

Case Studies in Resolution, Validation, and ...

Steve Ludtke
Baylor College of Medicine



My Assignment

- "We hope Steve will get into the nitty gritty of his comparison... even more than his excellent talk last winter at Hybrid Methods meeting. Practical solutions."
- Maybe I could re-refine our recent structures with the Gold Standard refinement and compare...
- NCMI: 72 EMDB structures in last 5 years
- Ok, maybe not ALL of them...

Gold Standard ?

- Refine all data together, split at the end, no refinement of halves before FSC
- Refine all data together, split at end, partial orientation redetermination of halves
- Split at the beginning, low-pass filtered same starting model, independent refinements with resolution-limited info
- Split at the beginning, randomized different starting models, independent refinements with arbitrary info

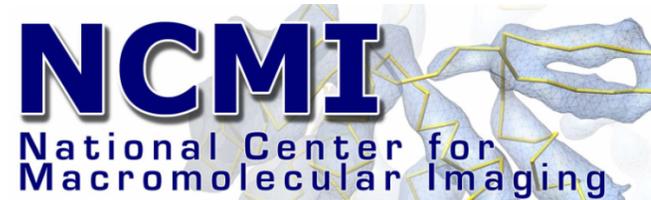
Gold Standard ?

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Molluscan Hemocyanin



Xinghong Dai
Qinfen Zhang

**South China Sea
Fisheries Research
Institute**

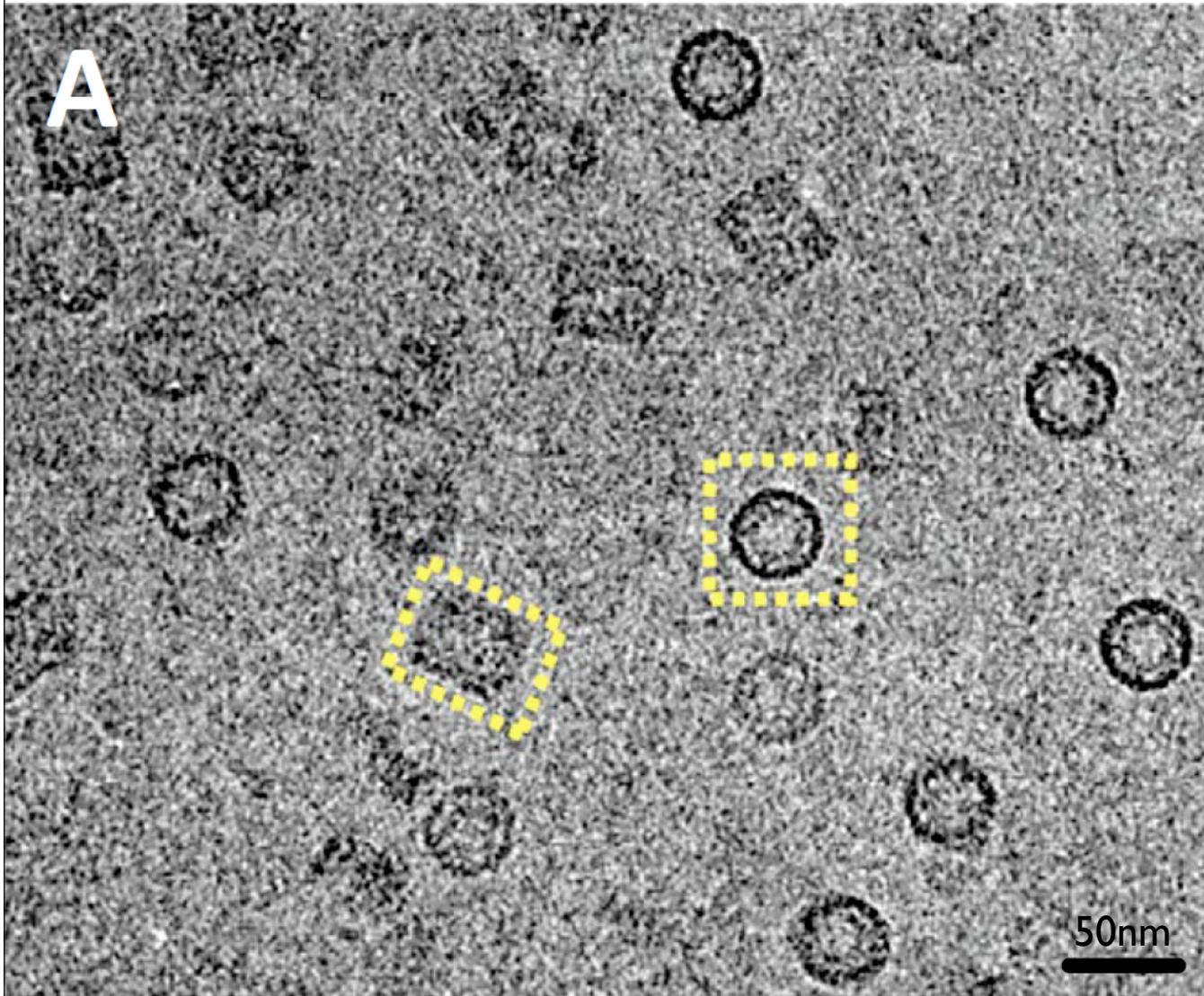
Jiangyong Wang

SKLBC10B05, NSFC, China
Guangdong Province Agricultural Project,
China

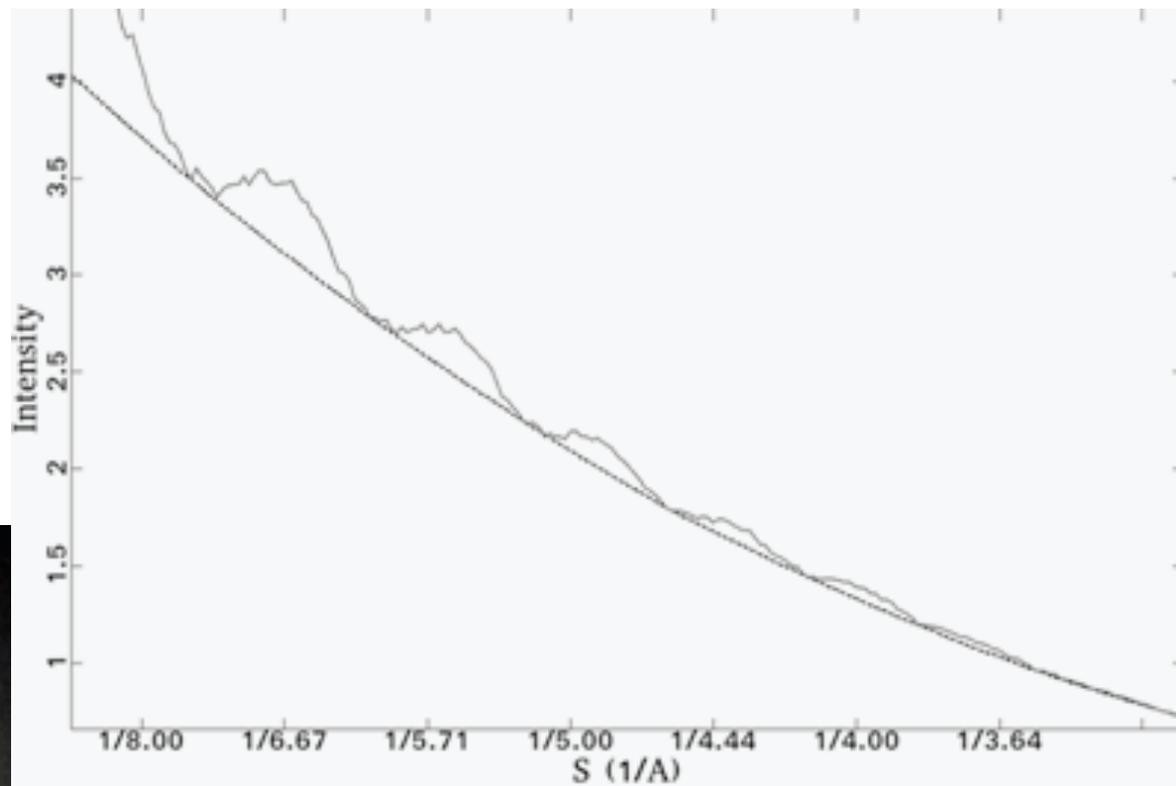
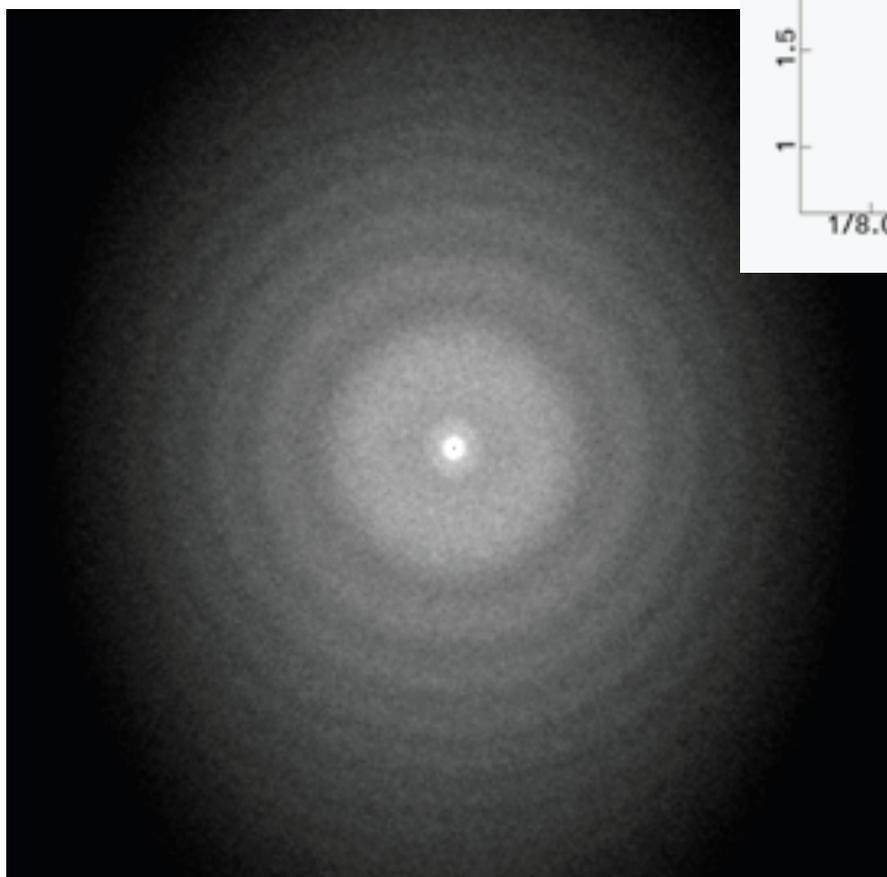
Wah Chiu
Michael Schmid
Yao Cong
Junjie Zhang
Donghua Chen

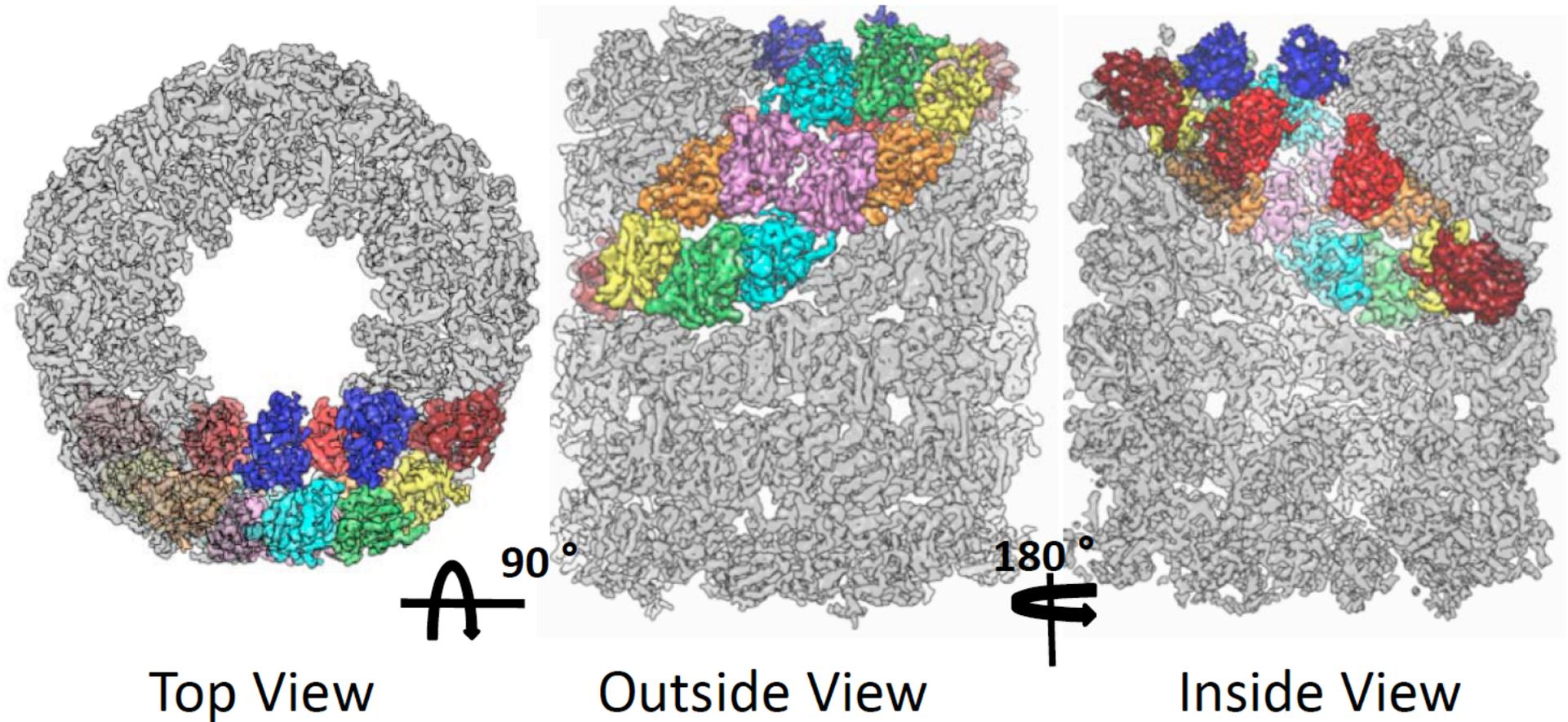
NIH grants (P41GM103832 and
PN2EY016525), USA

