

SIMONS ELECTRON
MICROSCOPY CENTER

NEW YORK STRUCTURAL BIOLOGY CENTER

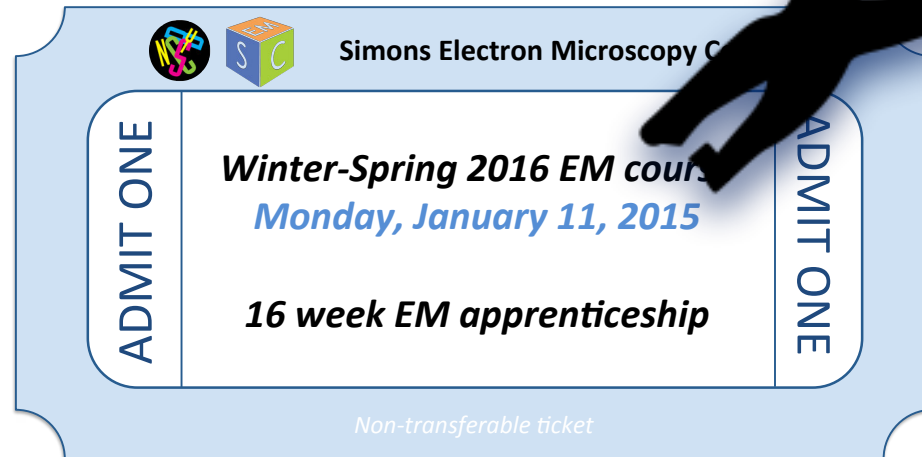
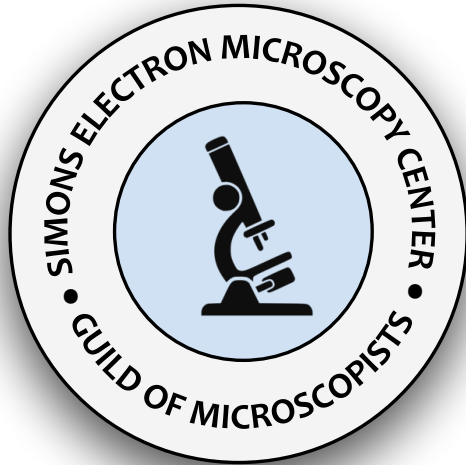


Winter-Spring 2016 EM Course

40 Min Intro + 10 min tour
11 Jan 2016

Art is science made clear.

from *Le coq et L'arlequin* by Jean Cocteau (1889 - 1963)



Art is science made clear.

from *Le coq et L'arlequin* by Jean Cocteau (1889 - 1963)



Painter's Studio
by Jan van der Straet (Stradanus) (Dutch, 1523-1604)



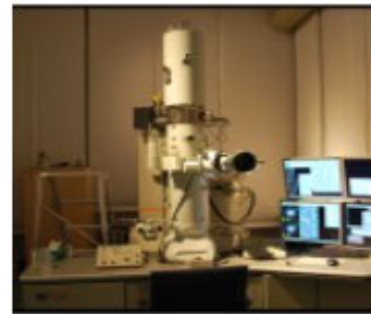
NEW YORK STRUCTURAL BIOLOGY CENTER



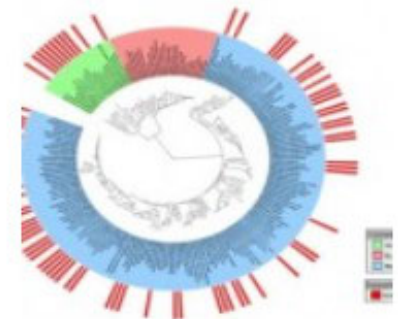
NMR



X-ray



EM



Protein Production



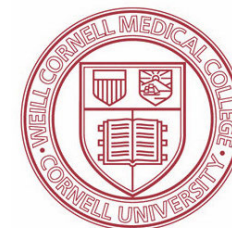
Driven by....



Memorial Sloan-Kettering
Cancer Center



**Mount
Sinai**



NYSBC non-member users



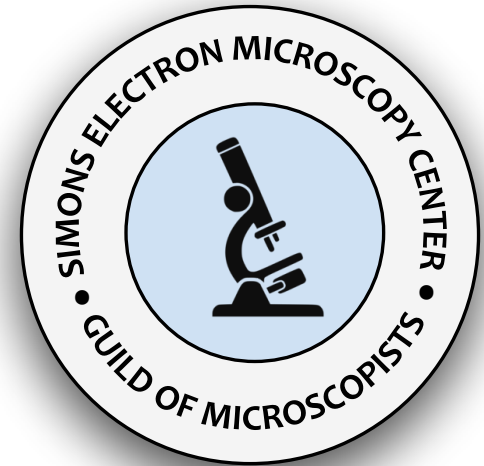
NRAMMM

**National Resource for Automated
Molecular Microscopy**

SIMONS FOUNDATION

Schedule

- *Welcome new students*
- Course logistics
 - Questionnaire
- Introduction to EM and the course
- Simons Electron Microscopy Center
 - SEMC training programs
 - NYSBC tour



Handouts

Logistics

Questionnaire

Syllabus



<http://semc.nysbc.org/course.html>



SIMONS
ELECTRON
MICROSCOPY
CENTER

NYSBC 

Renovation Updates
About SEMC

News/Events
Forums
Staff
Directions

New Users

Overview
Prior to
Start
Starting
Out
Training
Best Usage

Documentation
Publications
Instrumentation

Winter-Spring 2016 EM Course

Simons Electron Microscopy Center EM course

Electron microscopy in combination with image analysis is increasingly powerful in producing 3D structures of individual molecules and large macromolecular complexes that are unapproachable by other methods. This course is focused on the concepts and theories behind electron microscopy and will be taught in a reverse classroom format based on Grant Jensen's online course ([Getting Started in Cryo-EM \[https://cryo-em-course.caltech.edu/\]](https://cryo-em-course.caltech.edu/) from Caltech). Students will be responsible for watching these online lectures prior to class. Each week guest lecturers and SEMC staff lead discussions on the practice of solving molecular structures by electron microscopy.

The course will be held at the [New York Structural Biology Center](#) at 89 Convent Ave (133rd St).

Classes will be Mondays from 3:30-5:00 pm. On Wednesday at 3:30 pm we will screen the Jensen lectures that will be covered the following week.

To register for the course please fill out the following [application form](#).

[Course Syllabus:](#)

Classes in A-11 seminar room (Mon 3:30-5pm)

- **Jan 11** : Introduction & SEMC tour (short class) [Ed Eng & SEMC staff, NYSBC]
- **Jan 18** : No class - Martin Luther King
- **Jan 25** : Basic anatomy of the electron microscope [Christoph Wigge & Anchi Cheng, NYSBC]
- **Feb 1** : Fourier transforms and Image Formation [Bill Rice, NYSBC]

Feb 8 : Challenges in Electron EM & Sample Prep [Ed Eng & Anchi Cheng, NYSBC]

Video lectures

<http://cryo-em-course.caltech.edu/videos>

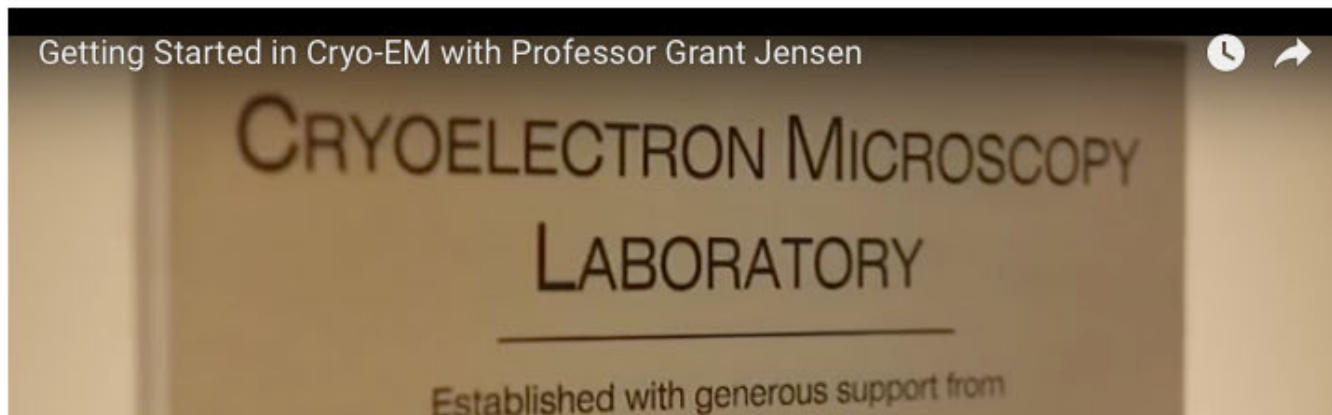
Caltech Getting Started in Cryo-EM

[Welcome](#) [Course Overview](#) [Outline](#) [Lecture Videos](#) [Instructor](#) [Links](#)

WELCOME TO THE COURSE

Before diving into the lecture videos, start by watching the [trailer](#) and reading the course [overview](#) and [outline](#).

We hope you enjoy learning about cryo-electron microscopy (cryo-EM)!



Class organization

Monday

3:30-5pm - A11 seminar room

1.5 hr class

30 min - Introduction by guest lecturer

15 min - Coffee break/informal conversation

45 min - Open ended discussion

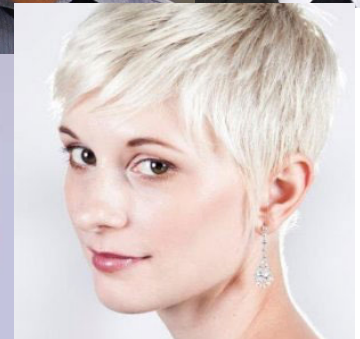
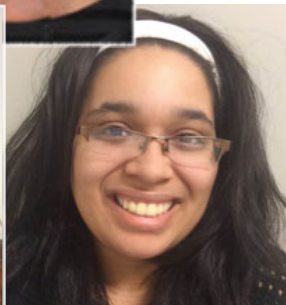
Wednesday *(optional)*

Starts at 3:30 *(or earlier if possible)* - SEMC conference room

Video screening/Recitation section

Jensen lectures that will be covered the next week will be played
SEMC lecturers will be available to assist with lecture topics

Team of Instructors



Class structure

Section 0: Course overview / Intro to EM

Section 7: EMDB, Validation methods & Fitting Atomic models

Section 1: Anatomy of an EM

Section 2: Fourier transforms and Image Formation

Section 3: Challenges in EM & Sample prep

Section 4: Tomography

Part I: ET

Part II: FIB-SEM

Section 5: Single Particle

Part I: SP Analysis & Sample prep

Part II: Data collection & Reconstruction

Part III: Additional topics & limitations

Section 6: 2D crystallography

Part I: 2dx

Part II: Helical

Question:

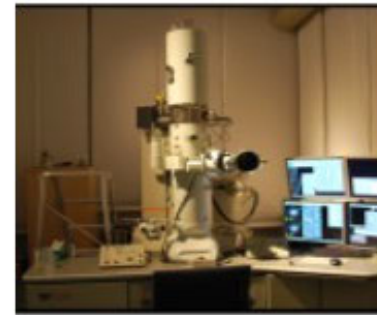
What biological systems are you interested in?



