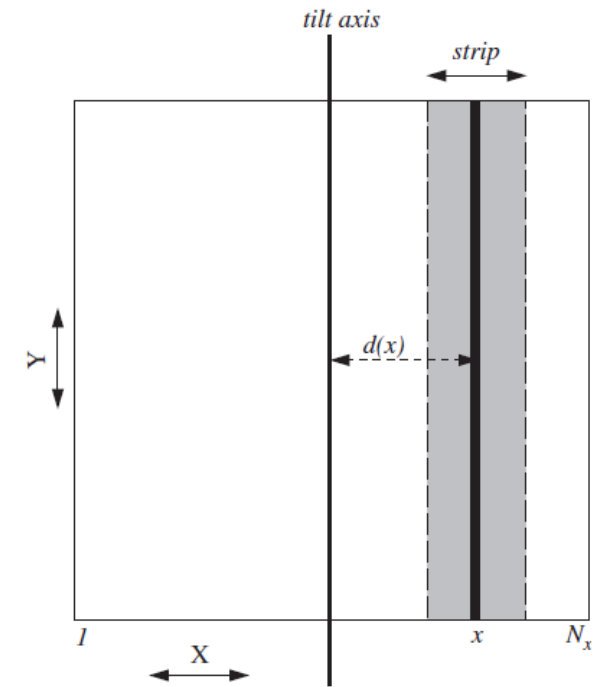
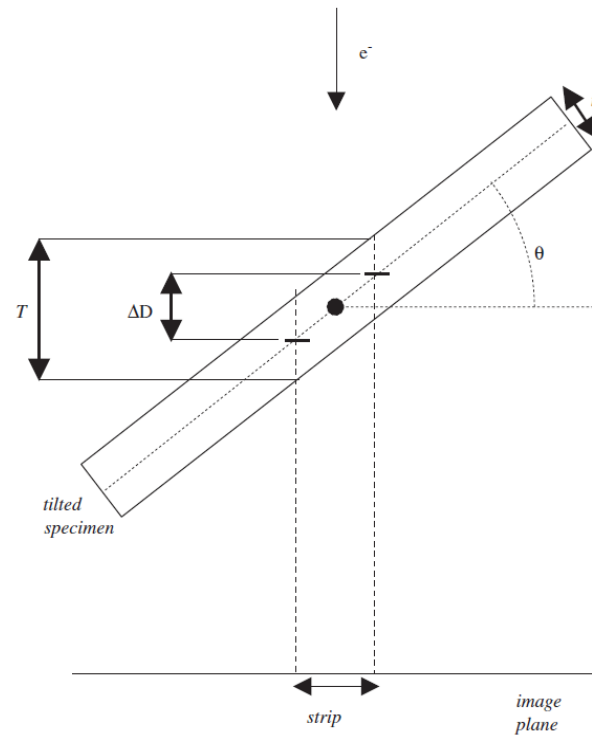
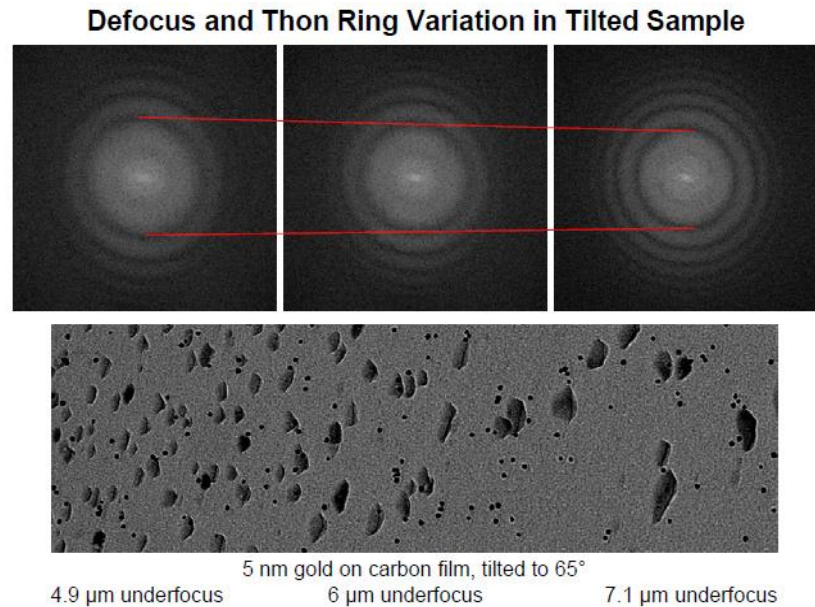