TACC (Computational Resources)

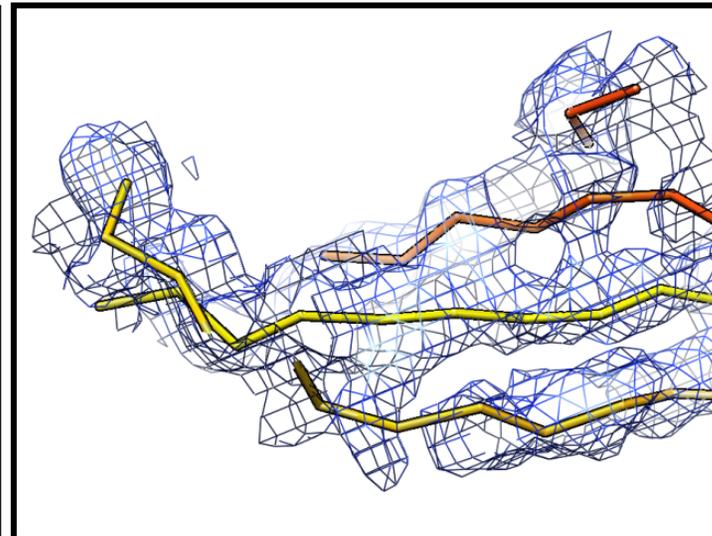
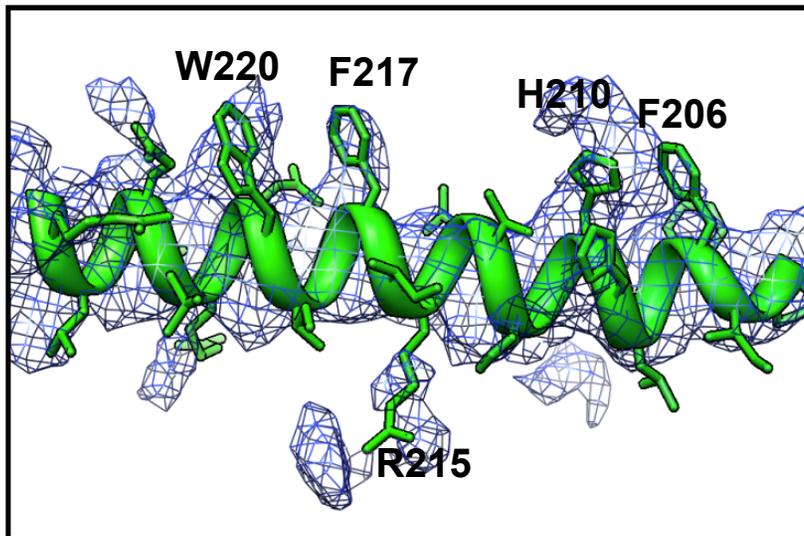
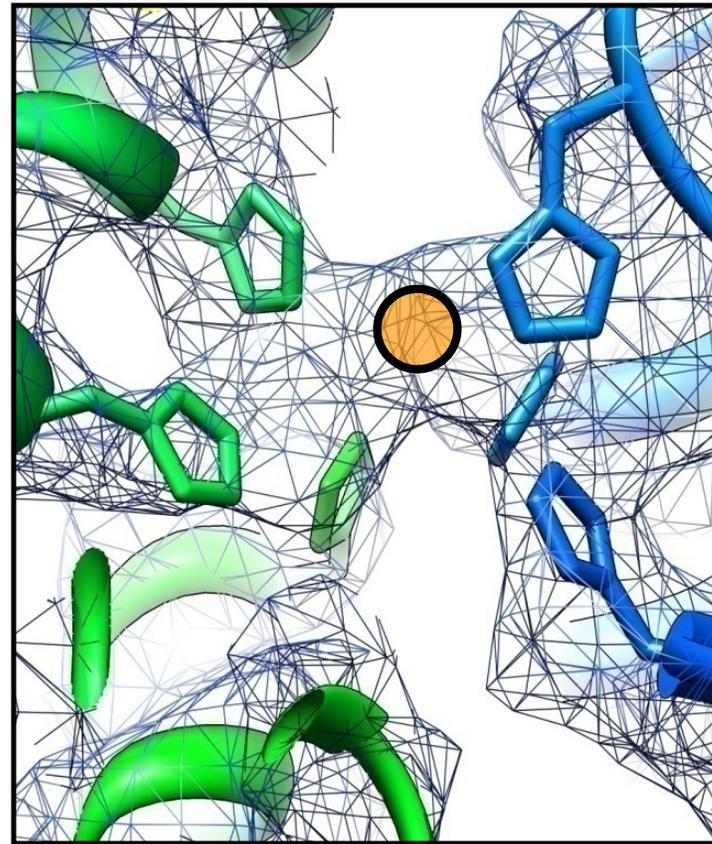
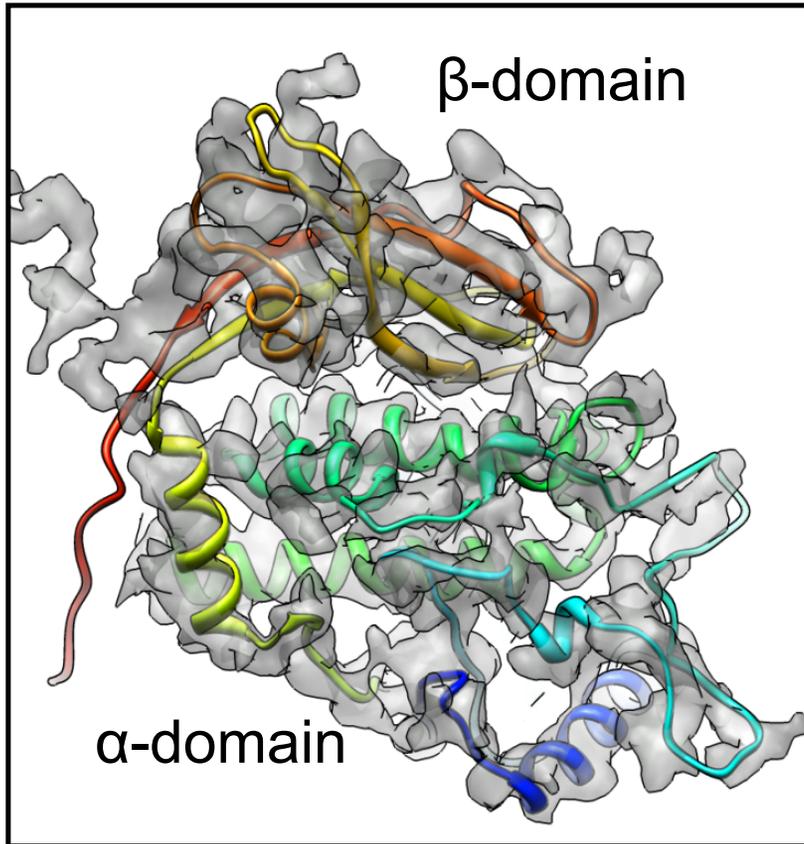


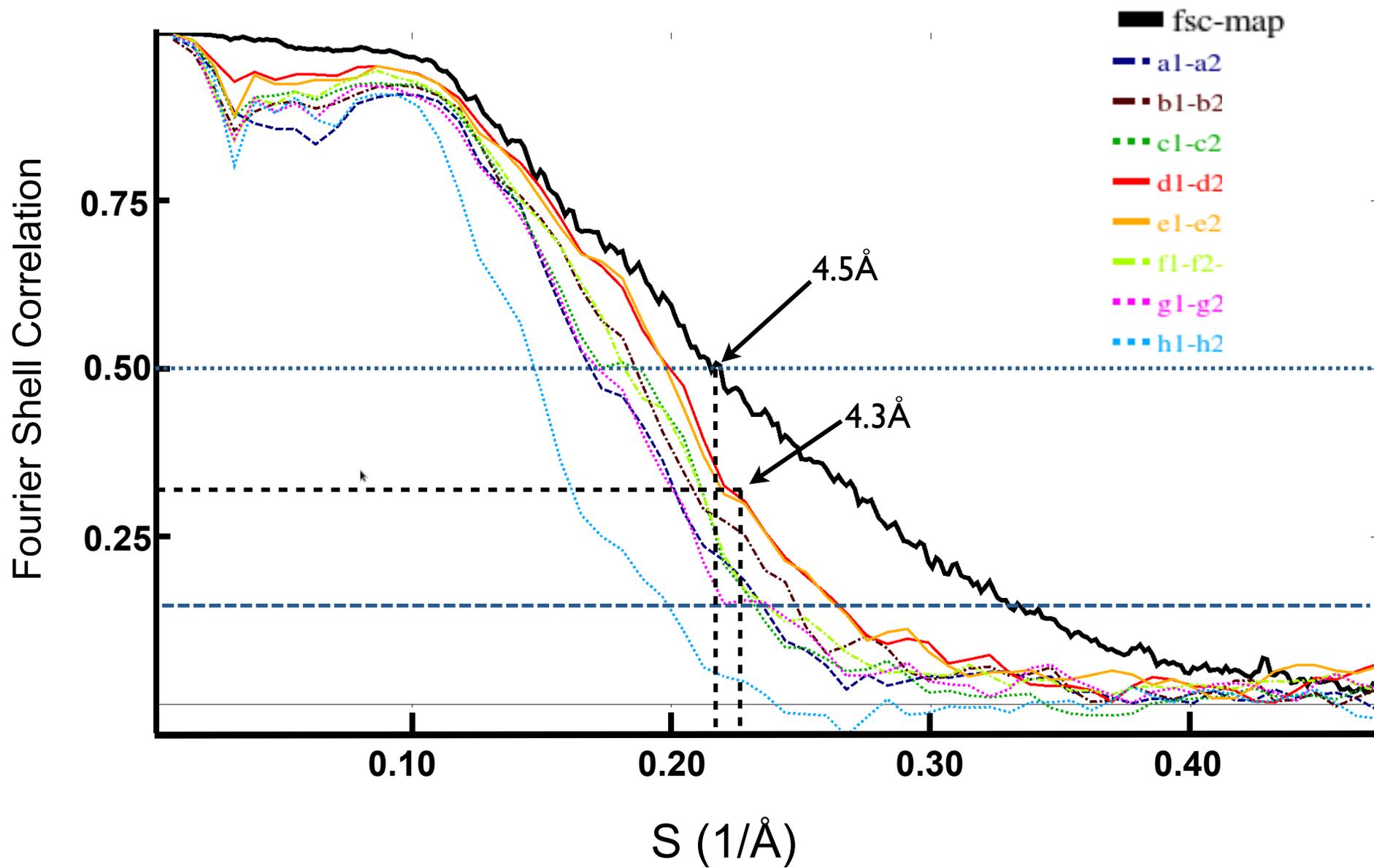
- JEOL3200SFF
- 300 keV
- SO-163/Nikon
- 28,641 Particles used
- 1.06 Å/pix
- D5 Symmetry
- Homo-dimer in each asym unit
- 8 pseudo-equivalent FUs per monomer
- ~8 MDa





D5 Symmetry x 2 subunits x 8 FUs
FUs have ~45% identity





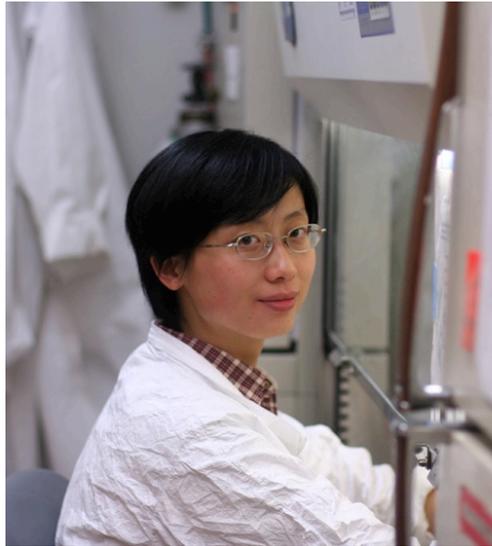
DARK

(Drosophila Apaf-I related killer)



