Transmission electron microscopy in structural Biology From specimen preparation to data collection







o.lambert@cbmn.u-bordeaux.fr





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Data collection Specimen Image with an Electron Microscope preparation Analysis 2D classes **Electron Beam** molecules **3D** reconstruction

Frozen-hydrated Molecules on EM grid Direct electron detector Captures projection image of of each molecule

> Model building & validation Structure deposition PDB

=





Hemoglobin 64 kDa 3.2 A R Danev, 2017



Biotin-SA C1

Streptavidin 52 kDa 3.2 A X Fan.... H-W Wang, 2019 Nat Commun



Riboswitch RNA 40 kDa 3.7 A Zhang.... W Chiu, 2019 Nat Commun

1 0

	PAC1R		GLP-1R-TAS	
	+VPP	-VPP	+ZLF	-ZLF
Data processing	•	*	•	
Micrographs	4,032	3,617	5,508	3,251
Micrographs after CTF	3,761	3,553	4,839	2,638
fits (retention)	(93%)	(98%)	(88%)	(81%)
Measured defocus [µm]	0.4 - 1.2	0.8-1.7	0.7 - 1.8	0.7 - 1.7
Picked particles [x10 ³]	2,446	3,012	3,246	1,490
(per micrograph)	(650)	(848)	(671)	(565)
Particles after	552	607	101	140
classification [x10 ³]	(220/)	(2017)	101	(0.4%)
(retention) (per	(23%)	(20%)	(5.0%)	(5.4%)
micrograph)	(147)	(1/1)	(37)	(53)
Resolution after CTF	2.12	2.02	2.02	2.99
refinement [Å]	3.12	2.83	2.83	
B-factor after CTF	127 5 (6 2)	120 1 (5 2)	124.0 (2.4)	124 2 (6 0)
refinement [Ų]	137.5 (0.2)	120.1 (5.3)	124.0 (2.4)	124.3 (0.9)
Particles to reach 3 Å				
after CTF refinement	958.0 (532)	241.5 (127)	78.0 (15)	150.1 (91)
[x10 ³]		. ,	. ,	
Resolution from 100k				
particles after CTF	3.58 (0.18)	3.22 (0.14)	2.95 (0.04)	3.09 (0.14)
refinement [Å]	/			
Resolution after				
polishing [Å]	2.99	2.69	2.72	2.87
B-factor after polishing				
[Å ²]	146.5 (3.4)	121.3 (2.8)	122.4 (4.9)	123.0 (3.5)
Particles to reach 3 Å				
after polishing [x10 ³]	487.0 (132)	116.7 (30)	41.1 (17)	/1.9 (21)
Resolution from 100k				
particles after polishing	3,34 (0.07)	3.04 (0.06)	2,82 (0.07)	2,93 (0.06)
[Å]	(()	

% particles needed for 3 A is less than 4%

.

Danev et al BioRxiv, 2020

How to reach high resolution in cryoEM with high efficacy?

and without spoiling money

Optimize Specimen preparation

Optimize data collection (Hardware and software)

Optimize image processing (software)





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Specimen preparation



Ciche Allorge de Mestres es Nore sejos

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Preparation regarding the size of biological samples

Dehydrated / stained specimen

Frozen hydrated/ unstained specimen

Thin Specimen : negative staining



freeze-plunging SPA -cryoEM



Thick Specimen : Plastic section

cryosection/FIB





Support : grid coated with thin amorphous carbon



Cryo EM: Holey carbon grid











Because the microscope column is under vacuum to maintain a coherent electron beam, WATER is forbidden.

Specimen must be introduced into EM either in a dehydrated form or in a "solid water" form









Phase Diagram of Water

Cryo-electron microscopy of vitrified specimens

JACQUES DUBOCHET¹, MARC ADRIAN², JIIN-JU CHANG³, JEAN-CLAUDE HOMO⁴, JEAN LEPAULT⁵, ALASDAIR W. McDOWALL⁶ and PATRICK SCHULTZ⁴

European Molecular Biology Laboratory (EMBL), Postfach 10. 2209, D-6900 Heidelberg, FRG





Fig. 2. Schematic view of a small part of a hexagonal ice crystal.

Vitrification of specimens:

Relationship between cooling speed and the size of the ice crystals



Hexagonal Ice (b) Cubic Ice

Density = 933 kg/m3 :Water expands during vitrification

liquid ethane : -88.7 °C / -183.3 °C Nitrogen: -196 °C / -210 °C

Vitreous ice forms by flash-cooling, is metastable and converts to crystalline ice:

- cubic ice, forms when vitreous ice is warmed up above -135°C \rightarrow keep samples below ~-135°C



Grid mounted on the Guillotine

Improve the sample distribution/stability

Plunging system

Home made



Transfer into cryoTEM

observation

Cryo-holder





Autoloader equipped instrument



Cryo EM: What do you expect ?



orientations

Cryo EM: What is a good cryo grid ?

