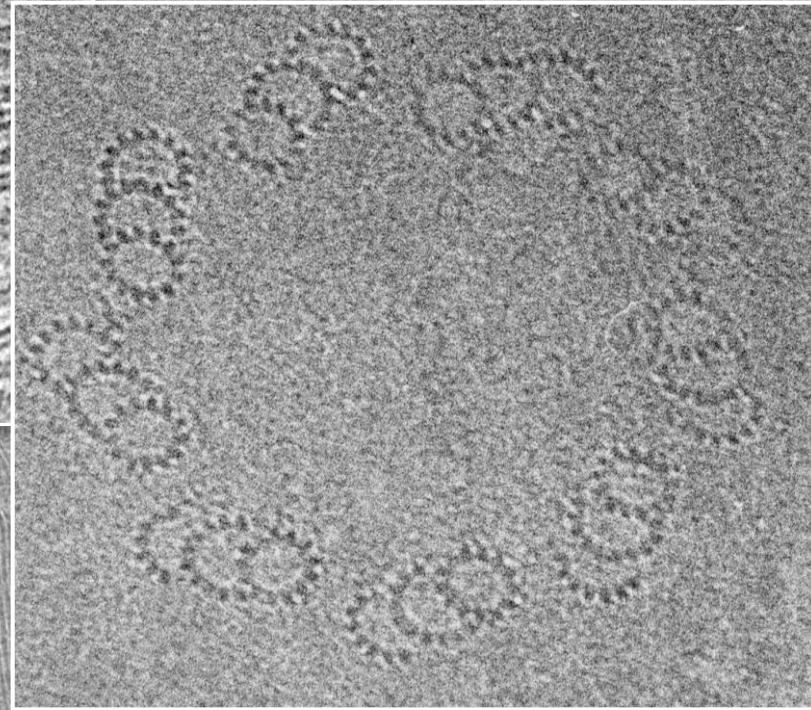
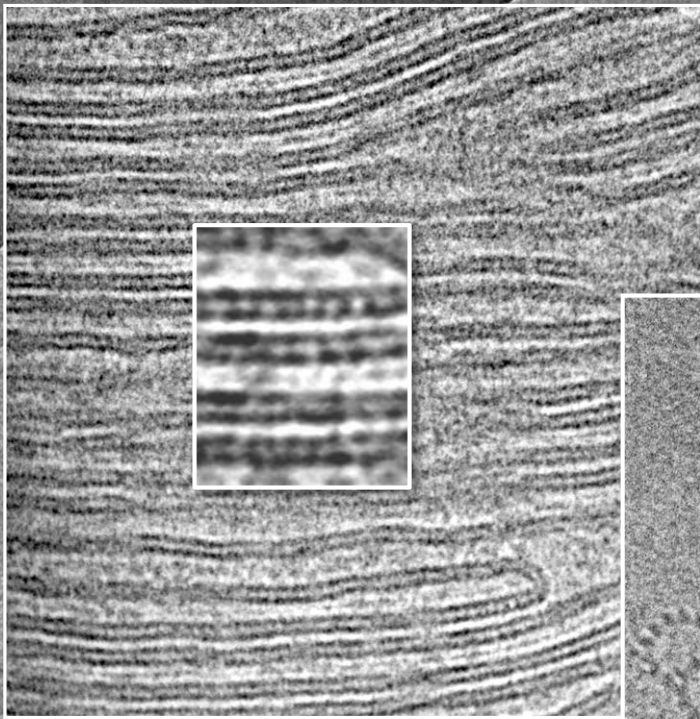


Structural biology *in situ* Cryo-Electron Microscopy of the Cell



Amélie Leforestier, Laboratoire de Physique des Solides, UPS, Orsay



Outline

SAMPLE PREPARATION

- vitrification of massive hydrated specimens
- thinning specimens(electron lucent)

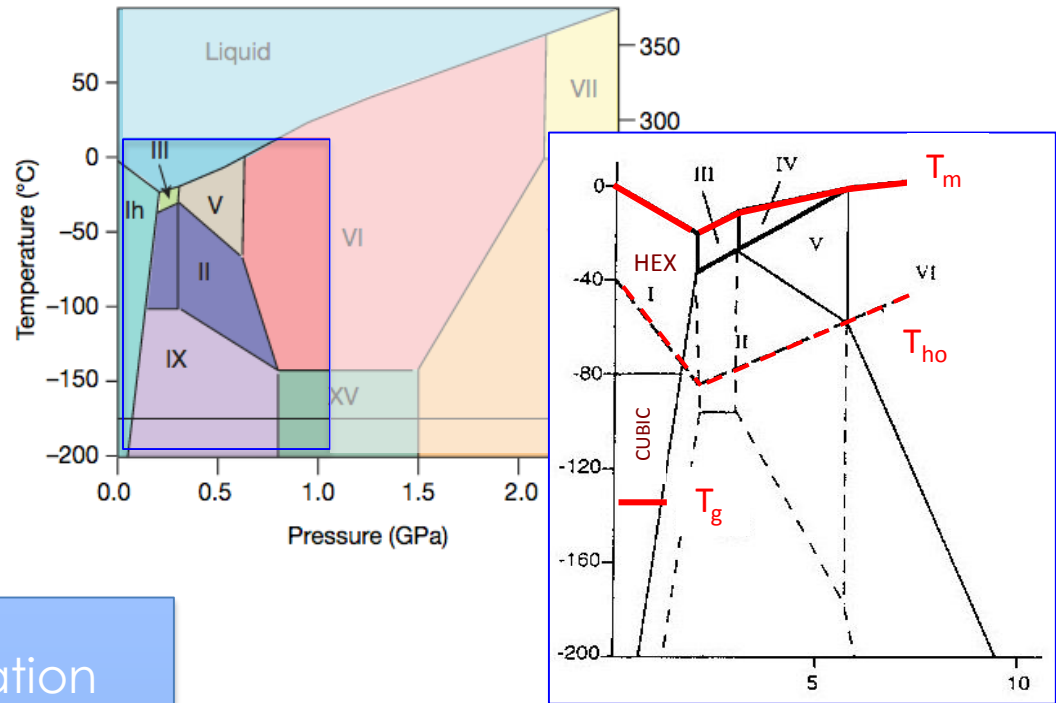
IMAGING

- a new cellular landscape
- 3D structures of unique objects: cryo-tomography
- targetting molecules of interest: cryoCLEM

OTHER CRYO-IMAGING METHODS

- cryoSTEM
- cryo X ray microscopy

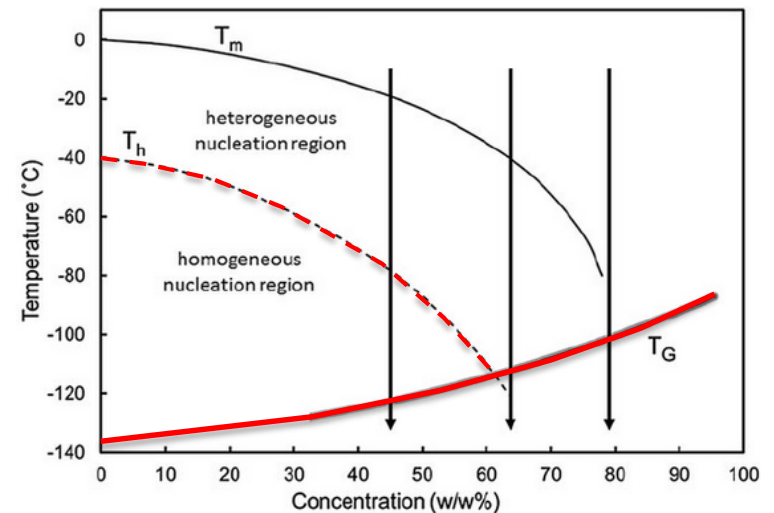
Vitrification



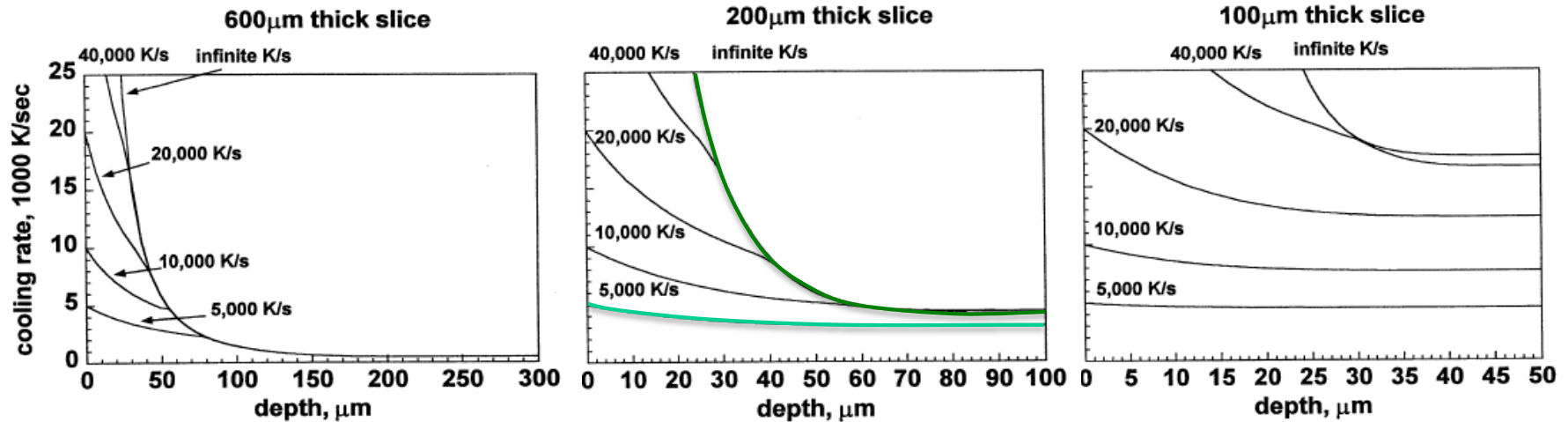
Cooling rate > crystallisation

$$\Delta T = T_{ho} - T_g$$

	100 % water	70% water
1 bar	10^5 - 10^6 Ks ⁻¹	10^4 Ks ⁻¹
2045 bars	10^4 Ks ⁻¹	10^2 - 10^3 Ks ⁻¹



Water & biological specimens: poor thermal conductors

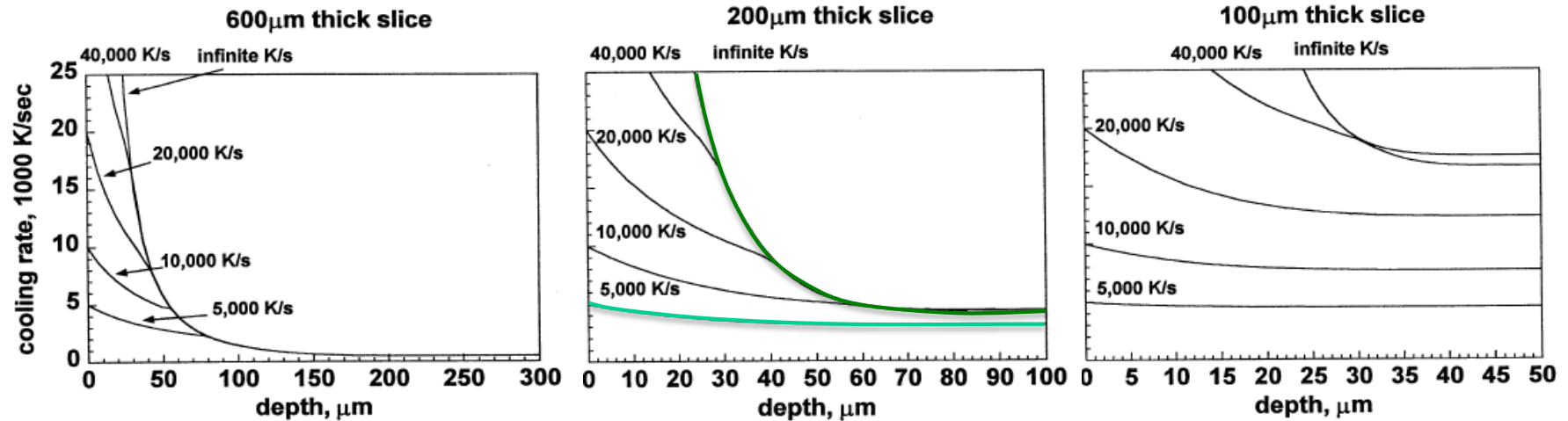


Studer et al, 1995

	100 % water	70% water
1 bar	10^5 - 10^6 Ks ⁻¹	$>10^4$ Ks ⁻¹
2045 bars	10^4 Ks ⁻¹	$>10^2$ - 10^3 Ks ⁻¹

+ nucleation & growth of ice crystals in deep zones = exothermic process, which in turn slow down cooling rate (Escaig, 1982)

Water & biological specimens: poor thermal conductors

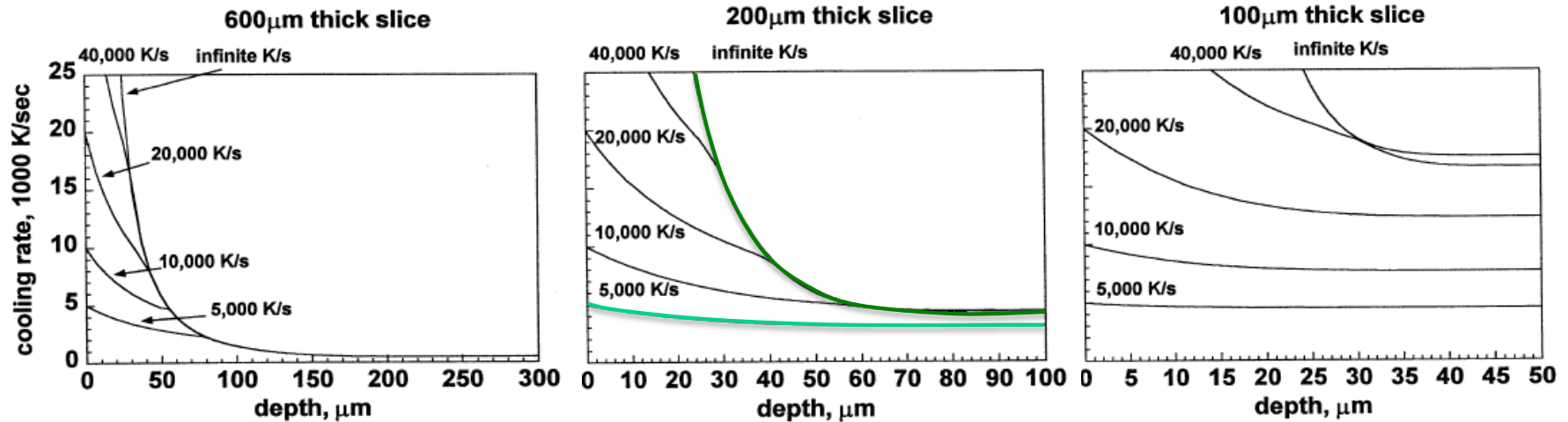


Studer et al, 1995

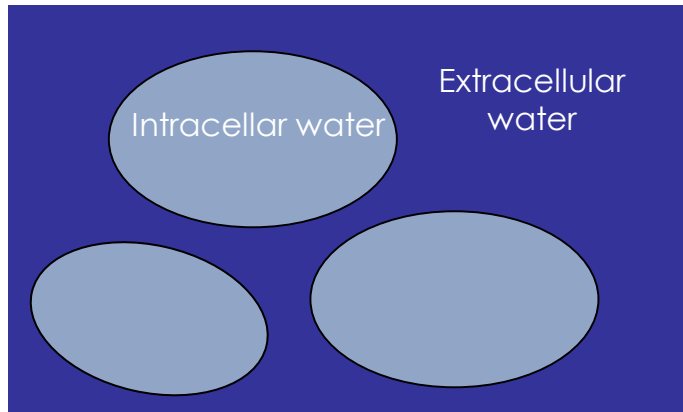
	100 % water	70% water
1 bar	10^5 - 10^6 Ks ⁻¹	$>10^4$ Ks ⁻¹
2045 bars	10^4 Ks ⁻¹	$>10^2$ - 10^3 Ks ⁻¹

No pure water bulk vitrification
Water content ≥ 80 %

Water & biological specimens: poor thermal conductors



Studer et al, 1995



Addition of cryo-protectants

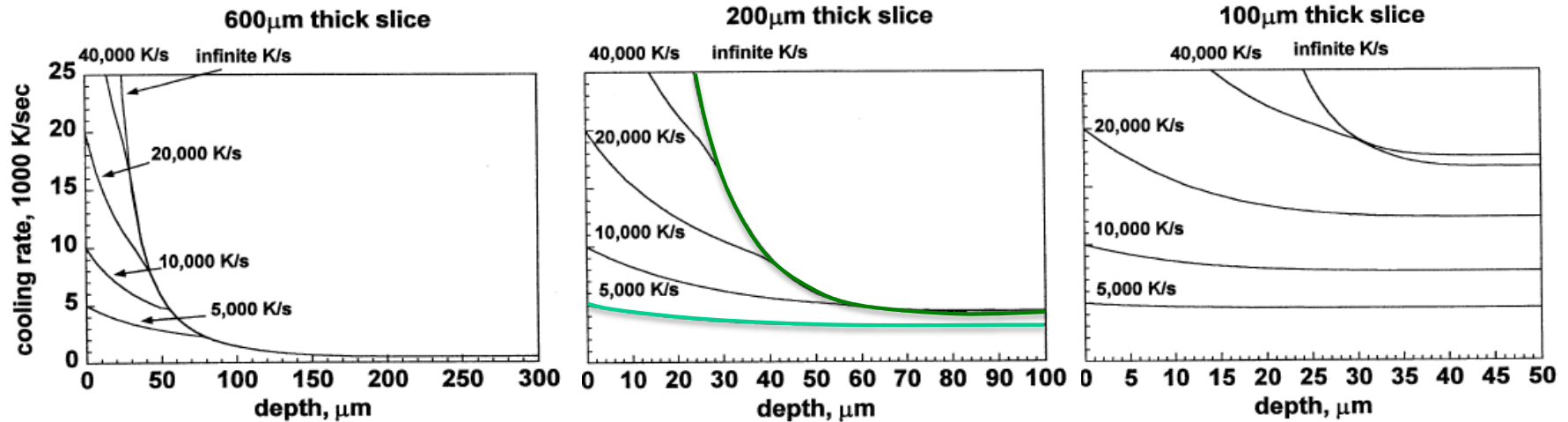
glycerol
glucose
threhalose

toxicity
sectioning
imaging

dextran
PEG
BSA

osmotic
stress

Water & biological specimens: poor thermal conductors



Studer et al, 1995

	100 % water	70% water
1 bar	10^5 - 10^6 Ks ⁻¹	$>10^4$ Ks ⁻¹
2045 bars	10^4 Ks ⁻¹	$>10^2$ - 10^3 Ks ⁻¹

@ 1 bar

Plunge Freezing
(ethane)

1-3 µm

Jet freezing ?
(ethane)

Slam Freezing
(helium)

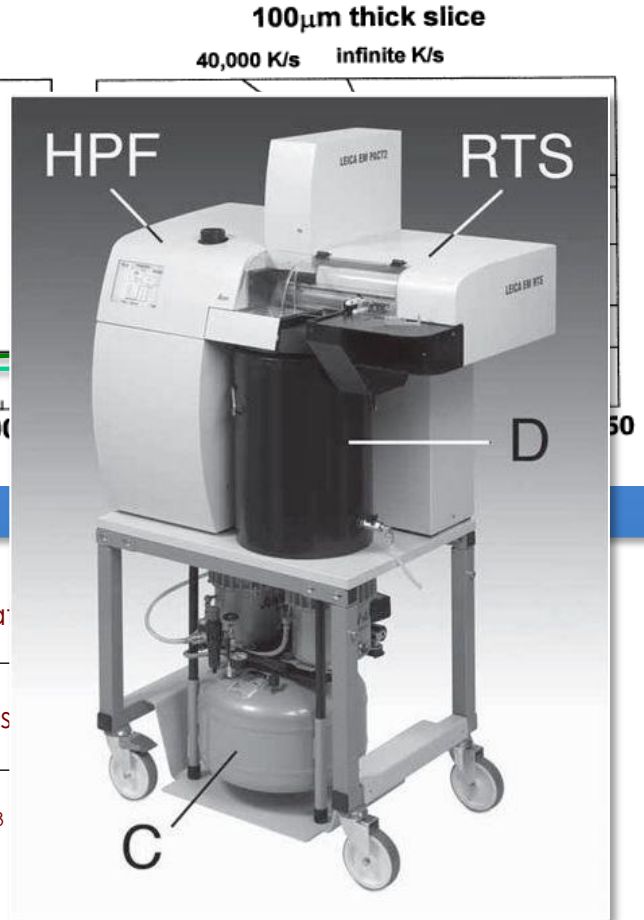
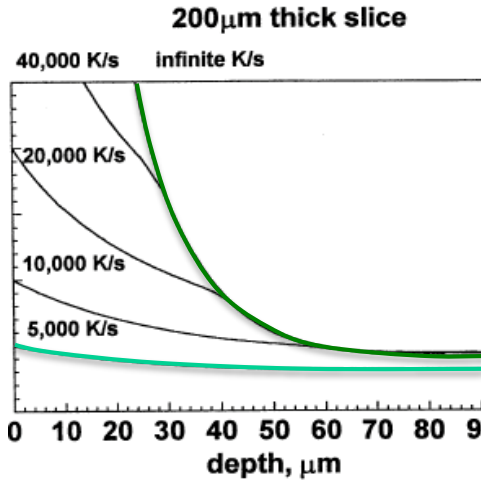
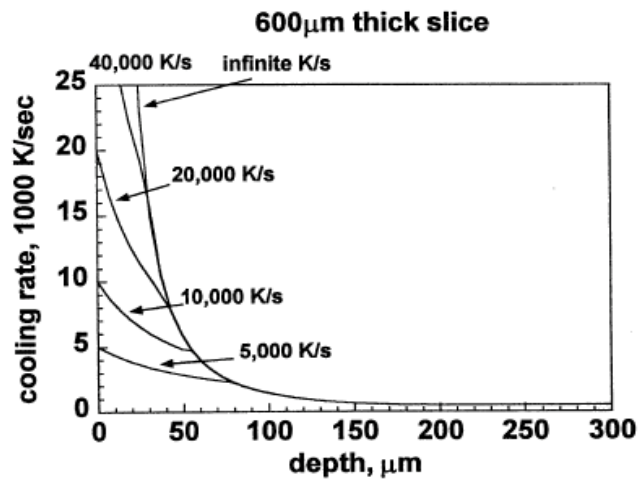
10-20 µm