School of Medicine

Acknowledgements



Shujun Yuan
Boston University School
of Medicine



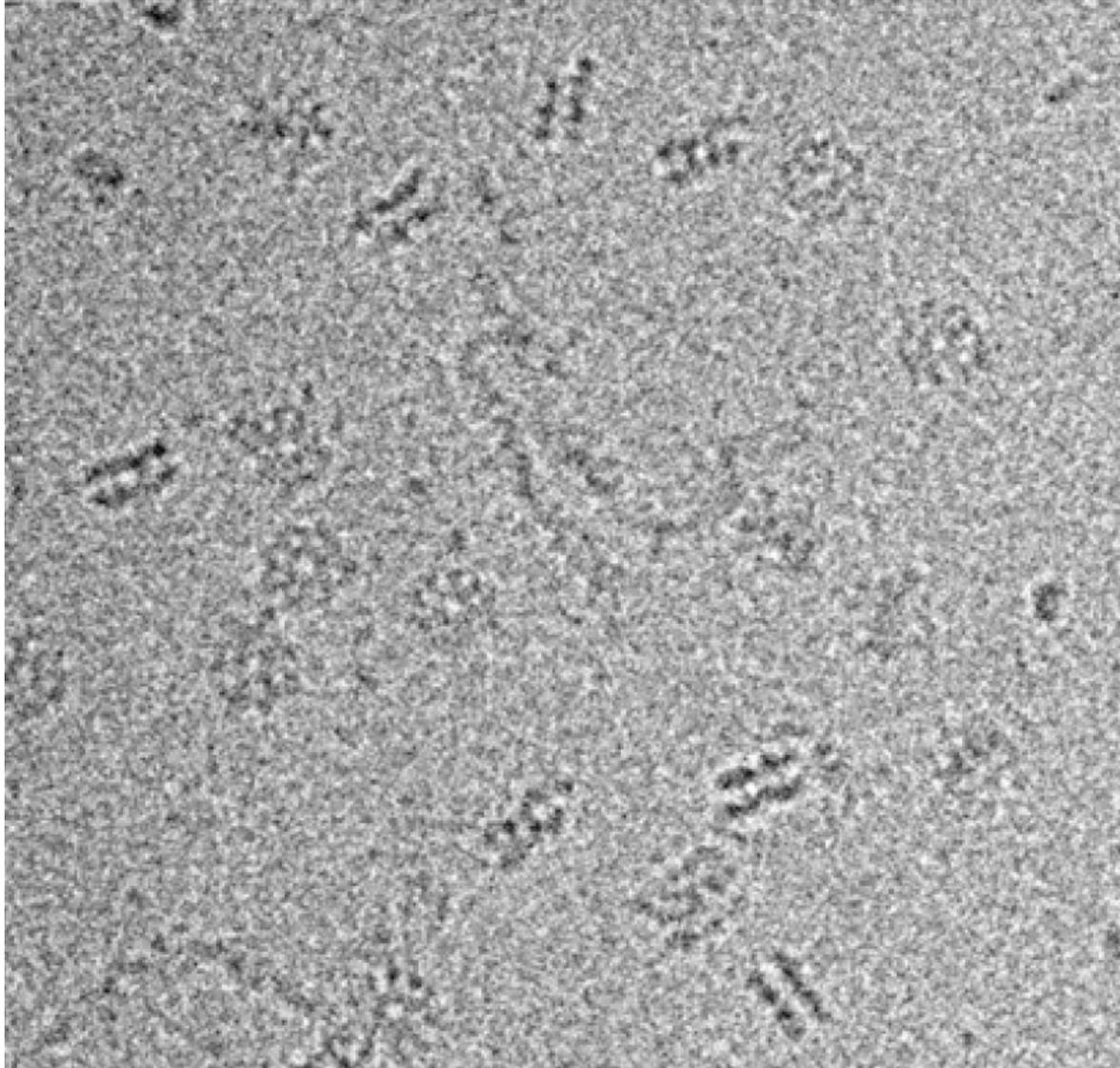
Maya Topf, Birkbeck
University of London



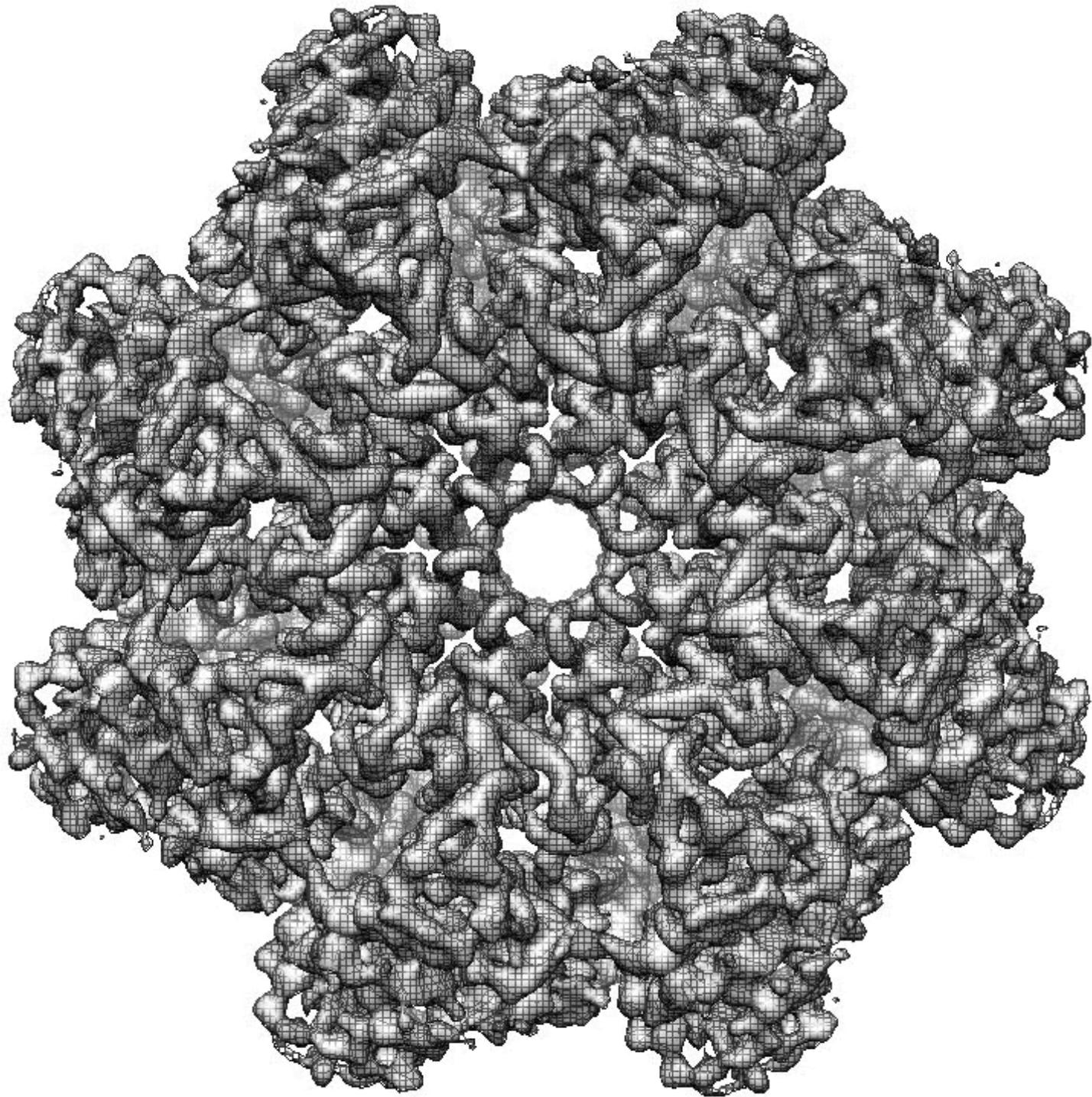
Christopher W. Akey
Boston University School
of Medicine

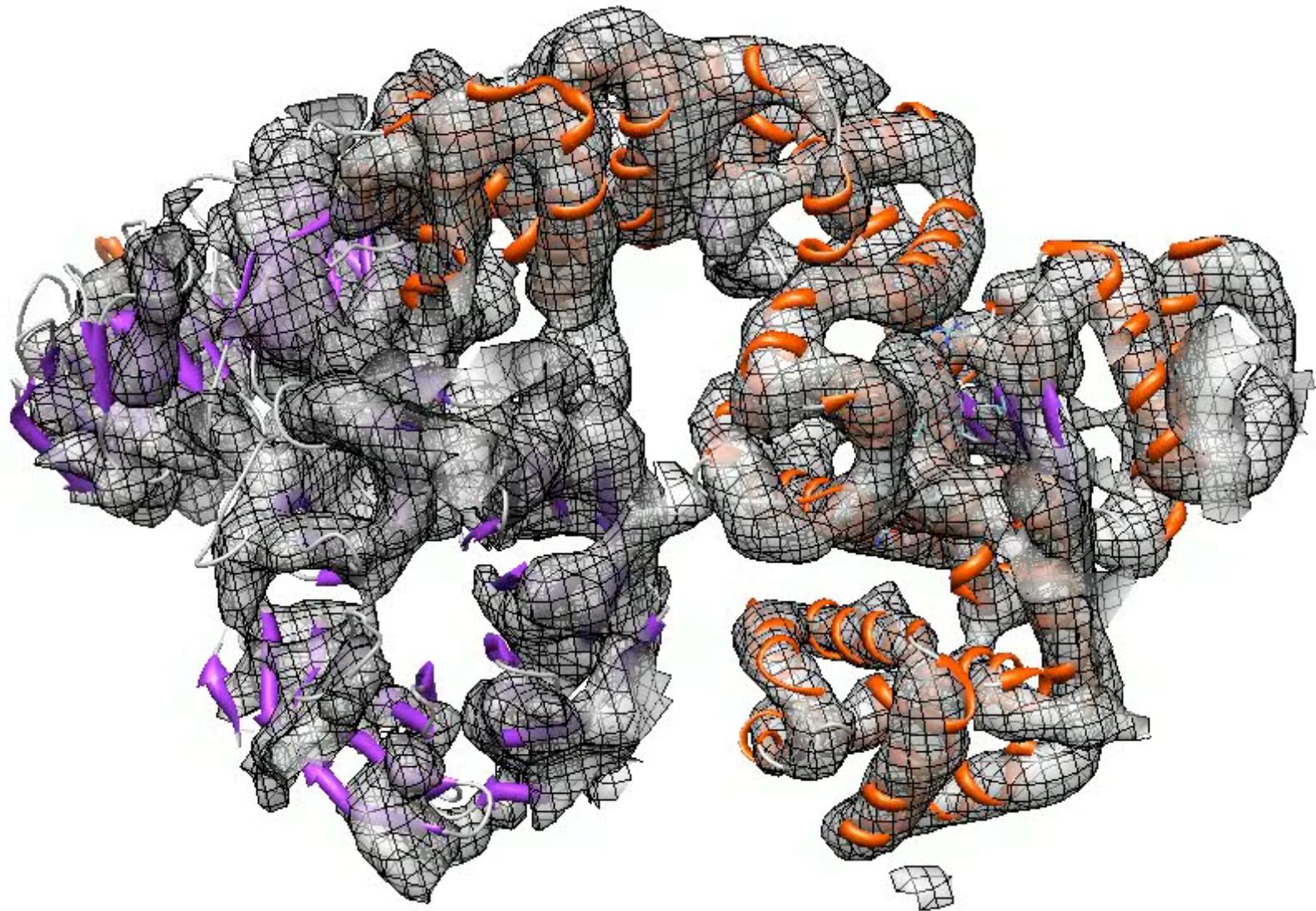
Research supported by NIHGMS

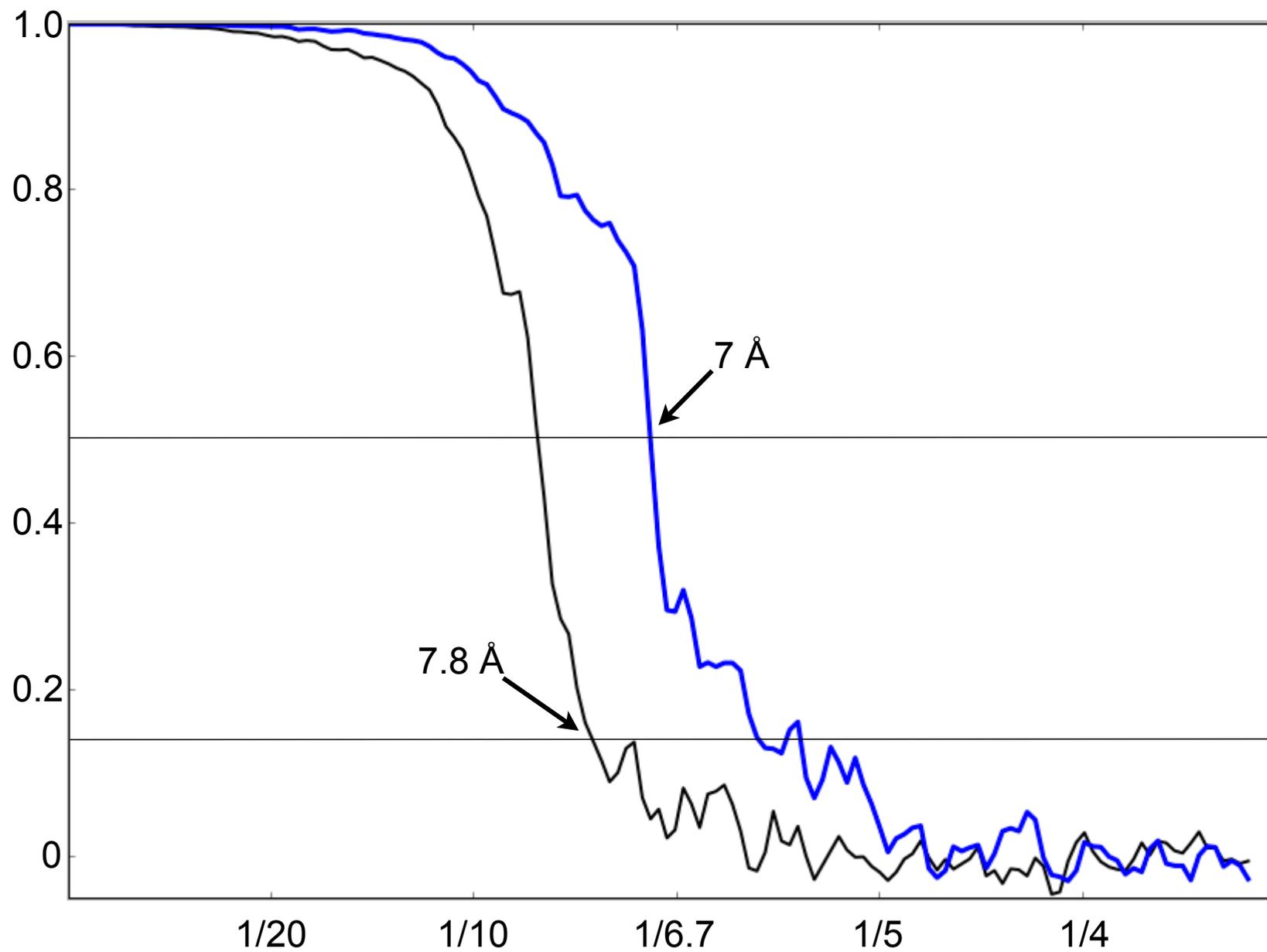




- Tecnai F20
- 160 kV
- 4k Tietz CCD
- 1.7 Å/pix
- D8 Symmetry
- ~48,000 particles
- ~2.5 MDa
- Homology
Modeling with
MODELLER