NMR

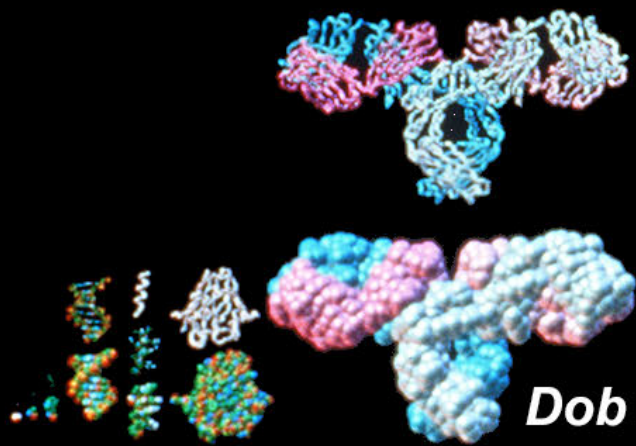


X-ray

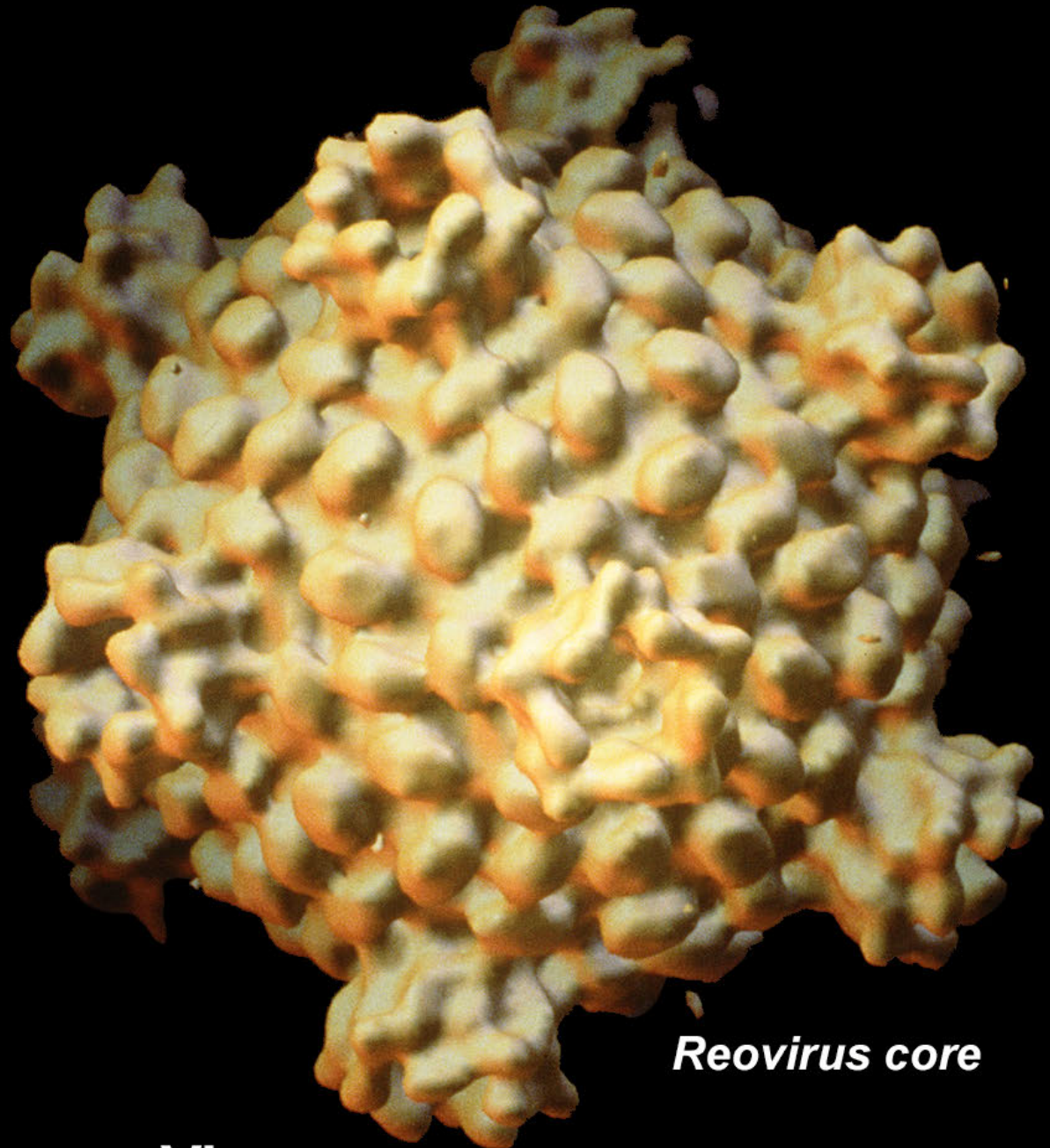


EM

The Scale of Biological Structures



Antibody

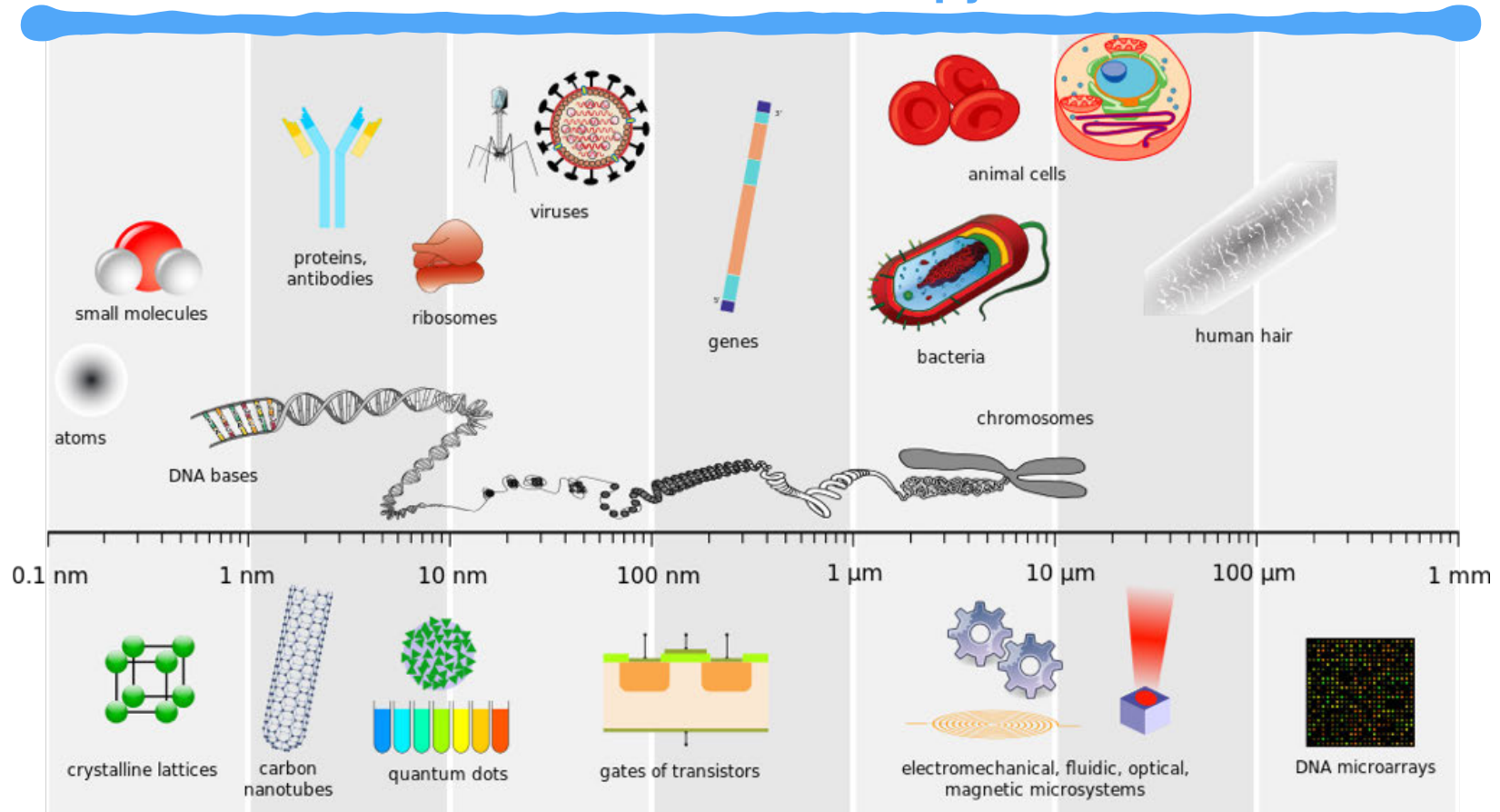


Reovirus core

Virus

Nanoscale: The scale of biological structures

Electron Microscopy



X-ray

Naked eye

NMR

Light microscopy

Class structure

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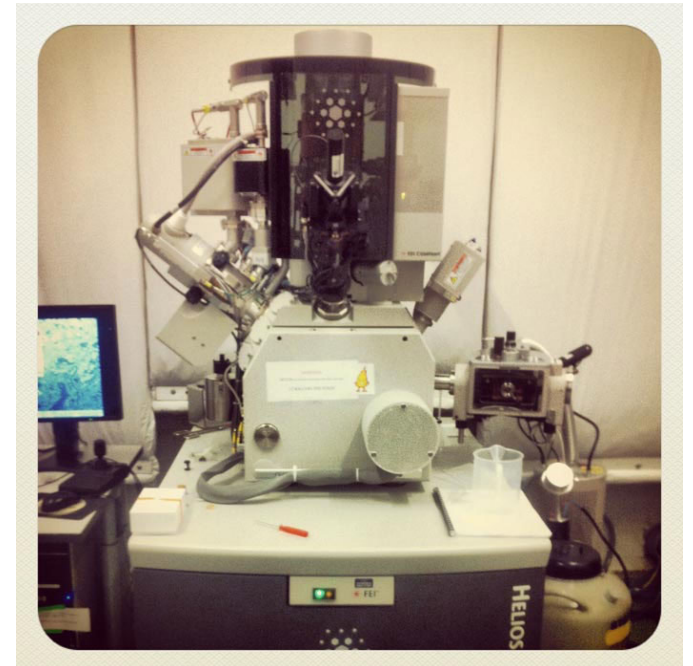
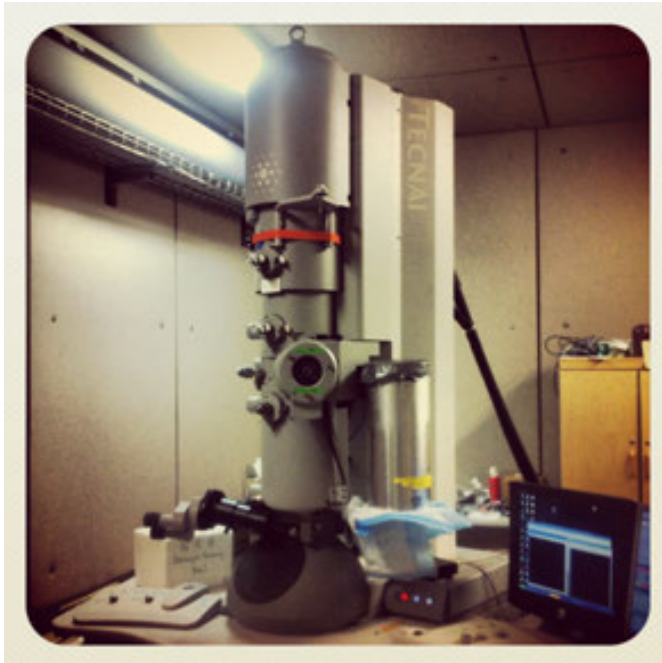
Comparison of a light microscope, TEM & SEM

Section 1: Anatomy of an EM

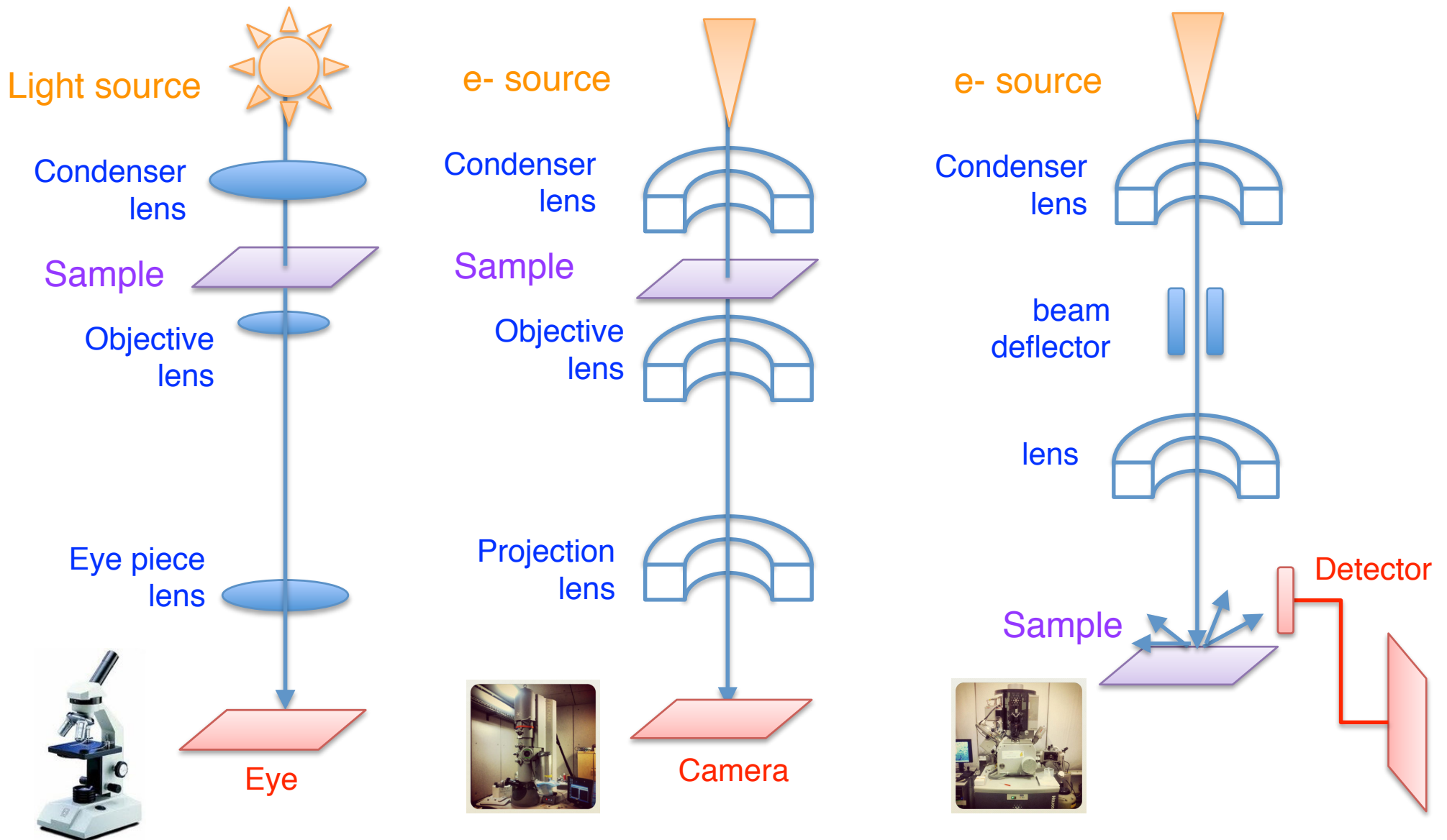
Christoph Wigge & Anchi Cheng [NYSBC]



Comparison of a light microscope, TEM & SEM



Comparison of a light microscope, TEM & SEM



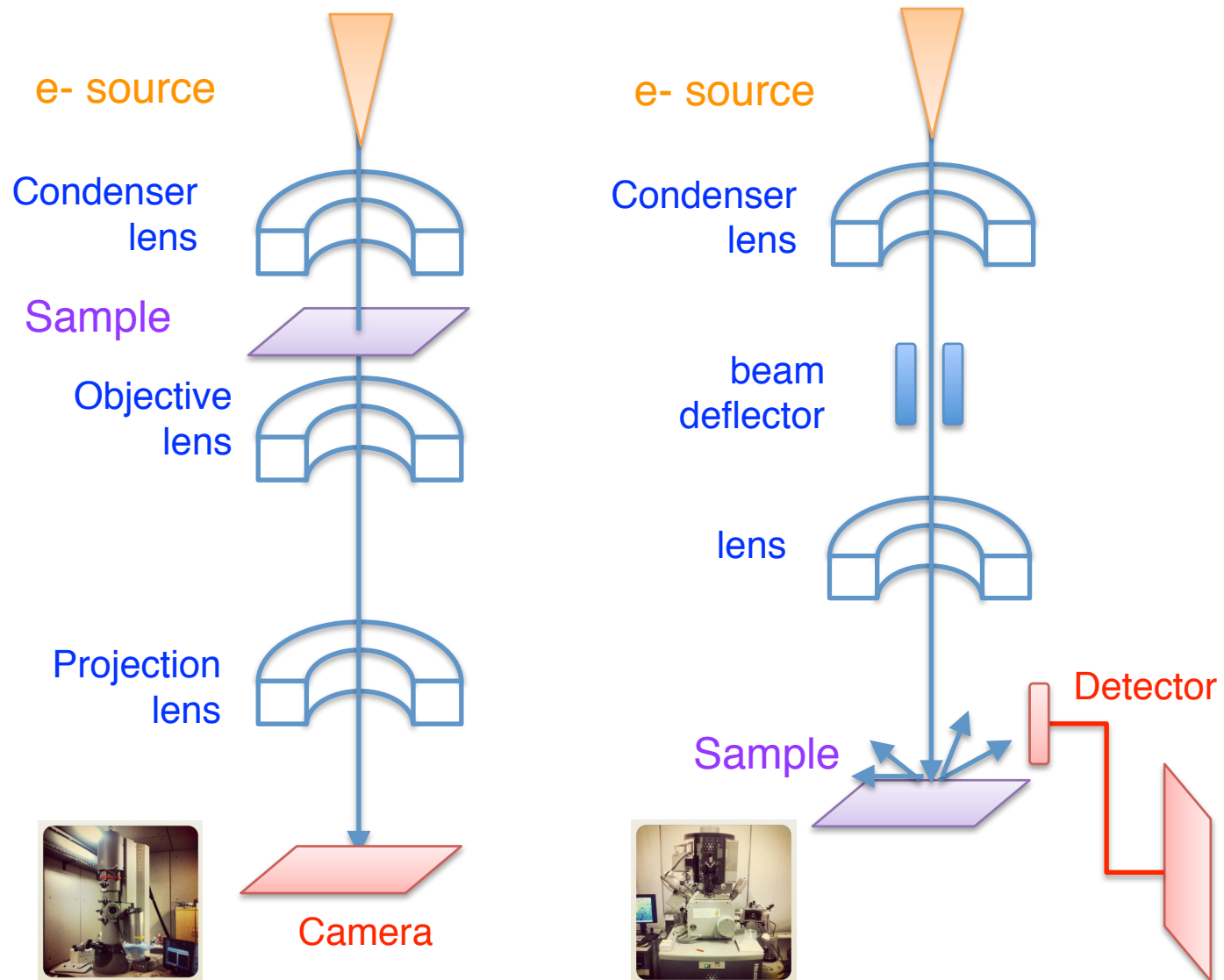
Obtaining a 3D structure from a 2D image

Section 2: Fourier transforms and Image Formation

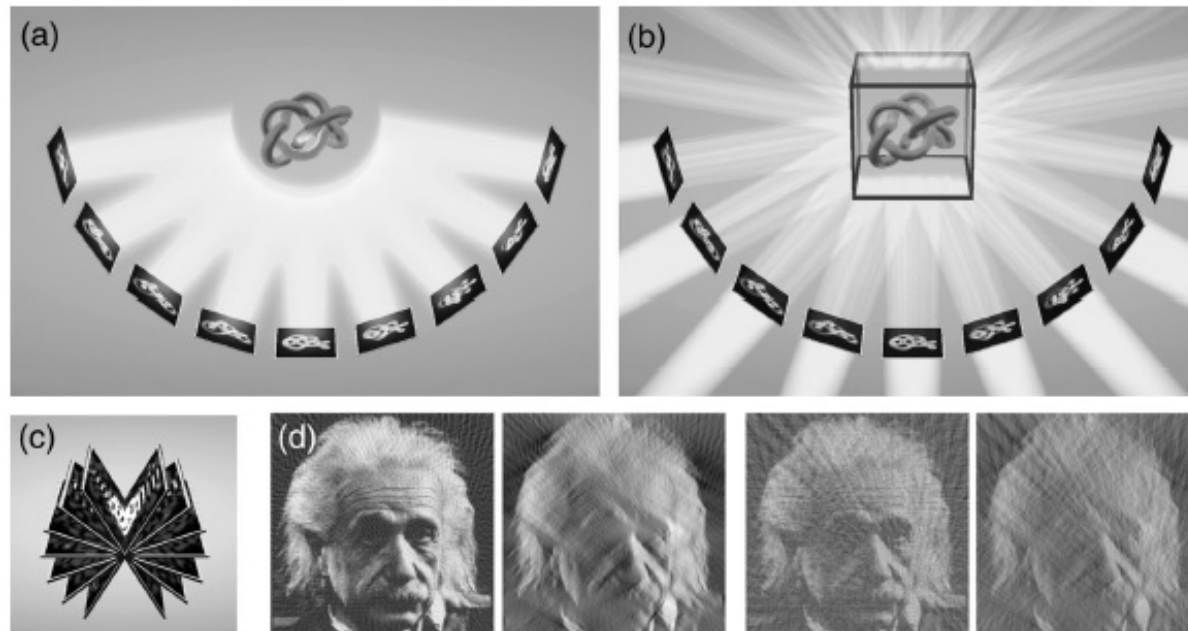
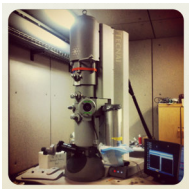
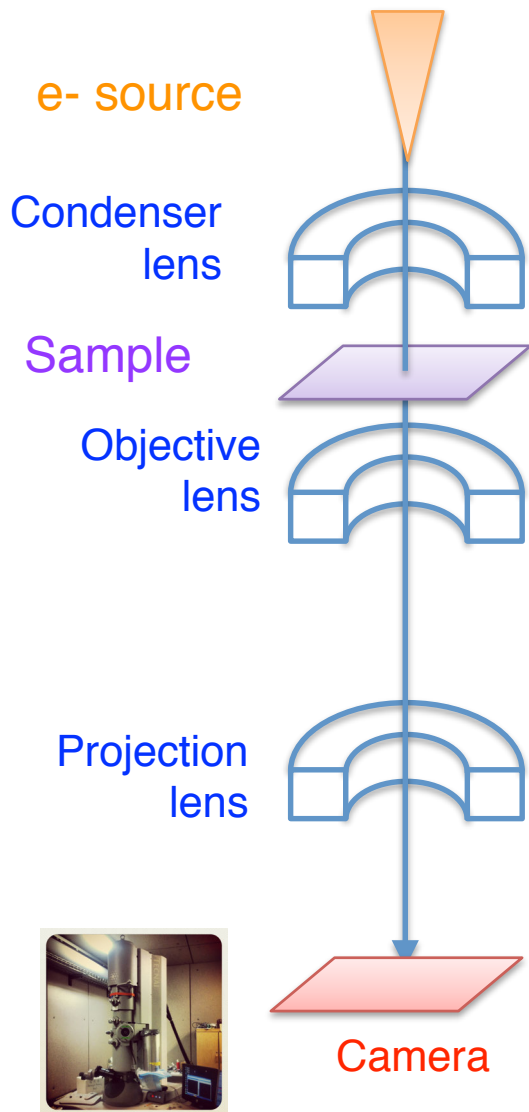
Bill Rice [NYSBC]



Obtaining a 3D structure from a 2D image

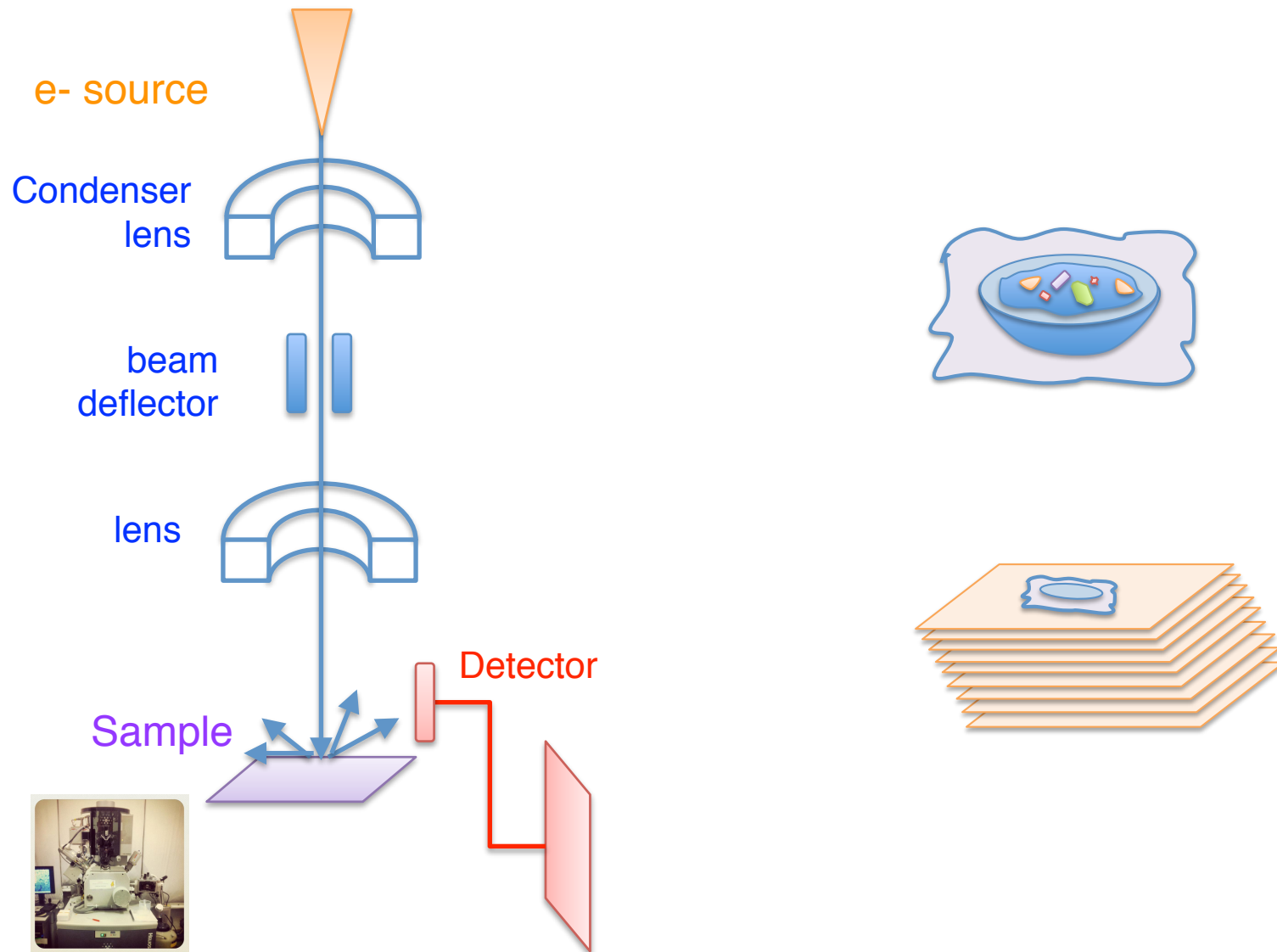


Obtaining a 3D structure from a 2D image



From W. Baumeister et al. [Trend in Cell Biology 9\(1999\)81](#)