@ 2045 bar

High Pressure Freezing
(HPF)

100-200 µm

Water & biological specimens: poor thermal conductors



Studer et al, 1995

	100 % water	70% water
1 bar	10^5 - 10^6 Ks ⁻¹	$>10^4$ Ks ⁻¹
2045 bars	10^4 Ks ⁻¹	$>10^2$ - 10^3 Ks ⁻¹

@ 1 bar

@ 2045 bar

Plunge Freezing
(ethane)

Slam Freezing
(helium)

High Pressure Freezing
(HPF)

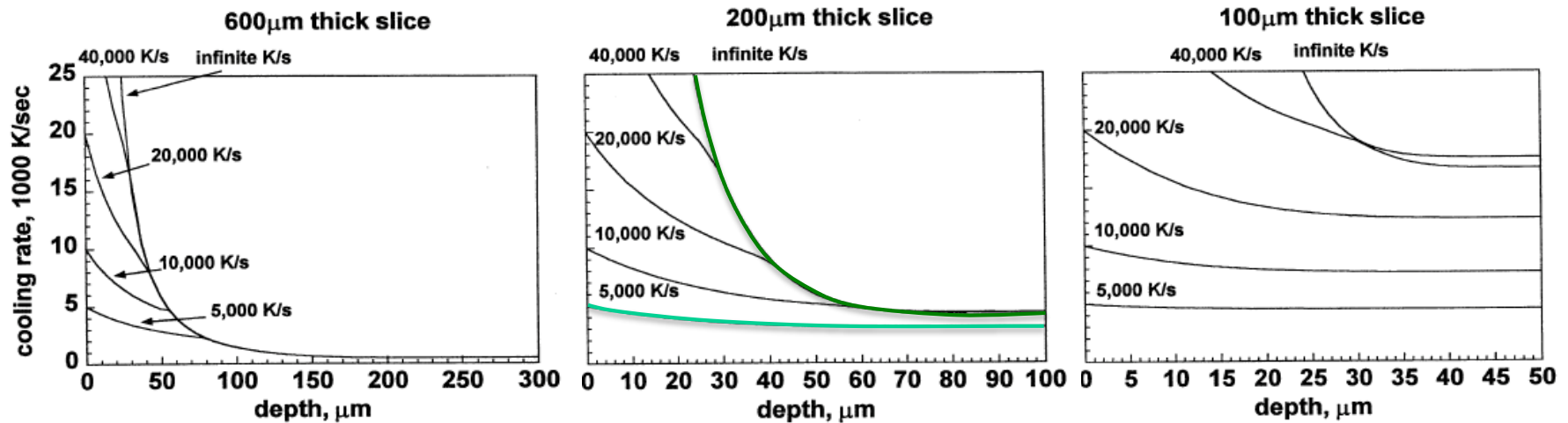
1-3 μ m

Jet freezing ?
(ethane)

10-20 μ m

100-200 μ m

Water & biological specimens: poor thermal conductors



Studer et al, 1995

cell extensions,
bacteria,
picoeukaryotes

@ 1 bar

Plunge Freezing
(ethane)

1-3 μm

isolated cells,
bacteria,
peripheral tissues

Slam Freezing
(helium)

10-20 μm

cells, tissues,
organs,
organisms

@ 2045 bar

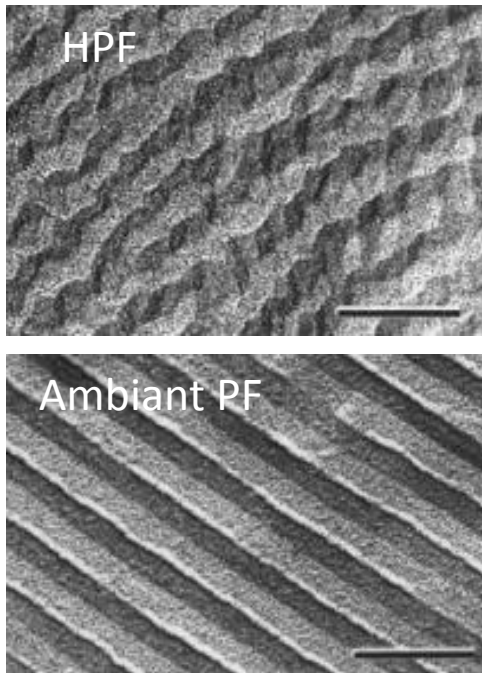
High Pressure Freezing
(HPF)

100-200 μm

Problems ?

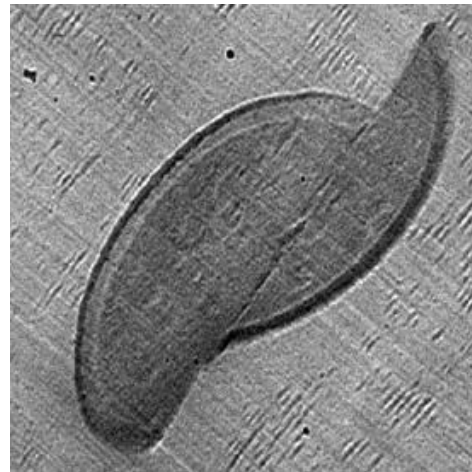
Phase transitions
(DNA, lipids)

Leforestier *et al*, 1992;
Semmler *et al*, 1995



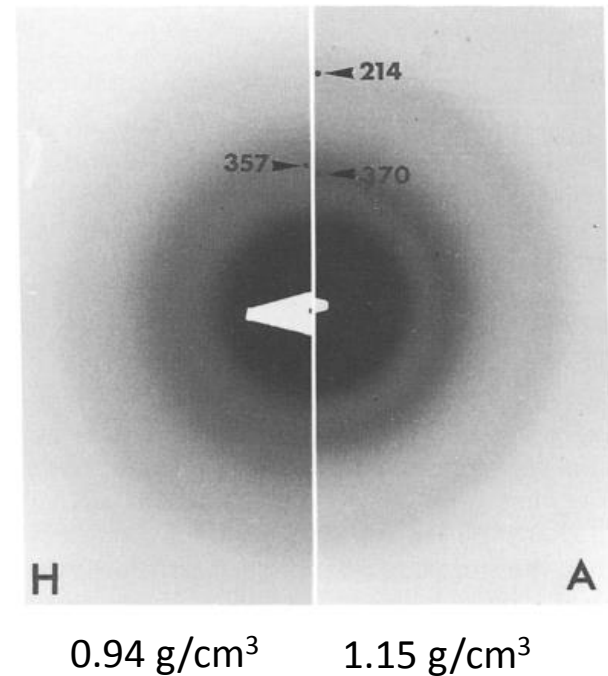
Cell techtonics

Dubochet *et al*, 2007



High density amorphous water
vs LDA

Richter, 1994

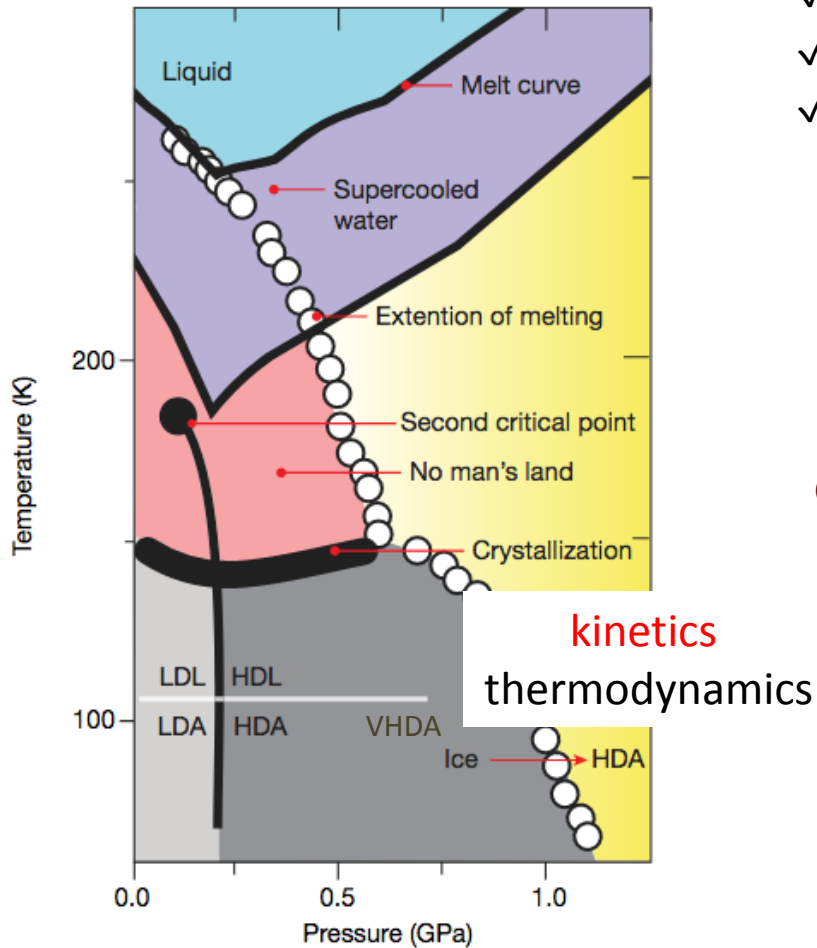


imaging

Vitreous does not (always) mean the native state is preserved

Problems, ... and perspectives ?

Voyage through water poly(a)morphs ?



Tulk et al, Nature 2019

- ✓ Transitions upon pressure changes
- ✓ Transitions upon temperature changes !
- ✓ Transitions upon beam irradiation



Check the state of water of your sample !

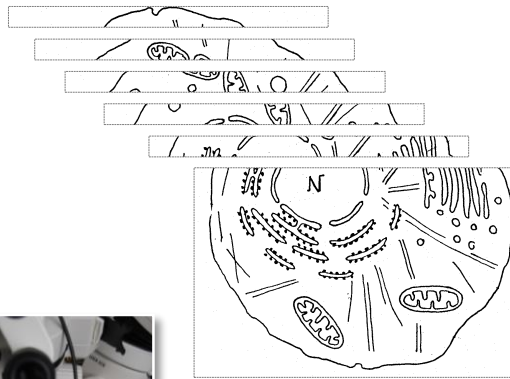


Pure water vitrification ?
Large volumes ?

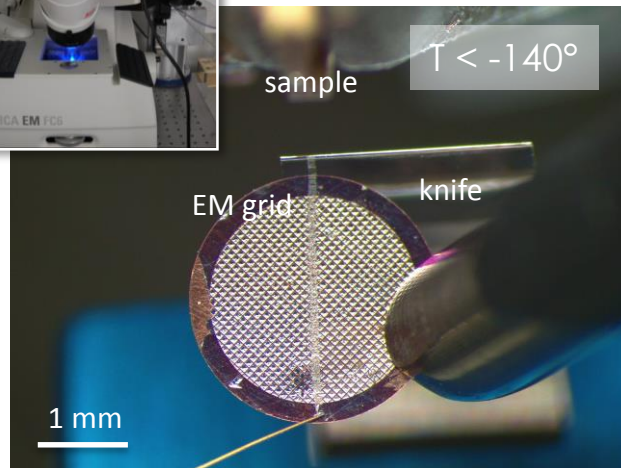
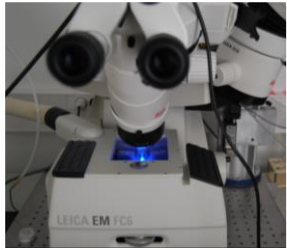
Obtaining a thin (electron lucent) specimen

Cryo-sectioning

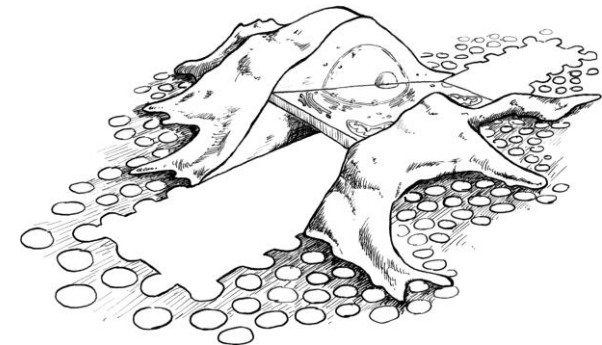
Cryo-Electron Microscopy Of Vitreous Sections



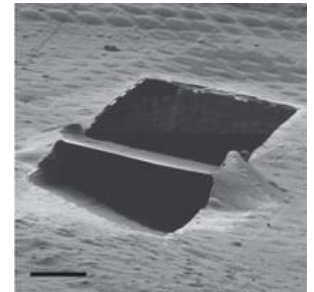
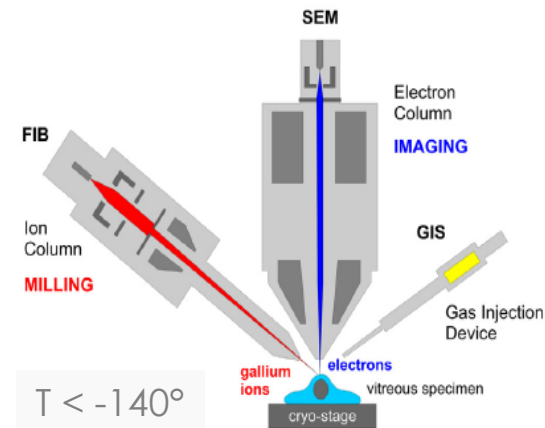
vitrified cells



Cryo-FIB milling



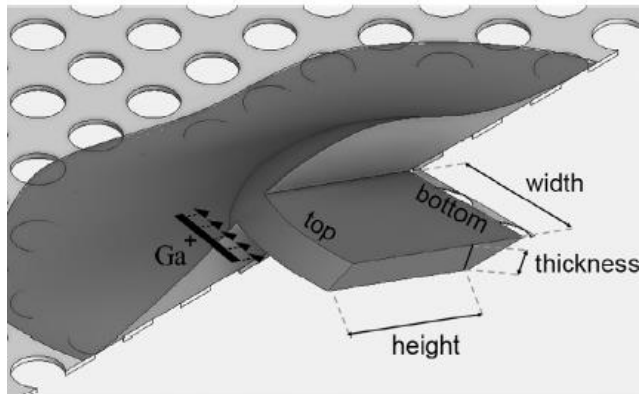
Villa et al, *Curr. Opin. Struct. Biol.*, 2013



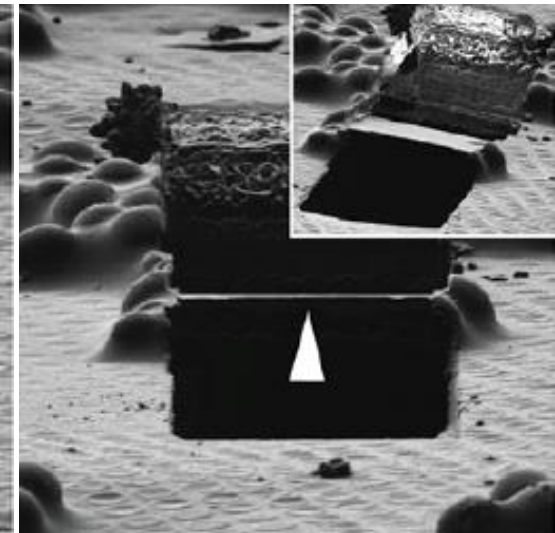
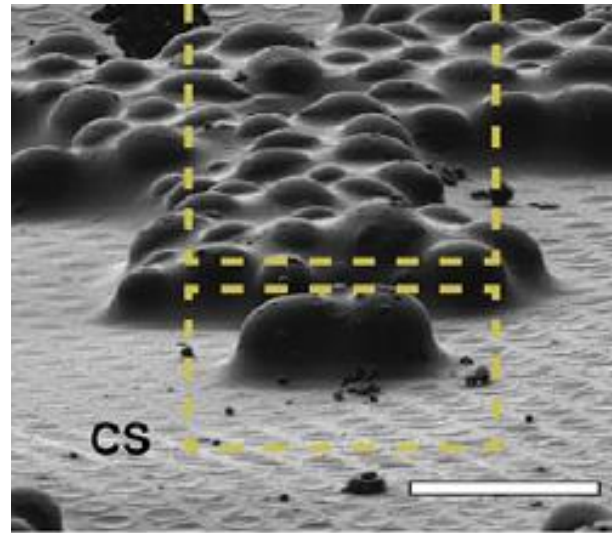
Cryo-FIB milling



Cells deposited/cultured on grids



Schaffer et al (2017) JSB, 197



lamella thickness
 $\geq 100-150$ nm

Cryo-FIB milli



J. Plitsko (Villa et al, 2013)

Cells deposited/cultured on grids

**Cryo-FIB milling of a
Chlamydomonas cell**

**Baumeister, MPI-Biochemistry
Schaffer et al., 2015
www.bio-protocol.org**

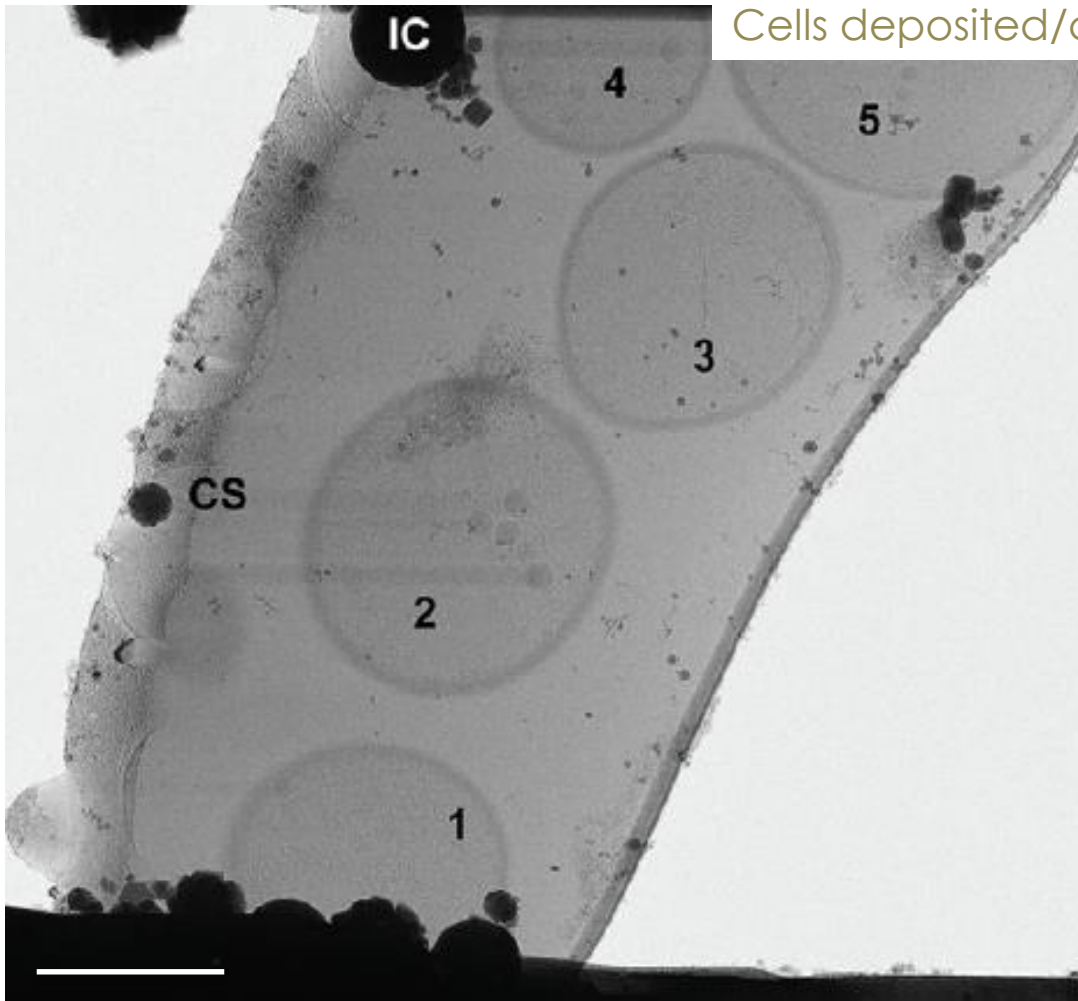
	HV	curr	dwell	HFW	tilt	mode	1 mm	
	5.00 kV	5.92 pA	1 µs	2.84 mm	17 °	SE	MPI für Biochemie	