IP3R Acknowledgements

UTHSC

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Serysheva Lab

Olga Popova

Thao Tran

Tri Le

Que Ngo

Penczek Lab

Zhengfan Yang

NCMI

Baylor College of Medicine

Ludtke Lab

John Flanagan

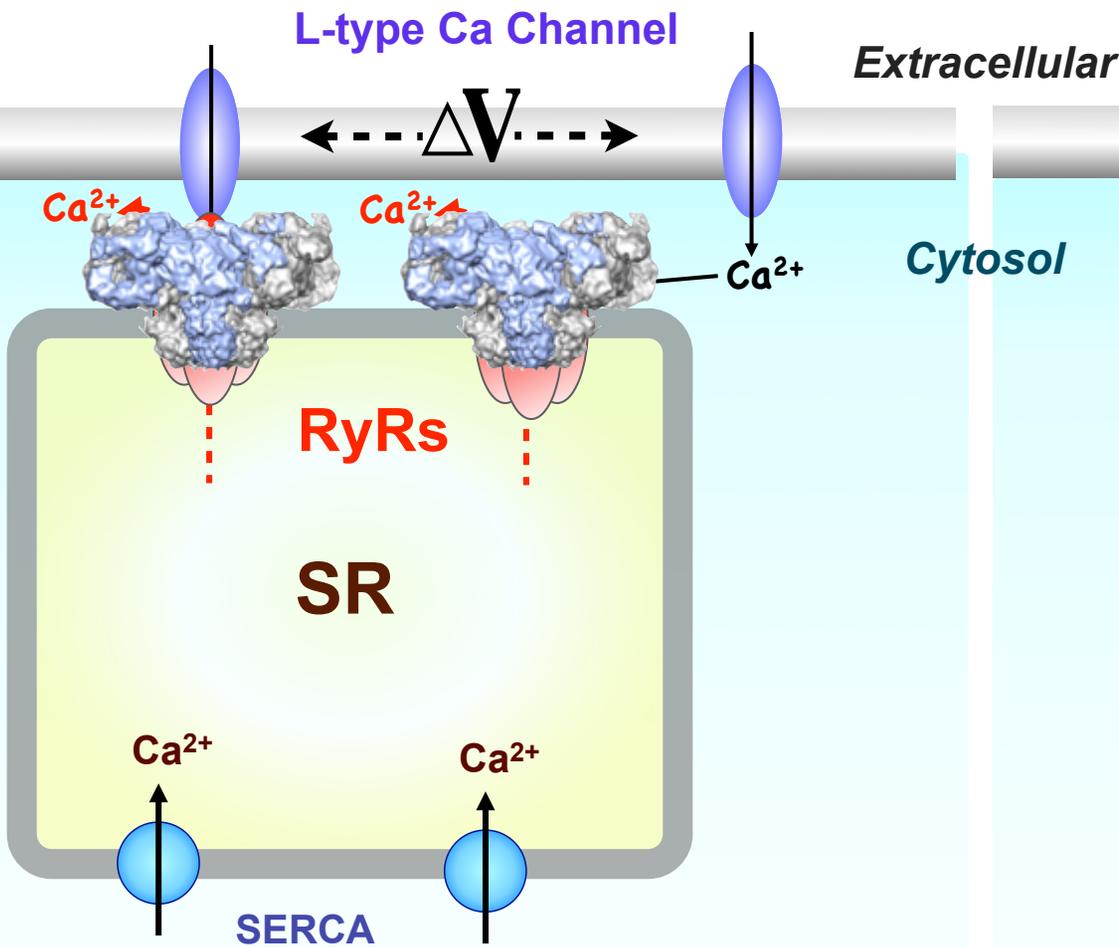
Chiu Lab

Matthew Baker

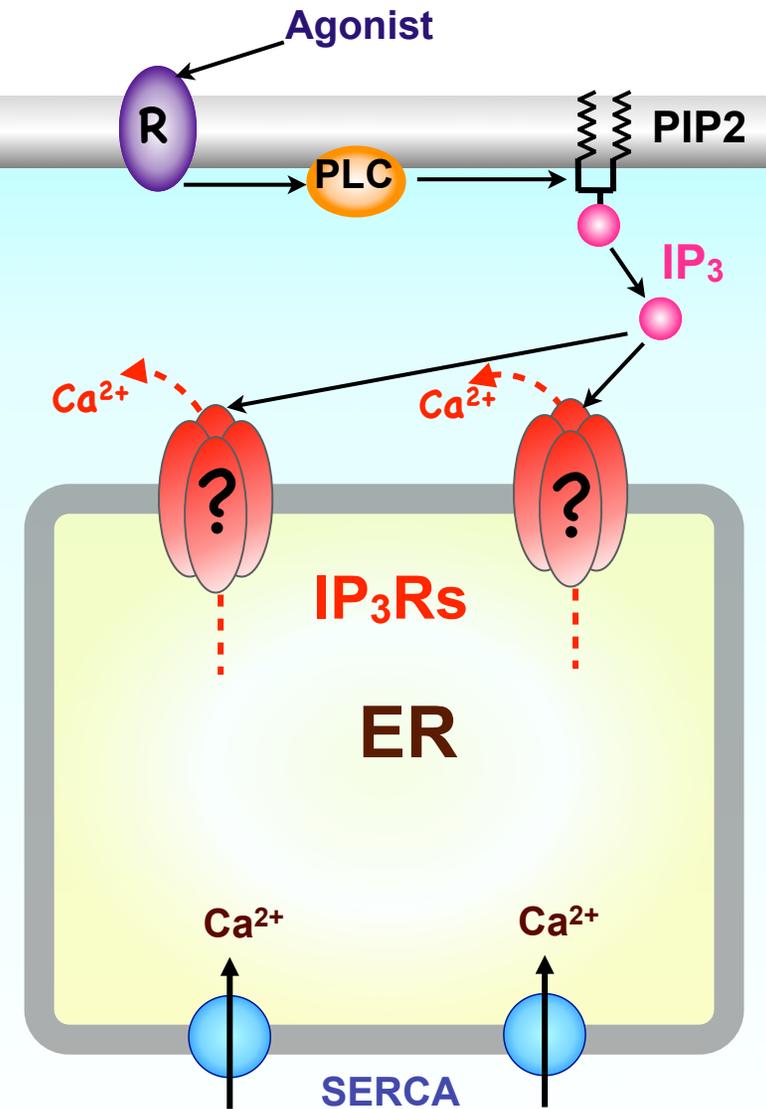


Two Families of Ca^{2+} Release Channels

Ryanodine Receptors/RyRs

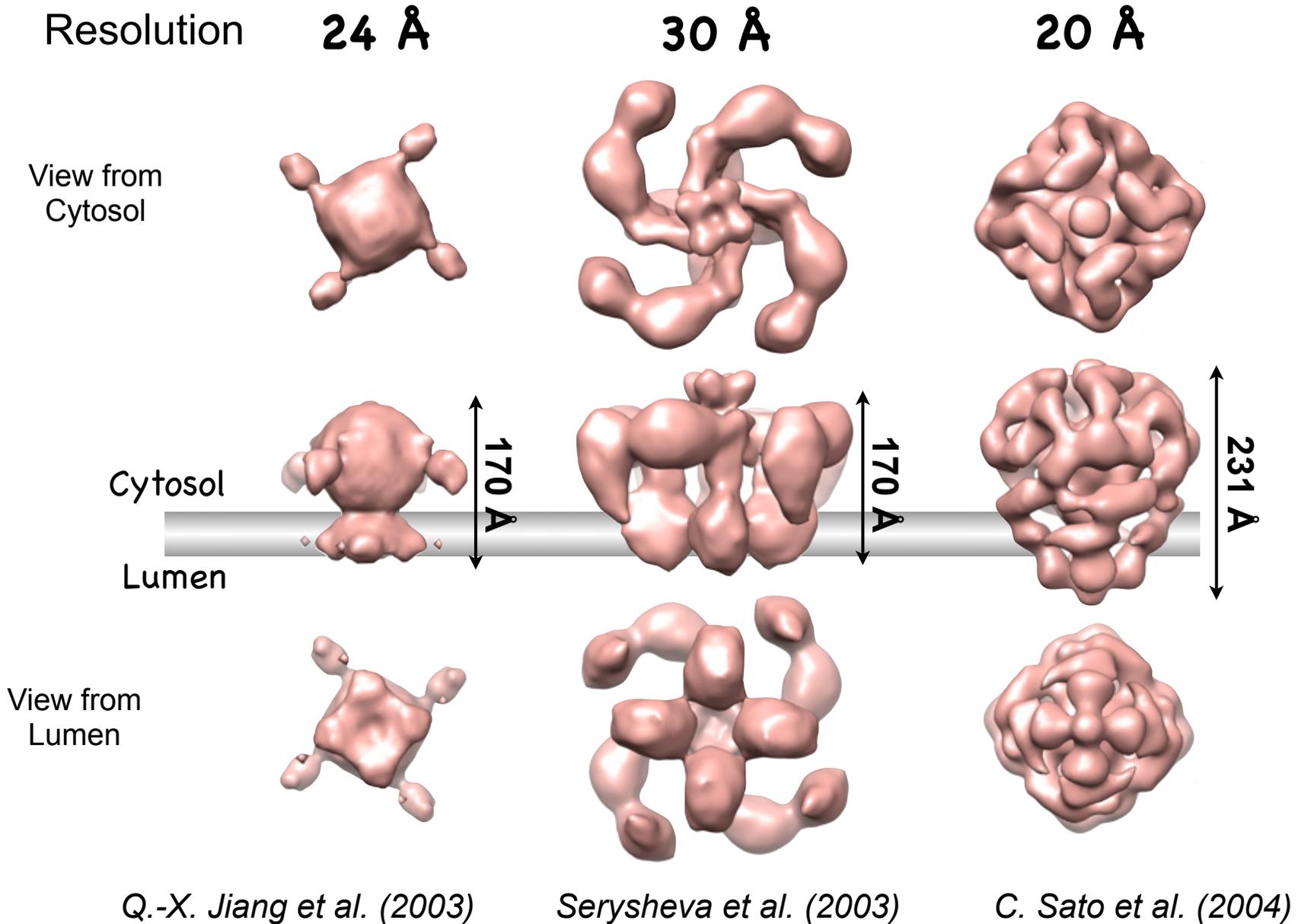


Inositol 1,4,5-Trisphosphate Receptors/IP₃Rs

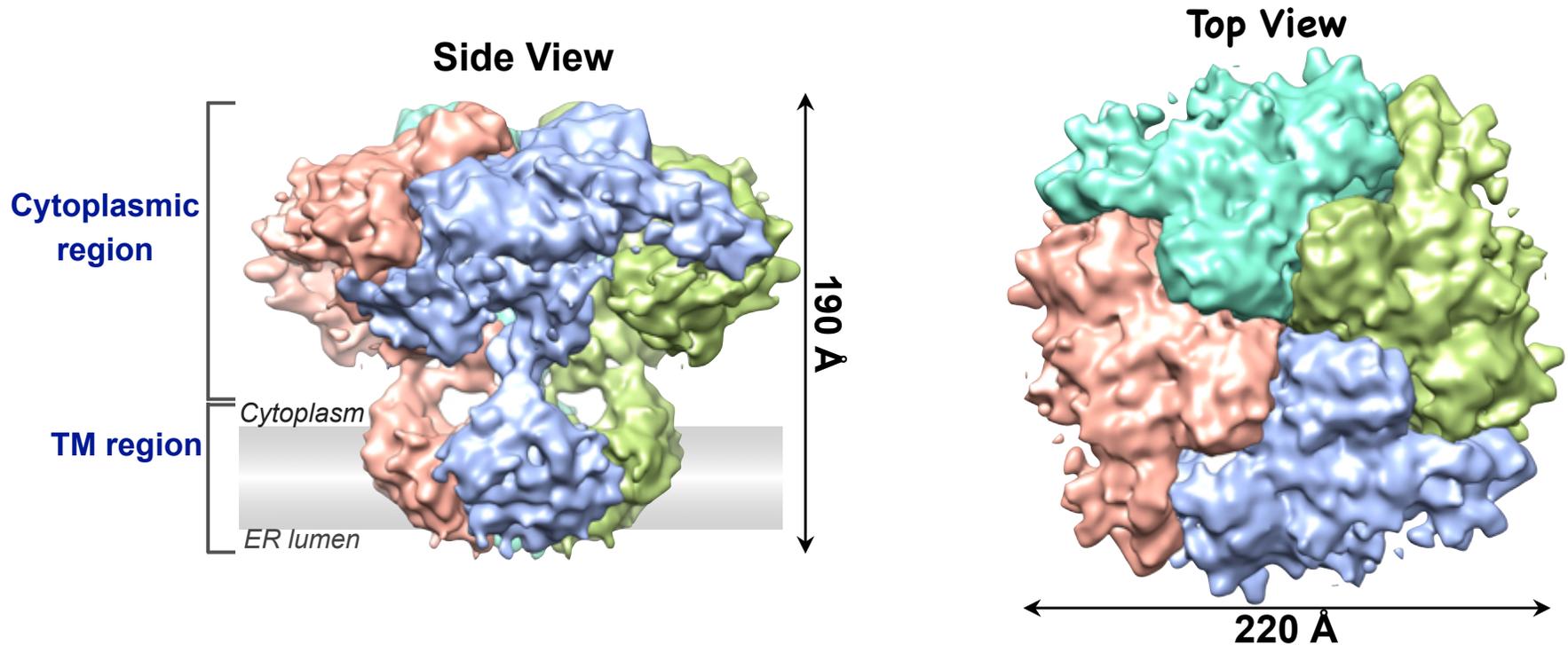


Slide Courtesy of Irina Serysheva

Cryo-EM Maps of IP₃R



The New Closed State IP₃R Map



Ludtke, Tran, Ngo, Moiseenkova-Bell, Chiu, and Serysheva. (2011). Structure. 19:1192-99.