Accumulated beam damage



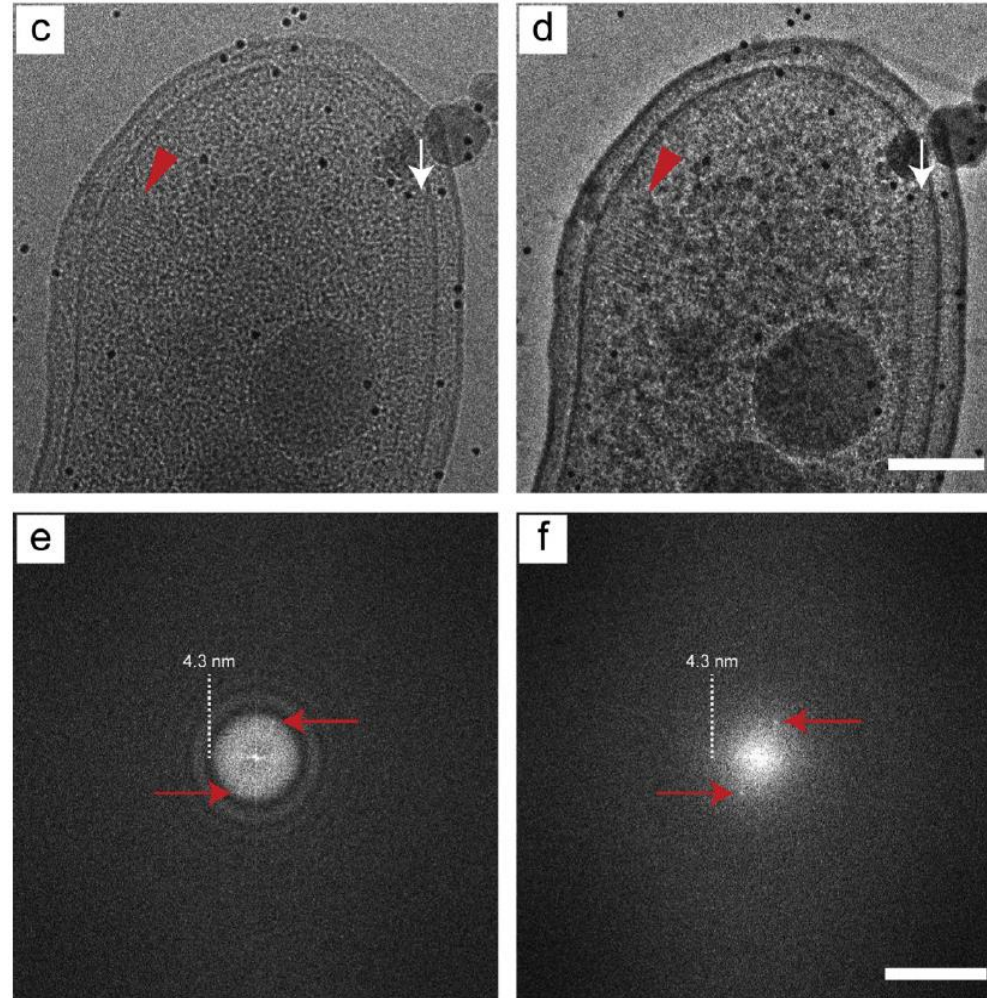
Grant & Grigorieff (2015) *eLife*. Measuring the optimal exposure for single particle cryo-EM using a 2.6 \AA reconstruction of rotavirus VP6.