Cryo-FIB milli



J. Plitsko (Villa et al, 2013)

Cells deposited/cultured on grids



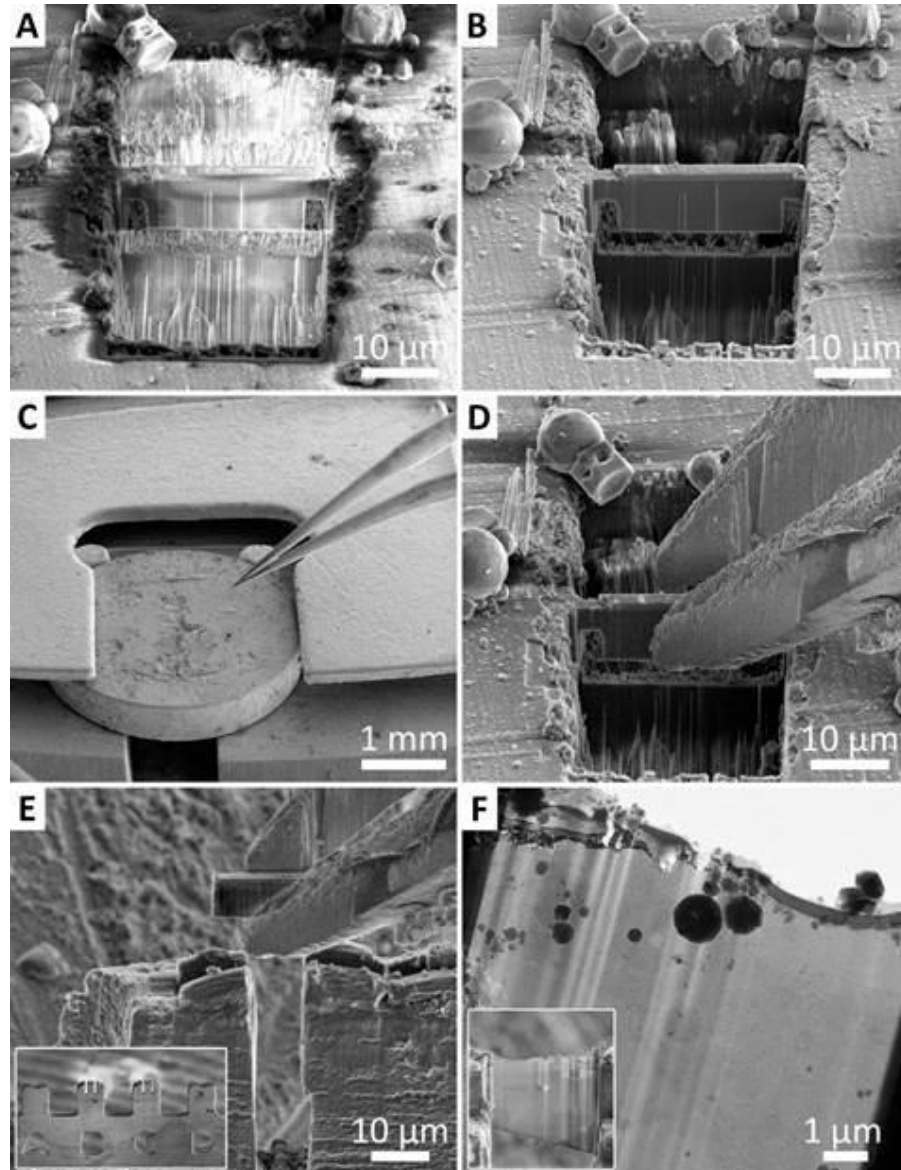
Cryo-FIB milling

Multicellular tissues & organisms: « lift out »

Mahamid et al (2015) J. Struct. Biol. 192, 262-269

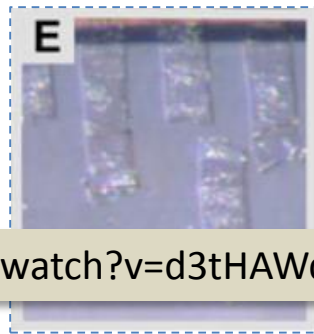
Hsieh et al (2014) J. Struct. Biol. 185, 32-41, 2014

Harapin et al (2015) Nature methods, 12, 634-636.

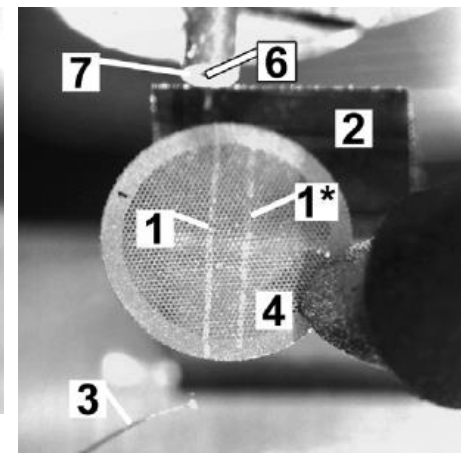
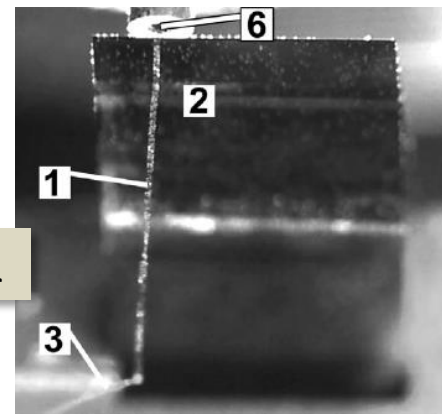


CEMOVIS

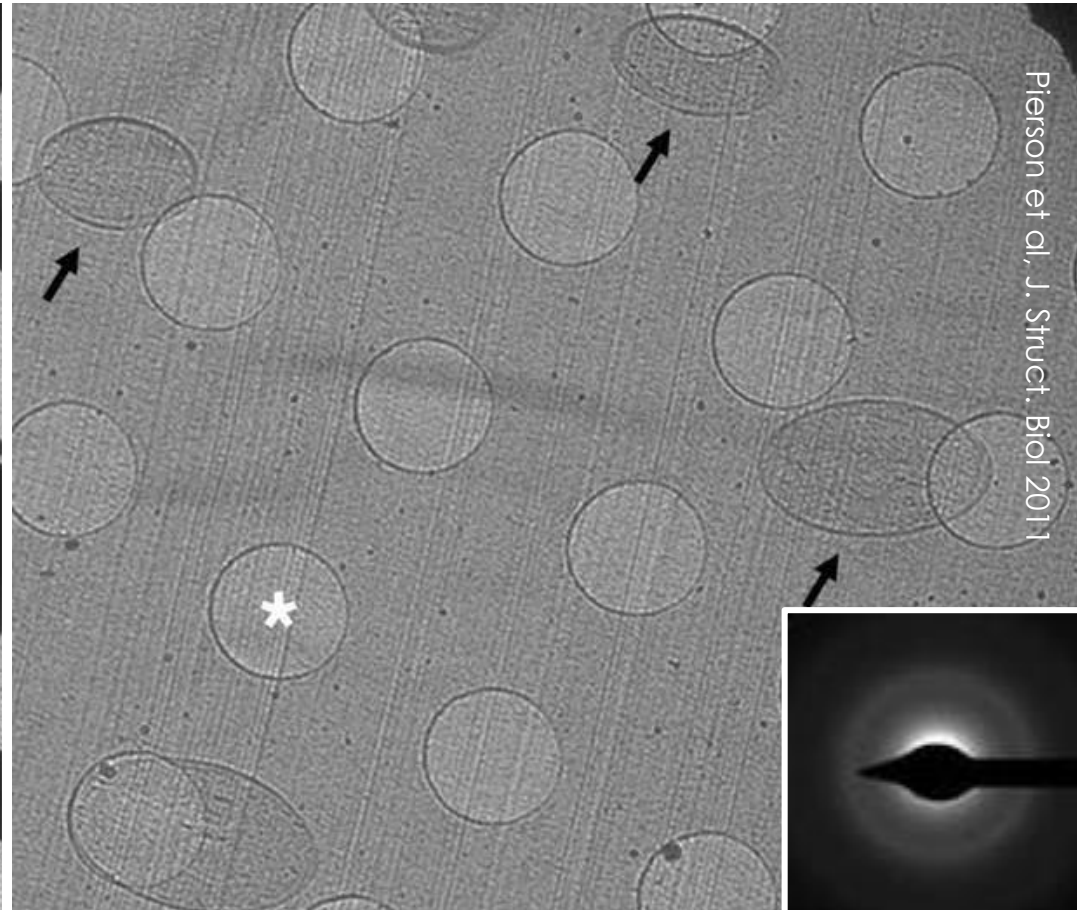
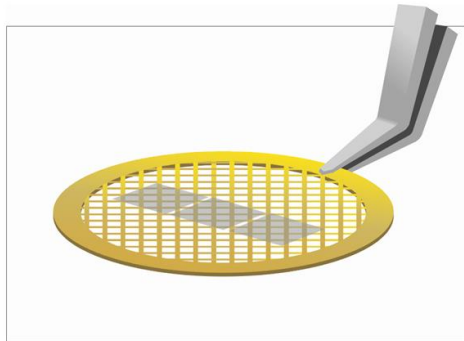
<https://www.youtube.com/watch?v=d3tHAWde1GQ>



Bouchet-Marquis et al
(2007) Biol. Cell, 99, 45



D. Studer et al (2014) J. Struct. Biol. 185, 125

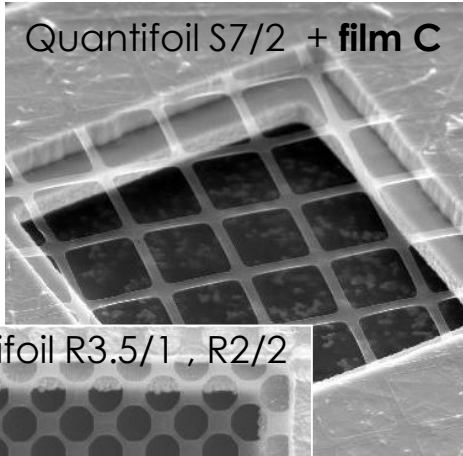


Pierson et al, J. Struct. Biol. 2011

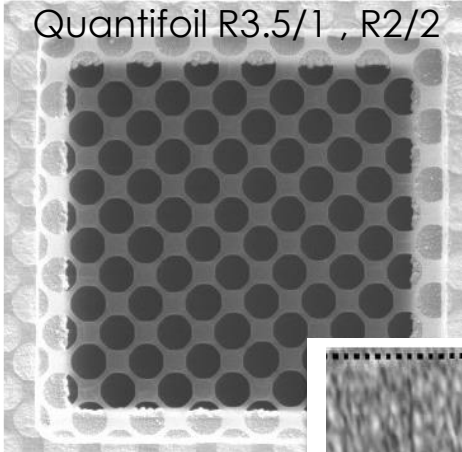
CEMOVIS: adhesion, flatness

Electrostatic press

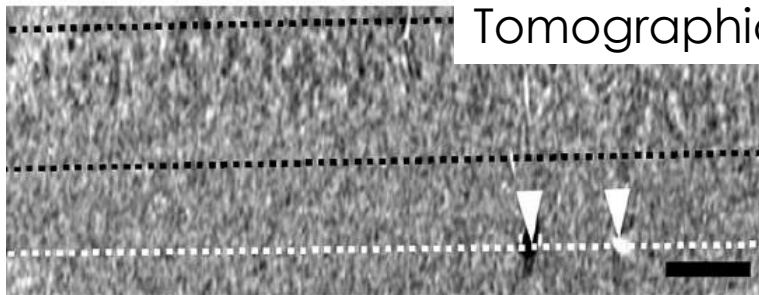
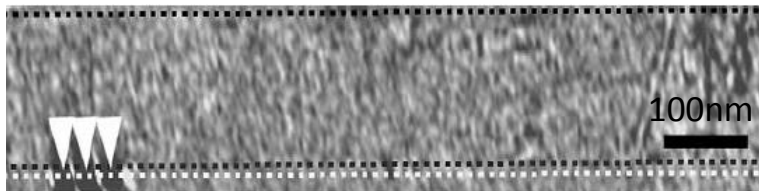
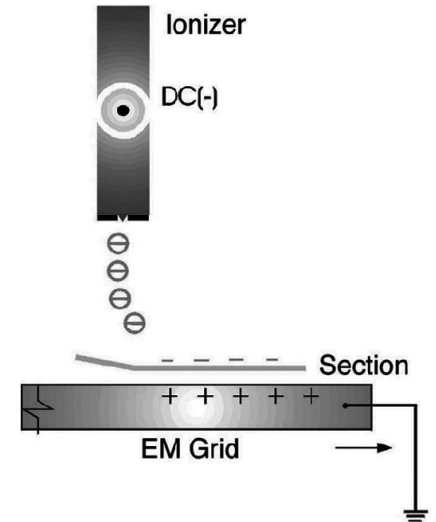
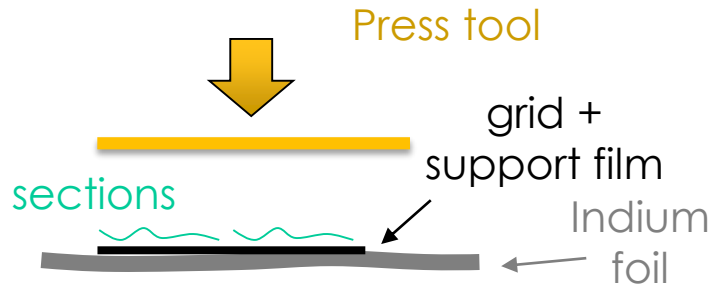
Quantifoil S7/2 + film C



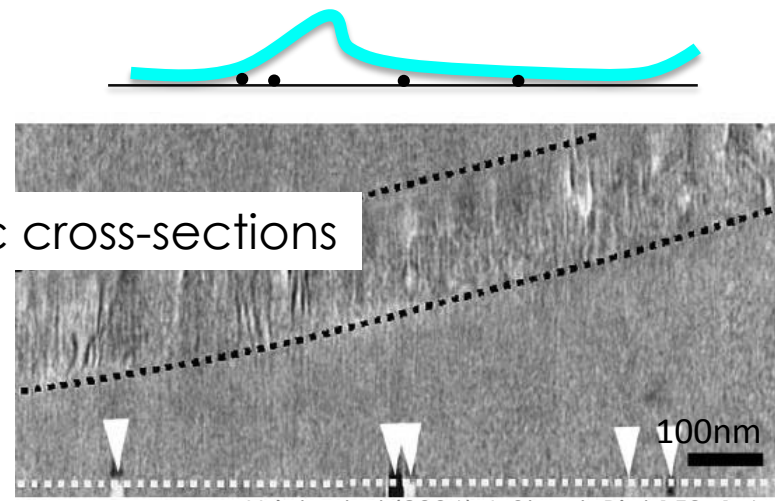
Quantifoil R3.5/1 , R2/2



Mechanical press



Tomographic cross-sections



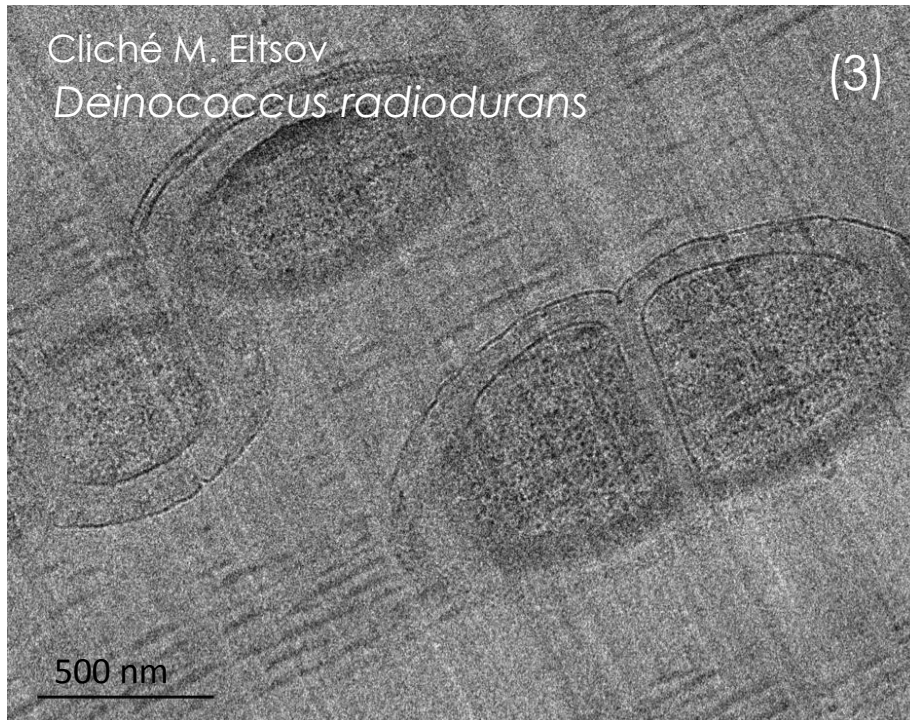
Hsieh et al (2006) J. Struct. Biol 153, 1-6

CEMOVIS: Problems & artefacts

- knife marks (1)
- chatter (2)
- crevasses (3)

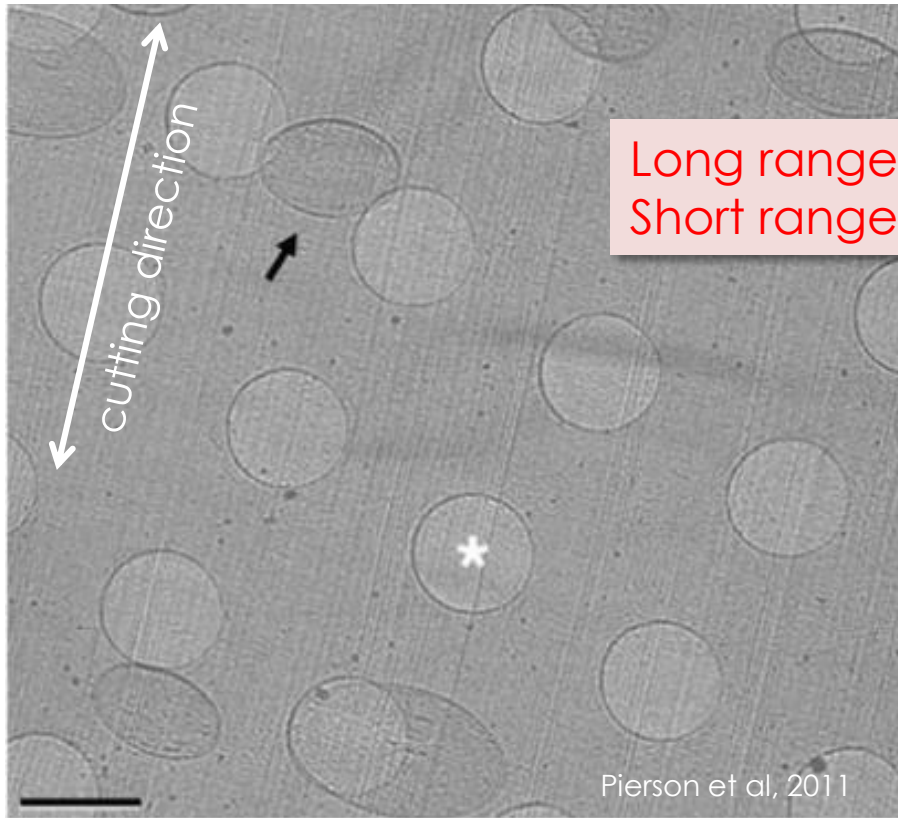
nature specimen
relative orientation molecules/section
thickness

- compression



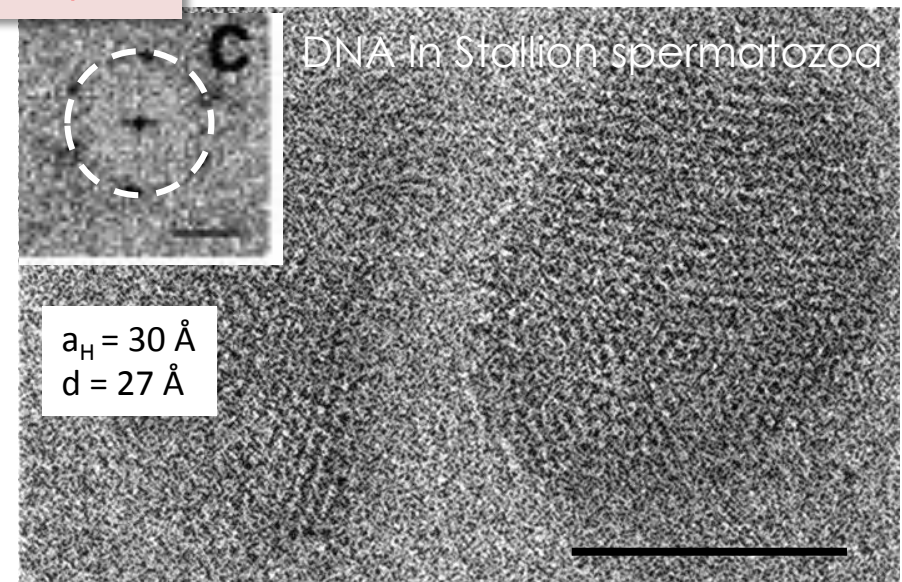
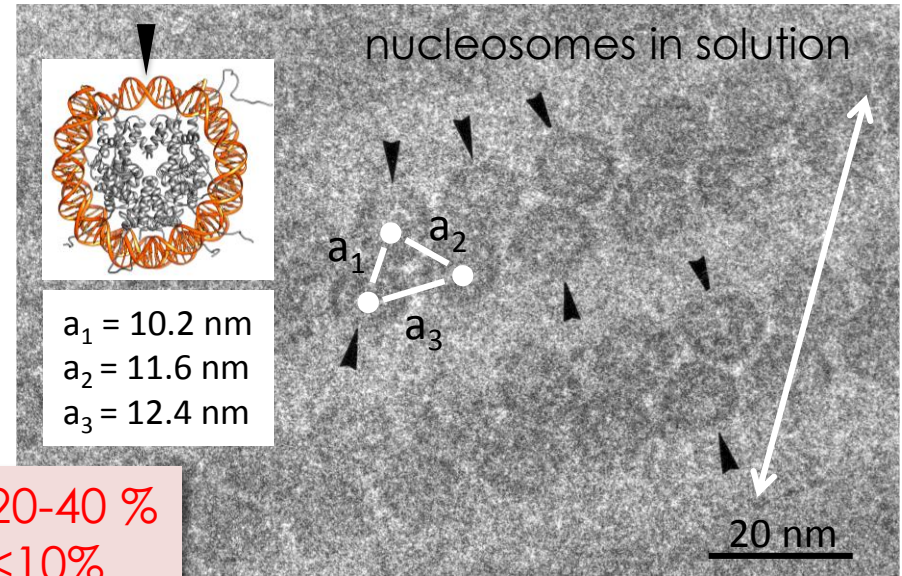
CEMOVIS: Compression ?