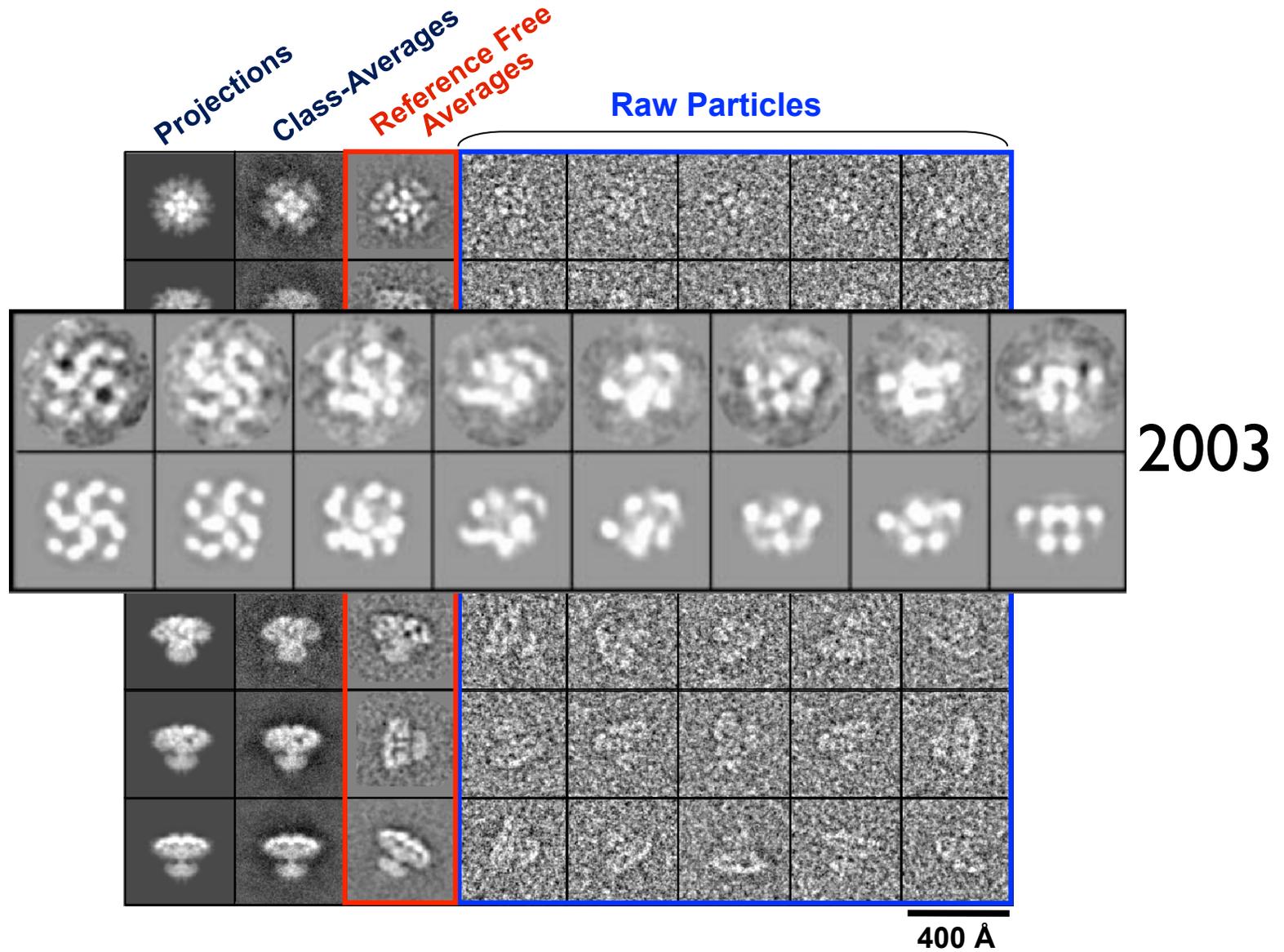
2003

Current Data (2011)
Functional Assay Performed

400 Å

Ludtke, Tran, Ngo, Moiseenkova-Bell, Chiu, and Serysheva. (2011). Structure. 19:1192-99.

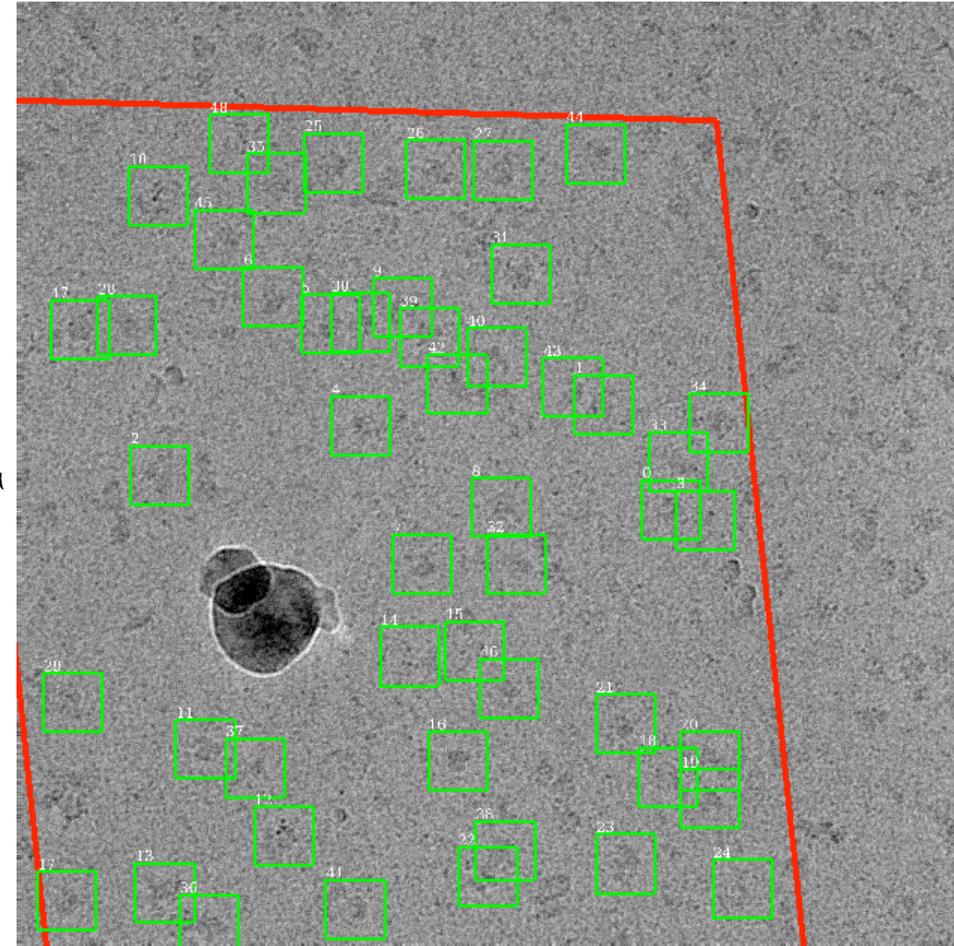
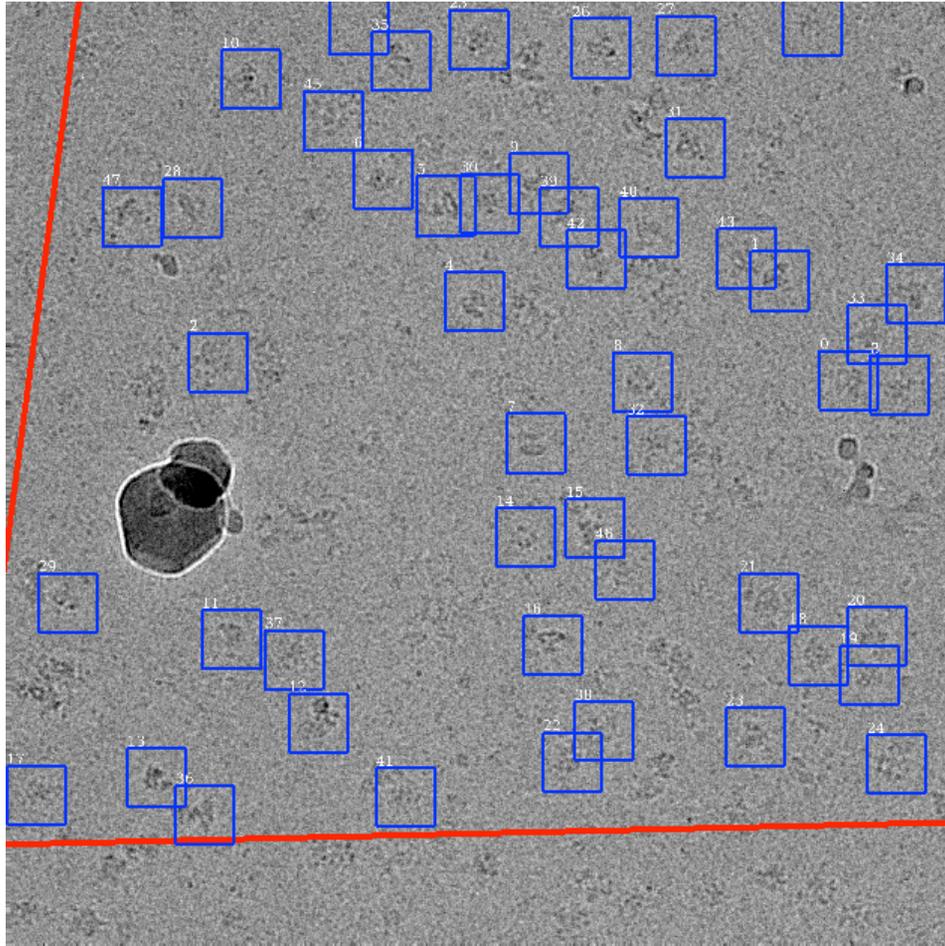
Self-consistency



Validation

1. Random Conical Tilt
2. Tilt Validation
3. Different Software Packages
4. "Gold Standard" Resolution

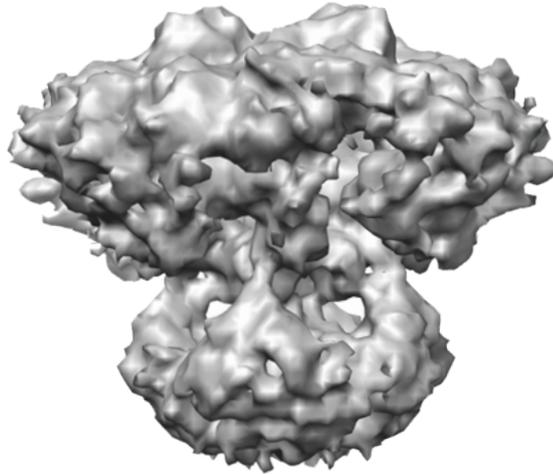
Method I: Random-Conical Tilt



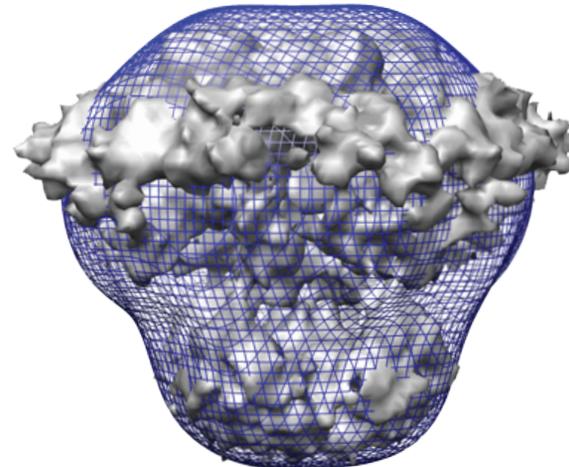
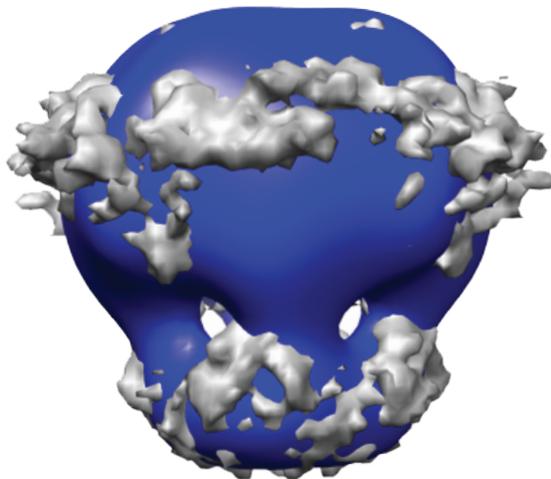
Radermacher, M., et.al. (1987). J Microsc.