Defocus gradient in tilts



Fernández and Crowther (2006) *Ultramicroscopy*. CTF determination and correction in electron cryotomography. https://bio3d.colorado.edu/RML_2017/2017_IMOD_PEET_Workshop/Lectures/CTFcorrInIMOD.pdf

CTF with phase plate

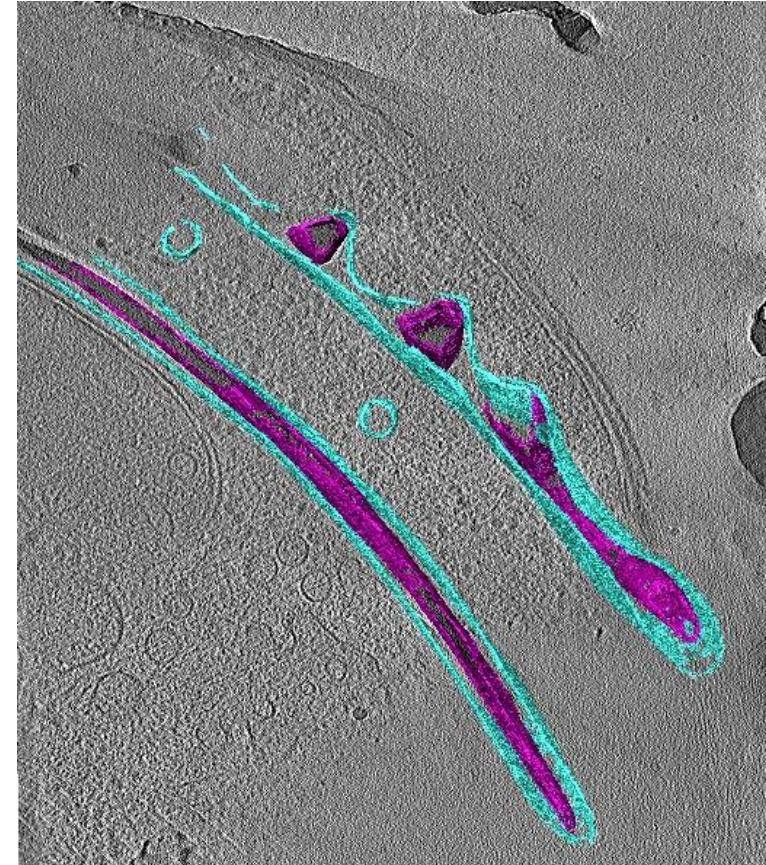
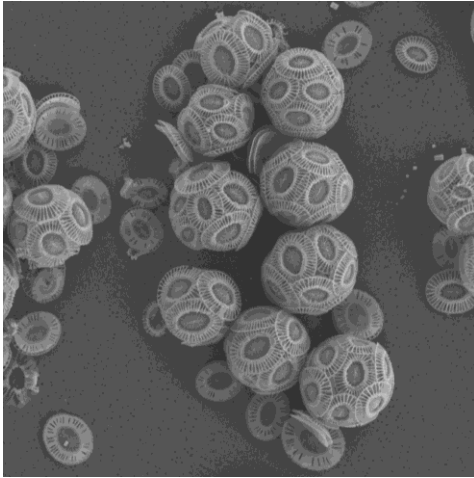


Fukuda et al (2015) *JSB*. Electron cryotomography of vitrified cells with a Volta phase plate