- nature of the specimen
- width of the specimen
- thickness
- scale



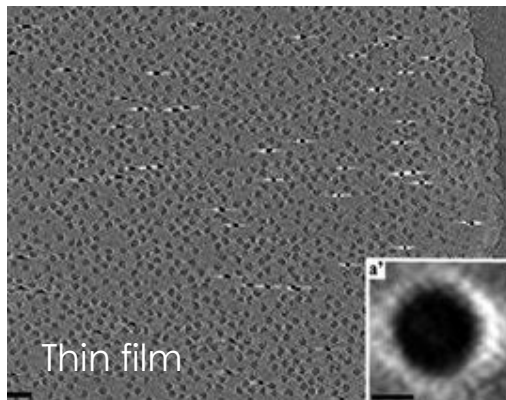
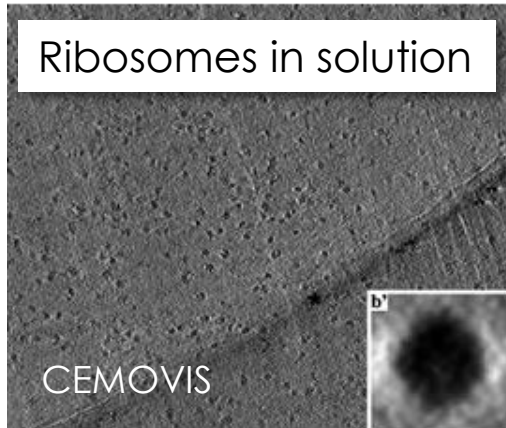
Long range 20-40 %
Short range <10%

Intermolecular spacing

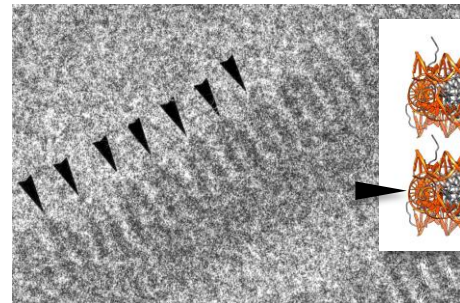
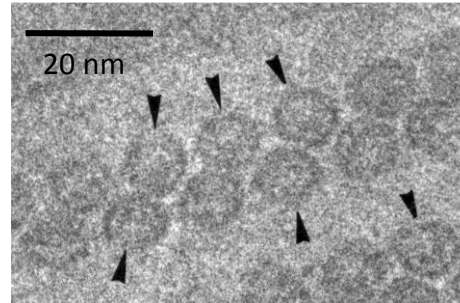


CEMOVIS: compression ?

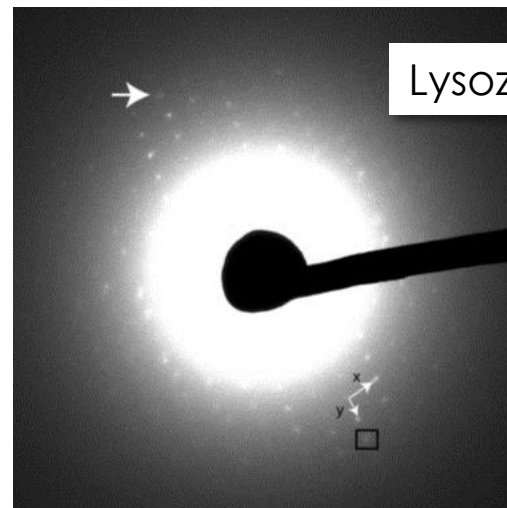
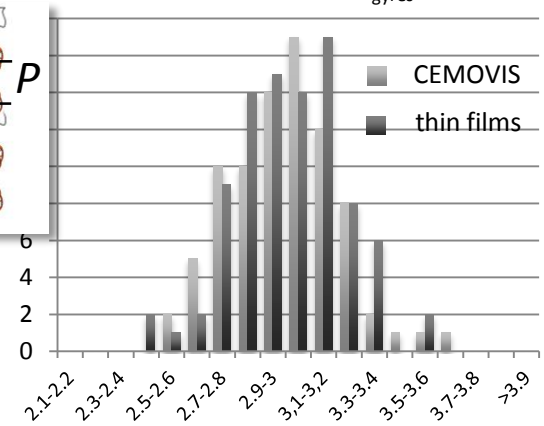
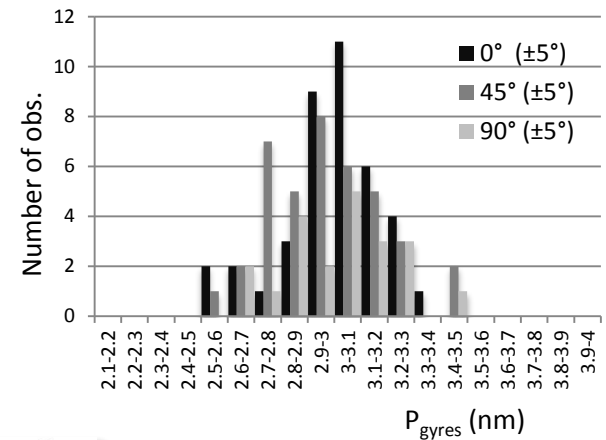
Nucleosomes



Pierson et al, JSB, 2011



Leforestier et al, Biophys. J., 2001
Eltssov et al, NAR, 2018



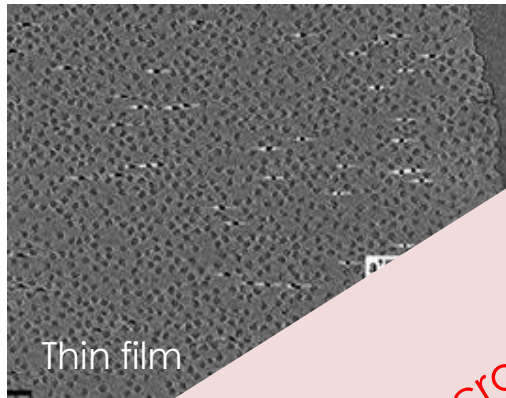
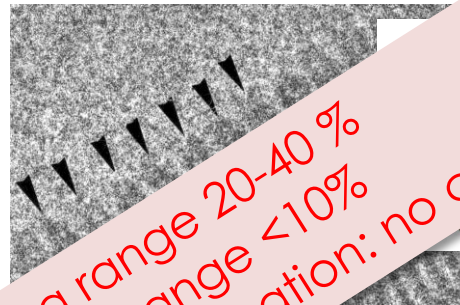
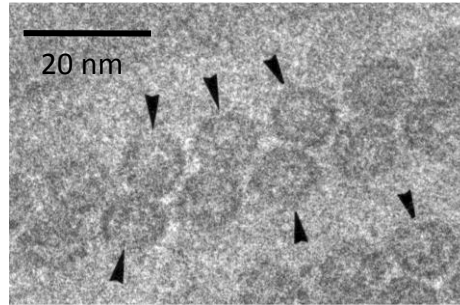
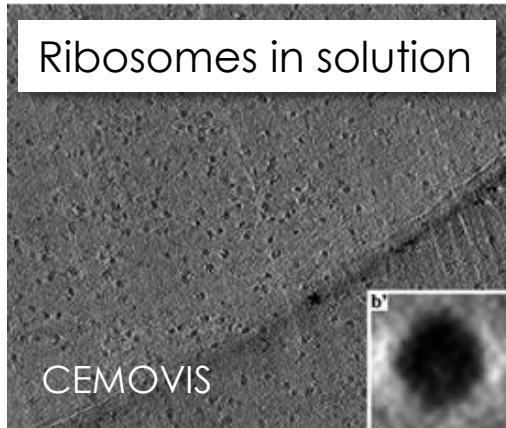
Lysozyme crystals

high resolution information 7.9 Å

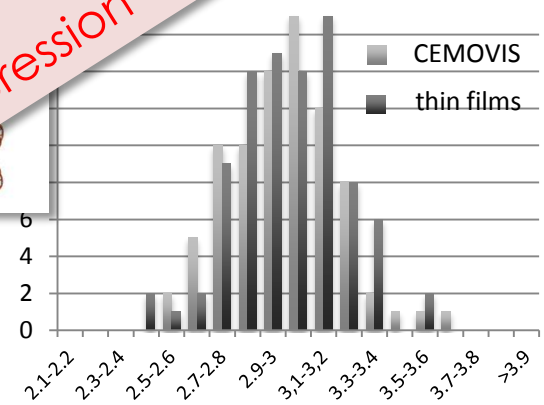
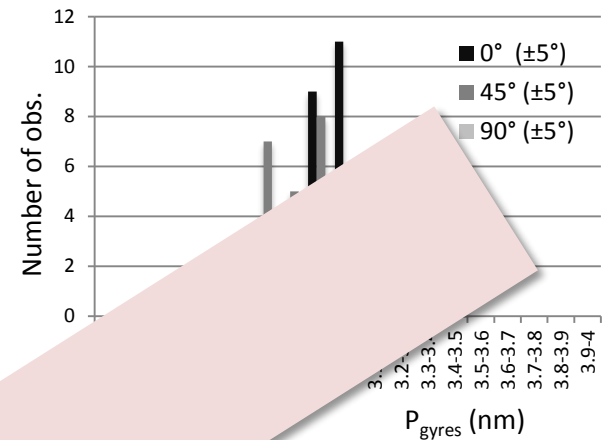
Sader et al, Ultramicroscopy 2009

CEMOVIS: compression ?

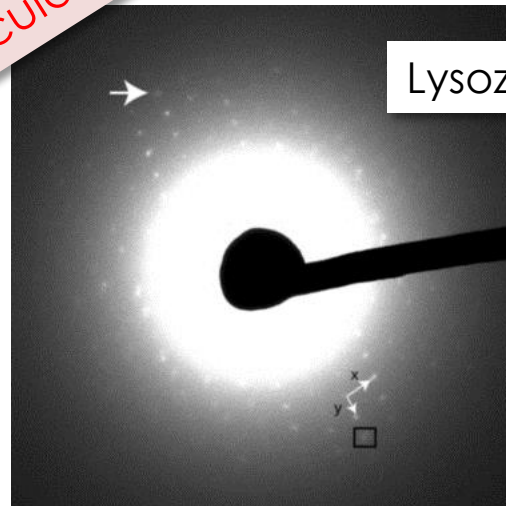
Nucleosomes



Pierson



Long range 20-40 %
Short range <10%
Macromolecular conformation: no compression



high resolution information 7.9 Å

Sader et al, Ultramicroscopy 2009

Pros & cons

Cryo-sectioning *versus* cryo-FIB milling ?

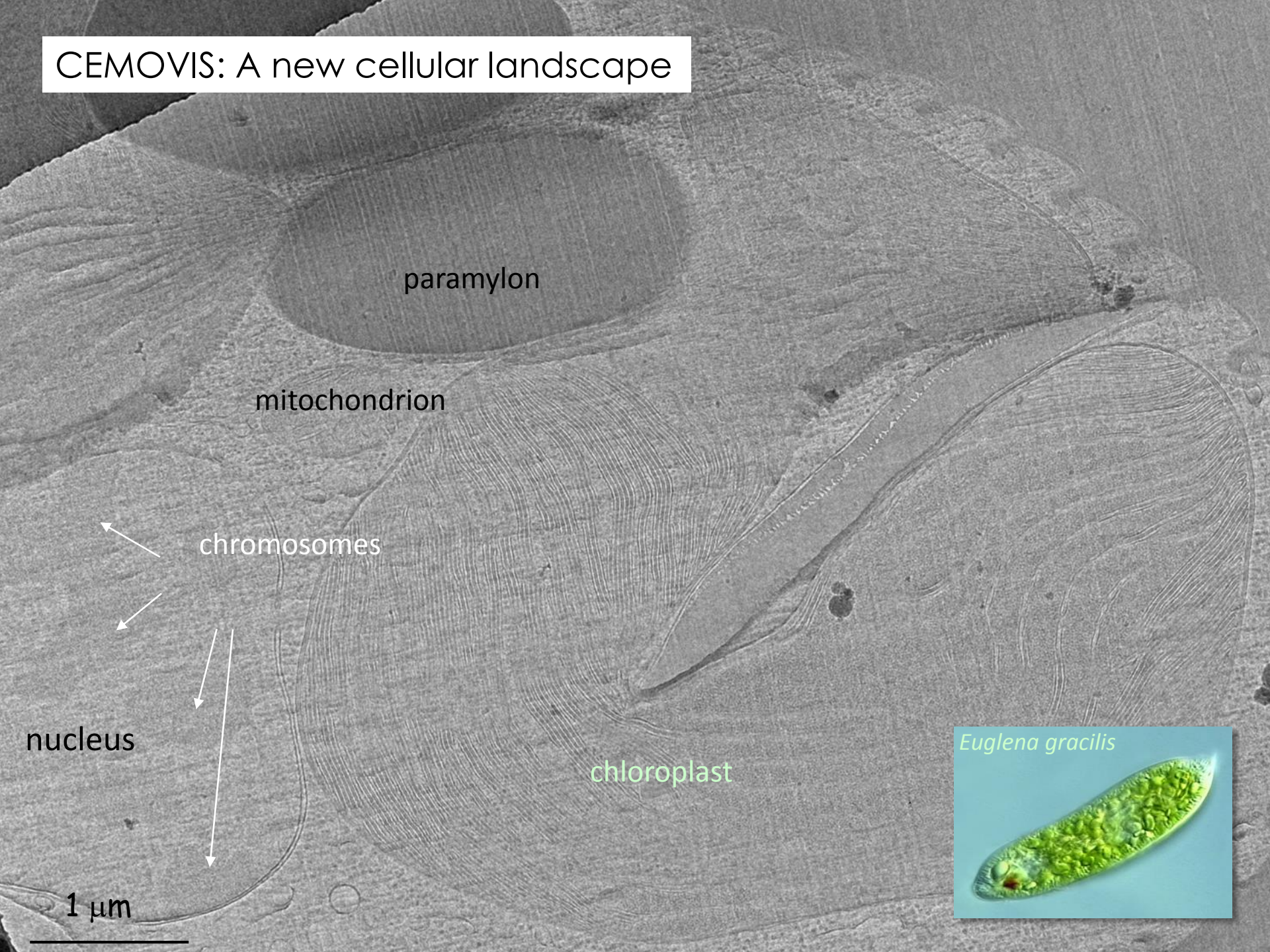
Technically demanding	YES	NO (?) / YES for tissue
Surface artifacts	YES crevasses ($e \geq 75\text{nm}$)	(YES)
Bulk artifacts	YES compression	NO
Serial sections	YES	NO
Surface of observation	50 x 150 μm	10 x 20 μm
Sample thickness	30 -300 (3000) nm	>150 nm
Imaging problems	YES flatness adhesion section-support	(YES) orientation for tomography

Pros & cons

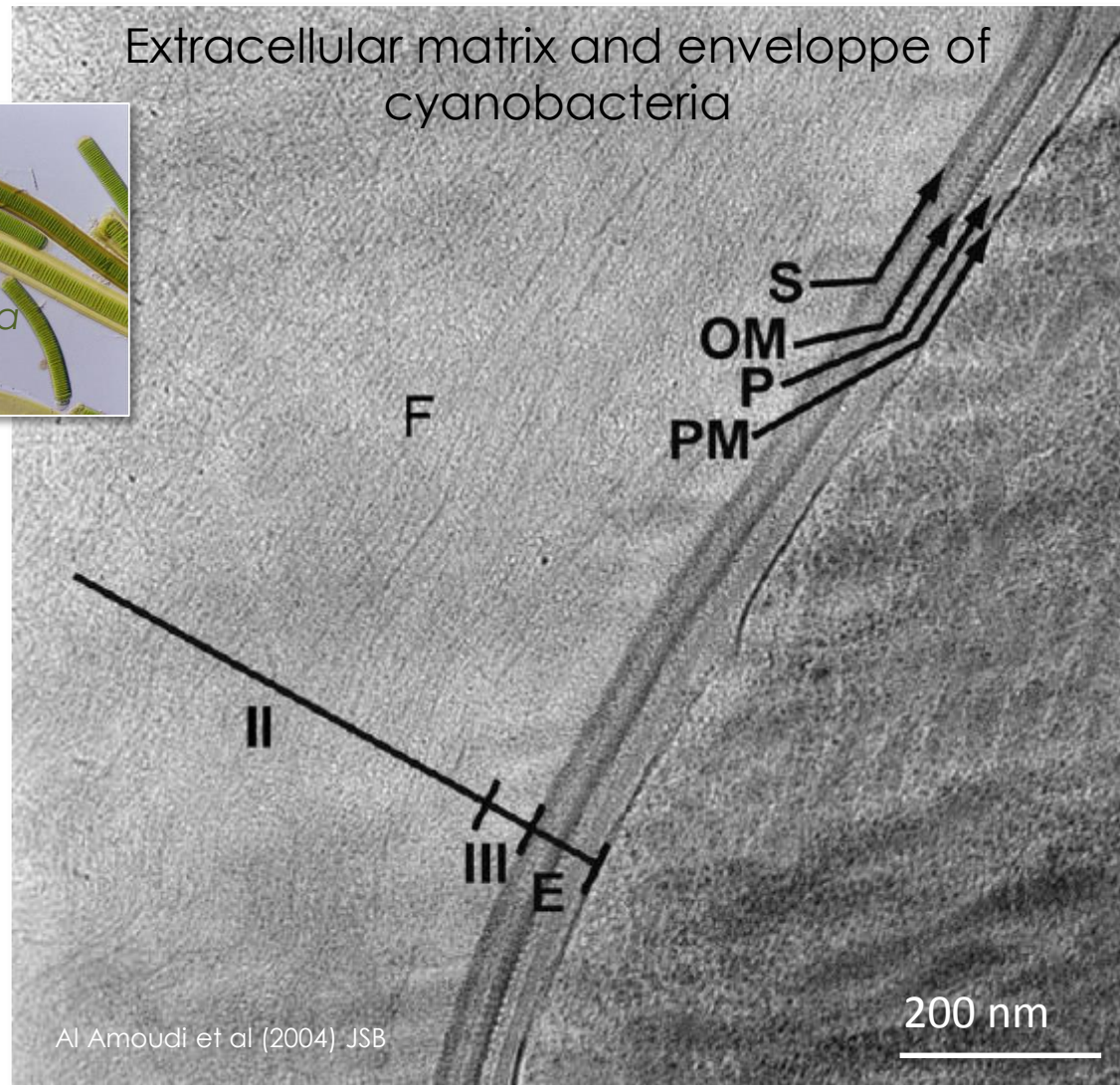
Cryo-sectioning *versus* cryo-FIB milling ?