Random-Conical Tilt

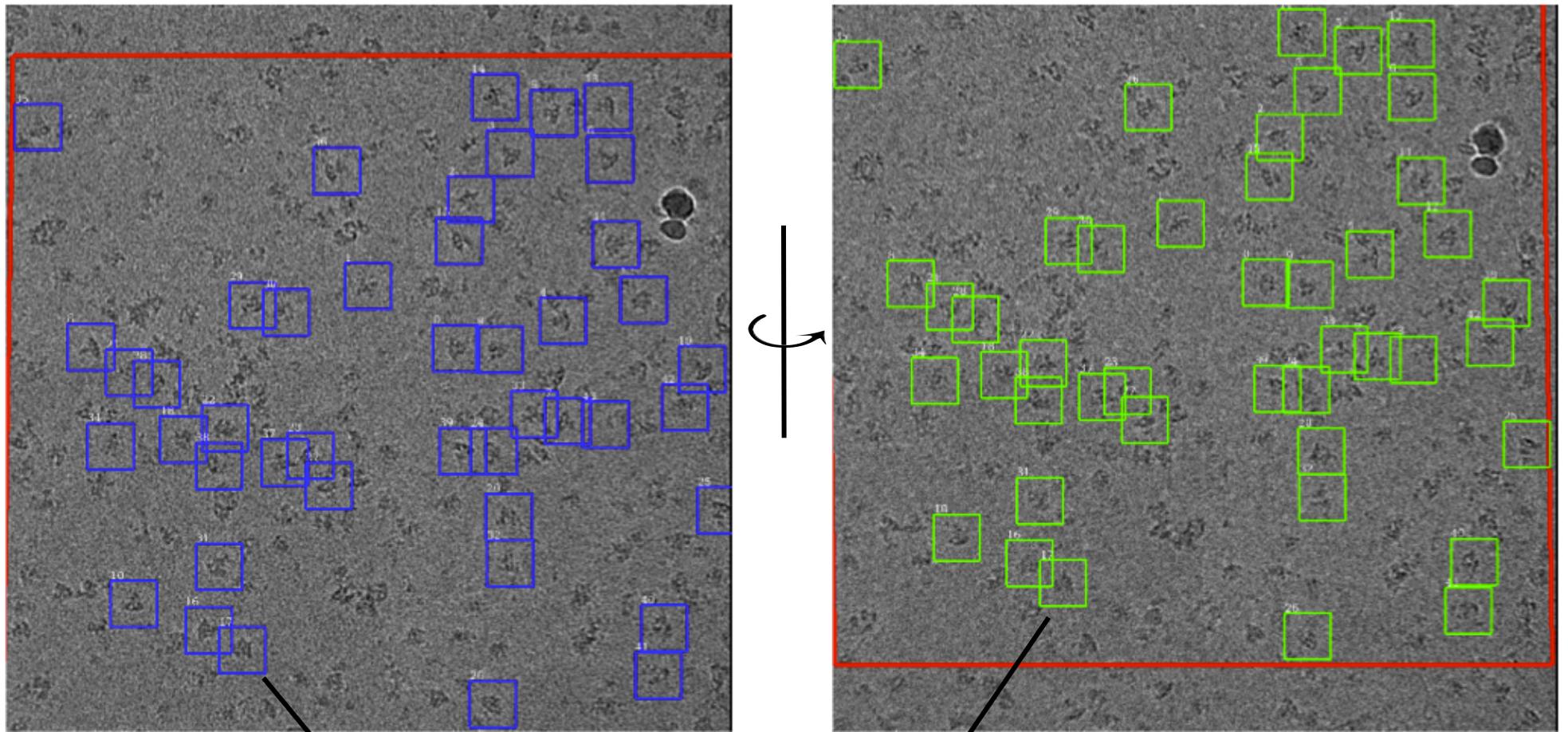
RCT Reconstruction



50° tilt



Tilt Validation

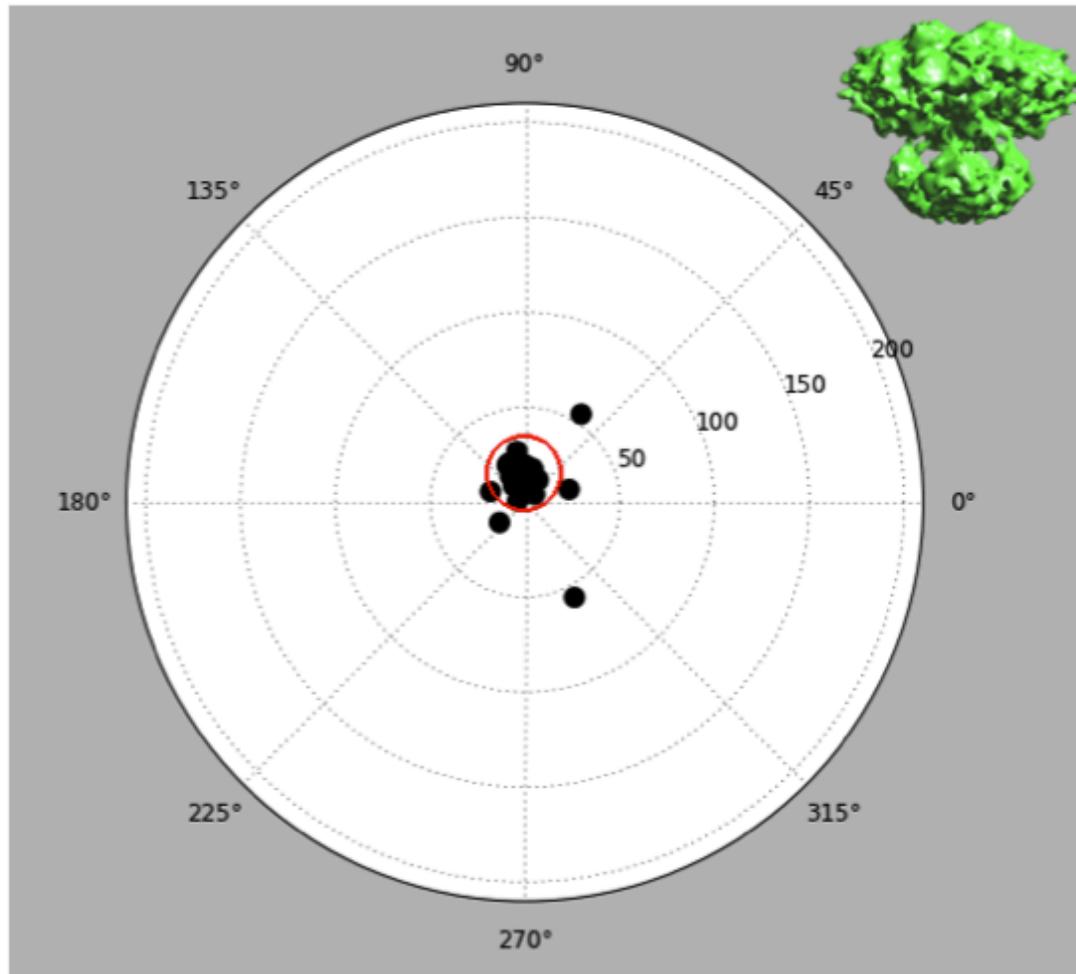


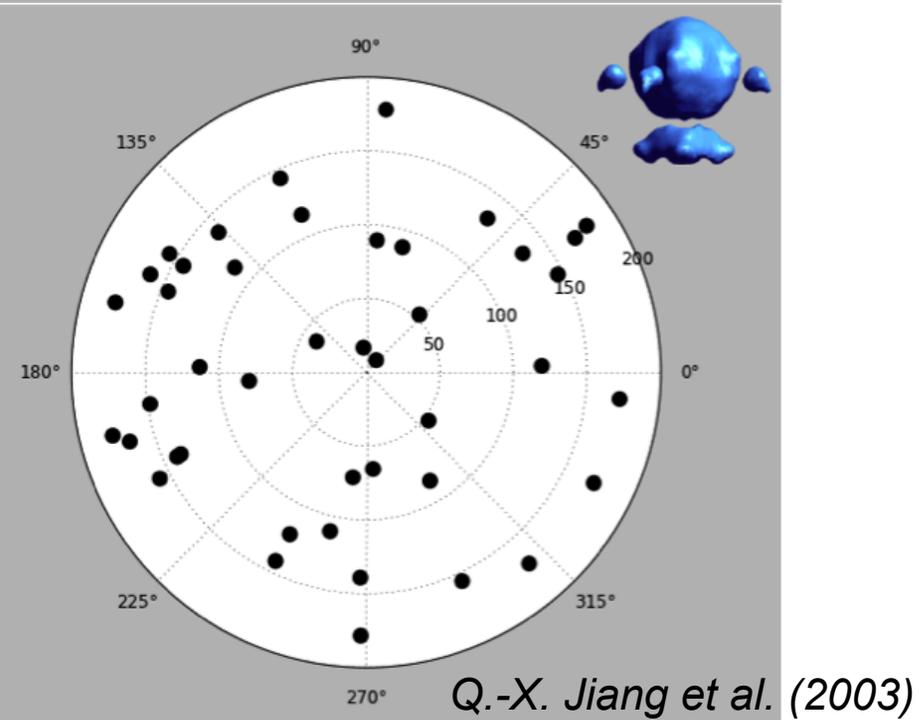
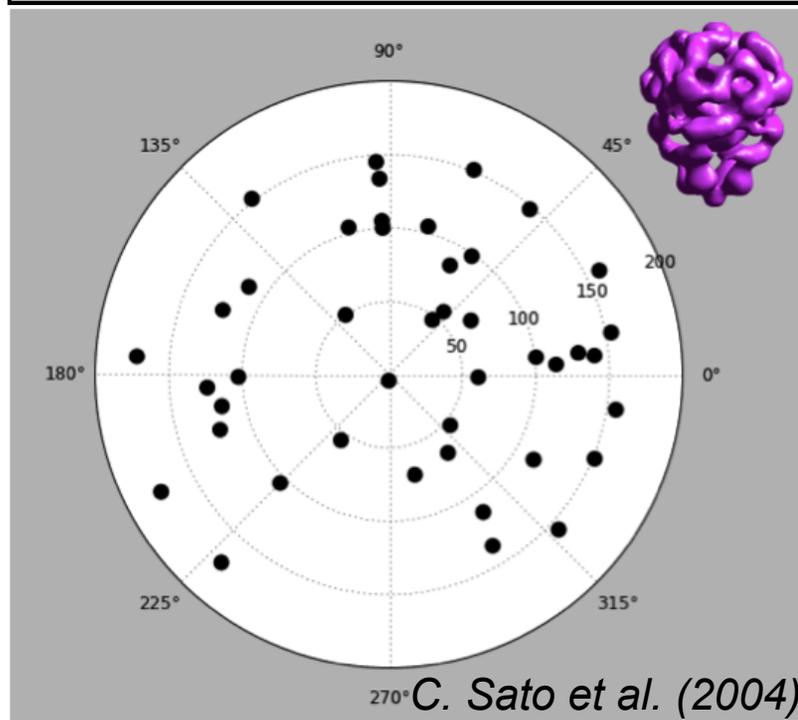
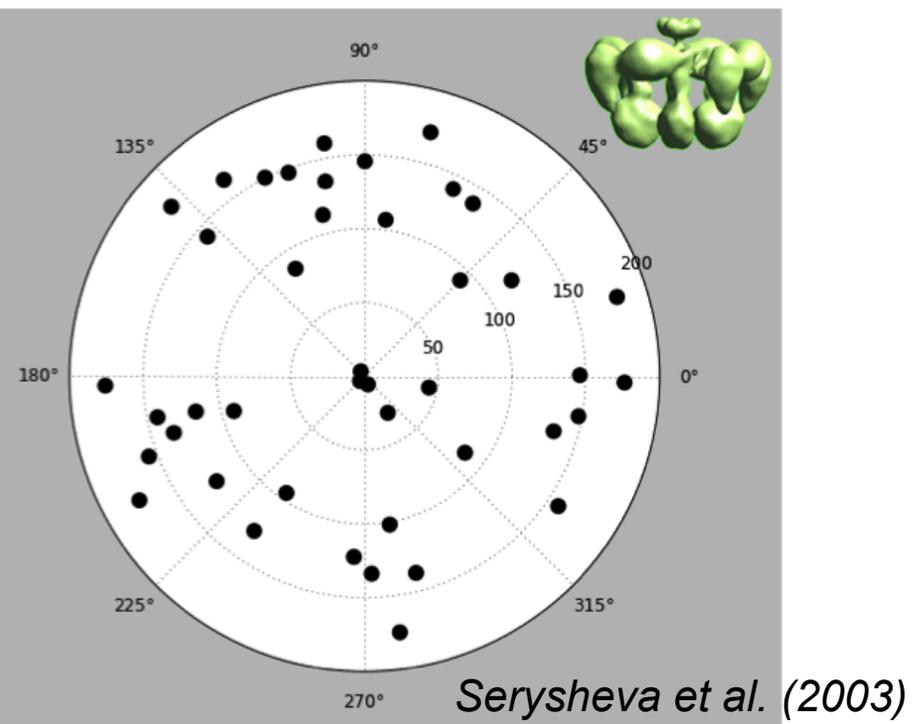
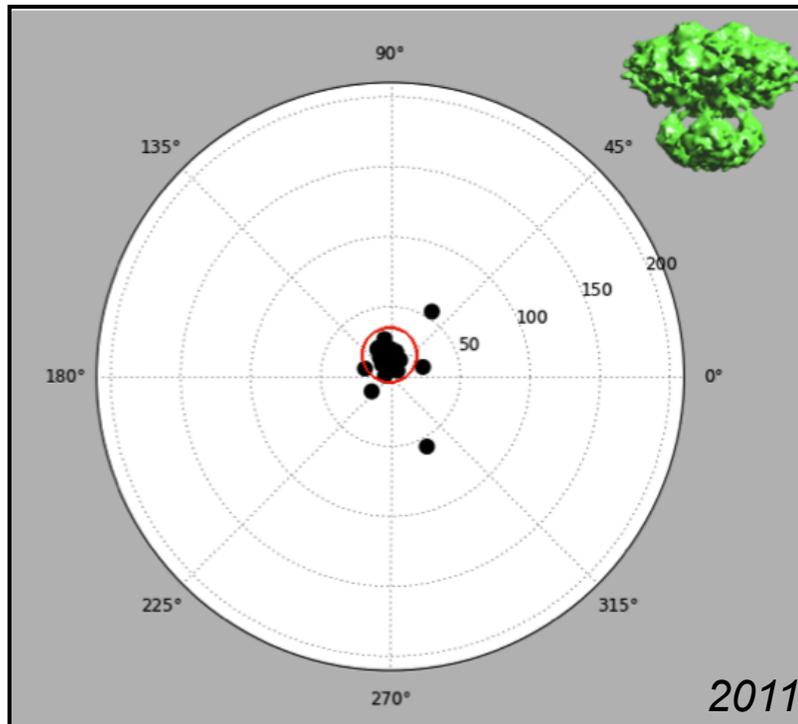
Find Orientation