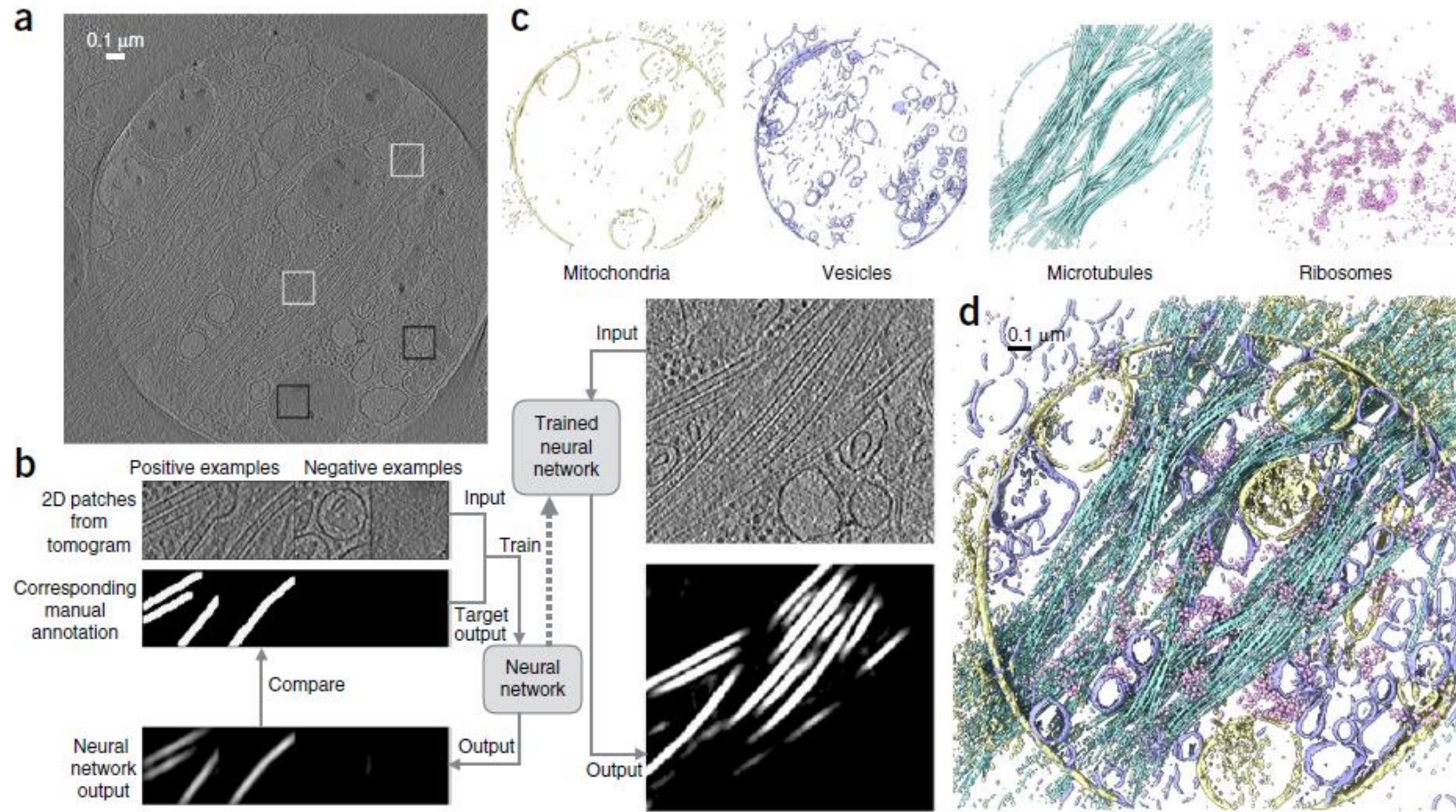
Interpretation of tomograms

- Manual segmentation
- Annotation with neuronal networks
- Template matching
- Sub-tomogram averaging
- Elemental characterization

Manual segmentation



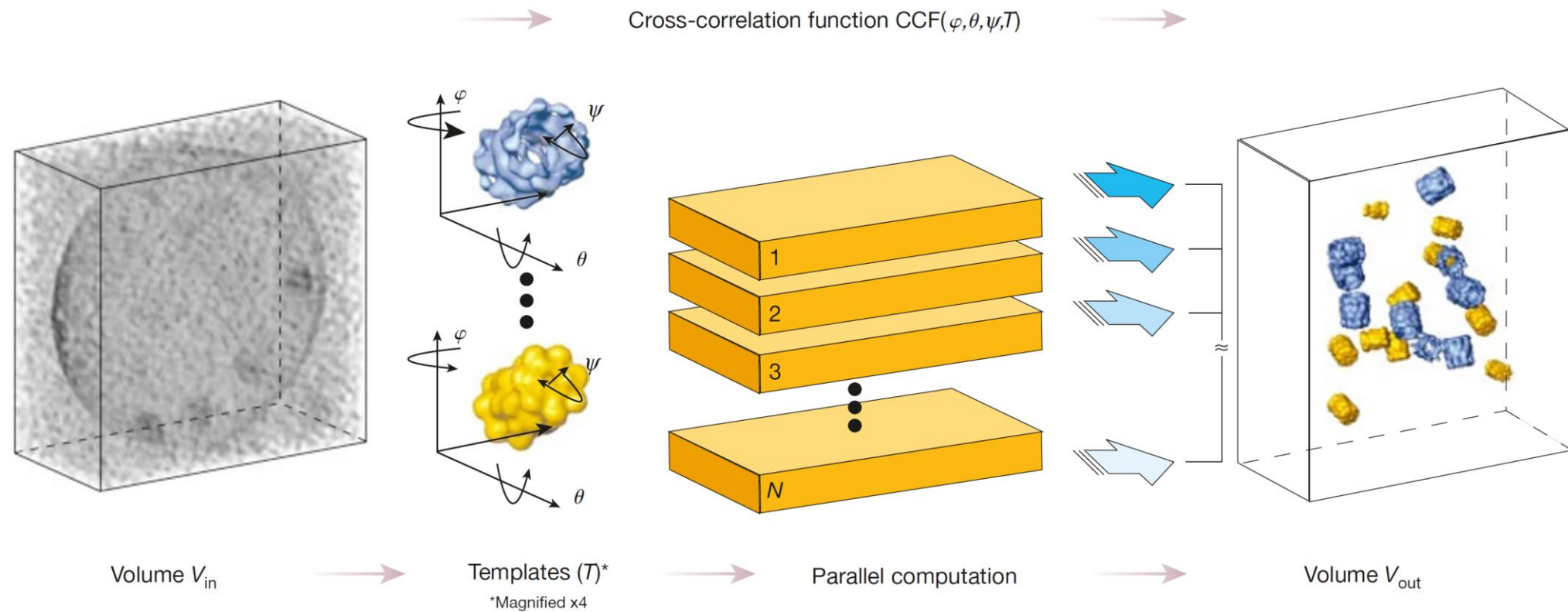
Tomogram annotation using neural networks