Technically demanding	YES	NO (?) / YES for tissue
Surface artifacts	YES crevasses ($e \geq 75\text{nm}$)	(YES)
Bulk artifacts	YES compression	NO
Serial sections	YES	NO
Surface of observation	50 x 150 μm	10 x 20 μm
Sample thickness	30 -300 (3000) nm	>150 nm
Imaging problems	YES flatness adhesion section support - new support films (graphene ?)	(YES) orientation for tomography

CEMOVIS: A new cellular landscape

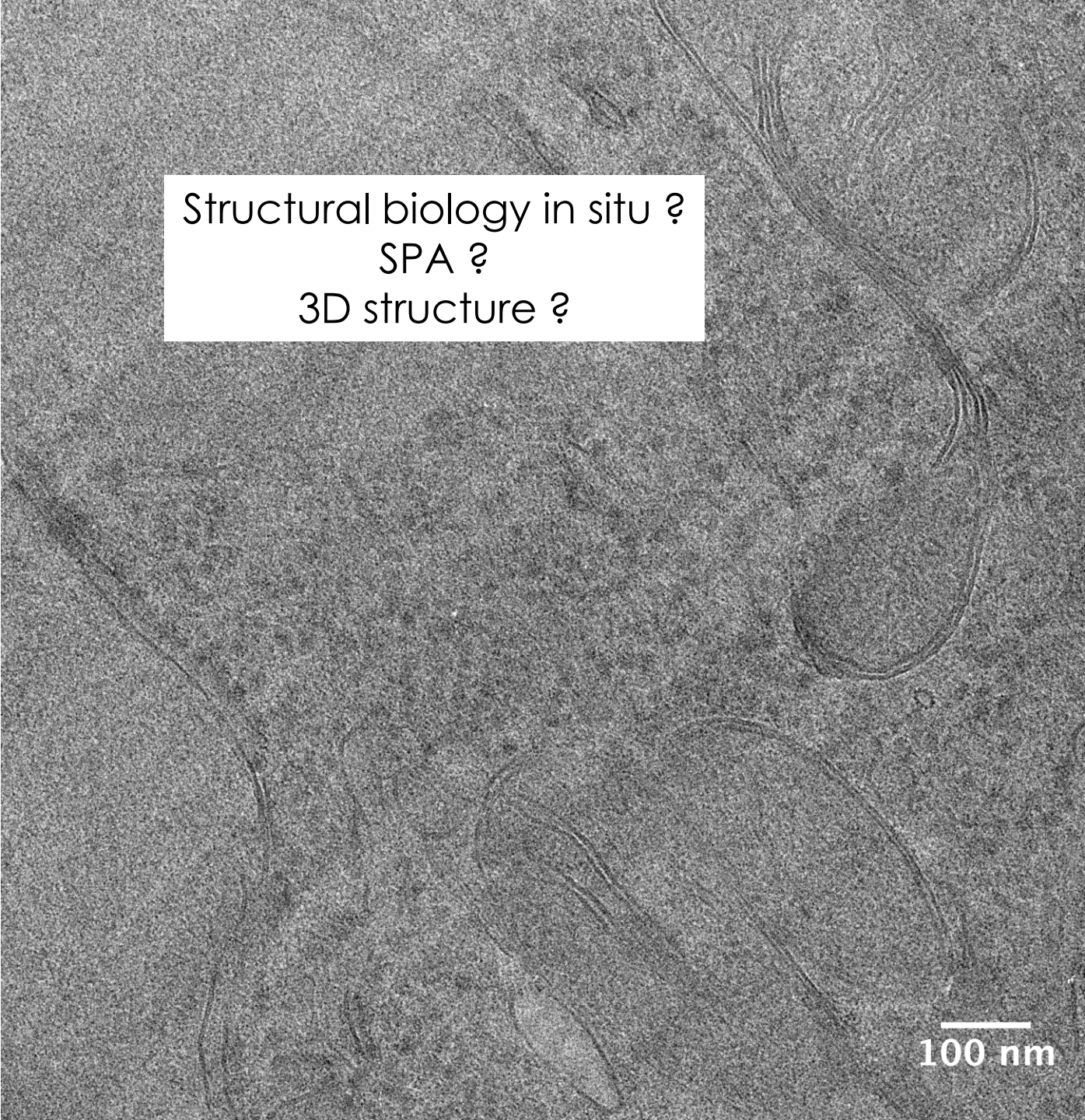


A new cellular landscape



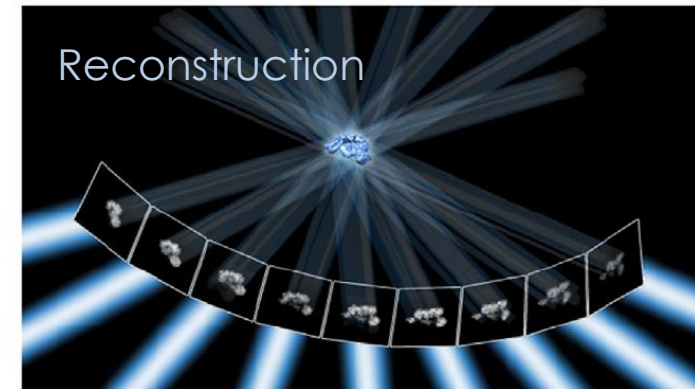
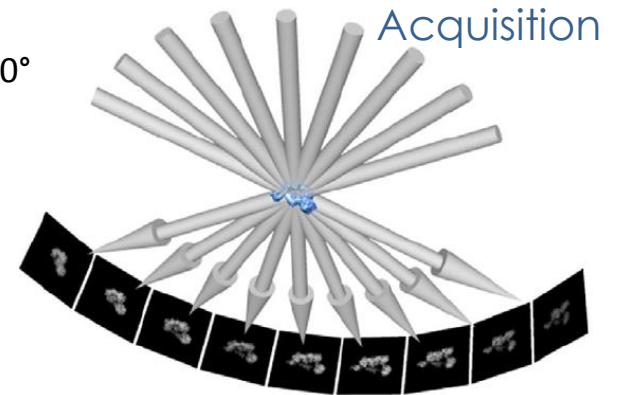
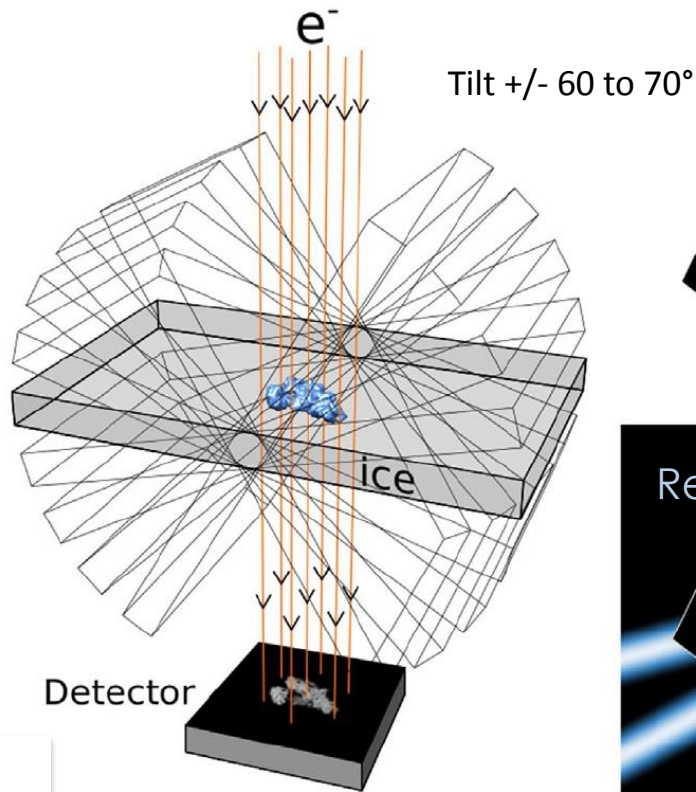
Imaging

Structural biology in situ ?
SPA ?
3D structure ?

A grayscale electron micrograph showing a cell with a nucleus and various organelles. A scale bar in the bottom right corner indicates 100 nm.

100 nm

3D structure by cryo-electron tomography

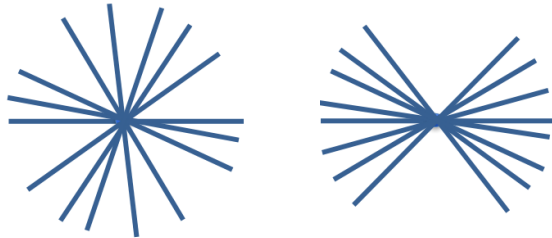


✓ Total electron dose

✓ Missing information

Single particle

Tomography



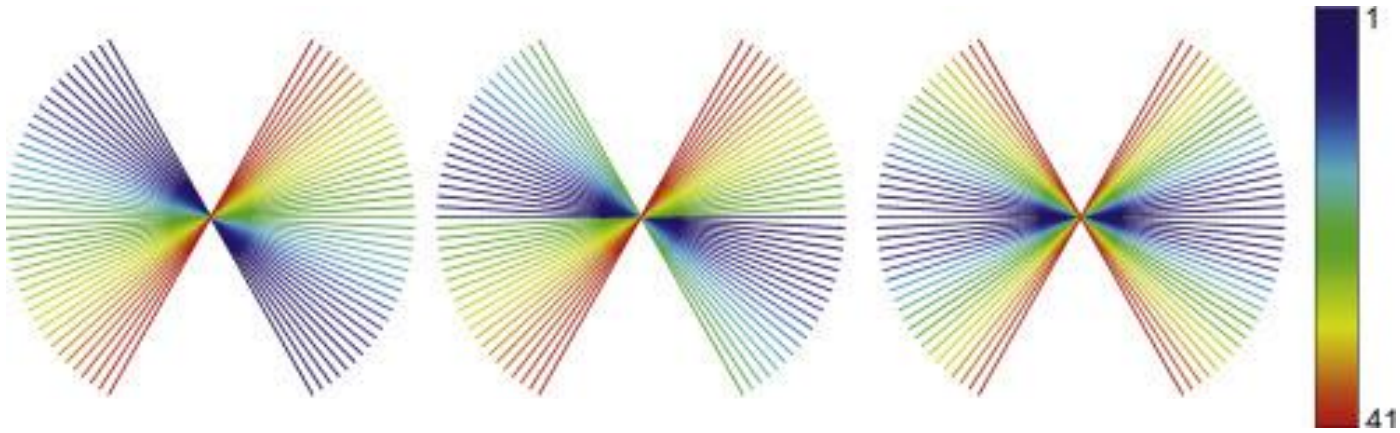
✓ CTF-correction (2D, 3D)

Acquisition schemes

Continuous

Bi-directional from 0

Dose symmetric



Hagen et al. JSB 2017

in-focus



« Phase plates »

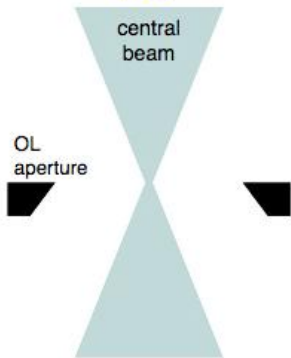
Volta phase plate in-focus



Frits Zernike (1888-1966)

(d)

Defocus Phase Contrast
DPC



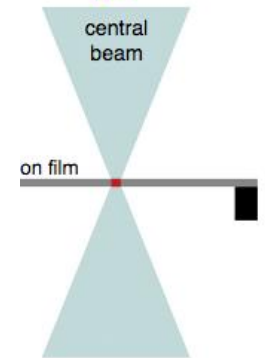
$$\sin(\gamma(\mathbf{k}))$$

Potentiel Volta
(interaction film-faisceau)

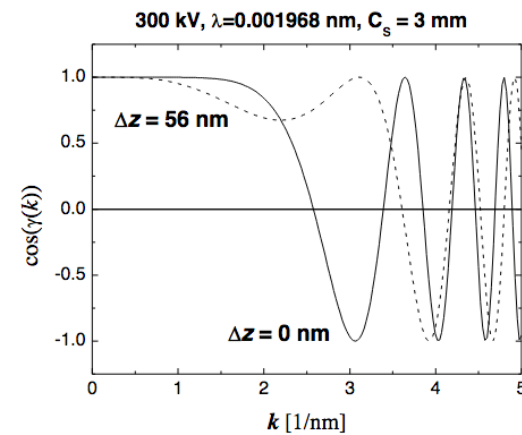
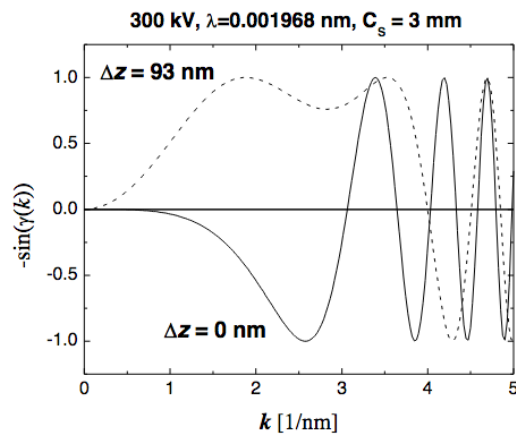
$$\cos(\gamma(\mathbf{k}))$$

(f)

Volta Phase Plate
VPP



Current Opinion in Structural Biology

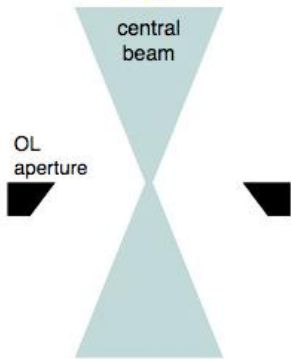


in-focus



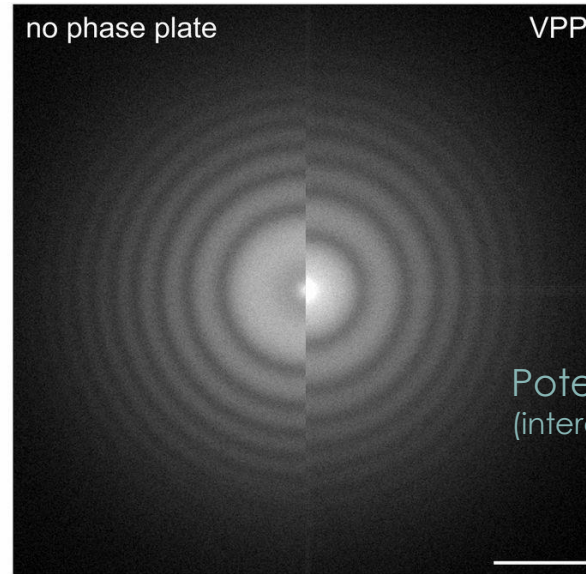
(d)

Defocus Phase Contrast
DPC



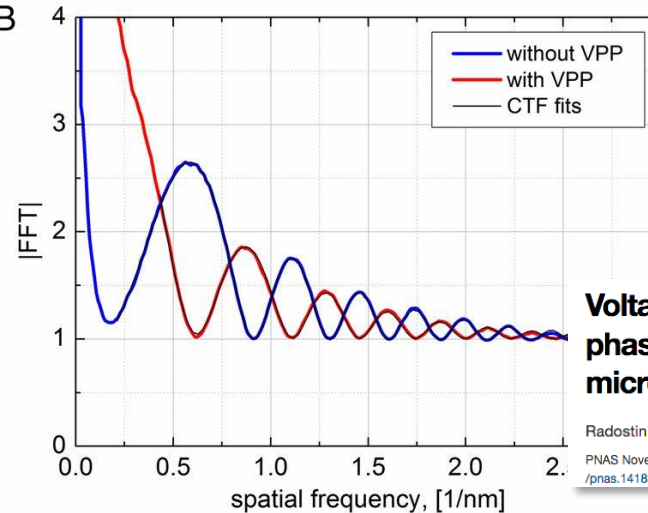
« Phase plates »

A



Potential Volta
(interaction film-faisceau)

B



Volta potential phase plate for in-focus phase contrast transmission electron microscopy

Radostin Danev, Bart Buijsse, Maryam Khoshouei, Jürgen M. Plitzko, and Wolfgang Baumeister
PNAS November 4, 2014 111 (44) 15635-15640; published ahead of print October 20, 2014 <https://doi.org/10.1073/pnas.1418377111>

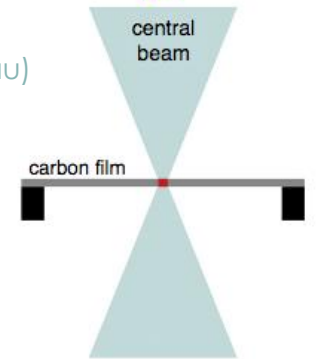
Volta phase plate in-focus



Frits Zernike (1888-1966)

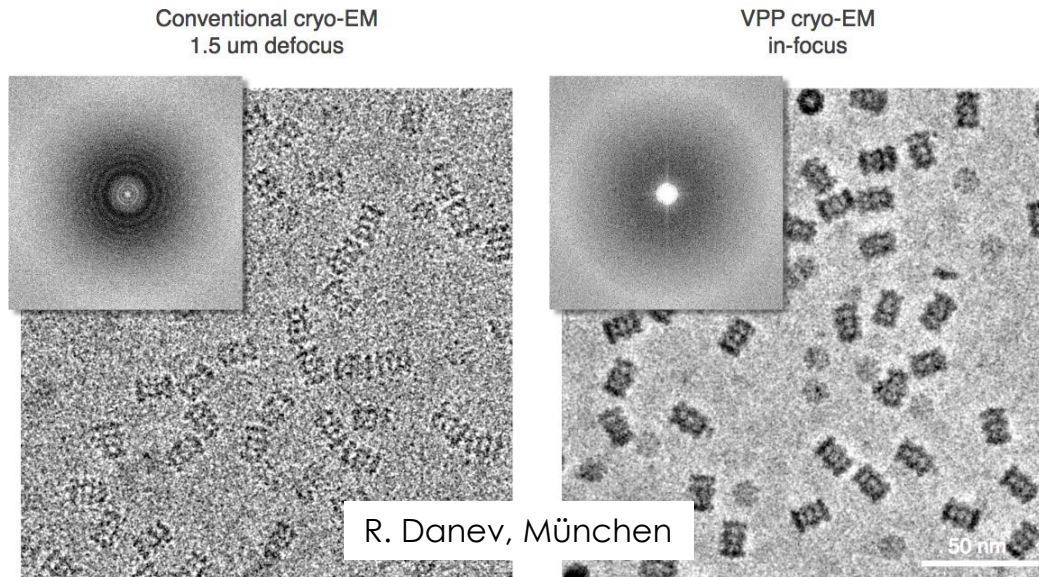
(f)

Volta Phase Plate
VPP



Current Opinion in Structural Biology

« Phase plates »



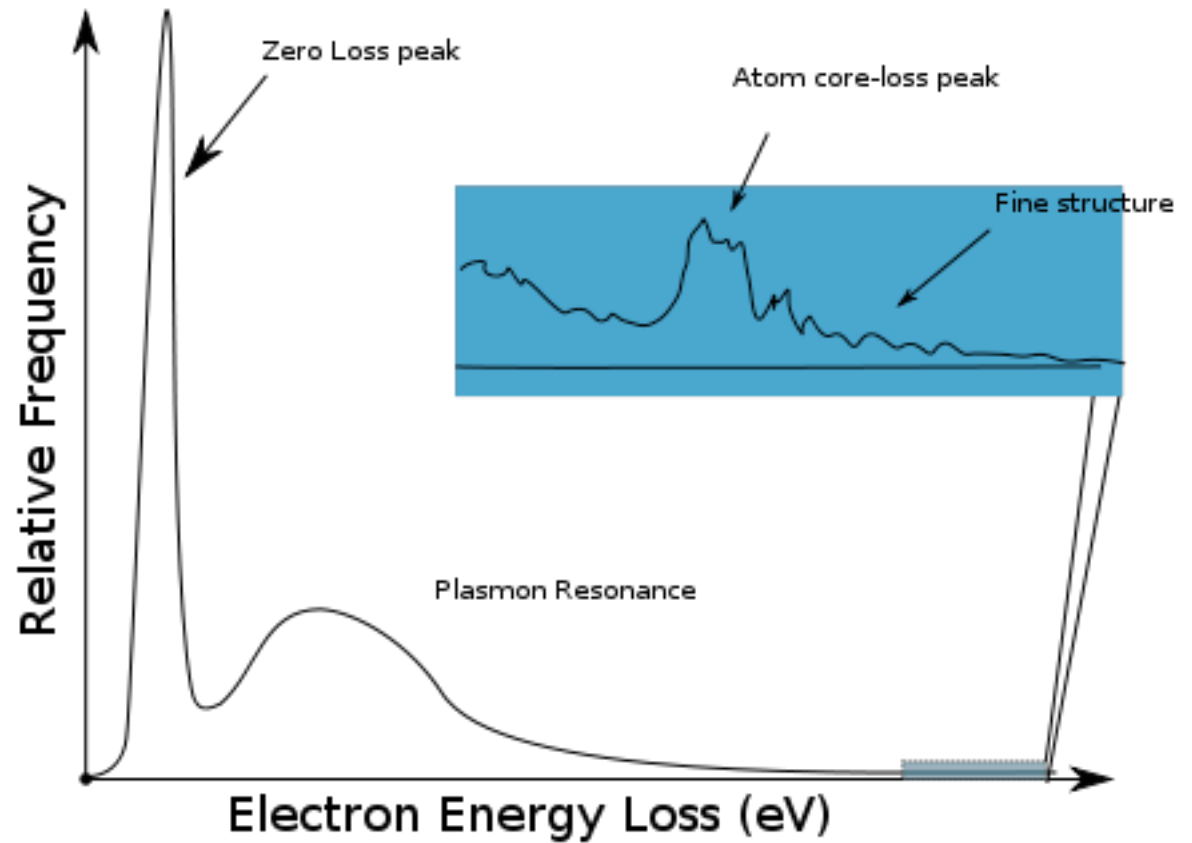
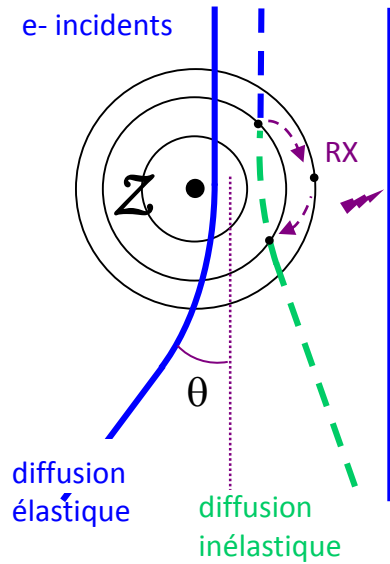
Volta potential phase plate for in-focus phase contrast transmission electron microscopy

Radostin Danev, Bart Buijsse, Maryam Khoshouei, Jürgen M. Plitzko, and Wolfgang Baumeister

PNAS November 4, 2014 111 (44) 15635-15640; published ahead of print October 20, 2014 <https://doi.org/10.1073/pnas.1418377111>