Find Orientation

Compare to Known Tilt

Method described in Rosenthal and Henderson, 2003 (JMB)

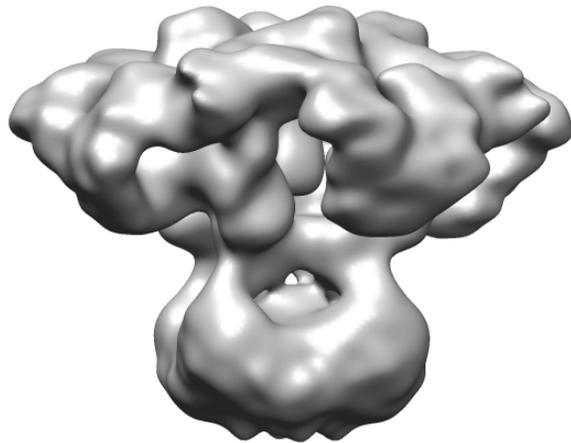




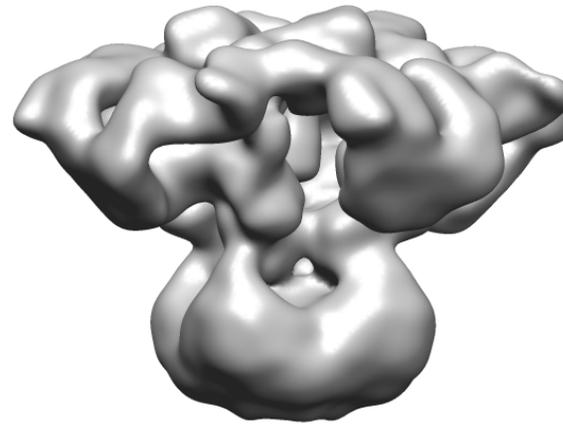
Tilt Validation

- Confirms quaternary structure
- Rough assessment of particle orientation uncertainty
- Could be used as a tool for eliminating bad particles