Good amorphous ice -not crystalline ice -no « leopard skin »pattern -no contamination

Appropriate ice thickness -typically as thin as possible

Clearly visible particles -particle size and shape -buffer composition -defocus,

Good particle distribution -in holes

-dense but particles not touching -randomly distributed orientations

© Guy Schoehn



Some points of vigilance



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Uneven Ice thickness



Rice et al, J struct Biol, 2018



Bridget Carragher Riccem2021

Particle distribution within the ice layer explored by tomography



Noble et al, Elife, 2018 D'Imprima et al, Elife, 2019

The vast majority of particles are localized to the air-water interface



At the air water interface, particles are damaged

Sample # Name	Example cross-sectional schematic diagram	Sample # Name	Example cross-sectional schematic diagram	Sample # Name	Example cross-sectional schematic diagram	Sample # Name	Example cross-sectional schematic diagram
1* 32 kDa Kinase	·····································	14* Neural Receptor	WORD	27* IDE	<u>سر ۵ مکړي يا سم ۳۵ و وا</u>	38*† Apoferritin (0.5 mg/mL)	
4*† Hemagglutinin	Bit manuficture and a second	17* Protein with Bound Lipids (deglycosylated)	E Transformer Contraction of Contrac	30** GDH	1 *** 11 * 11 * 11 * *** *** *** 11	39 *† Apoferritin with 0.5 mM TCEP	1000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
5* HIV-1 Trimer Complex 1	Mar San	18 Protein with Bound Lipids (glycosylated)		31*† _{GDH}		40 Protein with Carbon Over Holes	un site she de ature she
6* HIV-1 Trimer Complex 1		19* Lipo-protein		32*† GDH + 0.001% DDM (2.5 mg/mL)	a J. C. Almanna I Land	41 Protein and DNA Strands with Carbon Over Holes	and the bar a put at
7* HIV-1 Trimer Complex 2	North Street Str	20 GPCR	2 377 04 × 5000 42 83	33*† DnaB Helicase- helicase Loader	21	42*† T20S Proteasome	States and the state of the states of the st
10* Stick-like Protein 1		21*† Rabbit Muscle Aldolase (1mg/mL)		34*† Apoferritin	999 0 0 0 00 90 90 0 0 0 0 0 0 0 0 0 0	43* ⁺ T20S Proteasome	$= \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0$
12* Stick-like Protein 2	Enter & the first and	22*† Rabbit Muscle Aldolase (6mg/mL)		35*† Apoferritin	10 00 100 00 0 0 0 0 0 0 0 0 0 0 0 0 0	44*† T20S Proteasome	AT A A A A A A A A A A A A A A A A A A
13* Neural Receptor	a de la constante de la consta	25* Protein in Nanodisc (0.58 mg/mL)	E U COCCA CACACONTE B	36*† Apoferritin		45*† Mtb Proteasome	
				37*† Apoferritin (1.25 mg/mL)		46 Protein on Streptavidin	anadara & & a alla

Noble et al. Elife 2018

Need to keep our particles away from the air water interface

Support film (thin carbon, graphene)



Detergents or similar layers



D'Imprima et al, Elife, 2019

Other freezing machines

Diversification of methods for preparing grids





Droplet based

Ultrasonic spray 1-10μm (Rubenstein group) Gas pressurized spray (Muench group, Franck group Electrostatic spray 0.25-0.5 μm (Trinick group)

Inkjet printing 25µm Spotiton, Chameleon

Pin printing with a metal pen Vitrojet (Peters group) Capillary writing Cryowritter (Braun group Nuonex)

> Weissenberger G, 2021 Nature Methods



nature methods

BRIEF COMMUNICATION

https://doi.org/10.1038/s41592-020-0925-6

Check for updates

Time-resolved cryo-EM using Spotiton

Venkata P. Dandey^{1,7}, William C. Budell^{1,7}, Hui Wei¹, Daija Bobe¹, Kashyap Maruthi¹, Mykhailo Kopylov¹, Edward T. Eng¹, Peter A. Kahn², Jenny E. Hinshaw³, Nidhi Kundu³, Crina M. Nimigean^{®⁴}, Chen Fan⁴, Nattakan Sukomon⁴, Seth A. Darst^{®⁵}, Ruth M. Saecker⁵, James Chen⁵, Brandon Malone⁵, Clinton S. Potter^{1,6} and Bridget Carragher[®], ^{1,6}

NATURE METHODS | VOL 17 | SEPTEMBER 2020 | 897-900 |









Liang, et al. Structural basis for the mechanisms of human presequence protease conformational switch and substrate recognition. Research square 2020