Zero loss filtering



Zero loss filtering

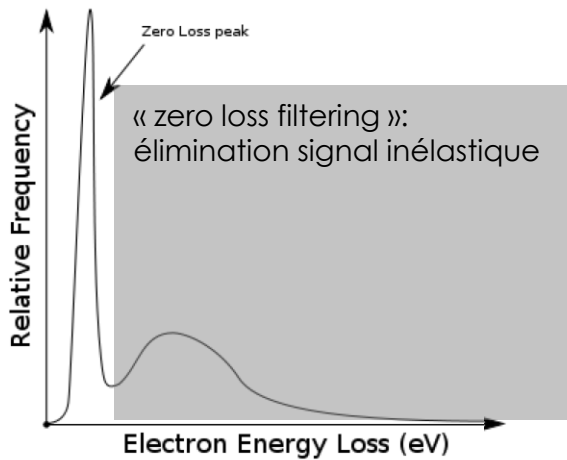
- thick specimen (> 150 nm)
- tomography

JEOL 2200FS

Thick specimen

50 nm

- filtre d'énergie



bacteriophage T5

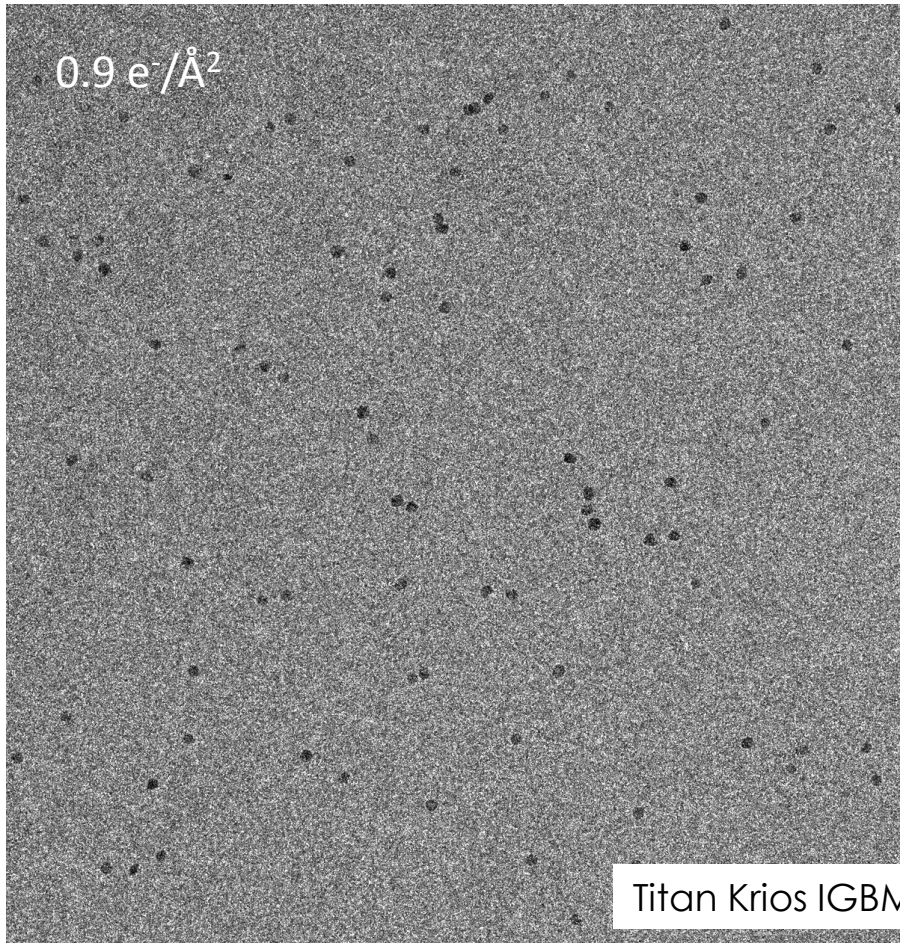
ADN

TMV

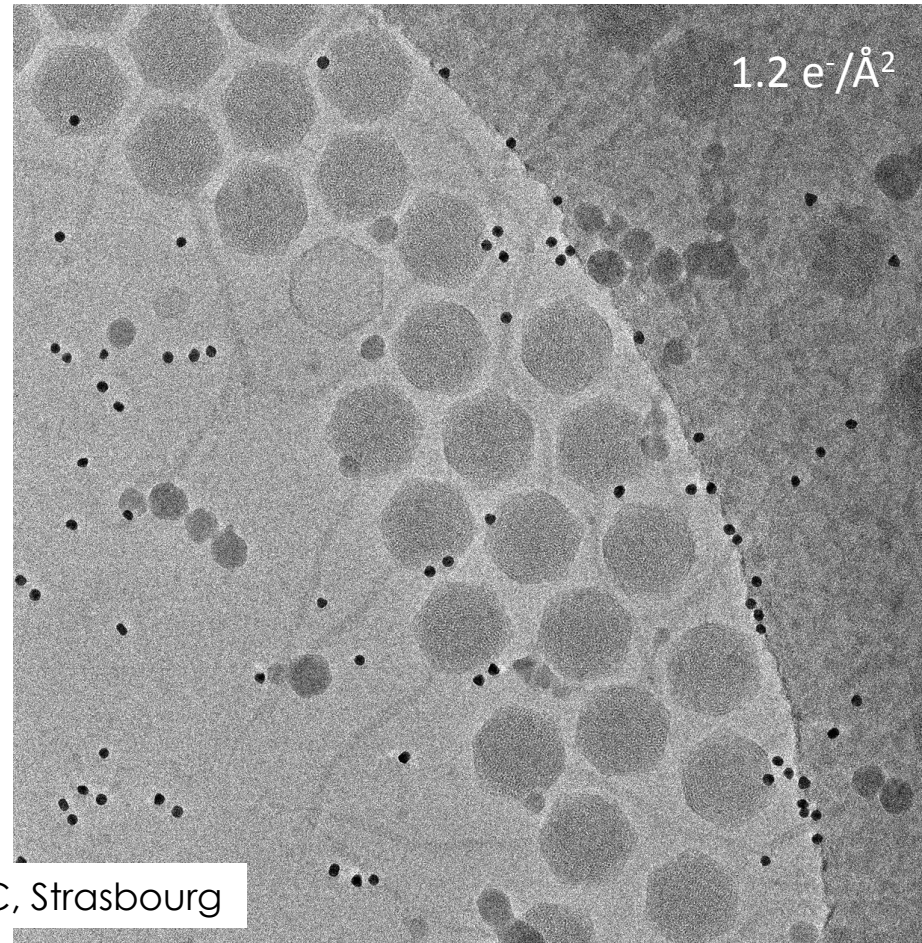
+ filtre d'énergie

« Volta Phase Plate » + energy filter

Conventional cryoEM
1 μm defocus

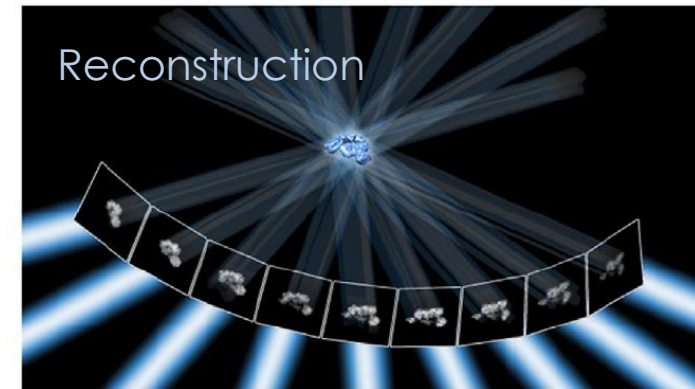
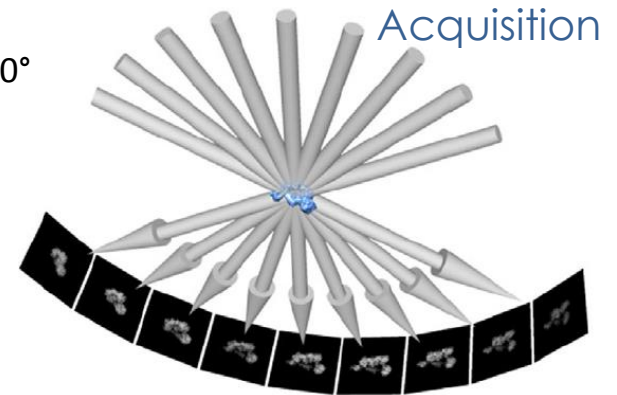
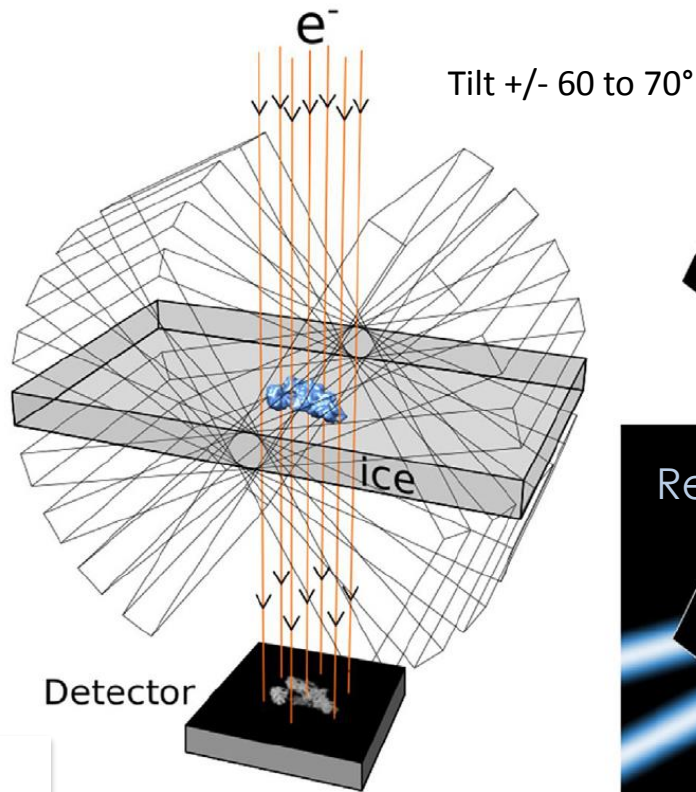


VPP cryoEM
In-focus + energy filter



Bacteriophage T5
(80 nm) + NP or (10 nm)

3D structure by cryo-electron tomography

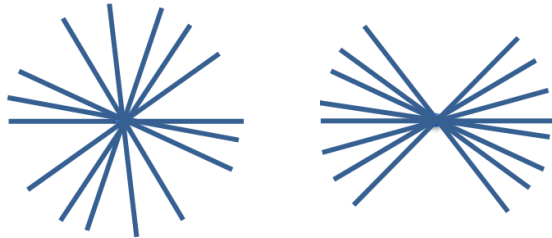


✓ Total electron dose

✓ Missing information

Single particle

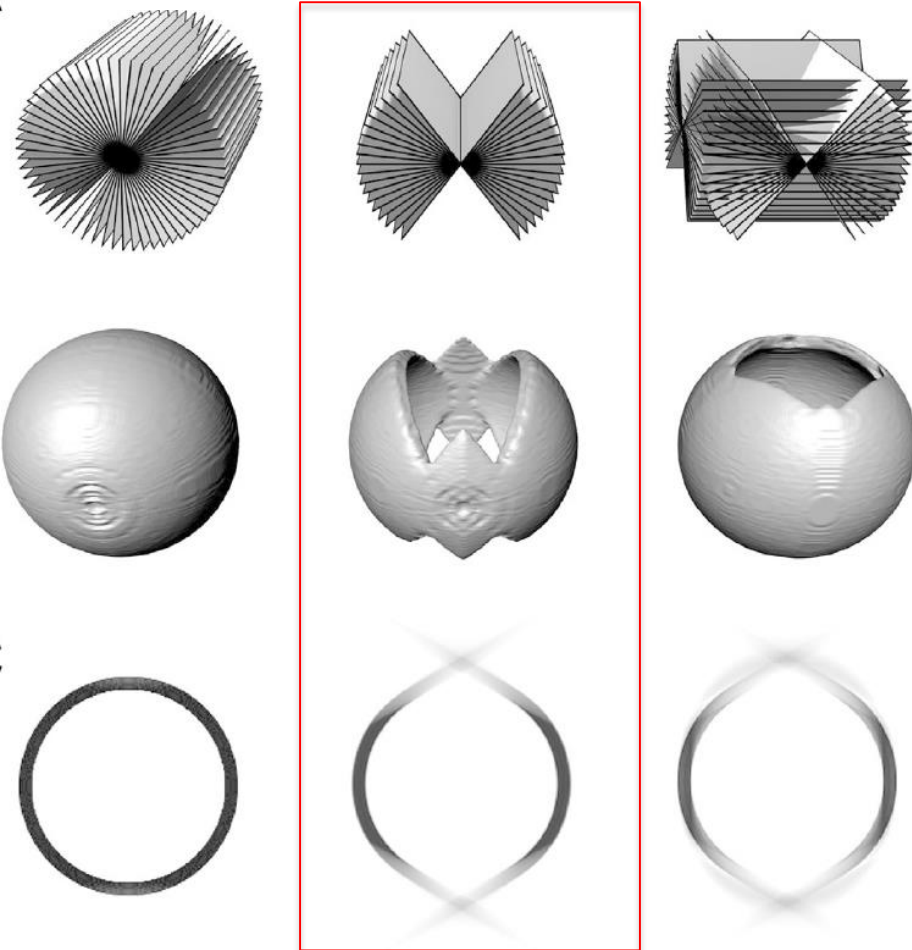
Tomography



✓ CTF-correction (2D, 3D)

« missing wedge », « missing cone »

R.I. Koning et al. / *Annals of Anatomy* 217 (2018) 82–96

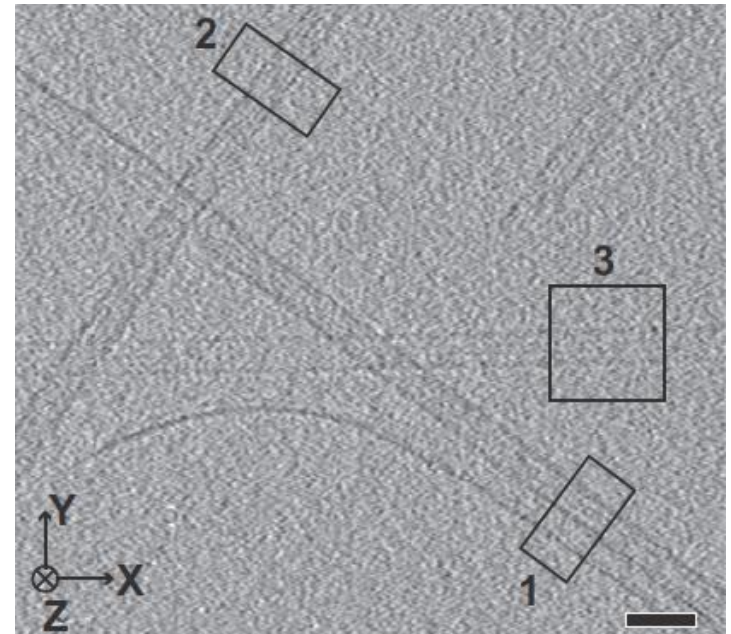


$$R_x = R_{2D}$$

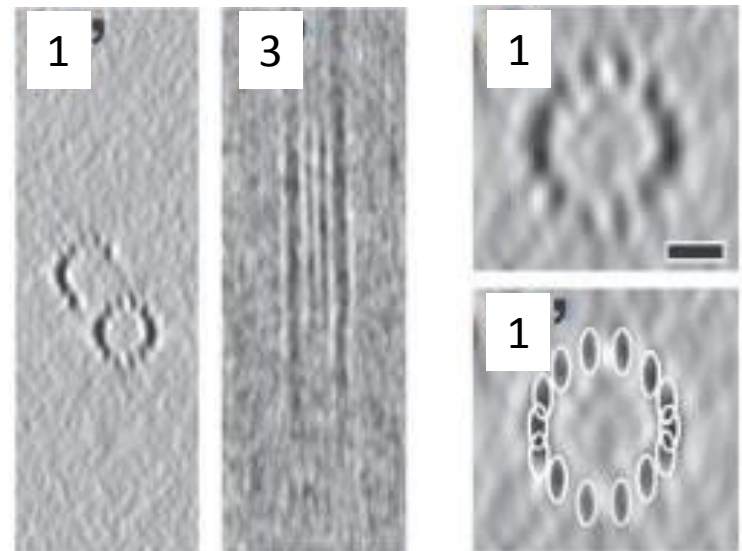
$$R_y = \pi D / N$$

$$R_z = f(\alpha) R_y$$

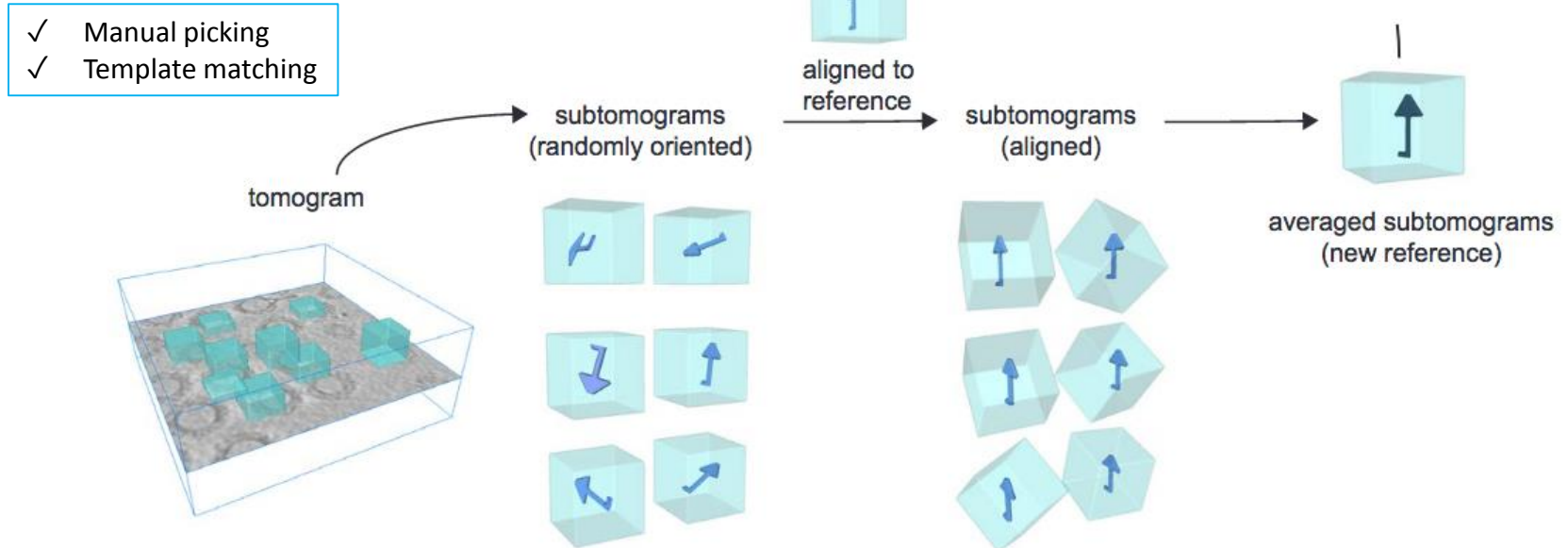
α max tilt angle,
D object diameter,
N $\approx$ number of images(angles)