Obtaining a 3D structure from a 2D image



How to make an EM ready sample

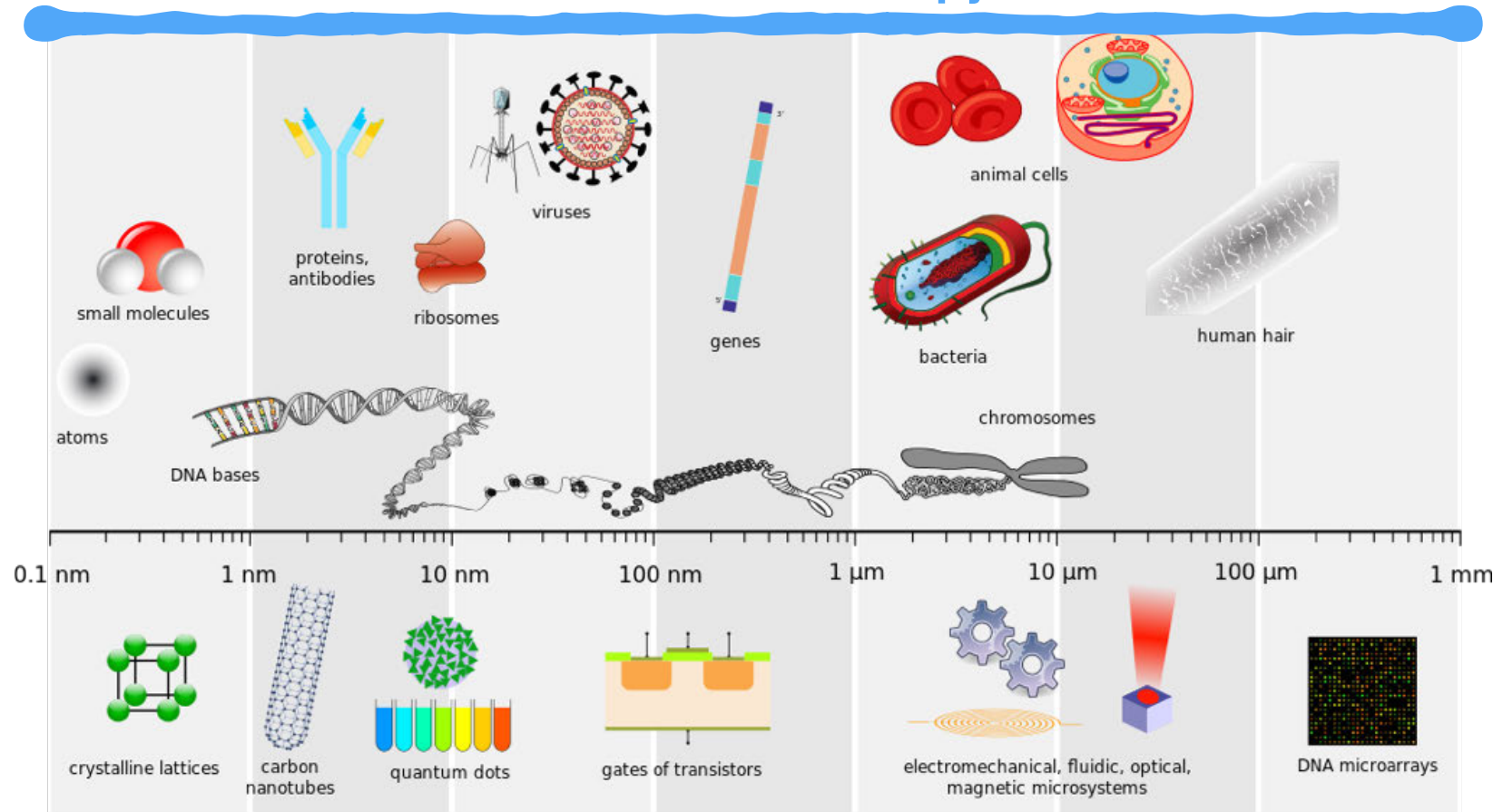
Section 3: Challenges in EM & Sample prep

Ed Eng & Ashleigh Raczkowski [NYSBC]



How to make an EM ready sample

Electron Microscopy



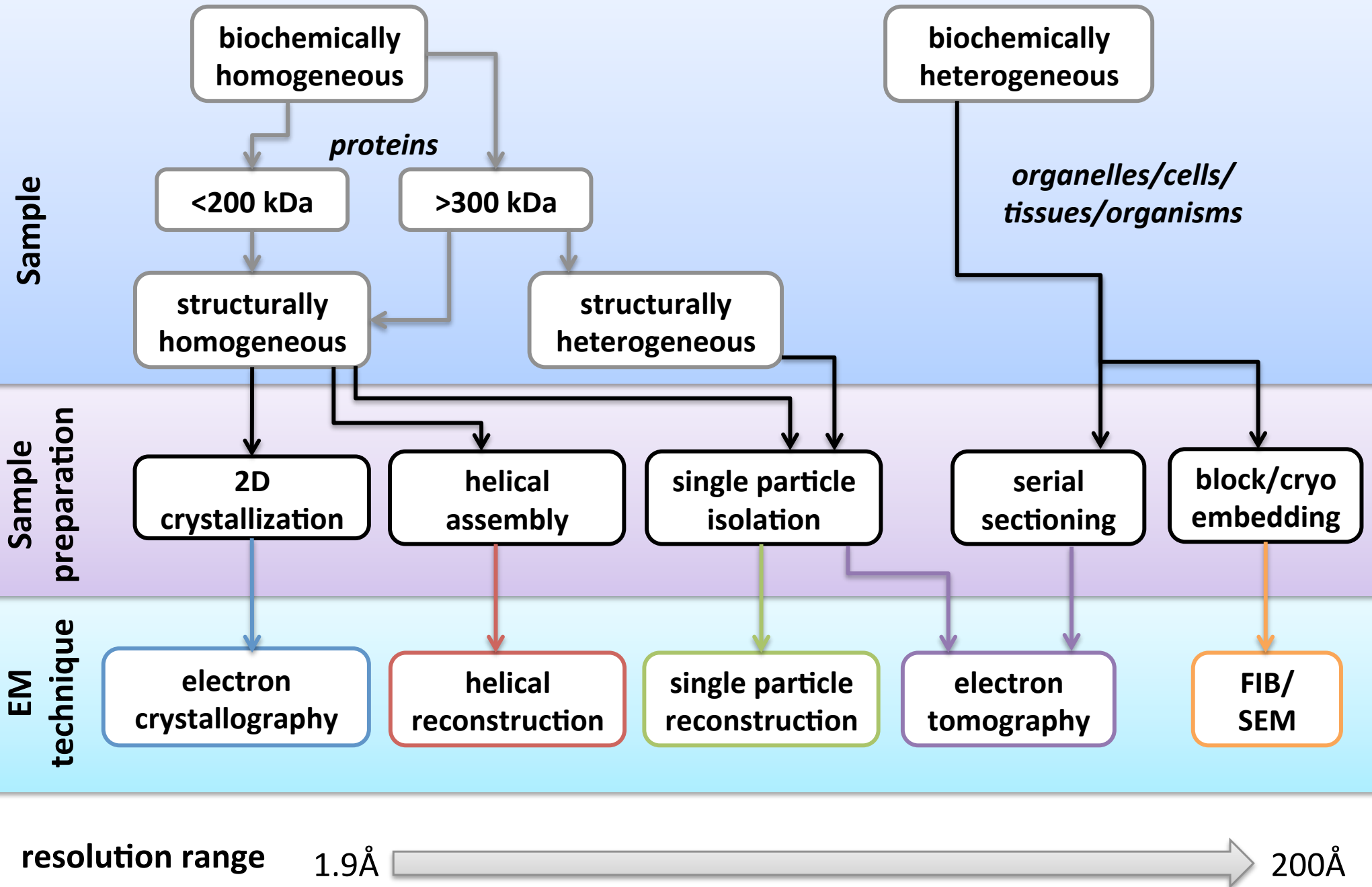
X-ray

Naked eye

NMR

Light microscopy

EM modalities



Class structure

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Section 7: EMDB, Validation methods & Fitting Atomic models

Looking at biochemically unique/heterogeneous
(pleiomorphic) samples

Section 4: Tomography

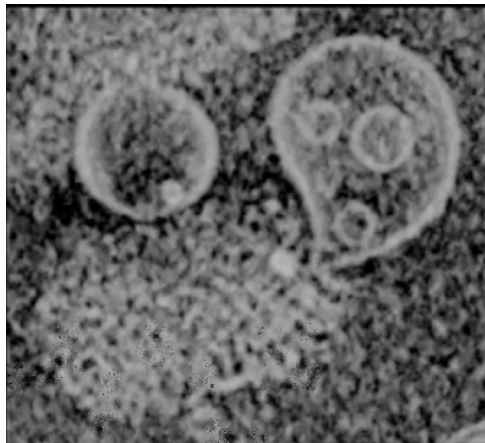
Part I: David Stokes [NYU]



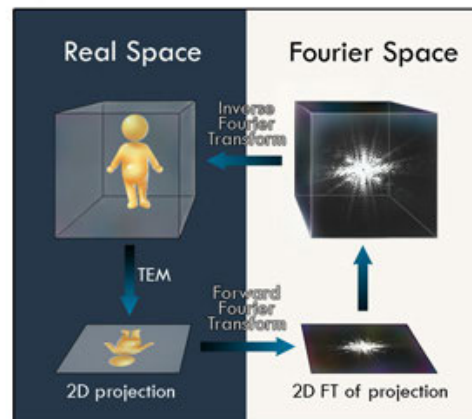
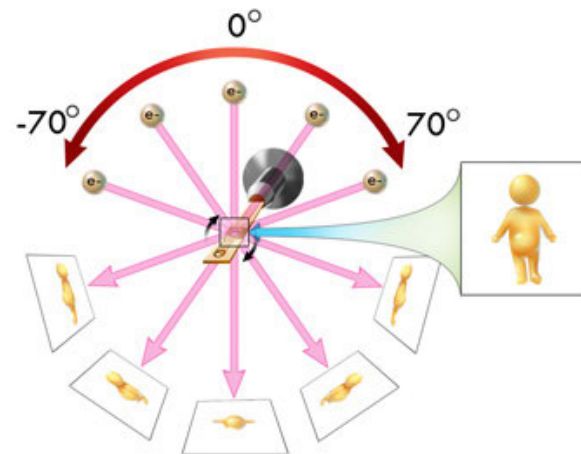
Part II: Bill & Christoph [NYSBC]



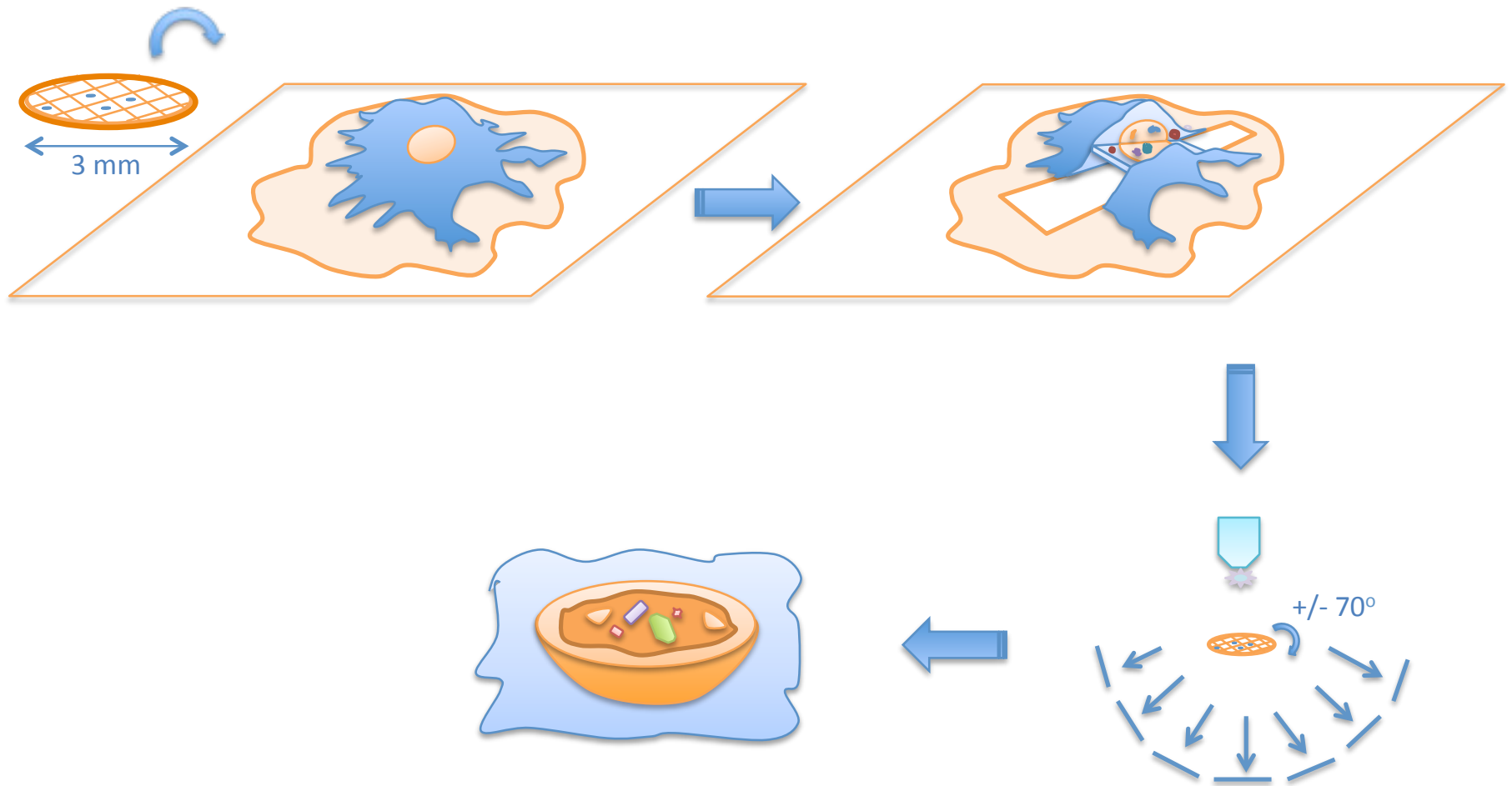
Looking at biochemically unique/heterogeneous (pleiomorphic) samples



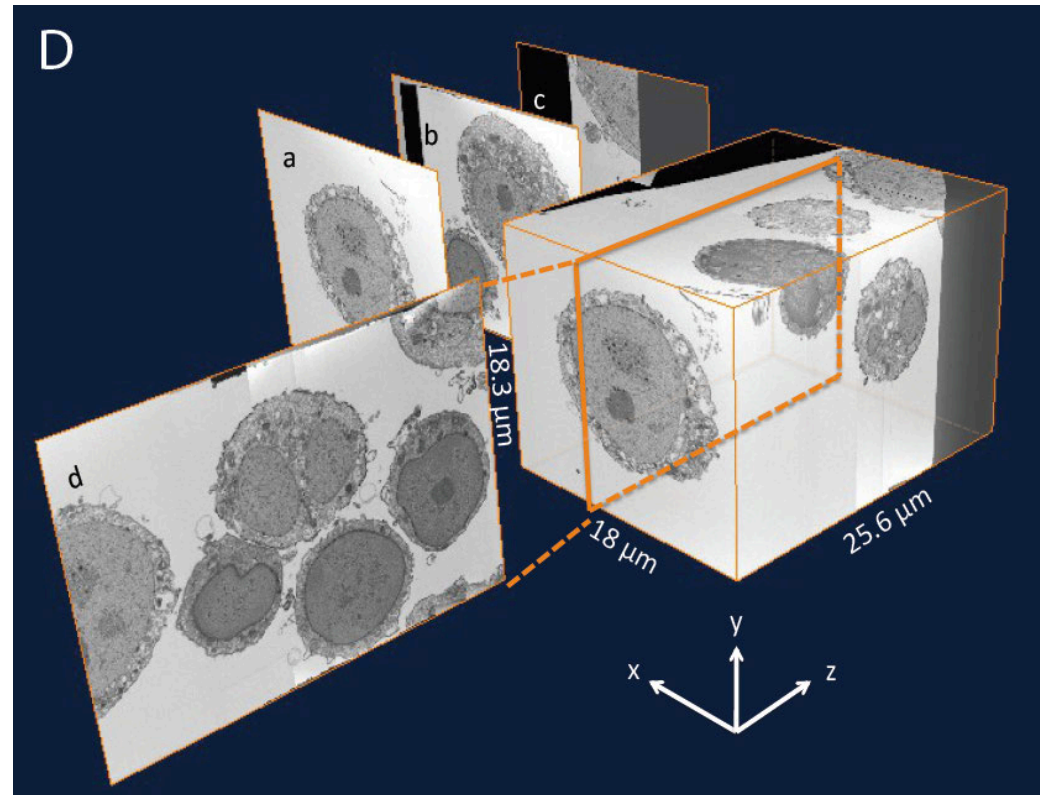
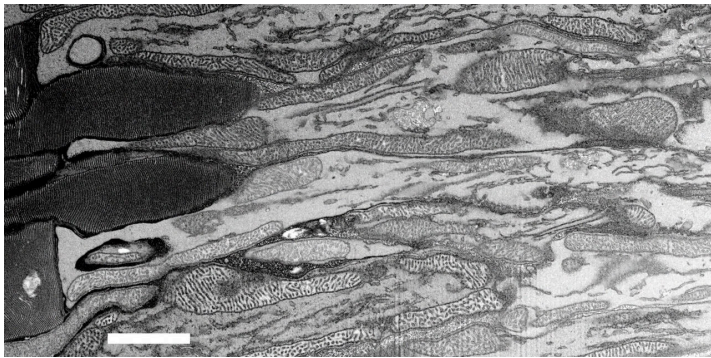
CryoET Cryo-electron Tomography