Beam-induced movement: Image blurring

Average of 60 frames



Average of 60 frames aligned in translation

Brilot et al., 2012 J. Struct. Biol



Cryo-EM with sub-1 Å specimen movement

Katerina Naydenova¹, Peipei Jia^{1,2}*, Christopher J. Russo¹† Science **370**, 223–226 (2020) 9 October 2020



holes 330 nm in diameter for 300-Å-thick ice

the ice never builds up enough stress to buckle during freezing or to deform under irradiation

Data collection



Cick & Biologie de Menterous et a Nacio espisi 2,8

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Electron microscopy in few words

- Electrons have much shorter wavelength than x-rays (~ 2pm~ 0.022 Å for 300 kV electrons
- Resolution not limited by wavelength
- . But resolution is degraded by lens defects, radiation damage, mechanical drift, specimen motion





Electron microscope : Principle



Image Formation: Phase contrast

Ice-embedded specimens of biological macro-molecules is well described by the "weakphase object" approximation The electron beam passing thorough the object (thin specimen) only suffers a modest phase shift, but its amplitude is effectively unchanged



Close to **focus**

-2 µm defocus





Images are intentionally taken out-of-focus in order to generate contrast (additional phase shift by changing the focal length)
➢ Contrast is modulated by defocus and lens aberrations

Spatial frequency dependent phase shift $\gamma(\nu)$ introduced by objective lens: Phase Contrast Transfer Fonction, Scherzer, (1949)

$$\sin\left[\frac{2\pi}{\lambda}\left(\frac{Cs\cdot\lambda^{4}\cdot\nu^{4}}{4}-\frac{\Delta f\cdot\lambda^{2}\cdot\nu^{2}}{2}\right)\right]$$



Cryo EM: Advantages and Drawbacks

Advantages : Hydrated state, High resolution, Small amount of sample Drawbacks : Low contrast, Highly sensitive to electron dose



Konig R et al., Annals of Anatomy, 2018, 217 82

300 kV FEG TITAN Krios, Parallel illumination, Automated collection, very stable stage, autoloader (12 grids)





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Cryo EM: Automated data acquisition

Example : Automated data acquisition software EPU (FEI)

Atlas = image of the EM grid



Improve collect speed: Fewer stage moves



Setup 30s stage move and settling 30s focus and other setting 5s image recording AFIS (Aberration-Free image shift) EPU TFS

Reduce total stage settling time



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Conversion electron into images

Film sensitive to electrons





Pixel size = 8 μm 1 image / s





14 μm 1 image / s

Direct Electron Detector

CMOS (complementary metal oxide semiconductor)





5 μm 20 images / s

Advantage of Direct Electron Detector vs CCD camera



Konig R et al., Annals of Anatomy, 2018, 217 82



CCDs move photogenerated charge from pixel to pixel and convert it to voltage at an output node. CMOS imagers convert charge to voltage inside each pixel.

Counting requires speed

Typical dose rate of 10 e⁻/pix/s.



40 frames per second: events overlap and cannot be resolved.



400 frames per second: events are resolved.

It takes 400 fps to resolve electrons at a dose rate of 10 e⁻/pix/s.

Counting mode

1. Electron enters detector



3. Charge collects in each pixel



Integration mode

2. Signal is scattered



4. Events reduced to the highest charge pixels



Counting mode Improved DQE

Detective quantum efficiency ≈ Sensitivity % incident electron converted in signal



 $DQE = (S/N)_{out}^2 / (S/N)_{in}^2$

Higher DQE for DED K2 summit (Gatan) Falcon II and III (FEI) DE-20 (Direct electron)

McMullan et al, 2014, and 2016

Movie acquisition

CMOS characteristic Rolling shutter : high speed read out 400 frames per second (for K2 camera)

(A)



Typically a movie of 40 frames 1 e/A2 /0.4 s 40 e/A2 Total 16 second **Dose fractioning**

Advantage of Movie acquisition: Correction for mechanical motion



Accessory equipments improving image quality and contrast

Monochromator, Cs corrector Energy filter Volta Phase Plate



zero-loss imaging mode removes the background noise due to inelastically scattered electrons

GIF Quantum Gatan Selectris TFS

Image contrast modulated by spatial filter





Frits Zernike (Wikipedia)











Volta Phase Plate

Radostin Danev, 2009 Ultramicroscopy, 2014 PNAS



1.5 um defocus



ZPP (2009)



Small (1µm) hole Thin amorphous carbon 20 nm that creates a $\frac{\pi}{2}$ shift

VPP Volta Phase Plate (2014)

Thin an Beam in by tem

Thin amorphous carbon 12 nm

Beam induced phase shift over time controlled

by temperature



Local changes in the properties of the carbon film that lead to changes in the inner and/or surface potentials (Volta Potential)



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