A. Guesdon et al. / *Journal of Structural Biology* 181 (2013) 169–178



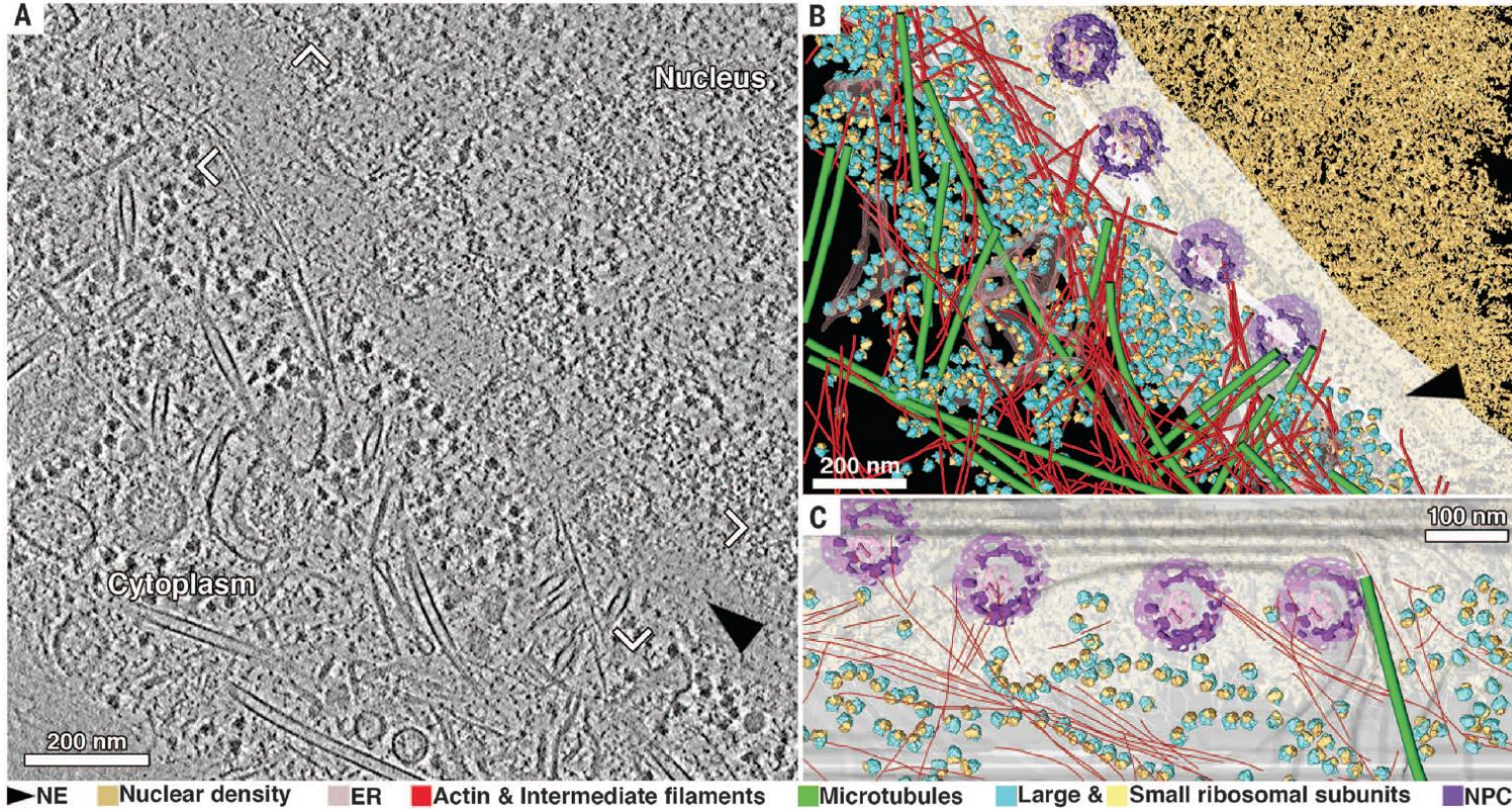
Sub-tomogram averaging



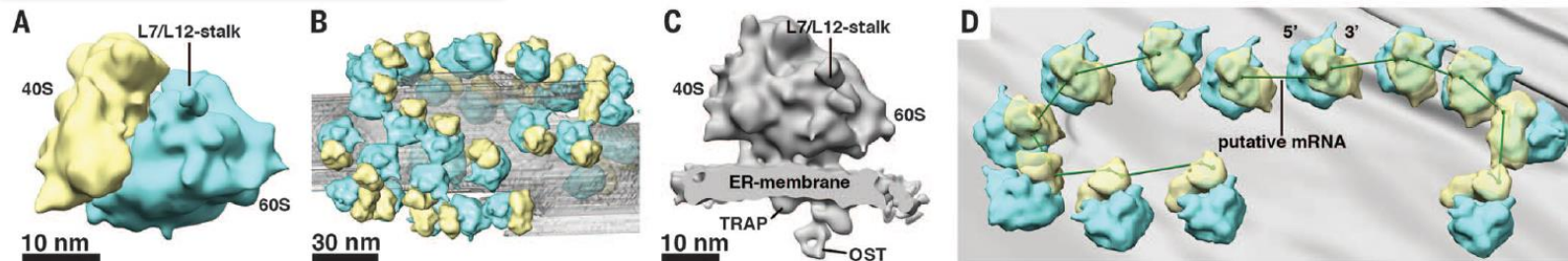
Wan, W., & Briggs, J. A. G. (2016). Cryo-electron tomography and subtomogram averaging. In *Methods in enzymology* (Vol. 579, pp. 329-367). Academic Press

« Molecular sociology »

Nuclear periphery (HeLa cell)

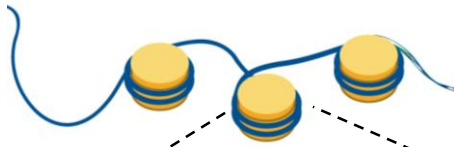


Sub-tomogram averaging

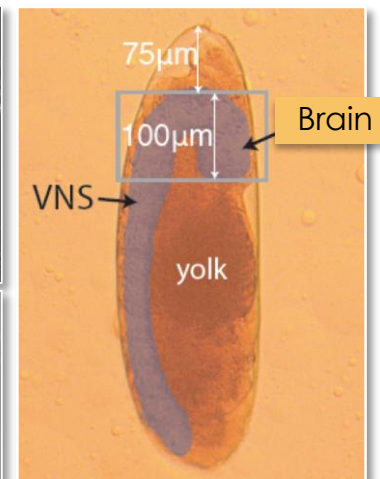
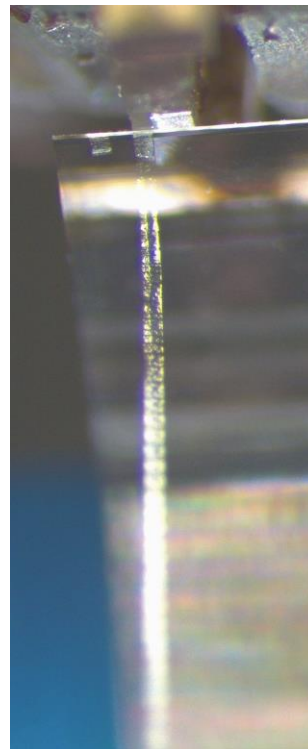
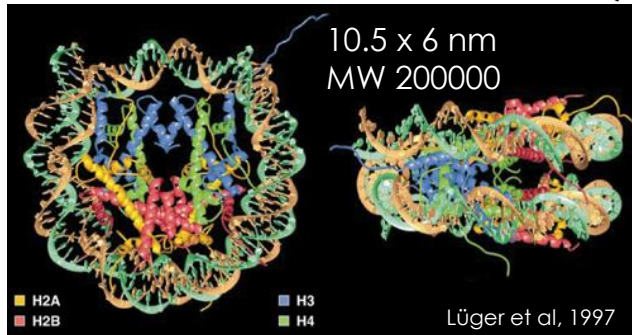


+VPP

Imaging the nucleosome in its cellular context



« bead-on-string »
chromatin filament



Drosophila embryo

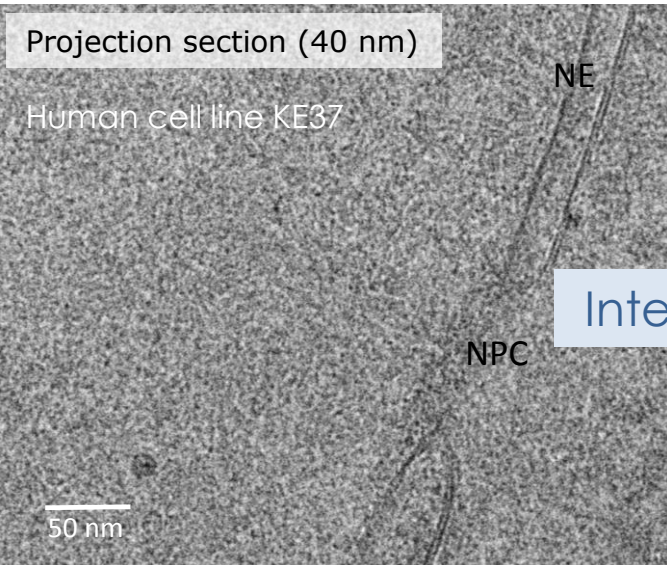


Mikhail Eltsov
Buchmann Institute, Frankfurt

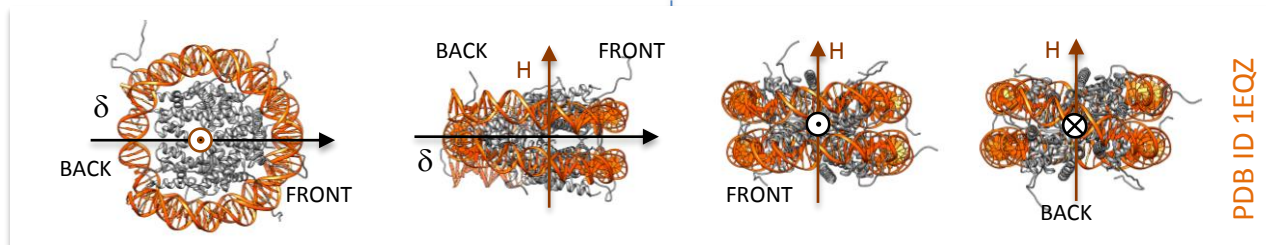
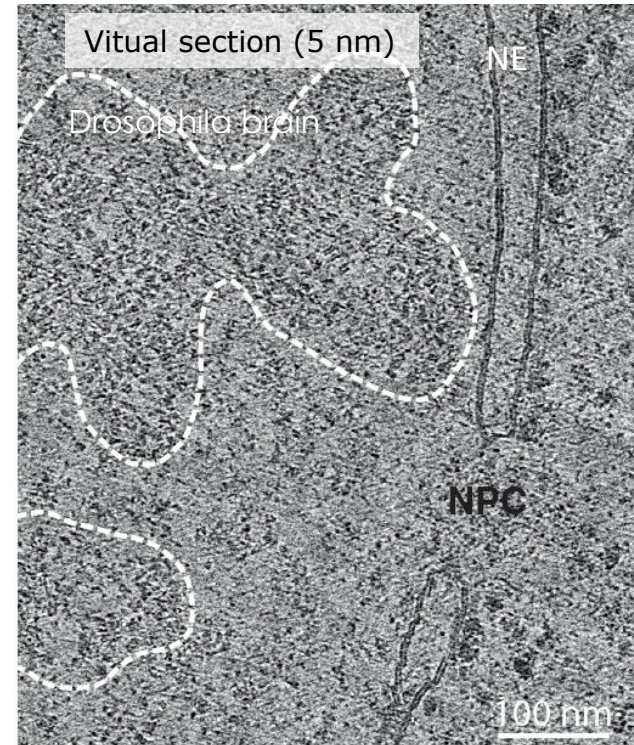


Diana Grew

Imaging the nucleosome in its cellular context



Interphase nuclei



2D imaging

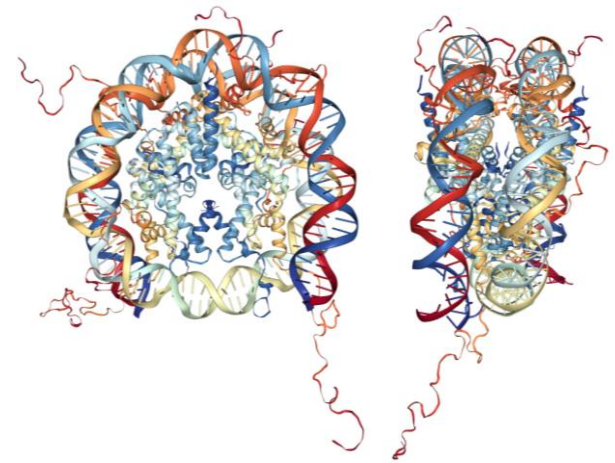
Tomography

Simulation of cryoEM nucleosomes

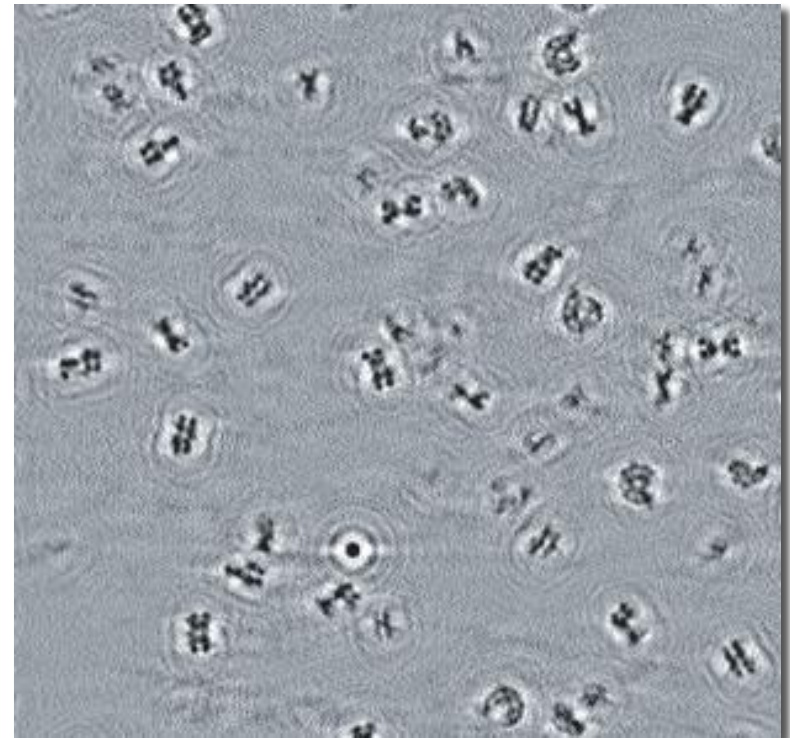
Nucleosome canonical structure PDB ID 1EQZ

CTF-modulated

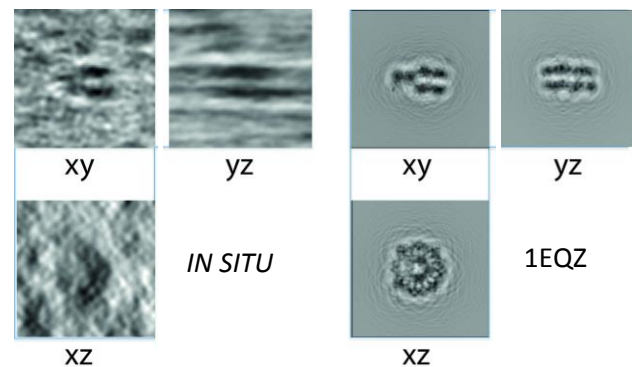
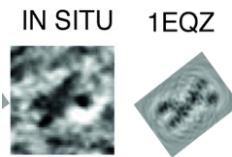
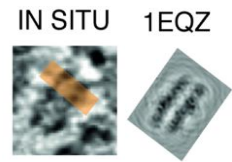
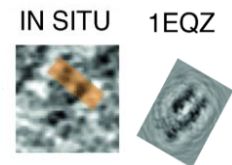
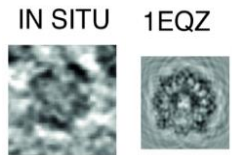
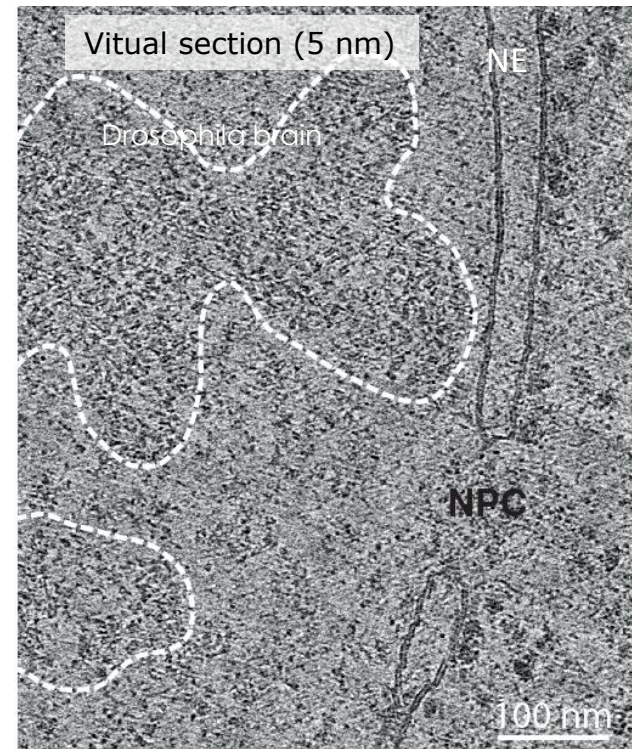
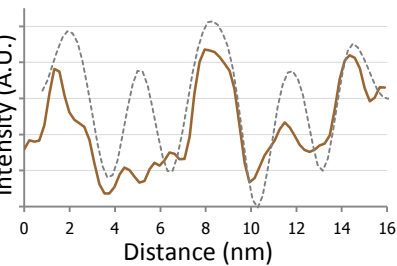
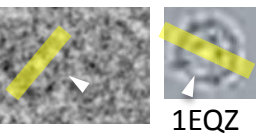
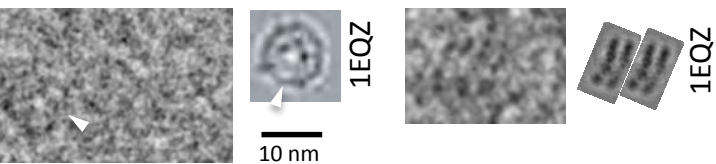
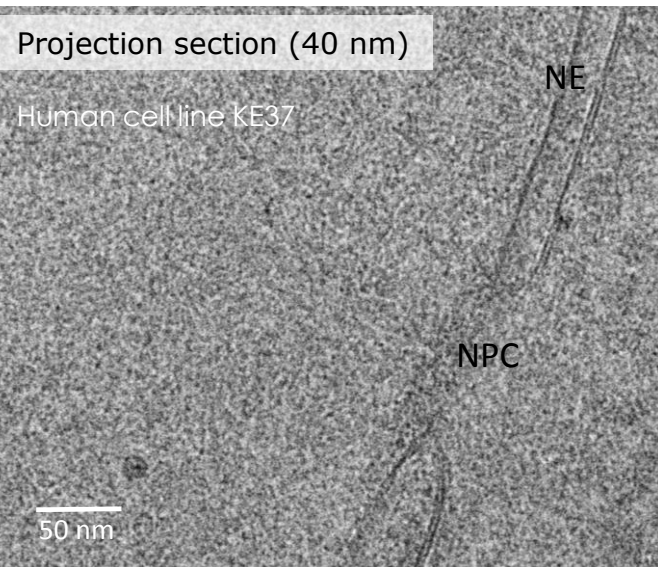
2D projections



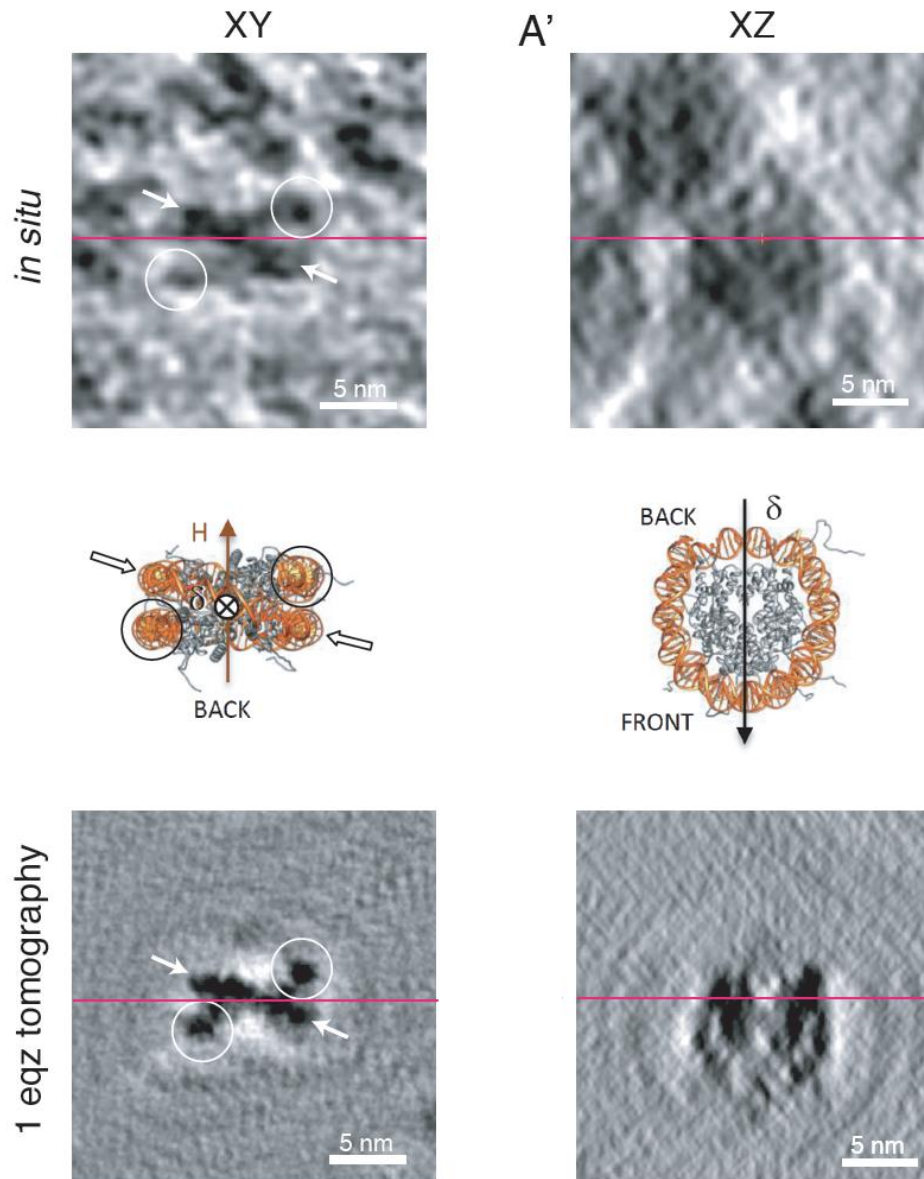
5-nm slices in simulated tomographic reconstructions



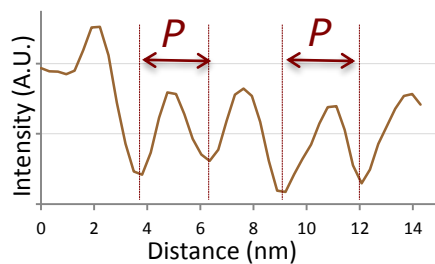
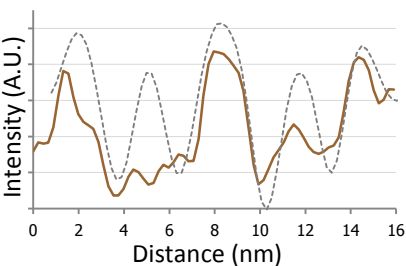
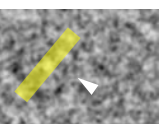
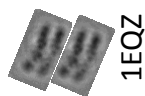
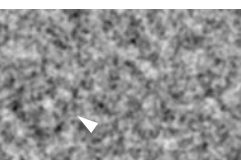
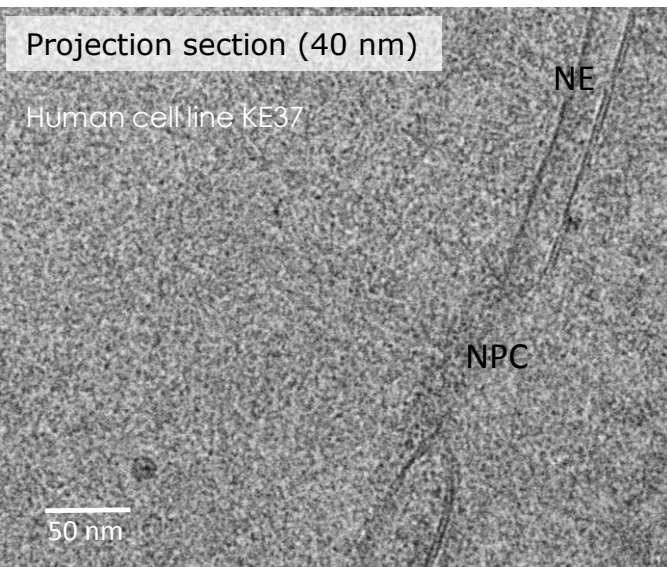
Can we visualise the nucleosome in its cellular context ?