Looking at biochemically unique/heterogeneous (pleiomorphic) samples



Looking at biochemically unique/heterogeneous (pleiomorphic) samples



Looking at ordered arrays and small macromolecules

Section 6: 2D crystallography

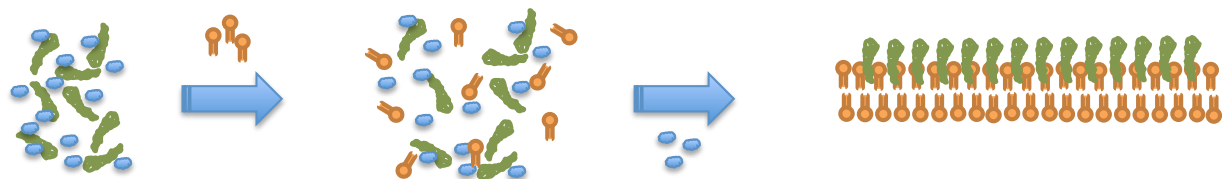
Part I: Iban Ubarretxena [MSSM]



Part II: Hernando Sosa [AECOM]



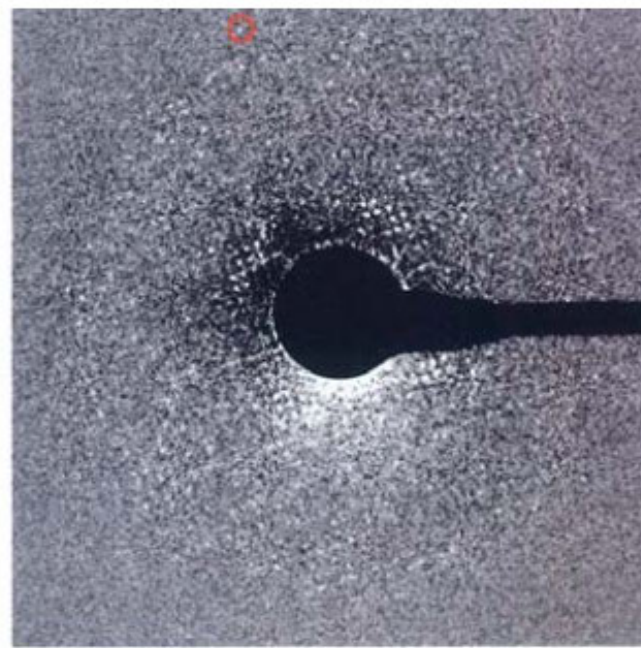
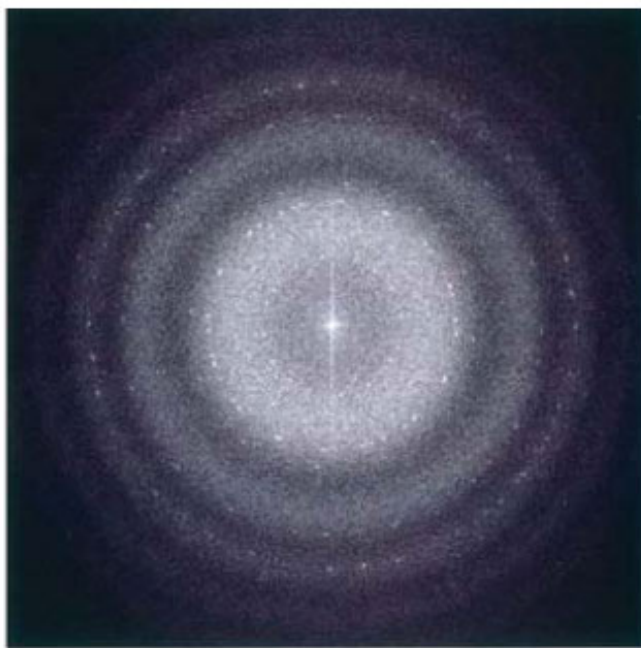
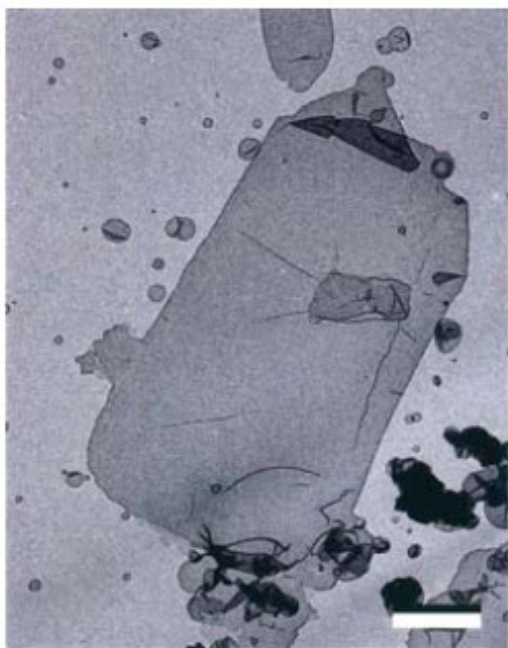
Looking at ordered arrays and small macromolecules



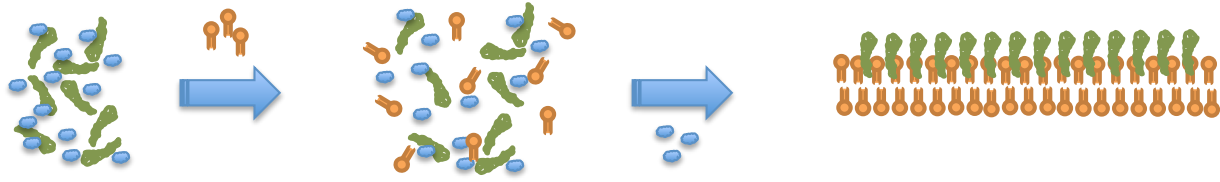
Membrane protein purified in detergent

Detergent solubilized lipids added

Different buffer components screened and detergent removed



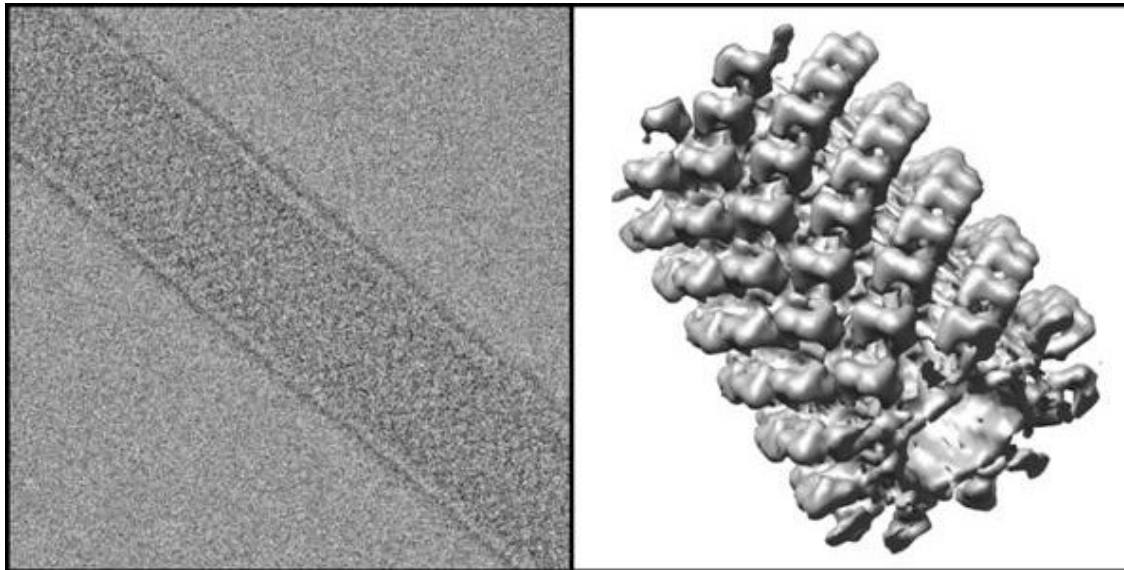
Looking at ordered arrays and small macromolecules



Membrane protein
purified in detergent

Detergent solubilized
lipids added

Different buffer components
screened and detergent removed

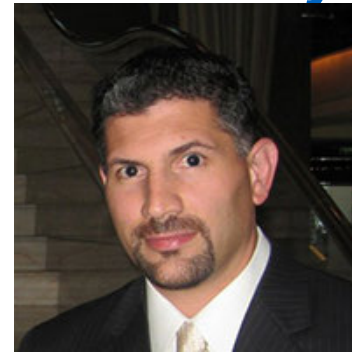


Section 5: Single Particle

Part I: Joachim Frank [CU]

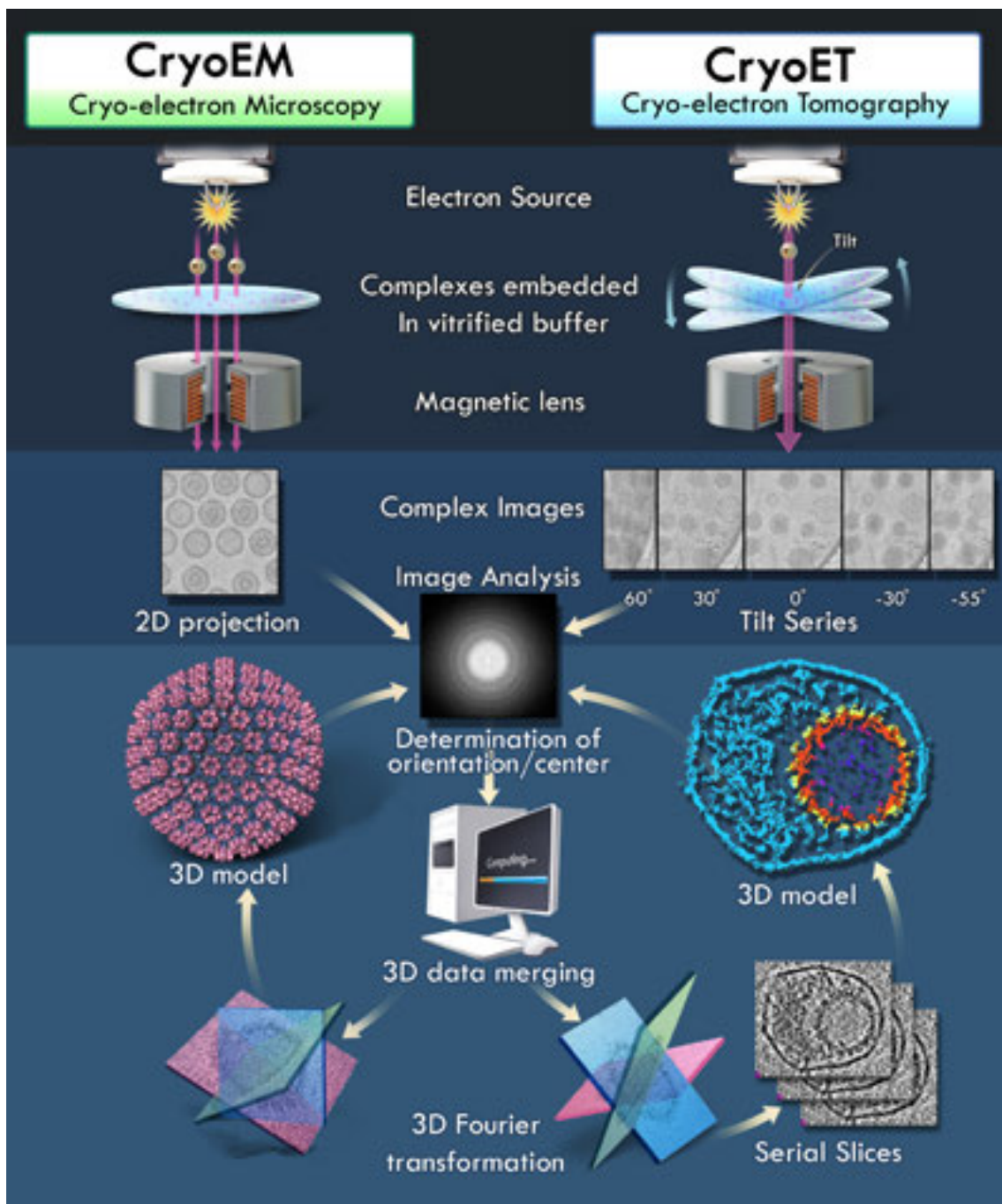


Part II: Amedee Des Georges & Reza Khayat [CUNY]

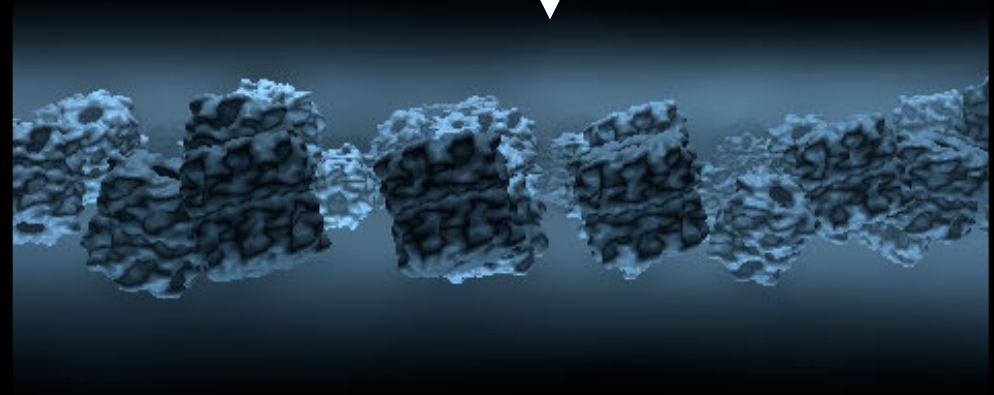
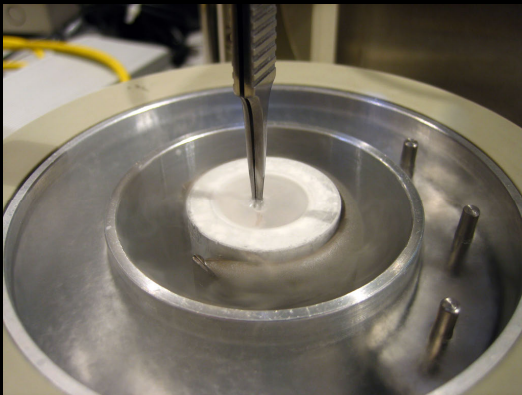
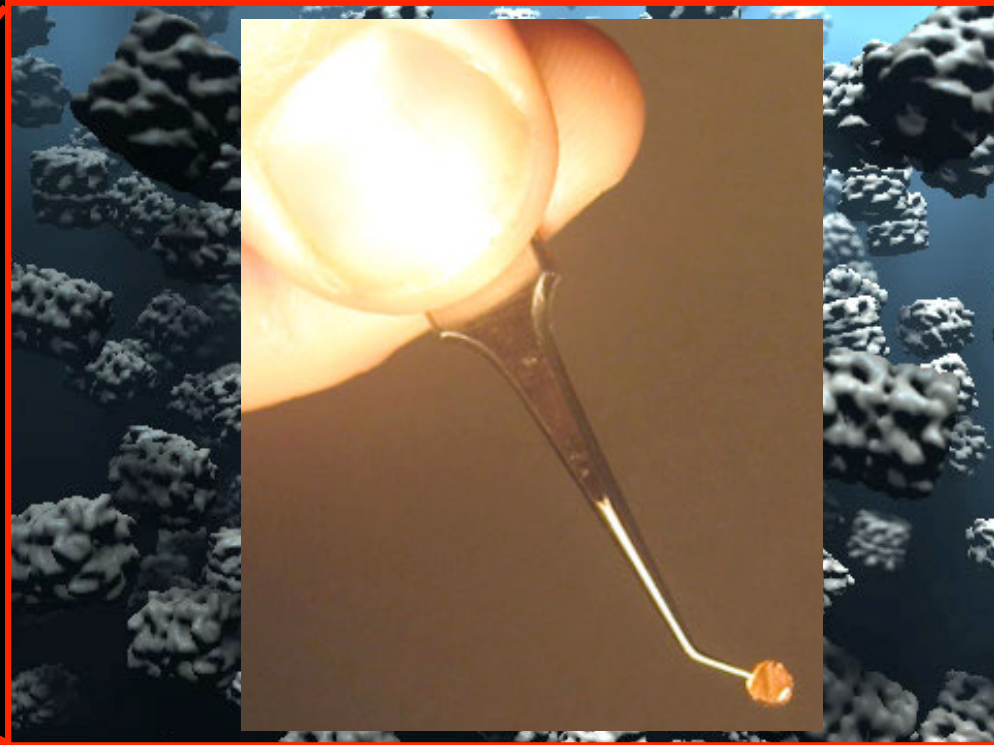


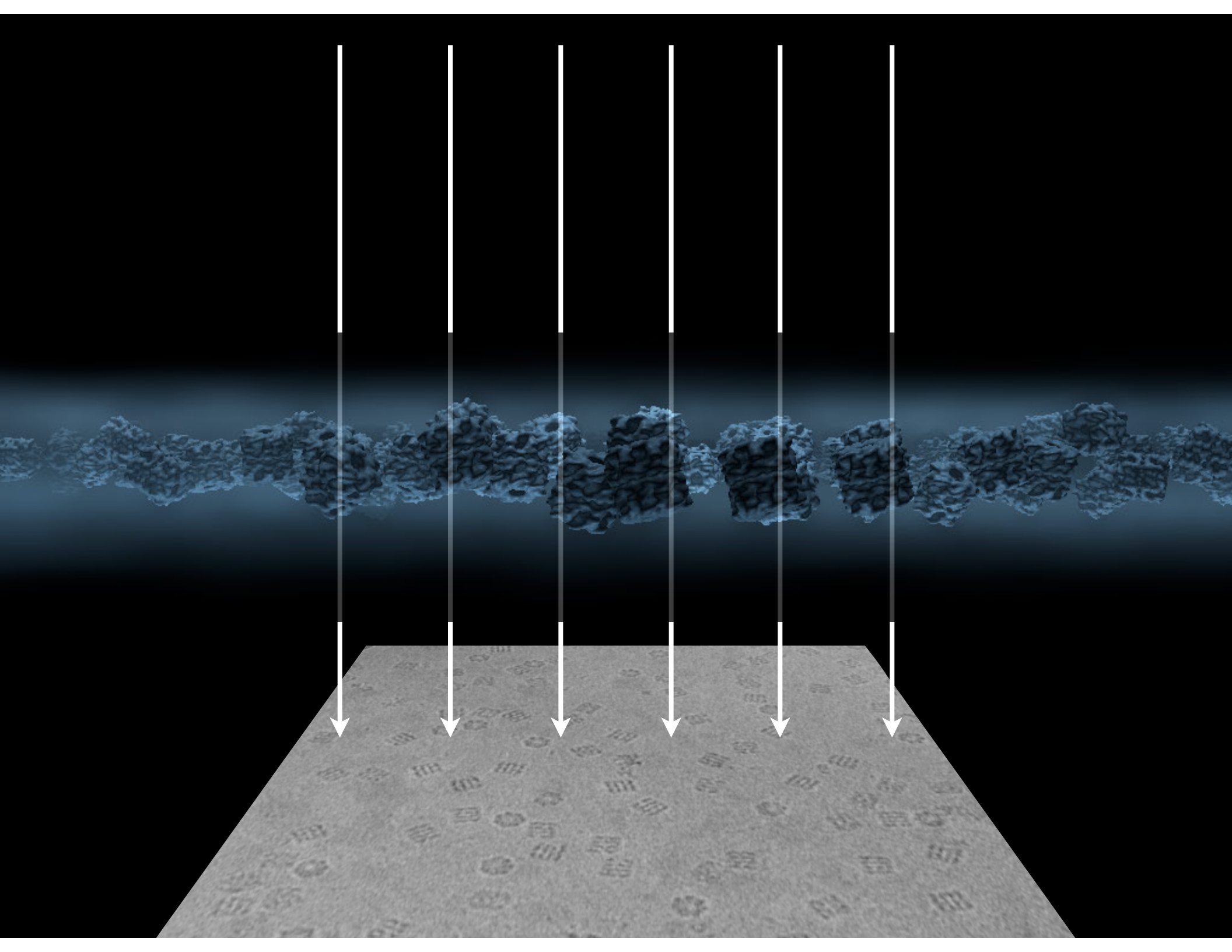
Part III: Yong Zi Tan, [CU/NYSBC]