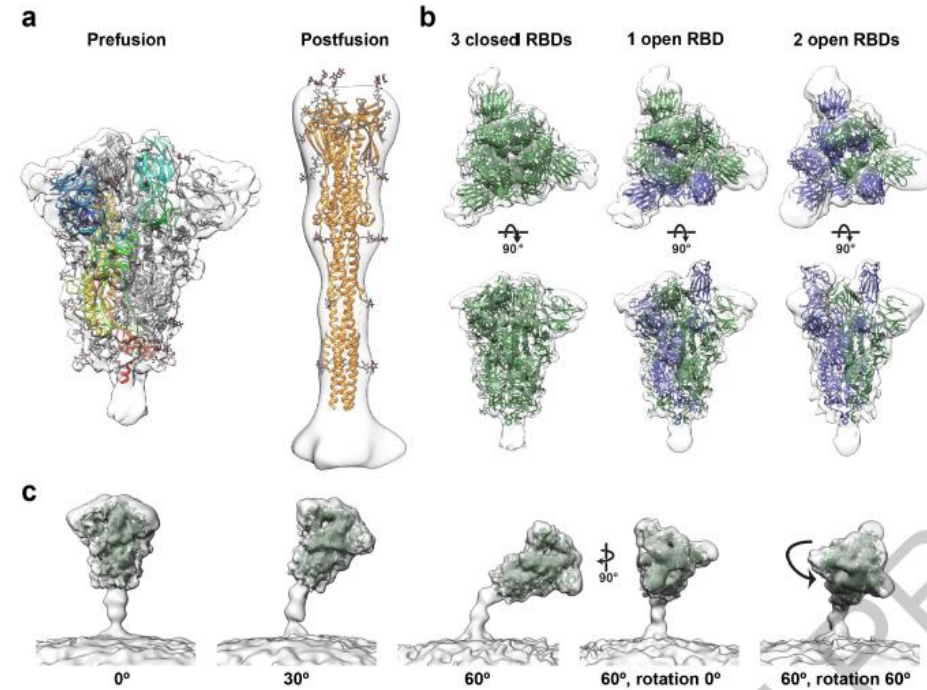
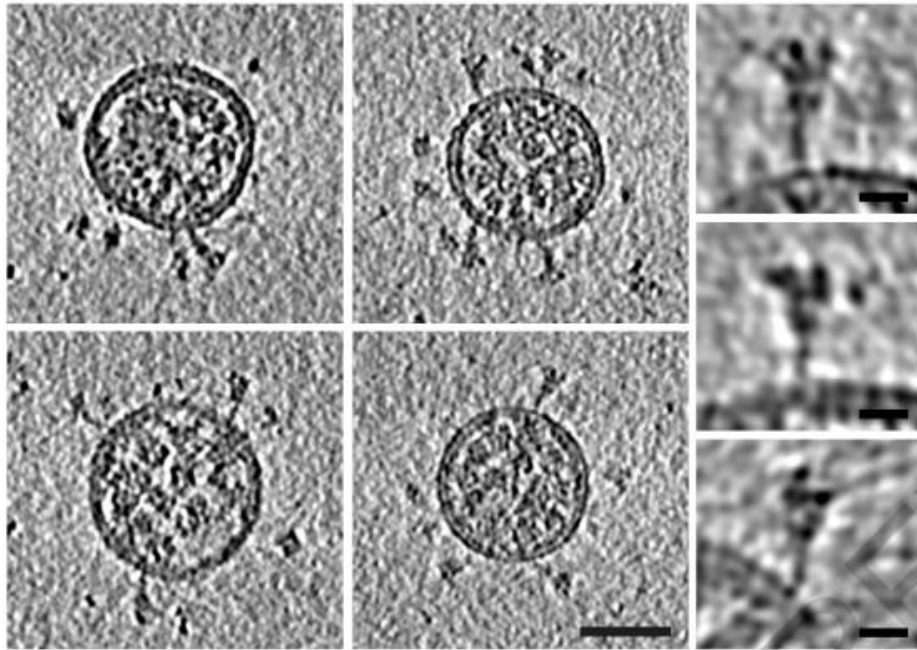
EMAN2 software