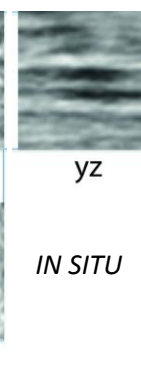
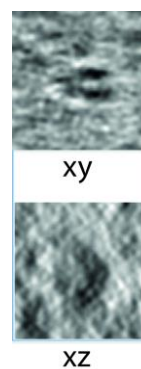
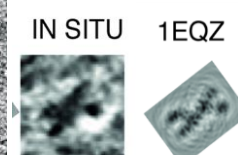
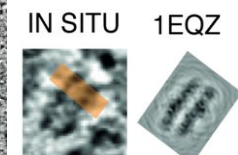
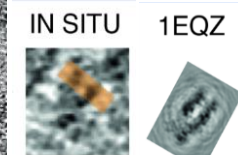
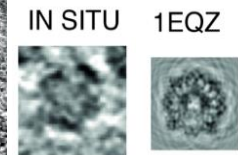
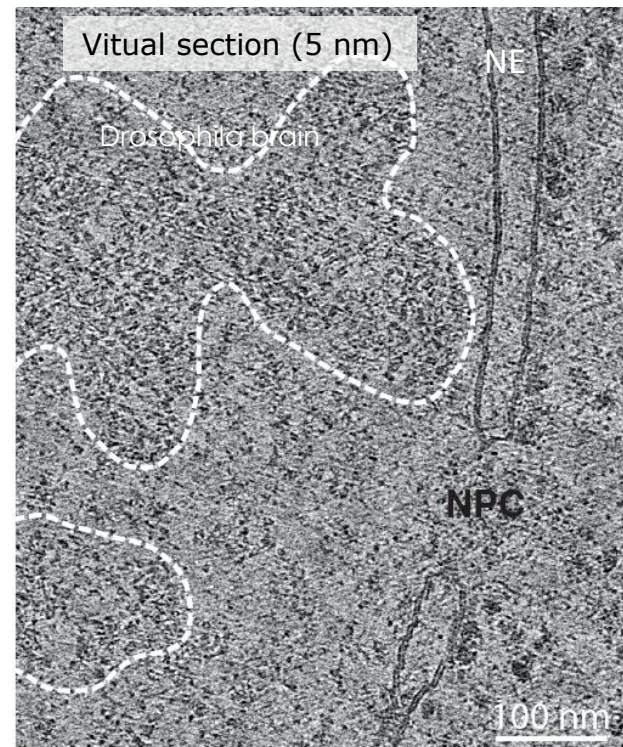
A left-handed DNA superhelix



Can we visualise the nucleosome in its cellular context ?

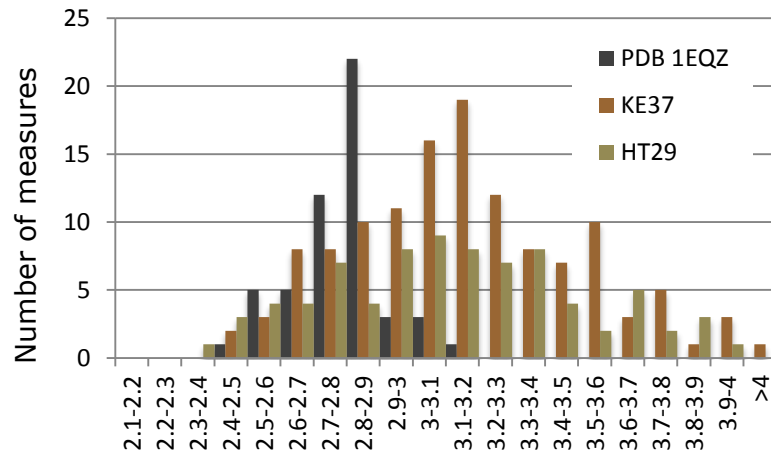


P-distances between DNA gyres

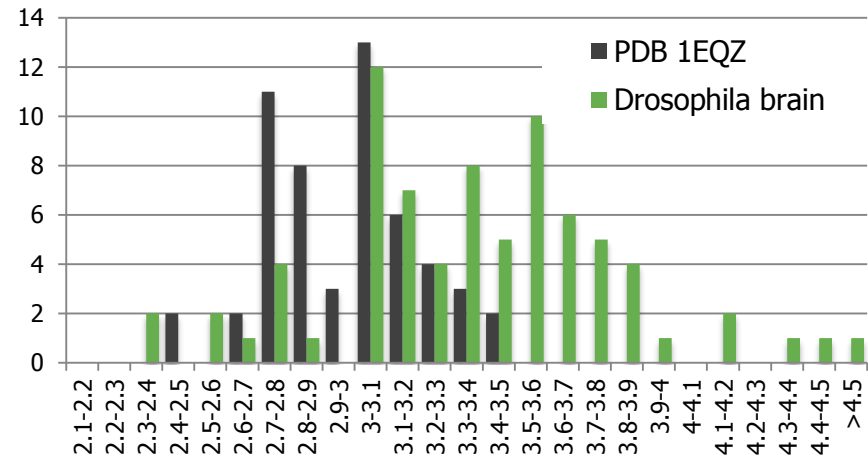


The nucleosome conformation in interphase nucleus is more open than the crystallographic structure.

2D imaging data

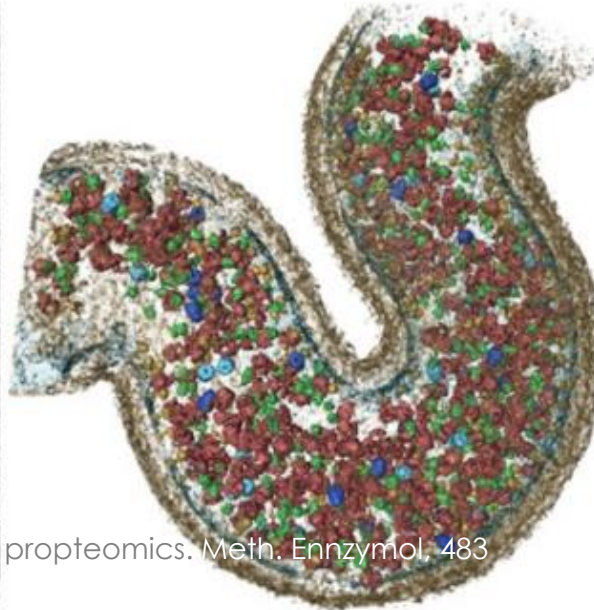
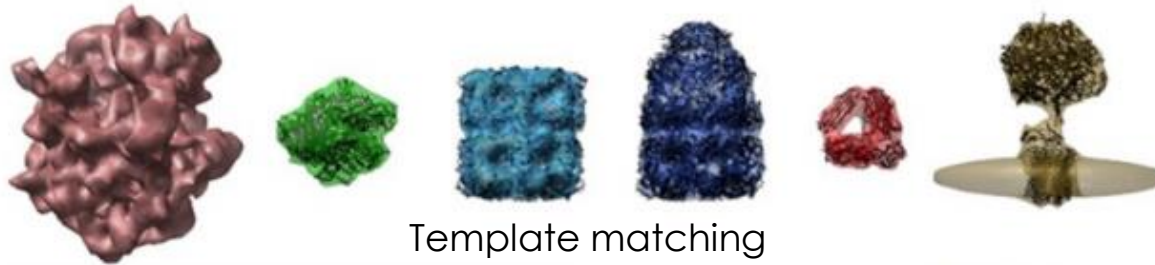


Cryo-tomo data



P-distance between DNA gyres (nm)

Targetting molecules of interest ?

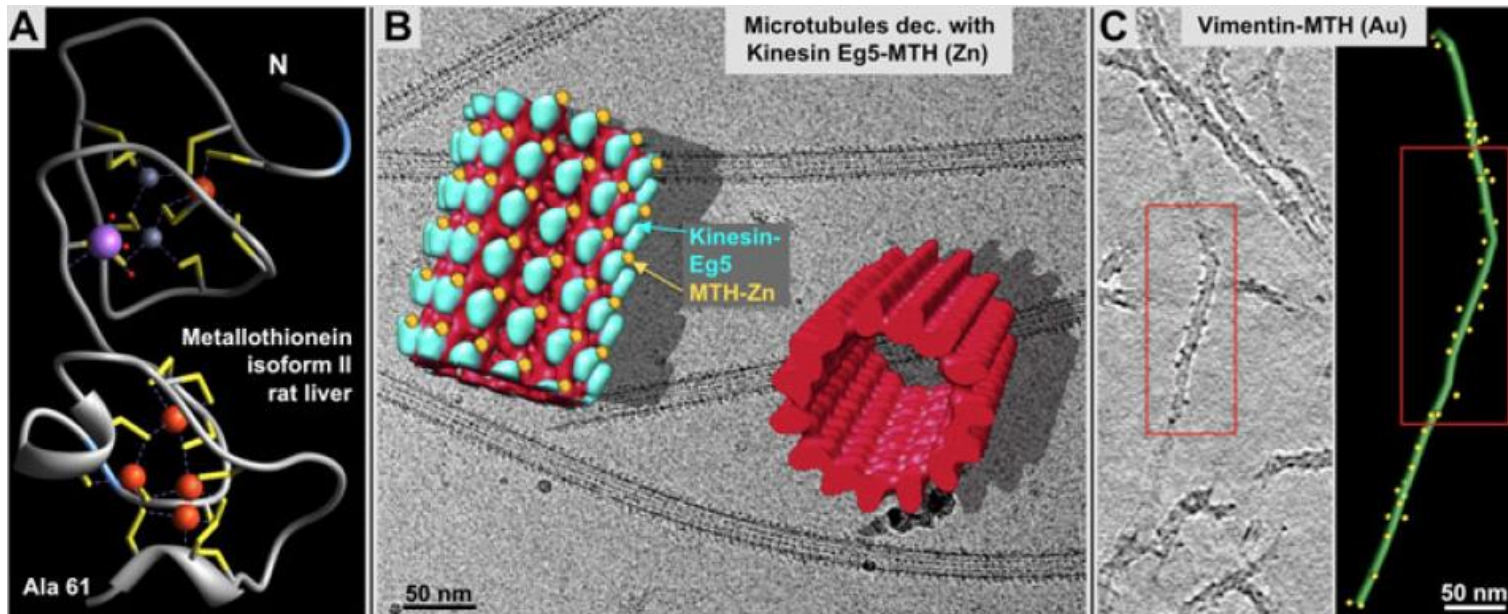


Förster, Han, & Beck (2010) Visual proteomics. Meth. Enzymol. 483

100 nm

Identification of macromolecules in the cellular (complex) context

Electron dense clonable labels ?



Proof of concept
metallothionein

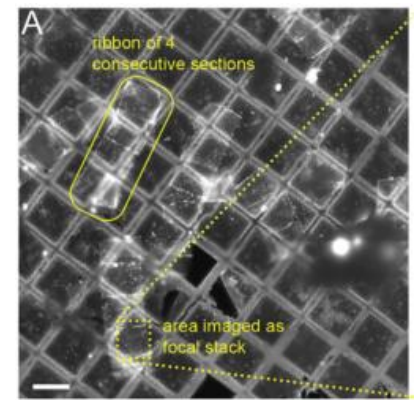
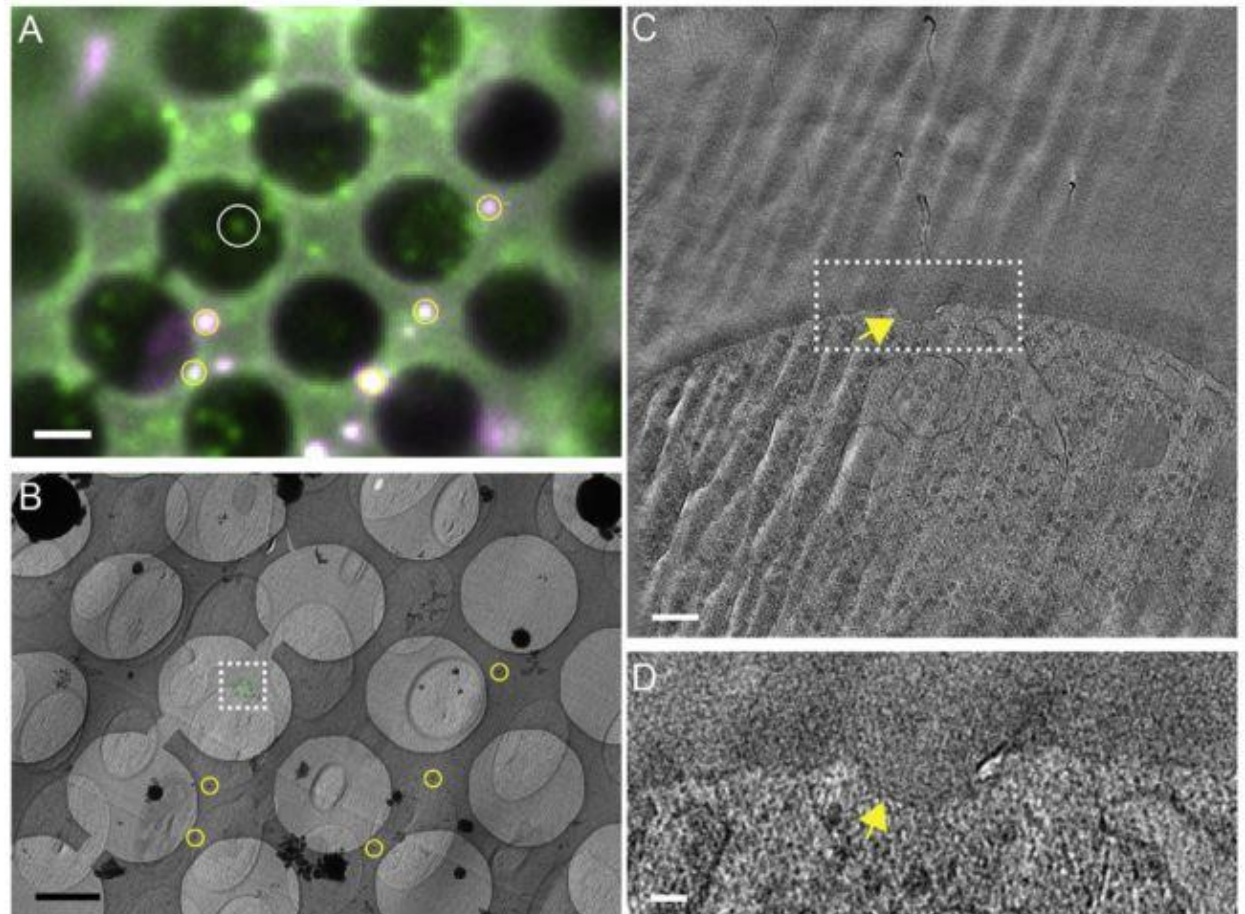
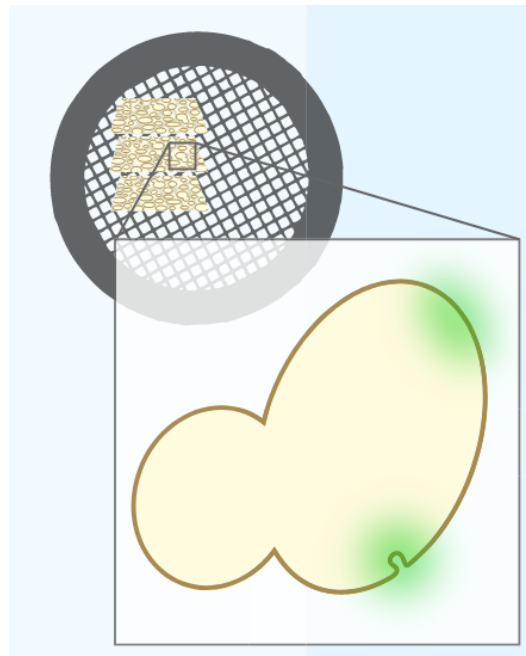
Mercogliano & De Rosier, 2004
Bouchet Marquis et al, 2012
Hirabayashi et al, 2014

Toxicity
Endogeneous metallothionein

Identification of macromolecules in the cellular (complex) context

Cryo-CLEM

- cryo-fluorescence microscopy
- cryo-EM/ET



Purified molecules in solution

Freezing
Imaging
CTF correction
SPA

Molecules in cells

Freezing
Thinning
Imaging: tomography
CTF correction
Tomogram reconstruction
Sub-tomogram averaging

Target/detect molecule of interest

. Dubochet, J., Adrian, M., Chang, J. J., Homo, J. C., Lepault, J., McDowell, A. W., & Schultz, P. (1988). Cryo-electron microscopy of vitrified specimens. *Quarterly reviews of biophysics*, 21(2), 129-228.

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- . Eltsov, M., Grewe, D., Lemercier, N., Frangakis, A., Livolant, F., & Leforestier, A. (2018). Nucleosome conformational variability in solution and in interphase nuclei evidenced by cryo-electron microscopy of vitreous sections. *Nucleic acids research*, 46(17), 9189-9200.
- . Dubochet, J., Zuber, B., Eltsov, M., Bouchet-Marquis, C., Al-Amoudi, A., & Livolant, F. (2007). How to “read” a vitreous section. *Methods in cell biology*, 79, 385-406.
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- . Sader, K., Studer, D., Zuber, B., Gnaegi, H., & Trinick, J. (2009). Preservation of high resolution protein structure by cryo-electron microscopy of vitreous sections. *Ultramicroscopy*, 110(1), 43-47.
- . Pierson, J., Fernández, J. J., Bos, E., Amini, S., Gnaegi, H., Vos, M., ... & Peters, P. J. (2010). Improving the technique of vitreous cryo-sectioning for cryo-electron tomography: electrostatic charging for section attachment and implementation of an anti-contamination glove box. *Journal of structural biology*, 169(2), 219-225.

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- . Studer, D., Graber, W., Al-Amoudi, A., & Eggli, P. (2001). A new approach for cryofixation by high-pressure freezing. *Journal of microscopy*, 203(3), 285-294.
- . Studer, D., Michel, M., Wohlwend, M., Hunziker, E. B., & Buschmann, M. D. (1995). Vitrification of articular cartilage by high-pressure freezing. *Journal of microscopy*, 179(3), 321-322.
- . Vanhecke, D., Graber, W., & Studer, D. (2008). Close-to-native ultrastructural preservation by high pressure freezing. *Methods in cell biology*, 88, 151-164.

CRYO-FIB Milling

- . Villa, E., Schaffer, M., Plitzko, J. M., & Baumeister, W. (2013). Opening windows into the cell: focused-ion-beam milling for cryo-electron tomography. *Current opinion in structural biology*, 23(5), 771-777..
- . Mahamid, J., Pfeffer, S., Schaffer, M., Villa, E., Danev, R., Cuellar, L. K., ... & Baumeister, W. (2016). Visualizing the molecular sociology at the HeLa cell nuclear periphery. *Science*, 351(6276), 969-972.

CRYO-TOMO

- Myasnikov, A. G., Afonina, Z. A., & Klaholz, B. P. (2013). Single particle and molecular assembly analysis of polyribosomes by single-and double-tilt cryo electron tomography. *ultramicroscopy*, 126, 33-39.
- Wan, W., & Briggs, J. A. G. (2016). Cryo-electron tomography and subtomogram averaging. In *Methods in enzymology* (Vol. 579, pp. 329-367). Academic Press.
- Hagen, W. J., Wan, W., & Briggs, J. A. (2017). Implementation of a cryo-electron tomography tilt-scheme optimized for high resolution subtomogram averaging. *Journal of structural biology*, 197(2), 191-198.
- Turonova, B., Schur, F. K., Wan, W., & Briggs, J. A. (2017). Efficient 3D-CTF correction for cryo-electron tomography using NovaCTF improves subtomogram averaging resolution to 3.4 angstrom. *Journal of structural biology*, 199(3), 187-195.