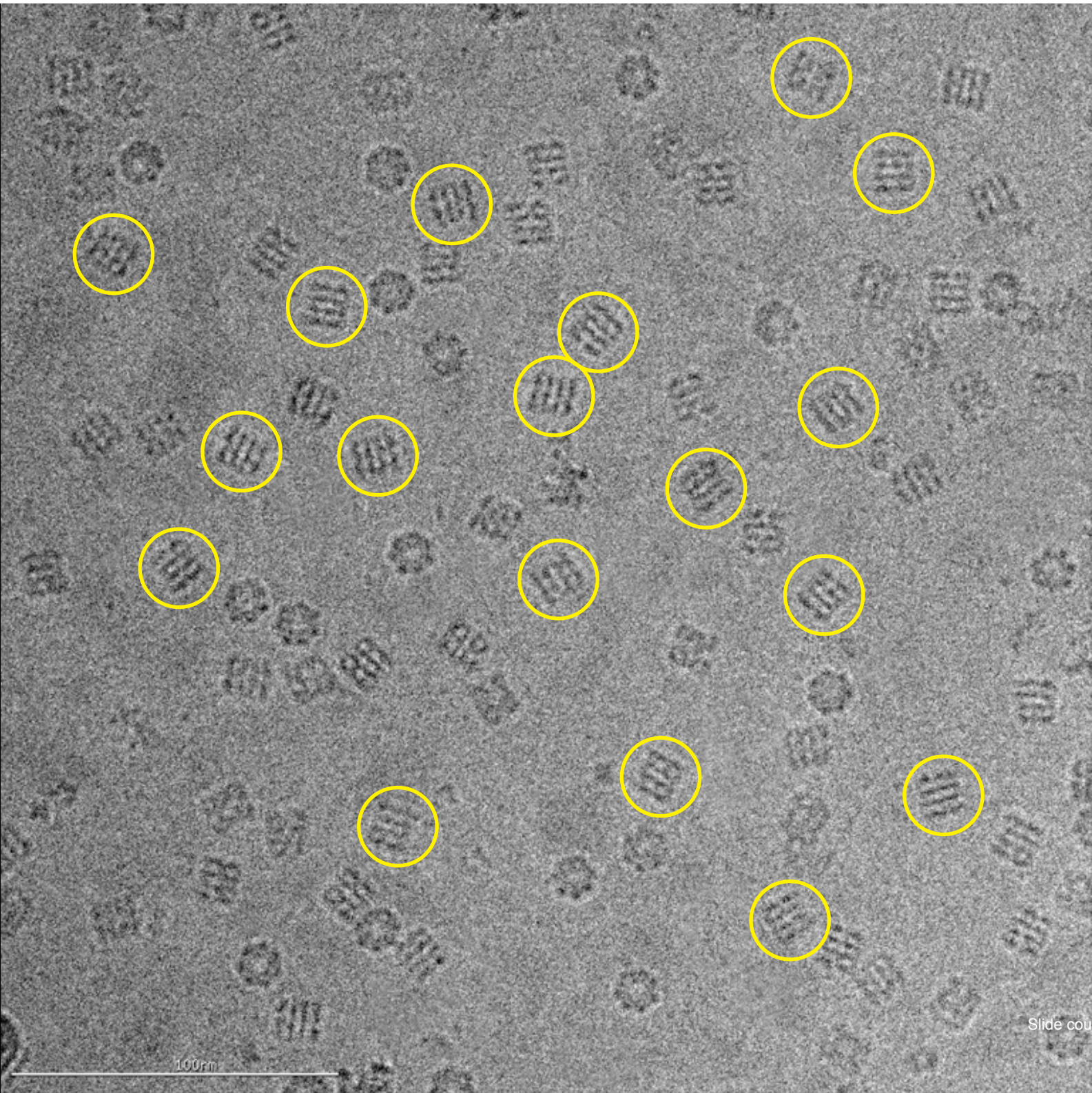




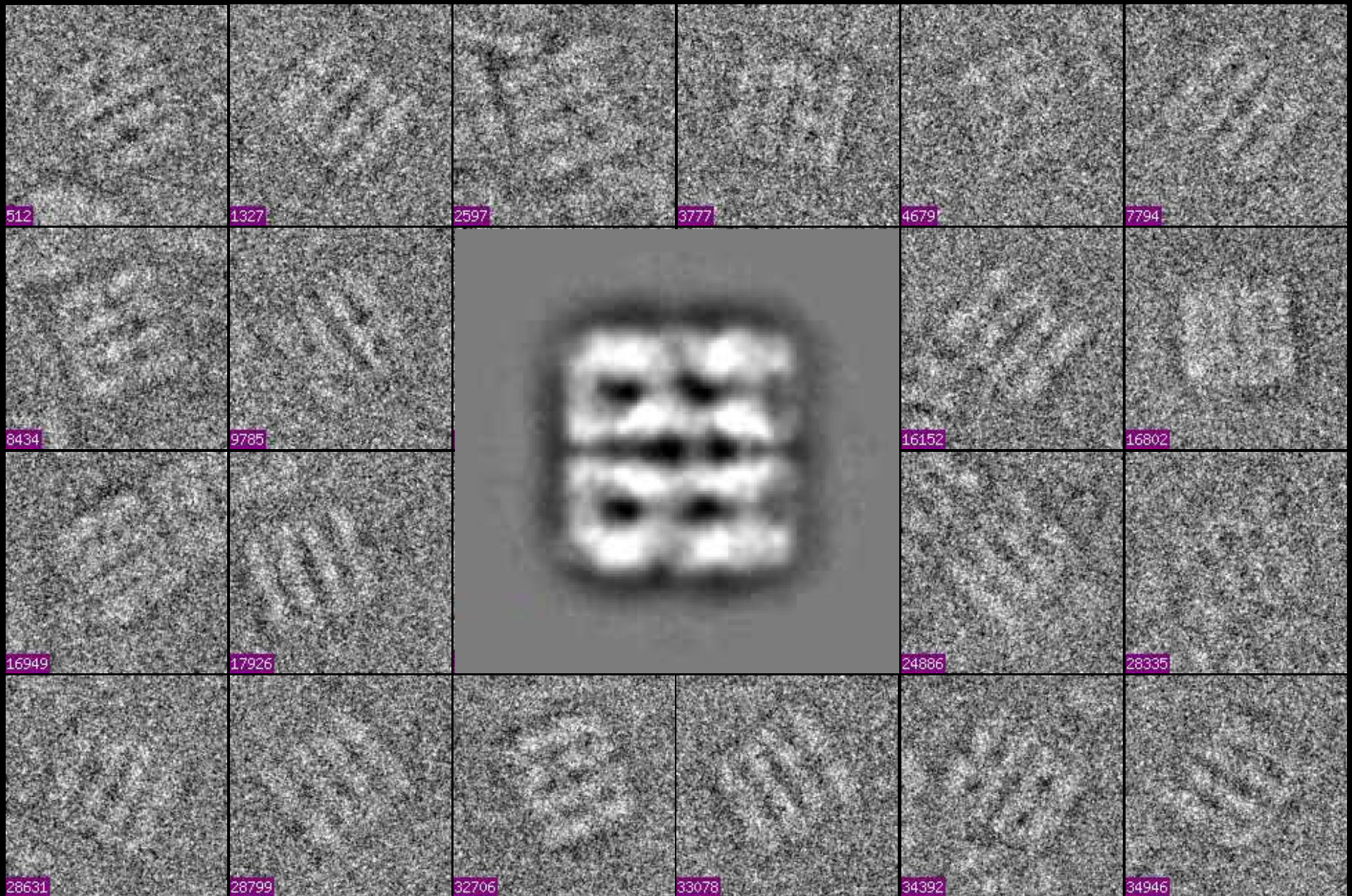
Vitrification process for CryoTEM

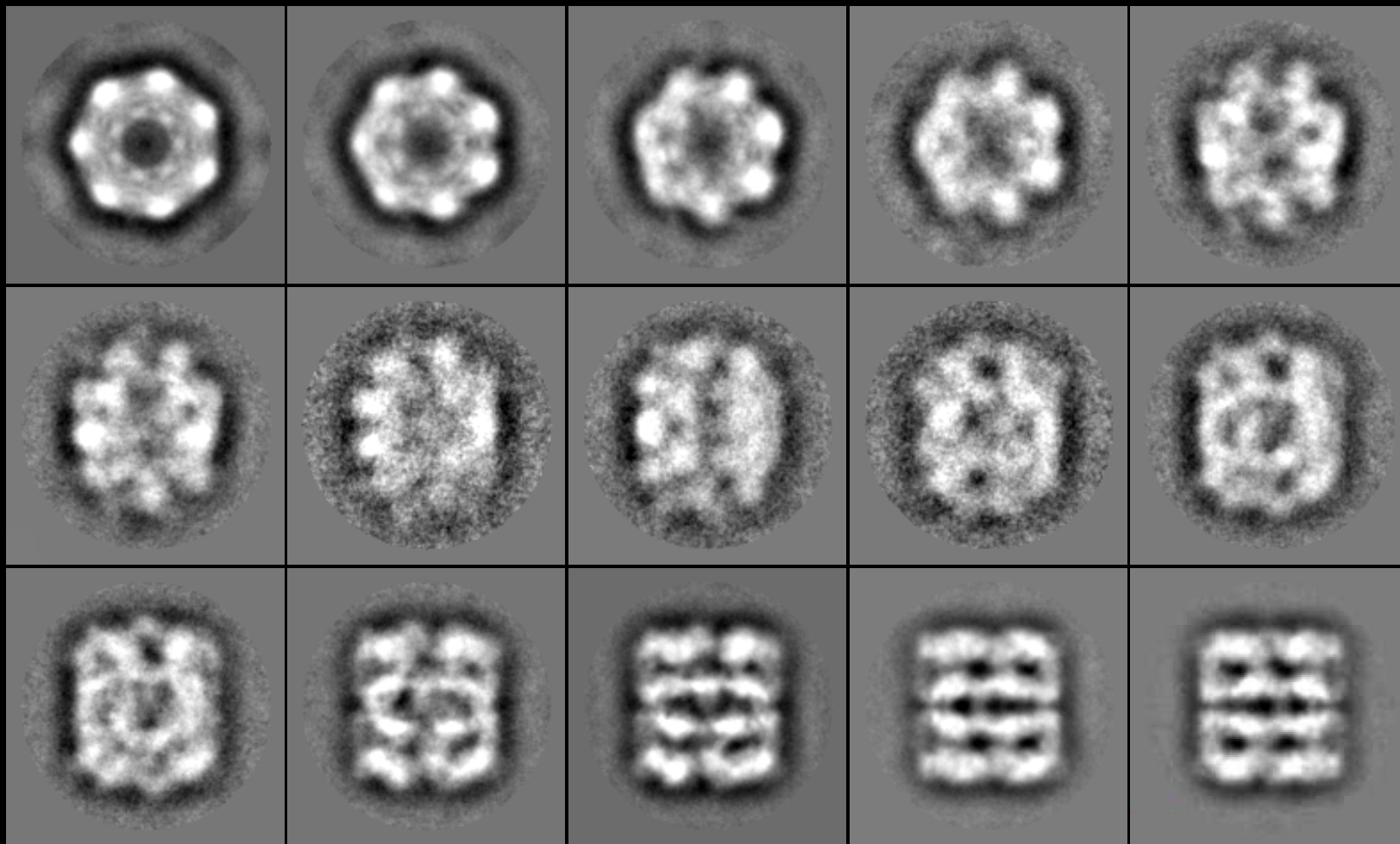


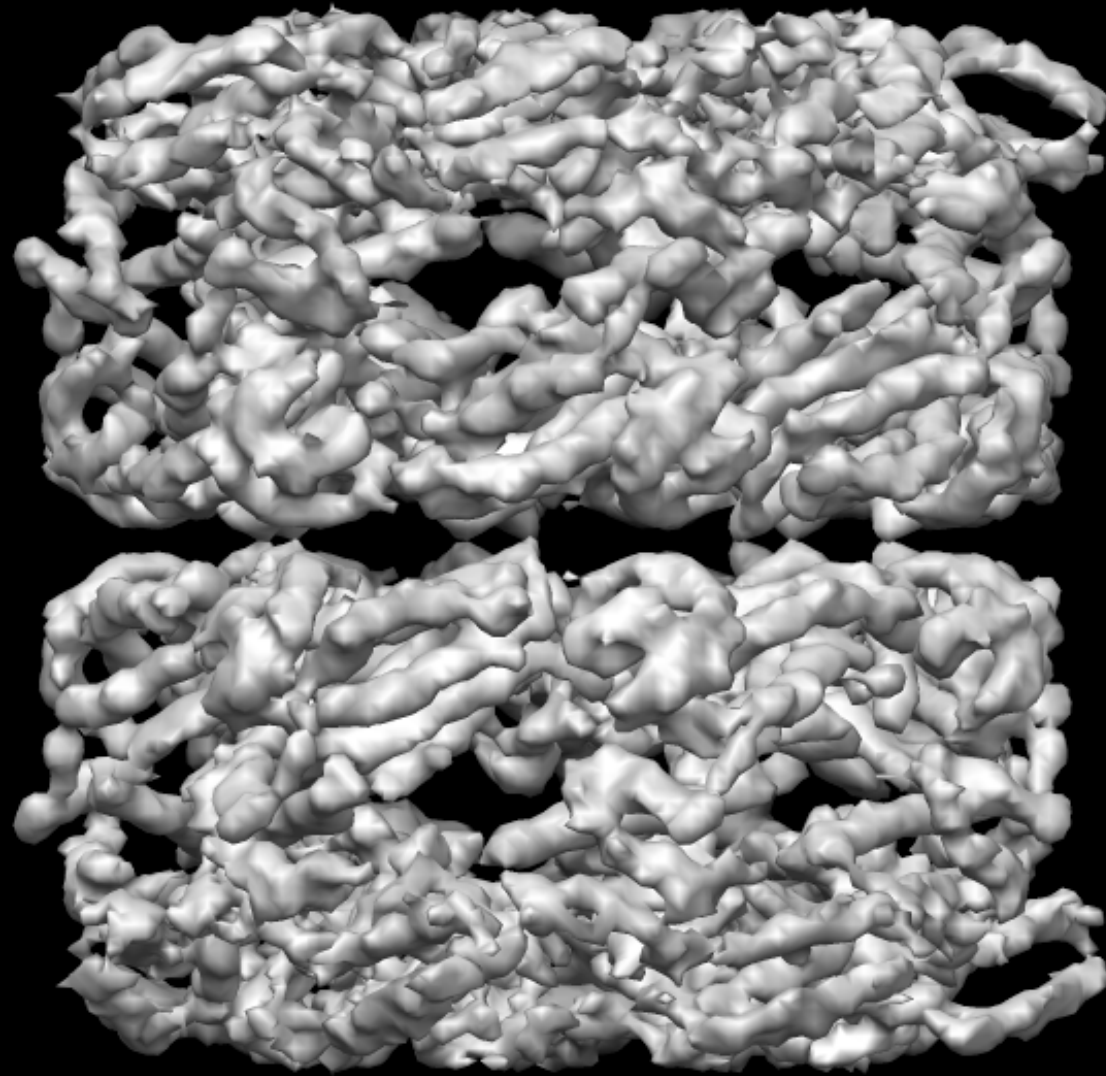


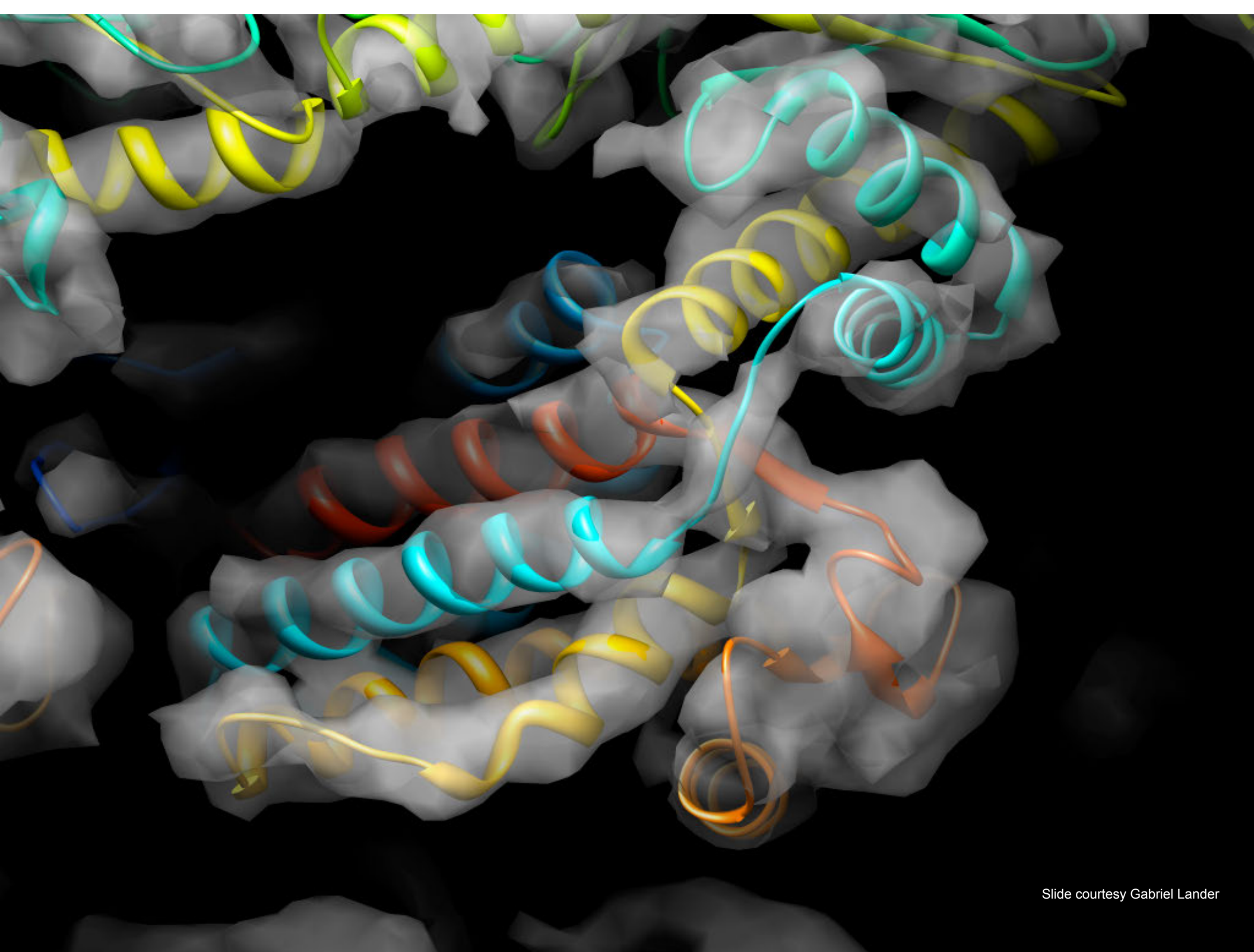


Slide courtesy Gabriel Lander

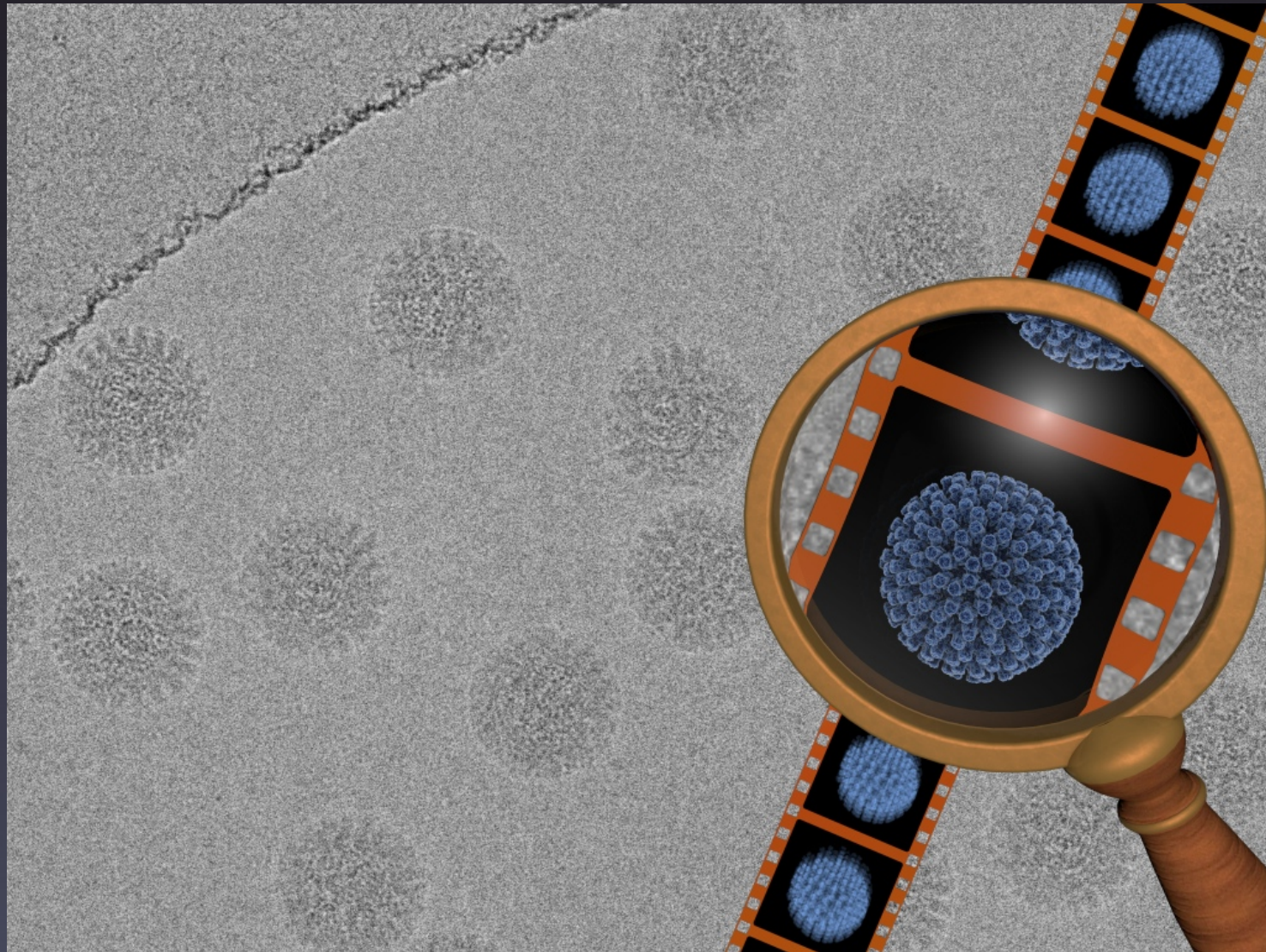








The Resolution Revolution!



Anchi Cheng



Melody
Campbell

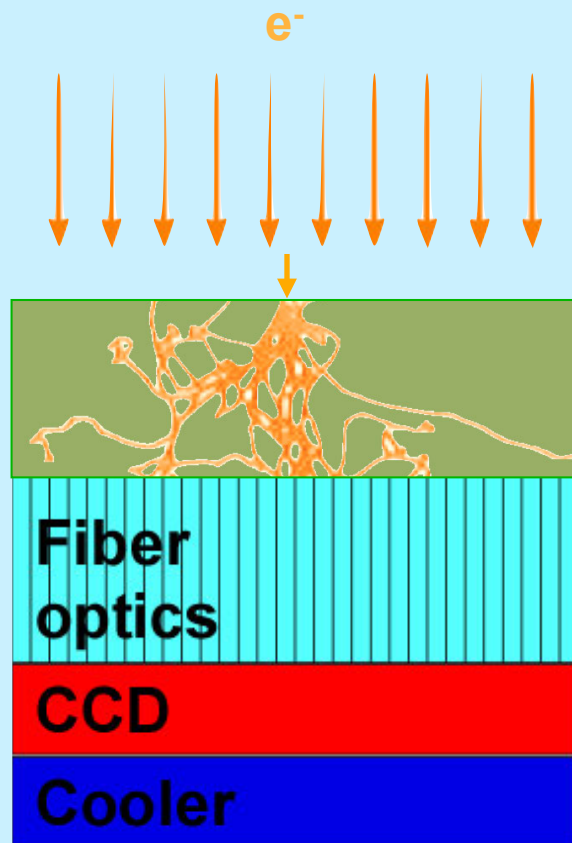
- Milazzo, A.C., Cheng, A., Moeller, A., Lyumkis, D., Jacovetty, E., Polukas, J., Ellisman, M.H., Xuong, N.H., Carragher, B., and Potter, C.S. (2011). Initial evaluation of a direct detection device for single particle cryo-electron microscopy. *J Struct Biol* 176, 404-408.
- Brilot, A.F., Chen, J.Z., Cheng, A., Pan, J., Harrison, S.C., Potter, C.S., Carragher, B., Henderson, R., and Grigorieff, N. (2012). Beam-induced motion of vitrified specimen on holey carbon film. *J Struct Biol* 177, 630-637.