Chen et al (2017) *Nature Methods*. Convolutional neural networks for automated annotation of cellular cryo-electron tomograms

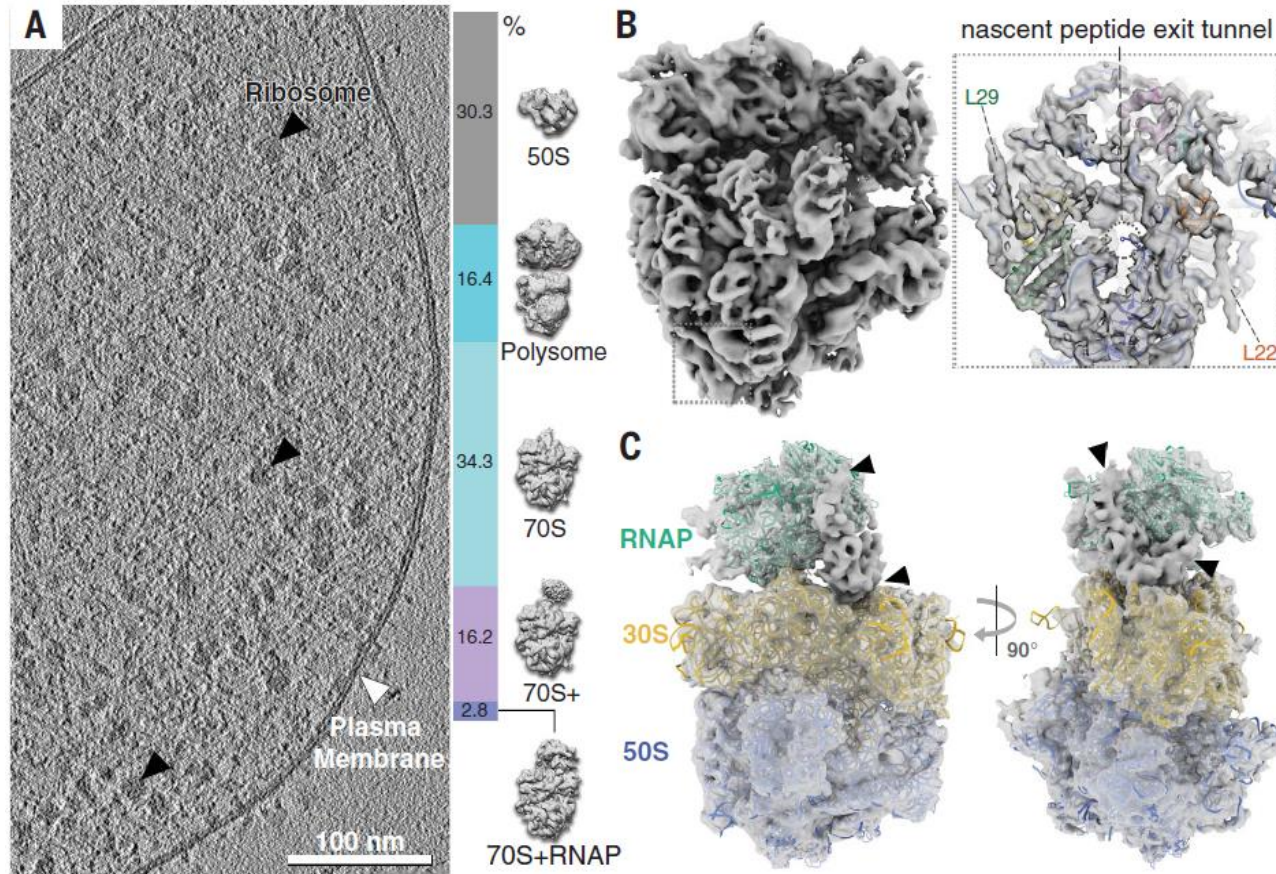
Template matching



Template matching and sub-tomogram averaging

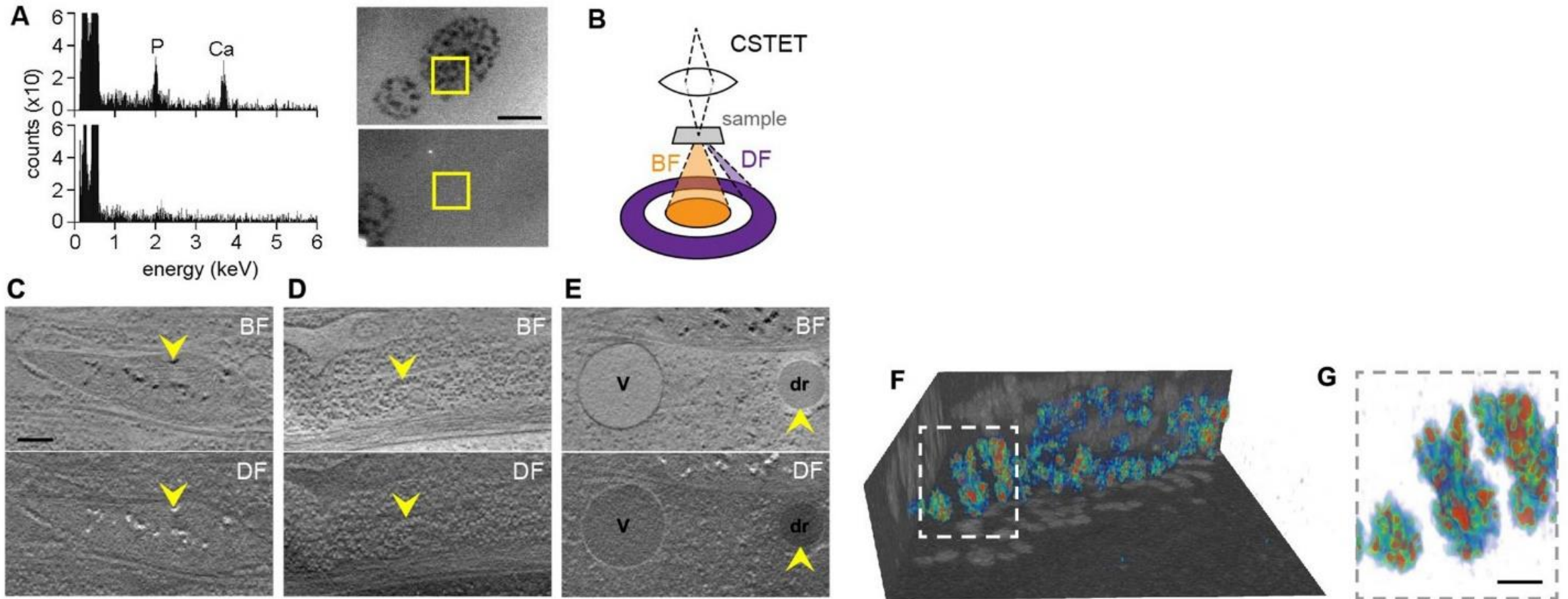


Template matching and sub-tomogram averaging



O'Reilly et al (2020) *Science*. In-cell architecture of an actively transcribing-translating expressome

Elemental characterization by cryo-STEM tomography



Sharon Grayer Wolf, Yael Mutsafi, Tali Dadosh, Tal Ilani, Zipora Lansky, Ben Horowitz, Sarah Rubin, Michael Elbaum, Deborah Fass (2017) *eLife*

Thank you!