- Campbell, M.G., Cheng, A., Brilot, A.F., Moeller, A., Lyumkis, D., Veessler, D., Pan, J., Harrison, S.C., Potter, C.S., Carragher, B., and Grigorieff, N. (2012). Movies of ice-embedded particles enhance resolution in electron cryo-microscopy. *Structure* 20, 1823-1828.



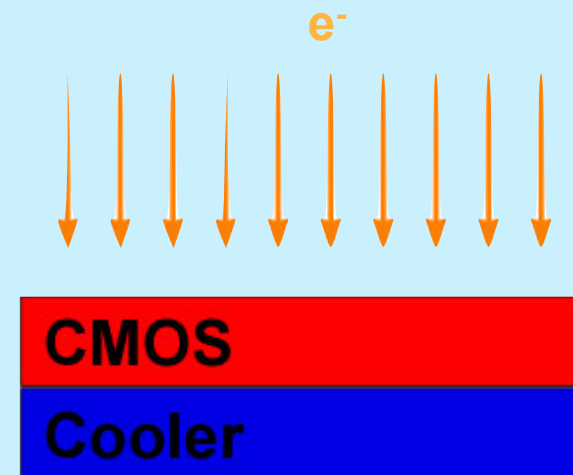
Niko Grigorieff

A new generation of cameras has improved the resolution and the efficiency of data collection

Charge Coupled Device (CCD)

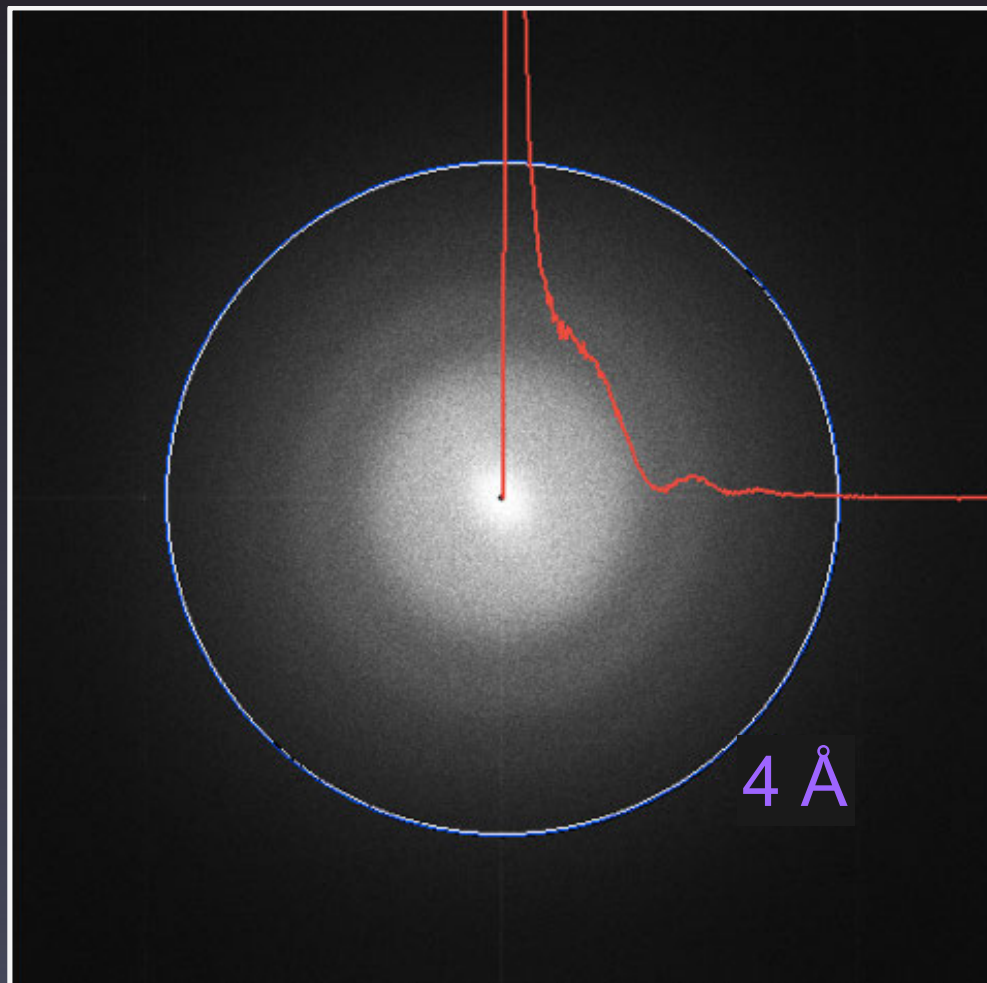


Direct Detection Device (DDD)



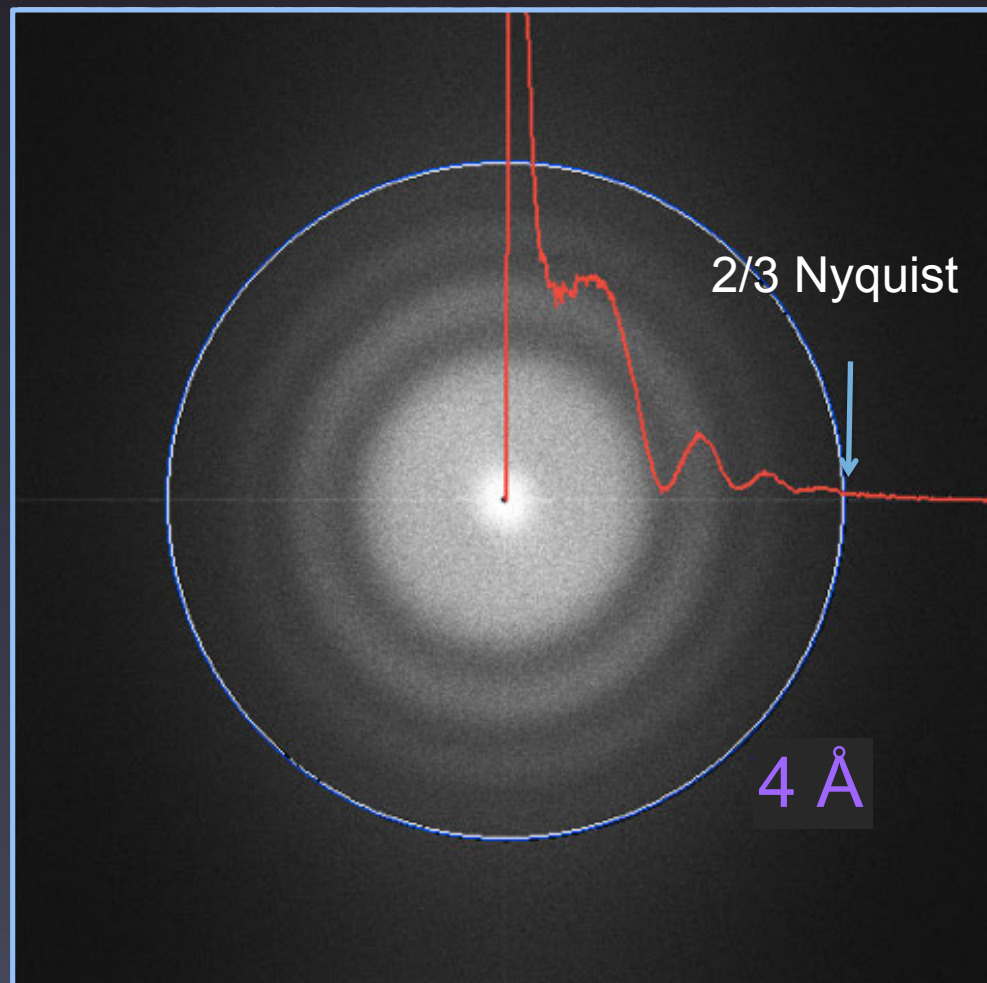
Improving the resolution: Detecting electrons instead of photons

CCD



1.37 Å/pixel

DDD



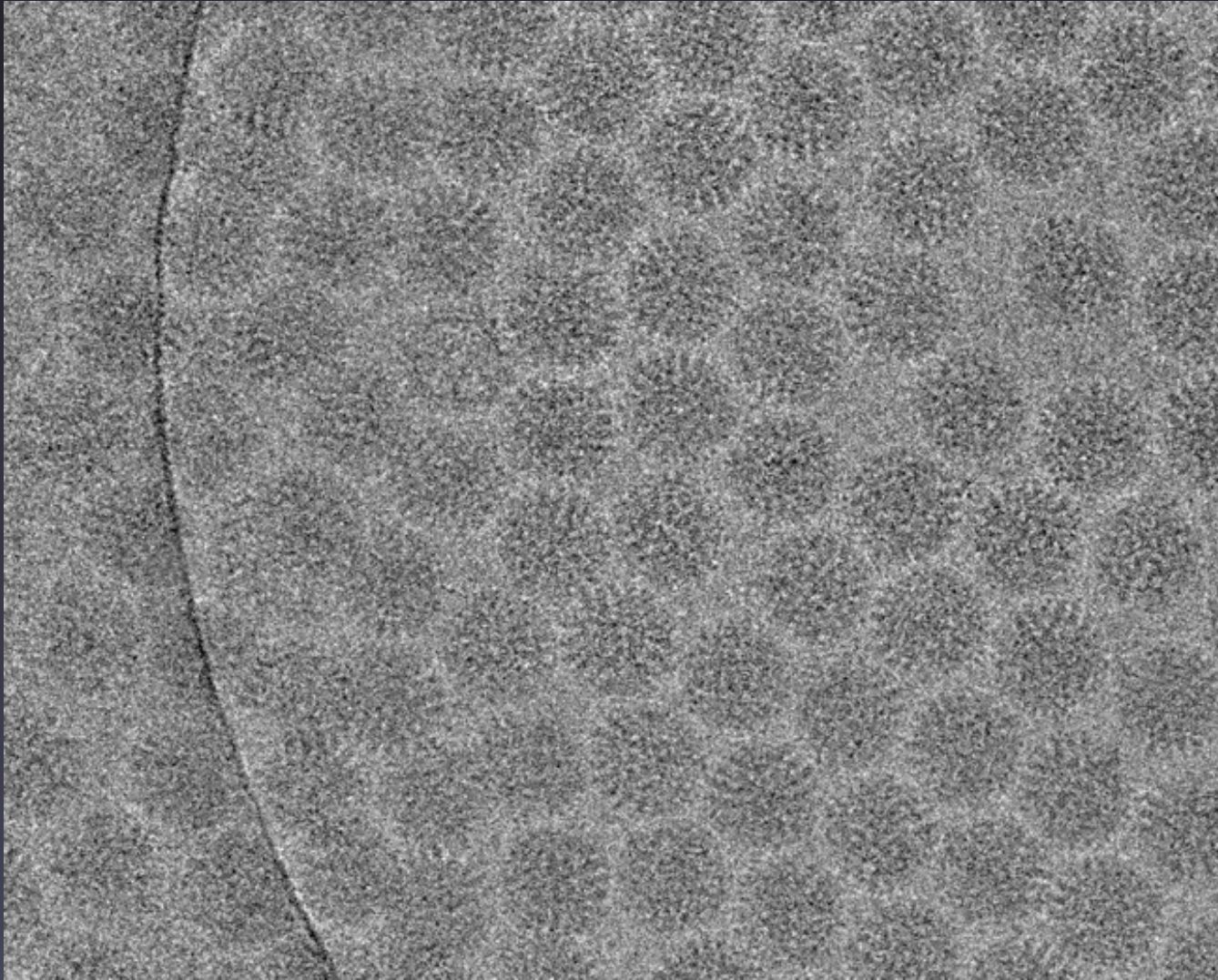
1.38 Å/pixel

200KeV ; 20 e-/Å² ; carbon film ; 3k x 3k image

Improving the resolution: Correcting for drift and beam induced motion



Improving the resolution: DDD records a set of frames (“movie”)



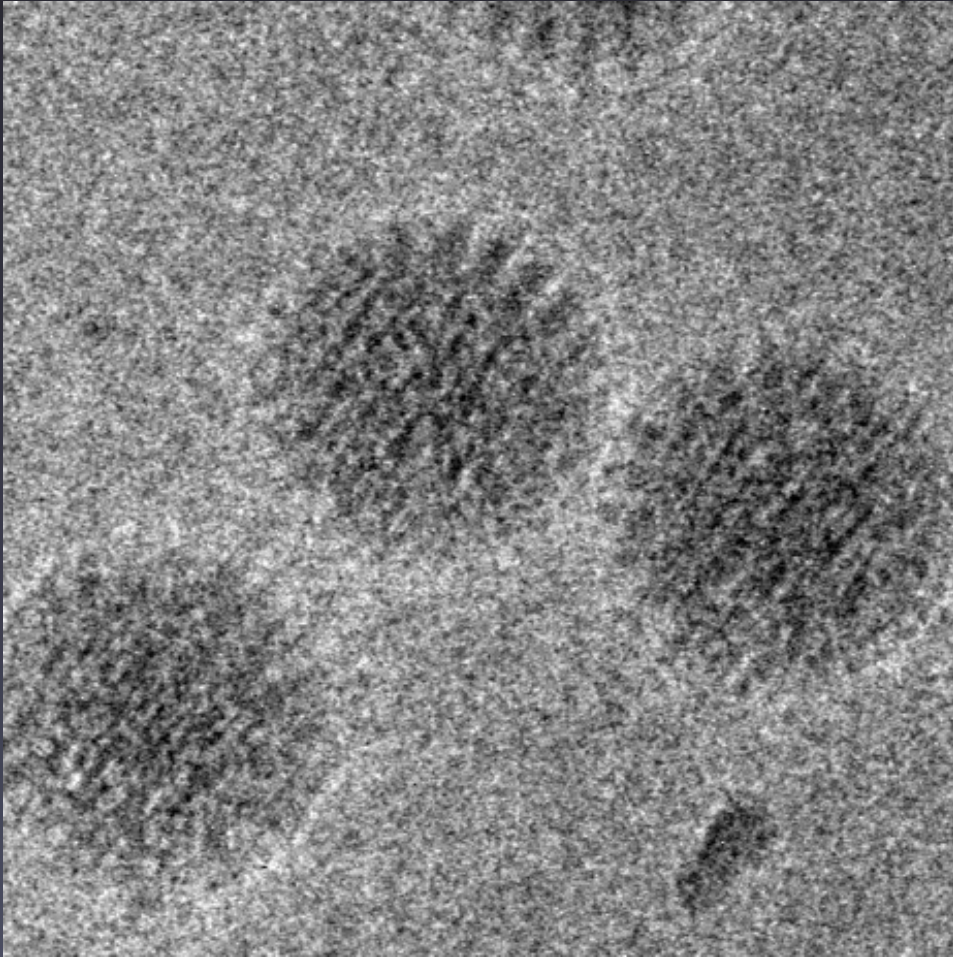
$0.5 \text{ e}^-/\text{\AA}^2/\text{frame}$

Image = Frame1 + Frame2 + Frame3 + Frame4 + Frame5

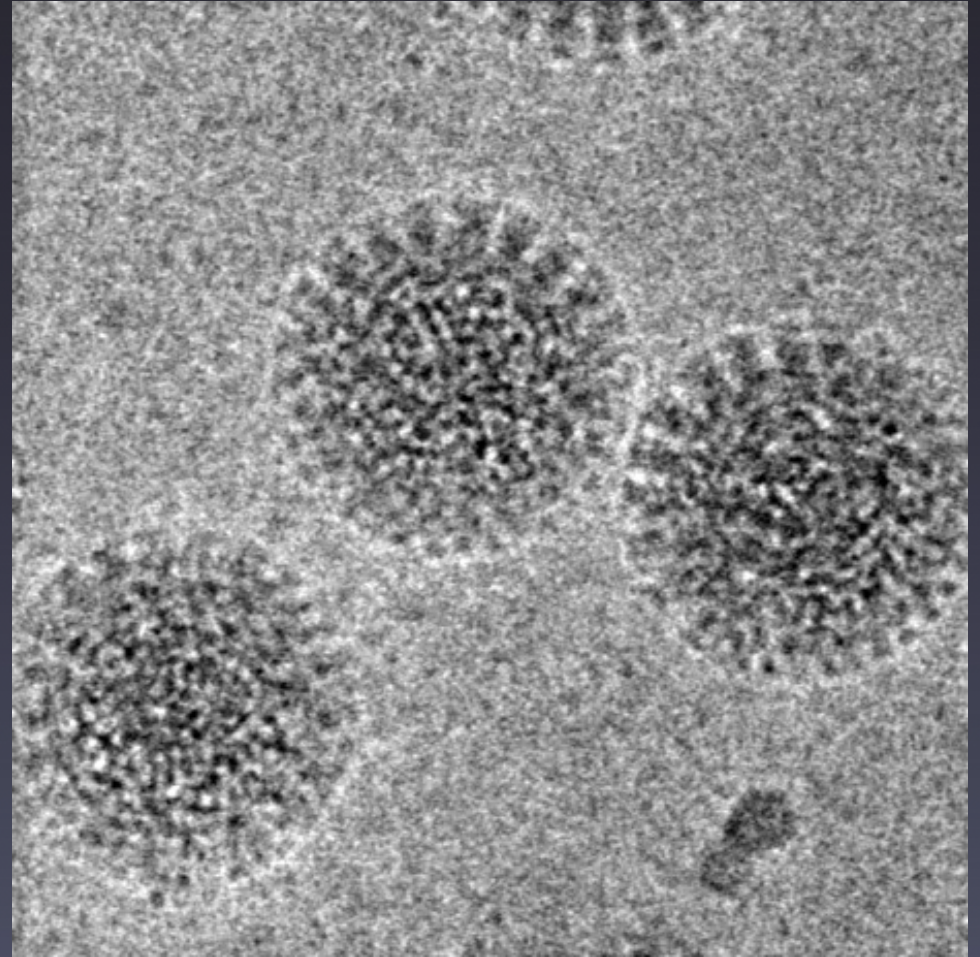
We can use DDD movies to examine (and correct) “beam induced motion”

Correcting for beam induced movement

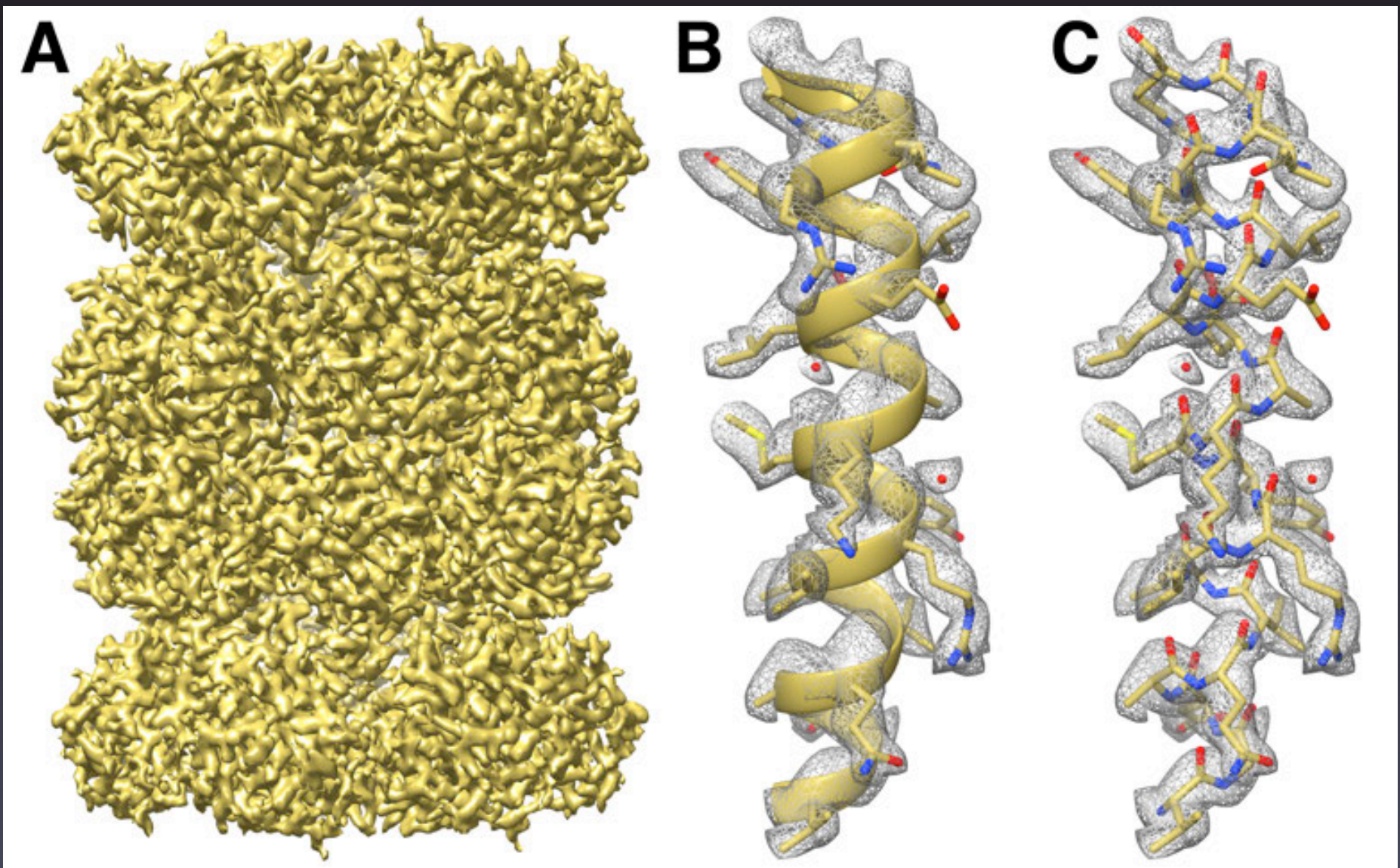
60-frame average
(no alignment)



60-frame average
(translational alignment)



2.8 Å resolution reconstruction of the 20 S proteasome



Melody
Campbell



David
Veesler

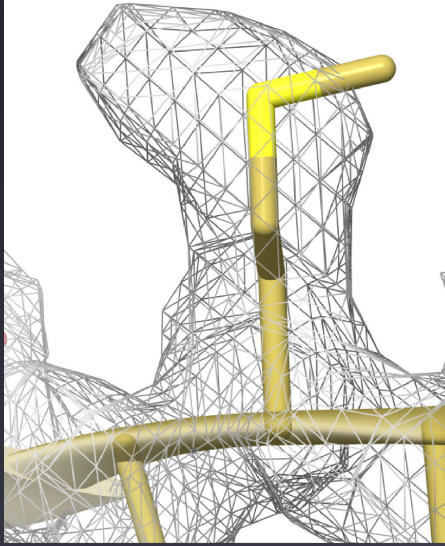


Anchi
Cheng

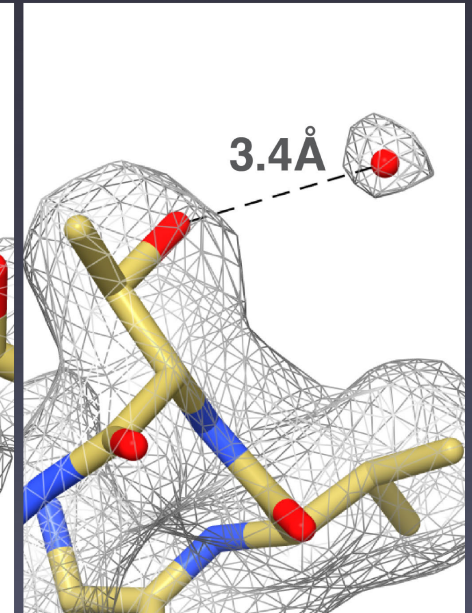
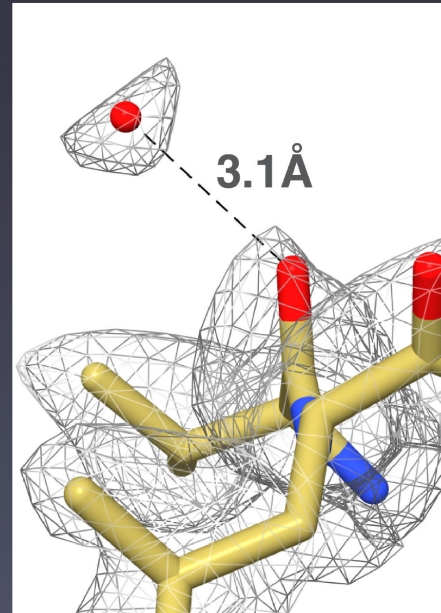
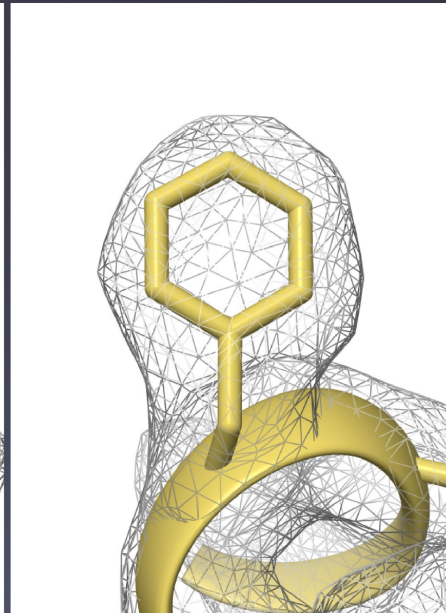
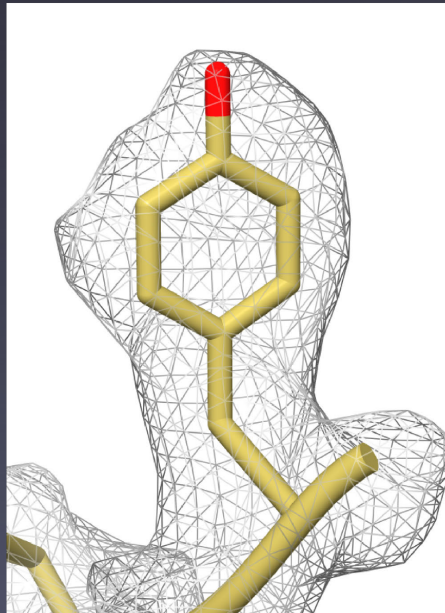
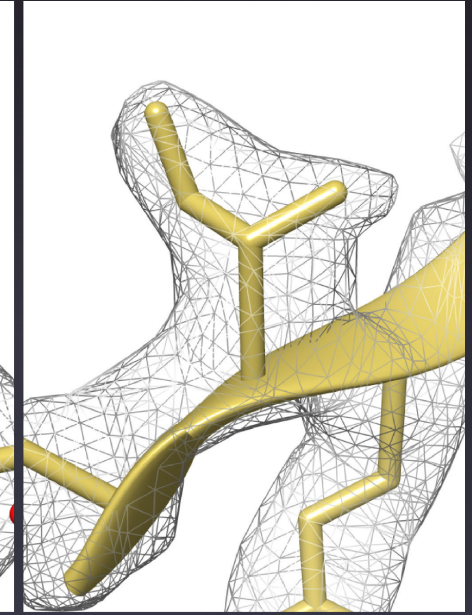
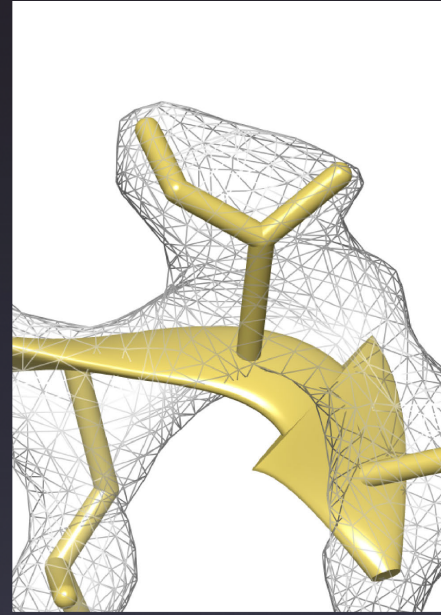
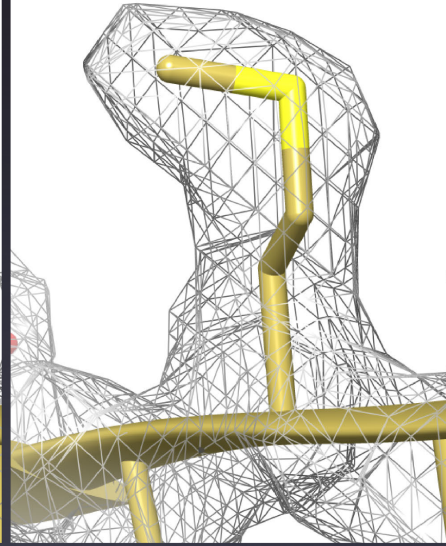
- Melody Campbell, David Veesler, Anchi Cheng, Bridget Carragher, and Clinton S. Potter (2015). 2.8 Å resolution reconstruction of the *Thermoplasma acidophilum* 20 S proteasome using cryo-electron microscopy. eLife.

2.8 Å resolution reconstruction of 20 S proteasome

X-Ray PDB 1PMA



EM EMD-6287



Class structure

Section 1: Anatomy of an EM

Christoph Wigge & Anchi Cheng [NY]

Section 2: Fourier transforms and Image Form

Bill Rice [NYSBC]

Section 3: Challenges in EM & Sample prep

Ed Eng & Ashleigh Raczkowski [NYSBC]

Section 4: Tomography

Part I: David Stokes [NYU]

Part II: Bill & Christoph [NYSBC]

Section 5: Single Particle

Part I: Joachim Frank [CU]

*Part II: Amedee Des Georges &
Reza Khayat [CUNY]*

Part III: Yong Zi Tan, [COLU/NYSBC]

Section 6: 2D crystallography

Part I: Iban Ubarretxena [MSSM]

Part II: Hernando Sosa [AECOM]

Section 7:



EMDataBank
Unified Data Resource for 3DEM

EMDB,
Cathy Lawson [Rutgers]



Validation methods
Tom Walz [RU]



situs.biomachina.org

Fitting Atomic models
Willy Wriggers
[Old Dominion University]

SEMC Forum
April 26 - noon



SIMONS ELECTRON MICROSCOPY CENTER

NEW YORK STRUCTURAL BIOLOGY CENTER



Painter's Studio
by Jan van der Straet (Stradanus) (Dutch, 1523-1604)



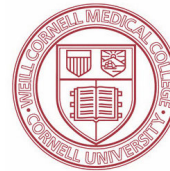
NEW YORK STRUCTURAL BIOLOGY CENTER



9 member institutions



Albert Einstein College of Medicine
OF YESHIVA UNIVERSITY



Member Institution Services

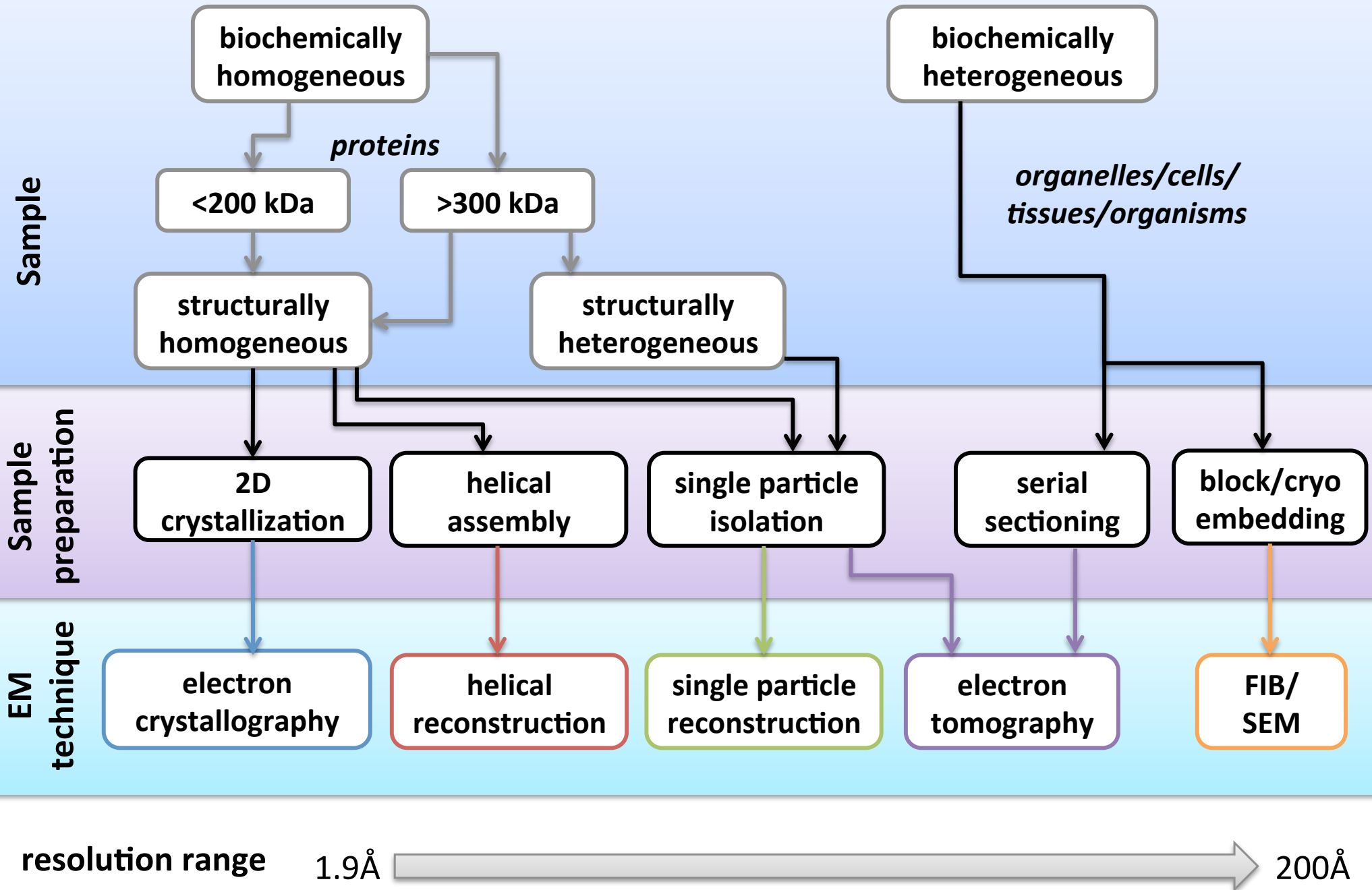
- Training in instrumentation and techniques, and individual instruction
- Assigned, dedicated instrument time

Additional services

(offered on a fee-for-service basis)

- Additional EM time (members) or access to EMs with staff assistance (non-members).
- EM starter kits and consumables

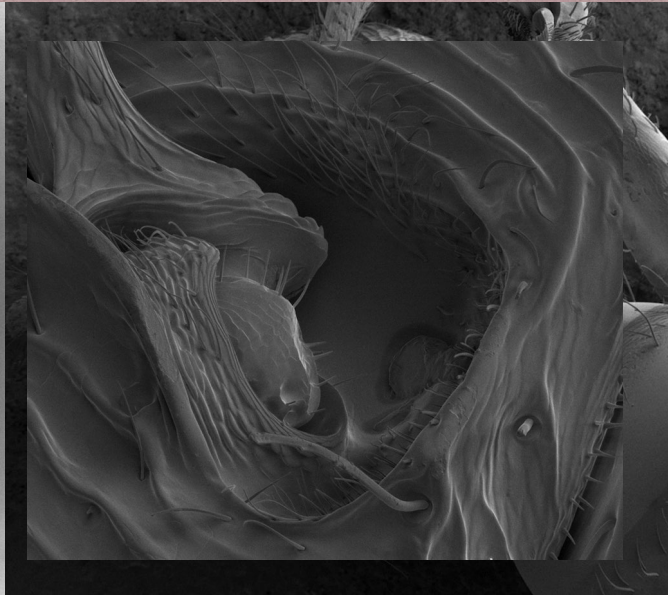
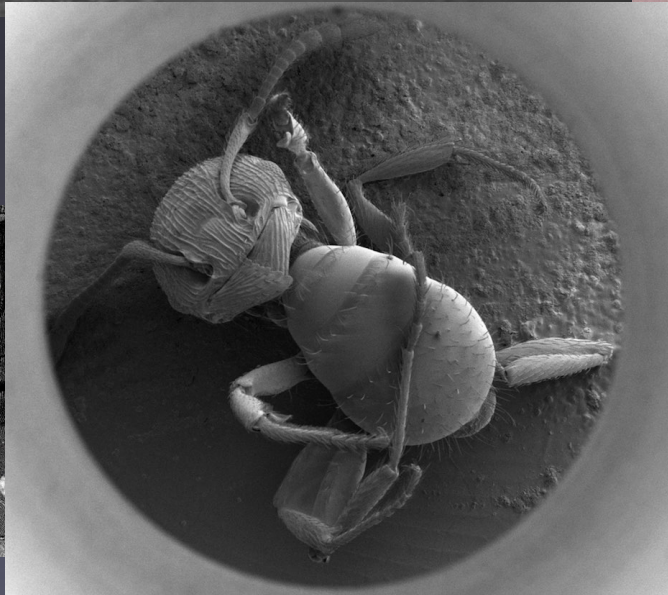
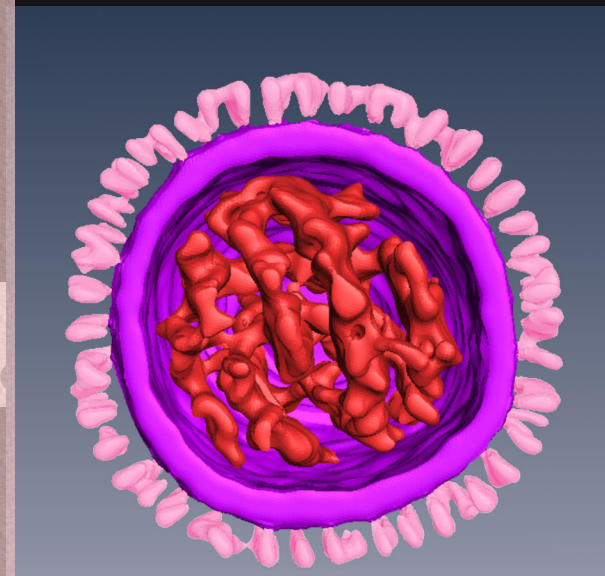
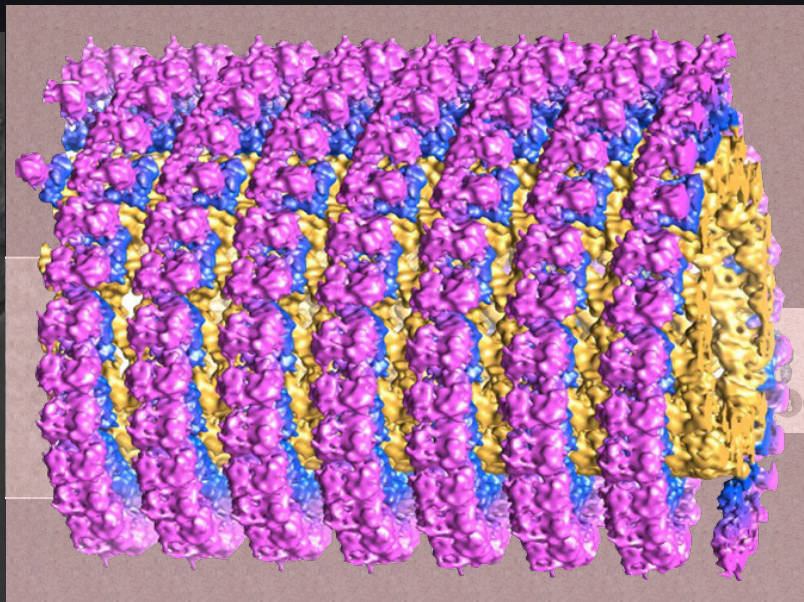
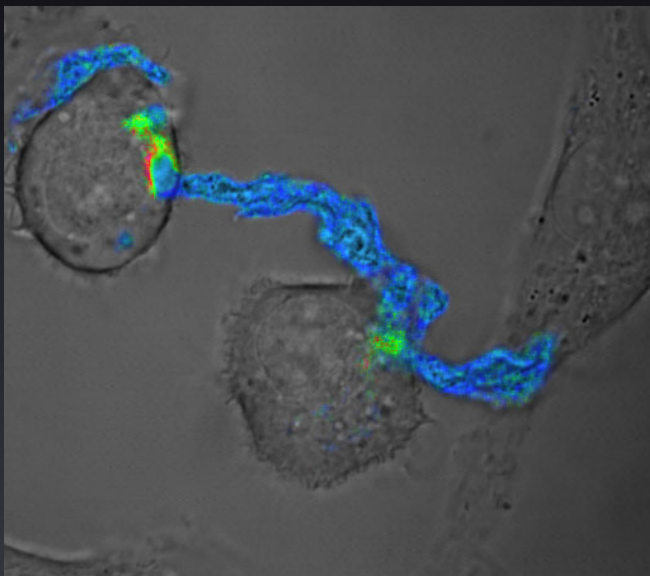
SEMC mission





The Simons Electron Microscopy Center

Focus on:



SEMC Training Programs

yearly

SEMC EM Course

Theory behind EM

starts Jan 11

quarterly

SEMC Appion workshop

Appion data processing practical

Jan 28

monthly

SEMC New User
Training

Sample preparation [neg-stain & cryo]
Leginon intro/use of screening microscopes

24-hr access test

All hours access test

Safety training

weekly

User Project Discussion
Meetings

Mon @ 11am
Thurs @3pm & @4pm

daily

Advanced Leginon use

Training for independent use of the
microscopes

Online registration



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MICROSCOPY
CENTER

NYSBC 

Renovation Updates
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Training

New user training [monthly]:

New users are required to attend a group new user training session before independent use of the facility. We offer these 1-day training sessions the beginning of each month from 9am to 4:30pm. The morning session will cover sample preparation (Negative-staining and Plunge Freezing). The afternoon session will cover basic TEM use (Loading samples and Introduction to Legicon). Also, for your convenience you may purchase a starter EM user kits from us.

Appion workshop [quarterly]:

<https://www.surveymonkey.com/r/AppionJanuary2016>

SEMC group members lead a workshop on the Appion single-particle data processing workflow. Appion is a "pipeline" for processing and analysis of EM images. Appion is integrated with Legicon data acquisition, but can also be used stand-alone after uploading images or particle stacks. Topics include analyzing the quality of your data collection, generation and refinement of 3D reconstructions, and validation methods.

Online materials

<http://semc.nysbc.org/start.html>



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About the Simons Electron Microscopy Center

The Simons Electron Microscopy Center provides expertise and resources for understanding both molecular and cellular structures. Molecular structure determination is enabled by high-end transmission electron microscopes (TEMs), direct detection cameras, and computational support for single particle analysis. Cellular structure determination is enabled by tomographic



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EM Directors



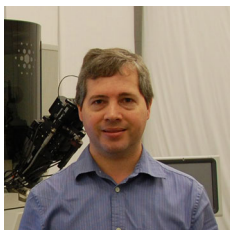
Bridget Carragher, Ph.D.



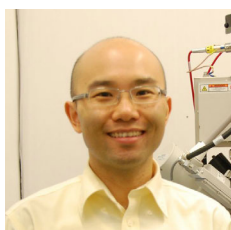
Clint Potter, Ph.D.

 @nysbc.org

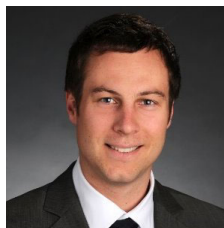
EM Staff



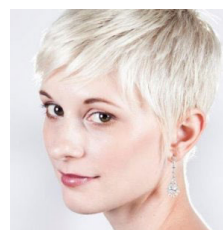
Bill Rice, Ph.D.
EM Manager



Ed Eng, Ph.D.
Scientist



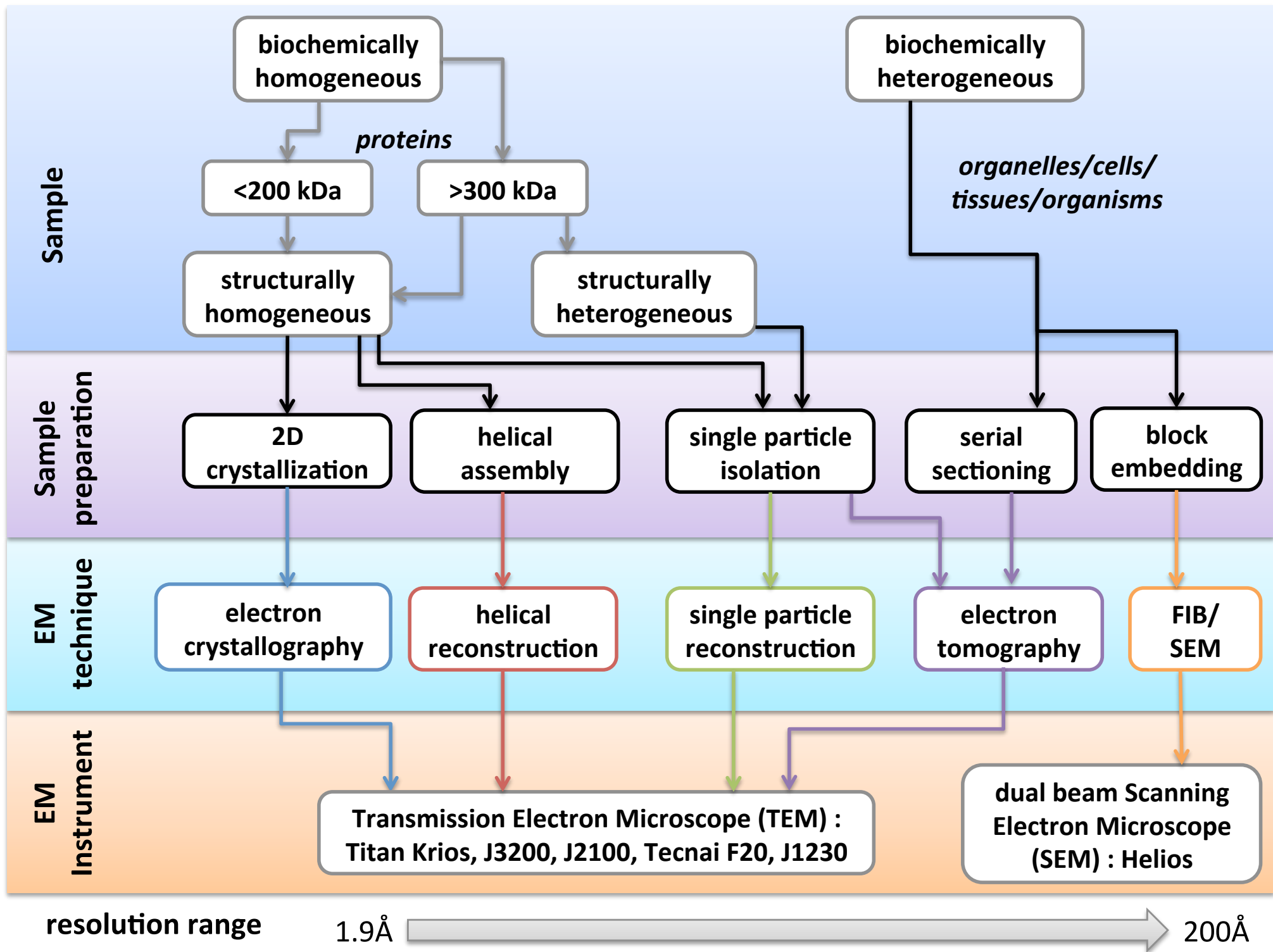
Christoph Wigge, Ph.D.
Scientist



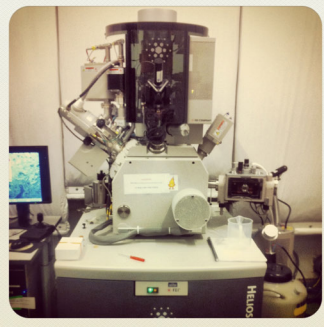
Ashleigh Raczkowski, B.S.
Technician



Kelsey Jordan, B.S.
Technician



Instrumentation



FEI Helios 650

+

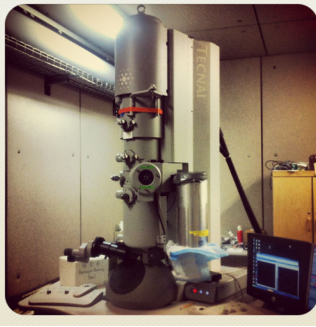
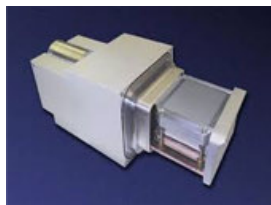
4K ETD, TLD, ICE



JEOL 1230

+

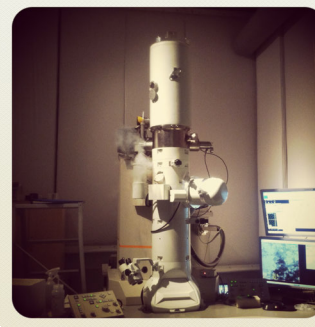
Gatan US4000
4K CCD



FEI Tecnai F20

+

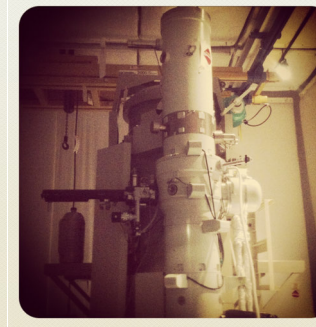
TVIPS F416
4K CMOS



JEOL 2100F

+

Gatan
K2 Summit
Direct Detector



JEOL 3200FSC

+

Direct Electron
DE-20
Direct Detector



FEI Titan Krios

+

FEI
Falcon 2->3
Direct Detector

Coming soon

Schedule

- *Welcome new students*
- *Course logistics*
 - *Questionnaire*
 - *Other SEMC training programs*
- *Introduction to EM*
- **NYSBC tour**



Andy Warhol's New York studio circa 1960s



Jeff Koons's New York studio