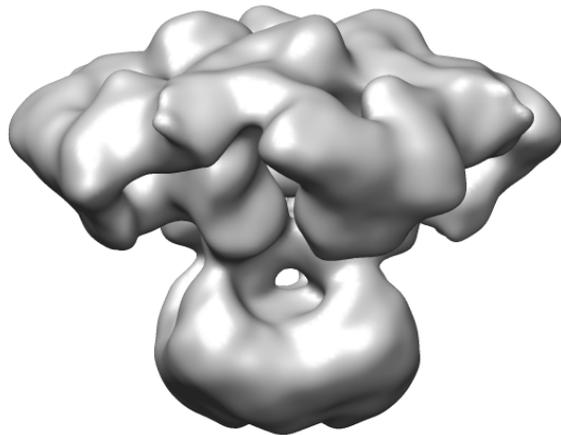
EMAN2



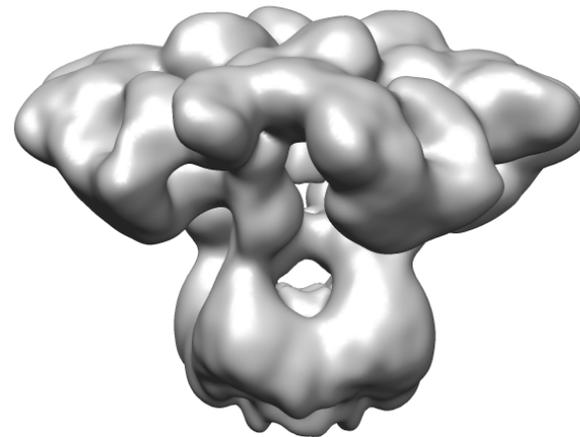
RELION

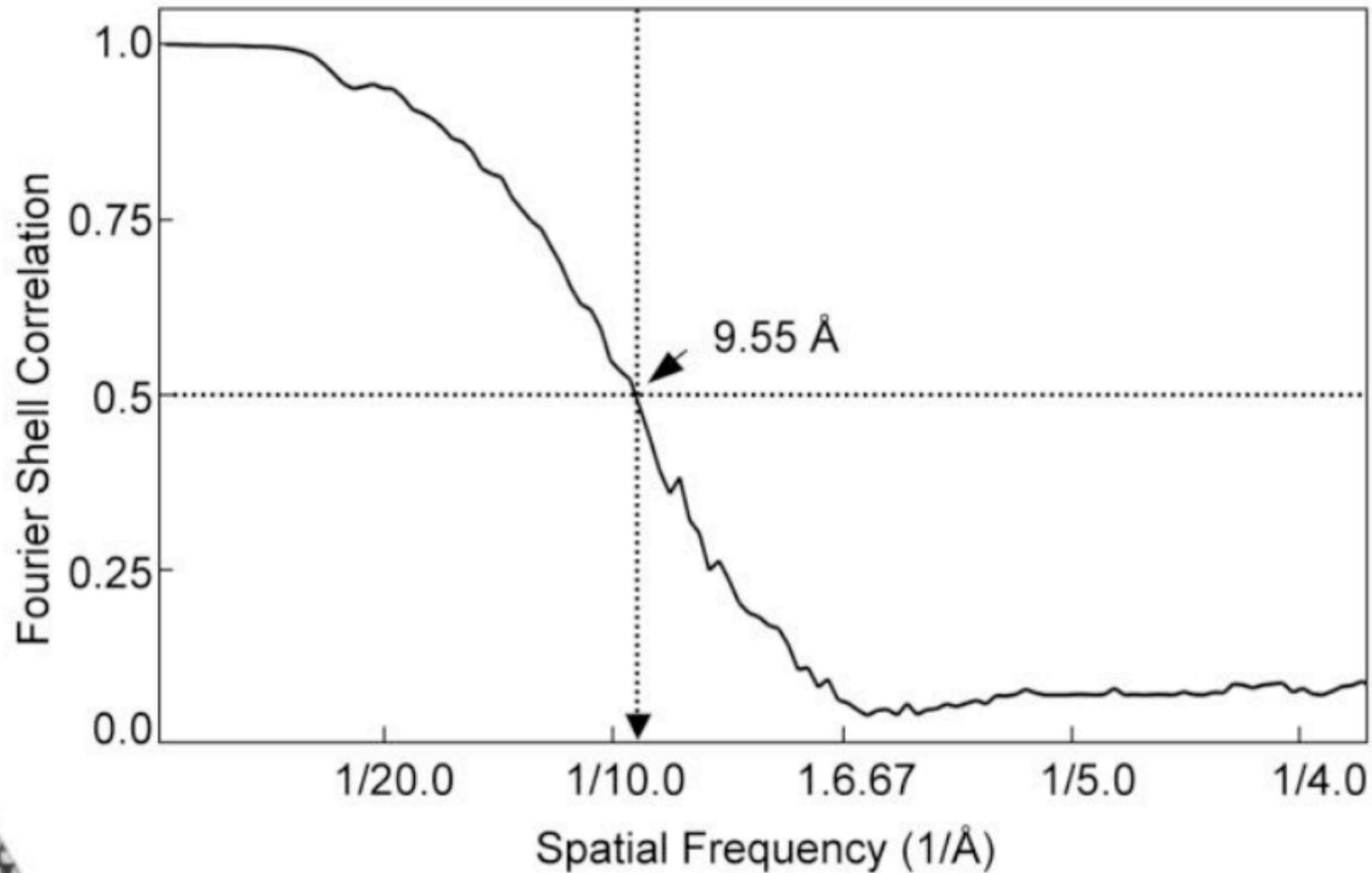


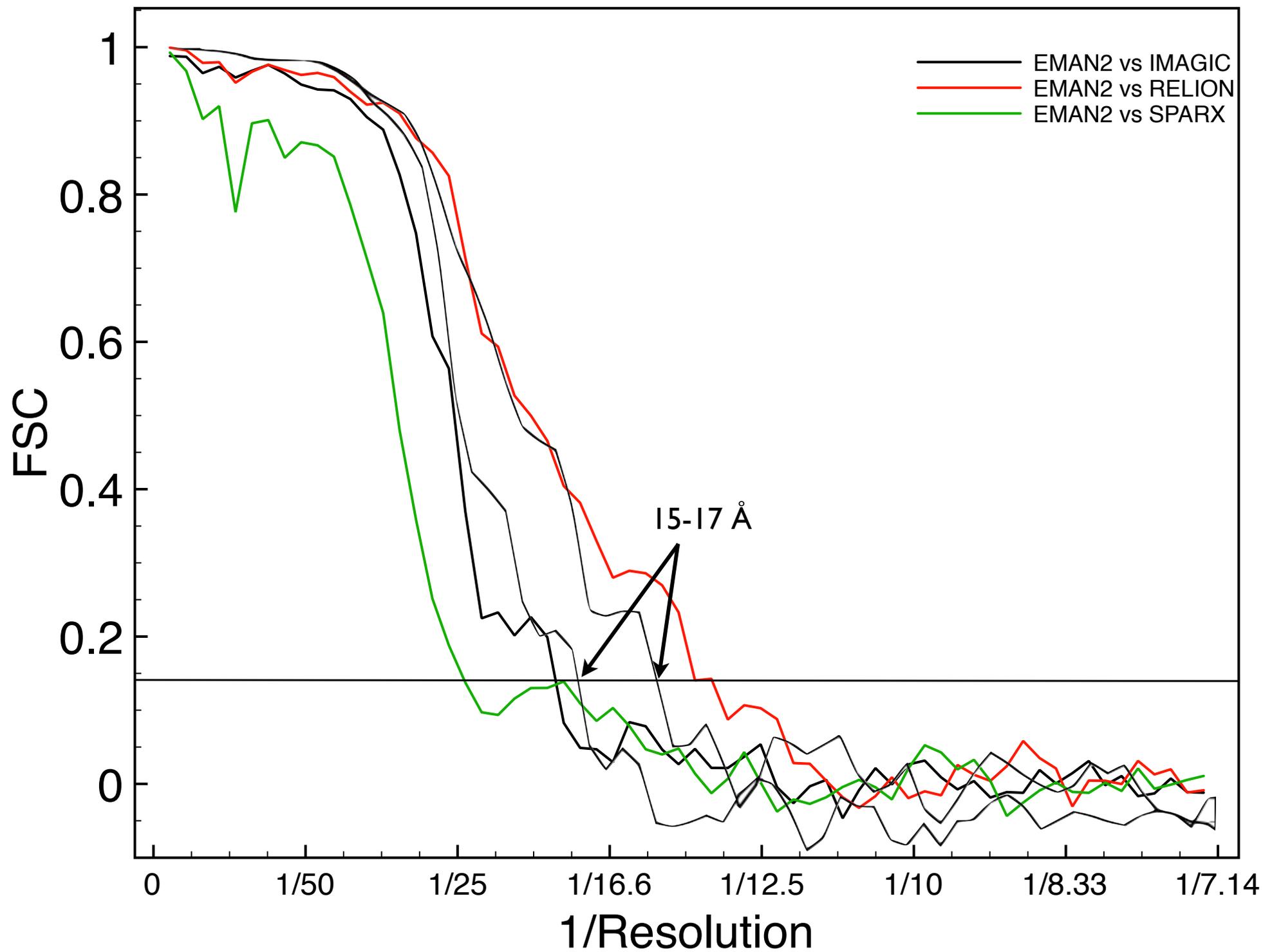
IMAGIC



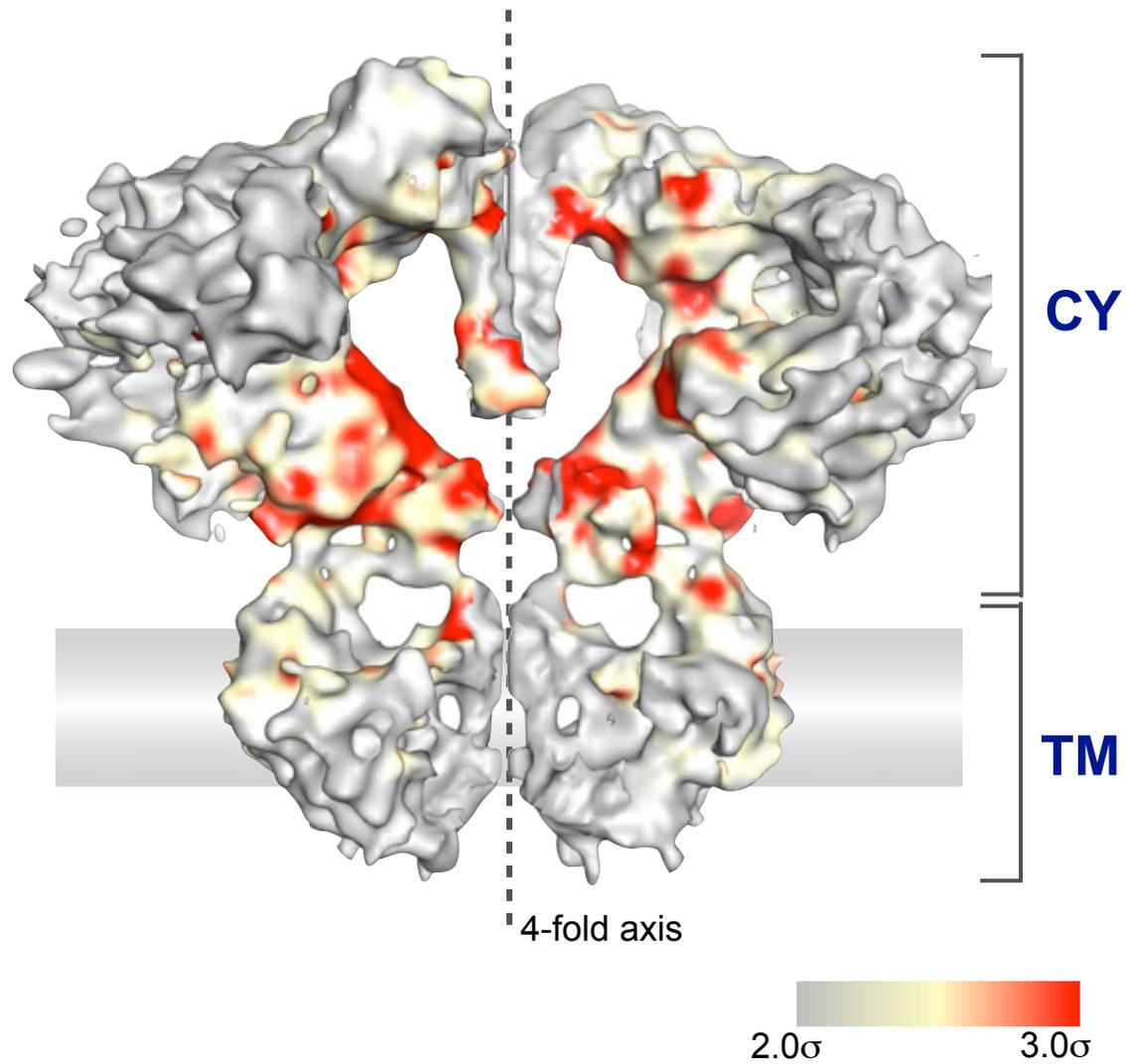
SPARX



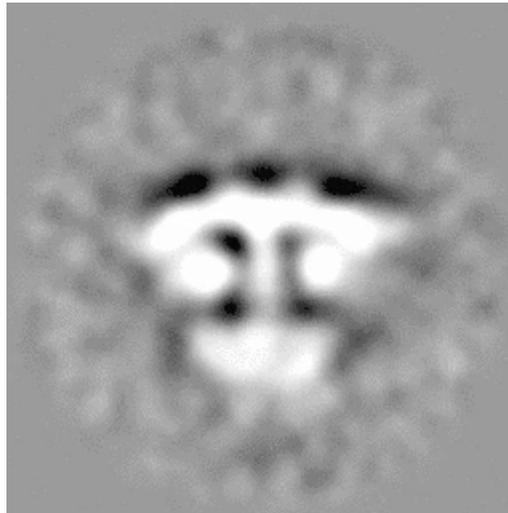
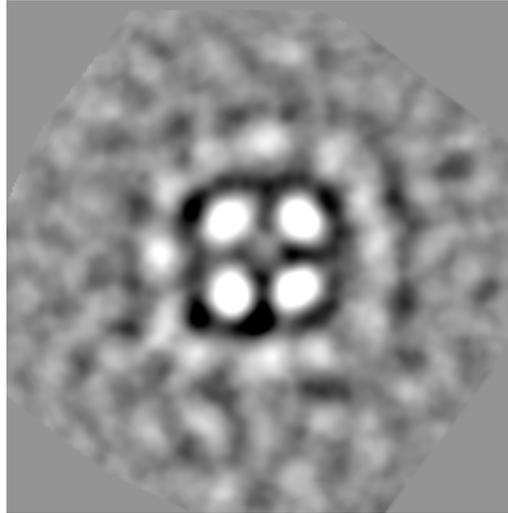




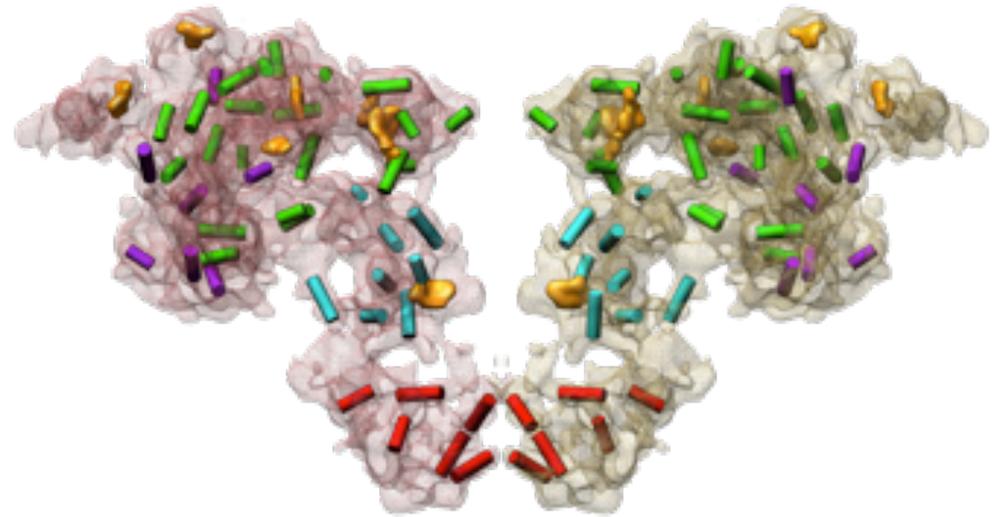
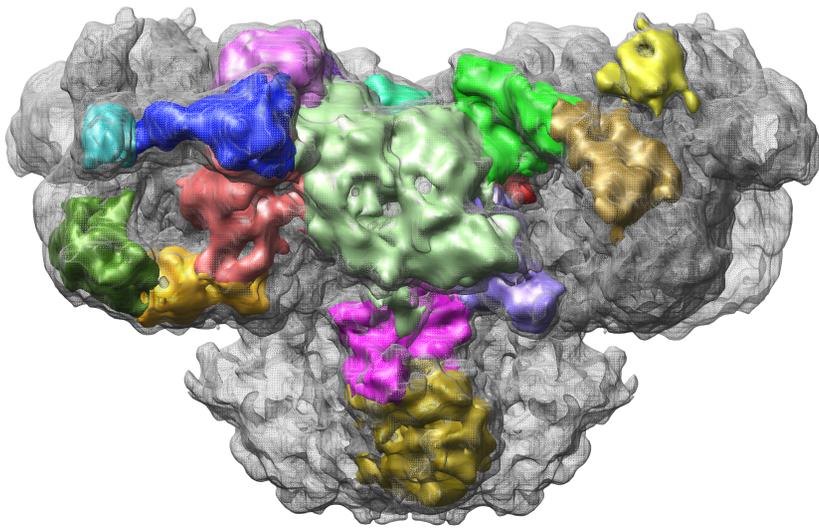
3-D Variance Map



IP₃R



Ca²⁺ Release Channel



Per-Particle SSNR

Image Evaluation

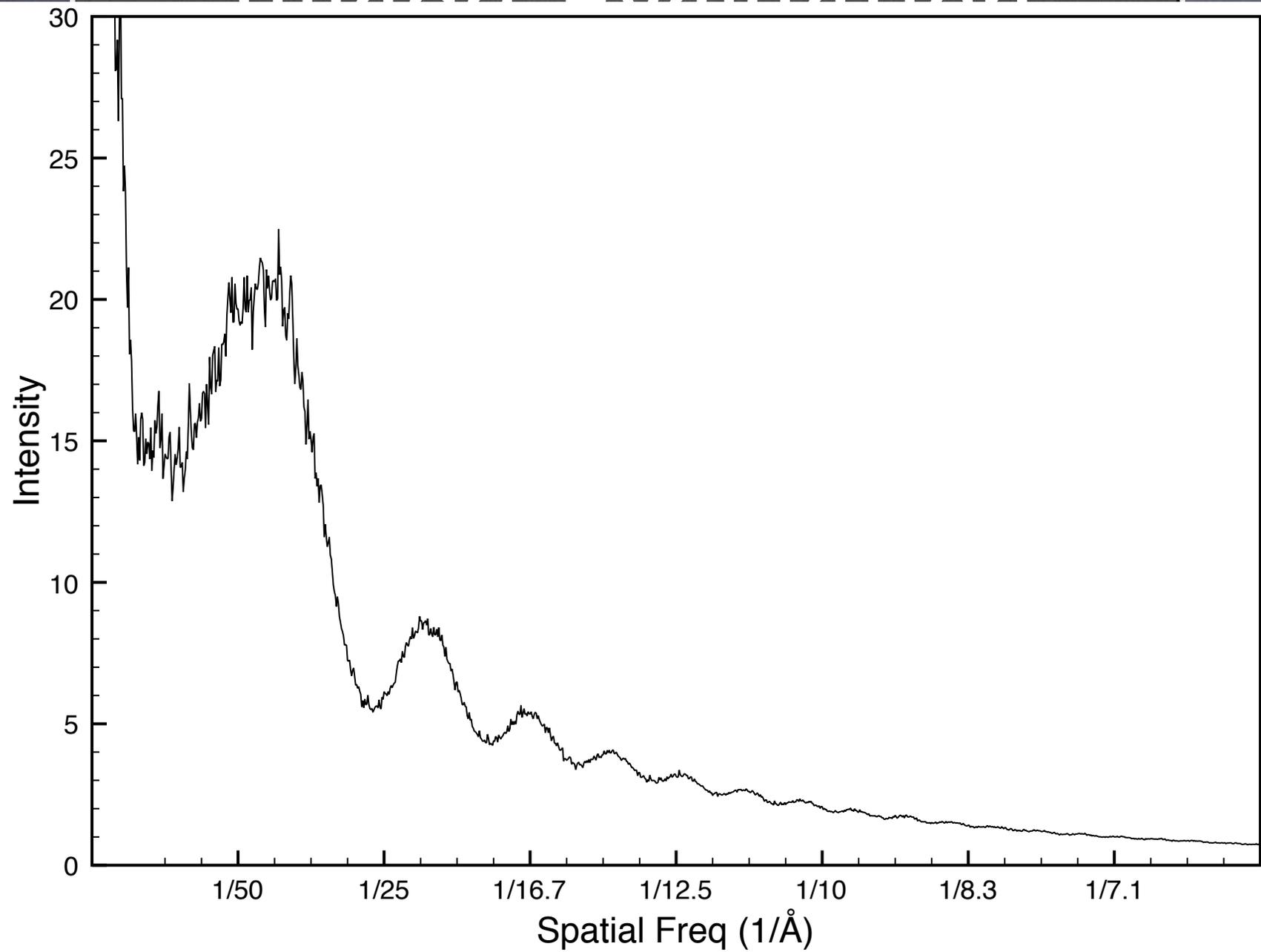
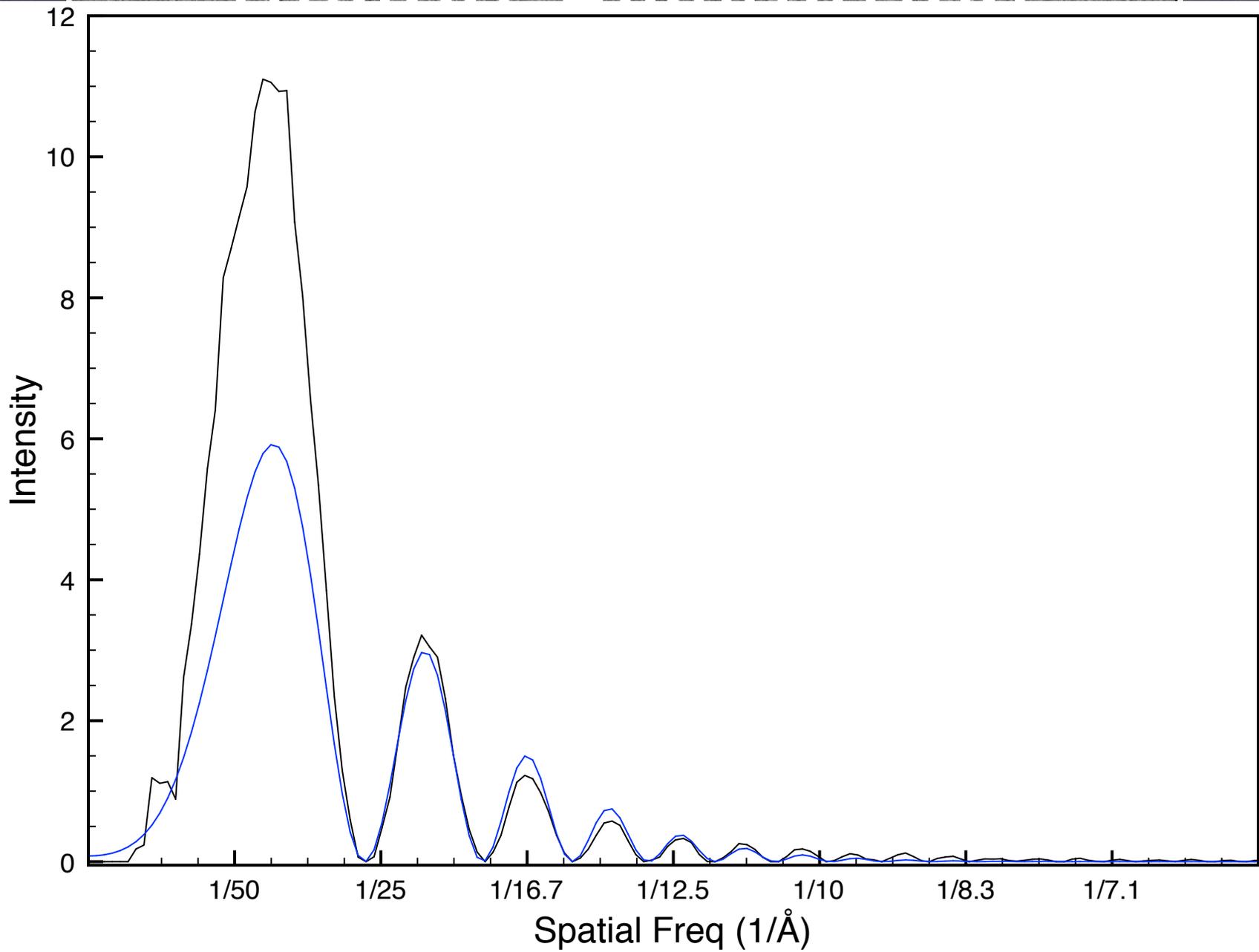
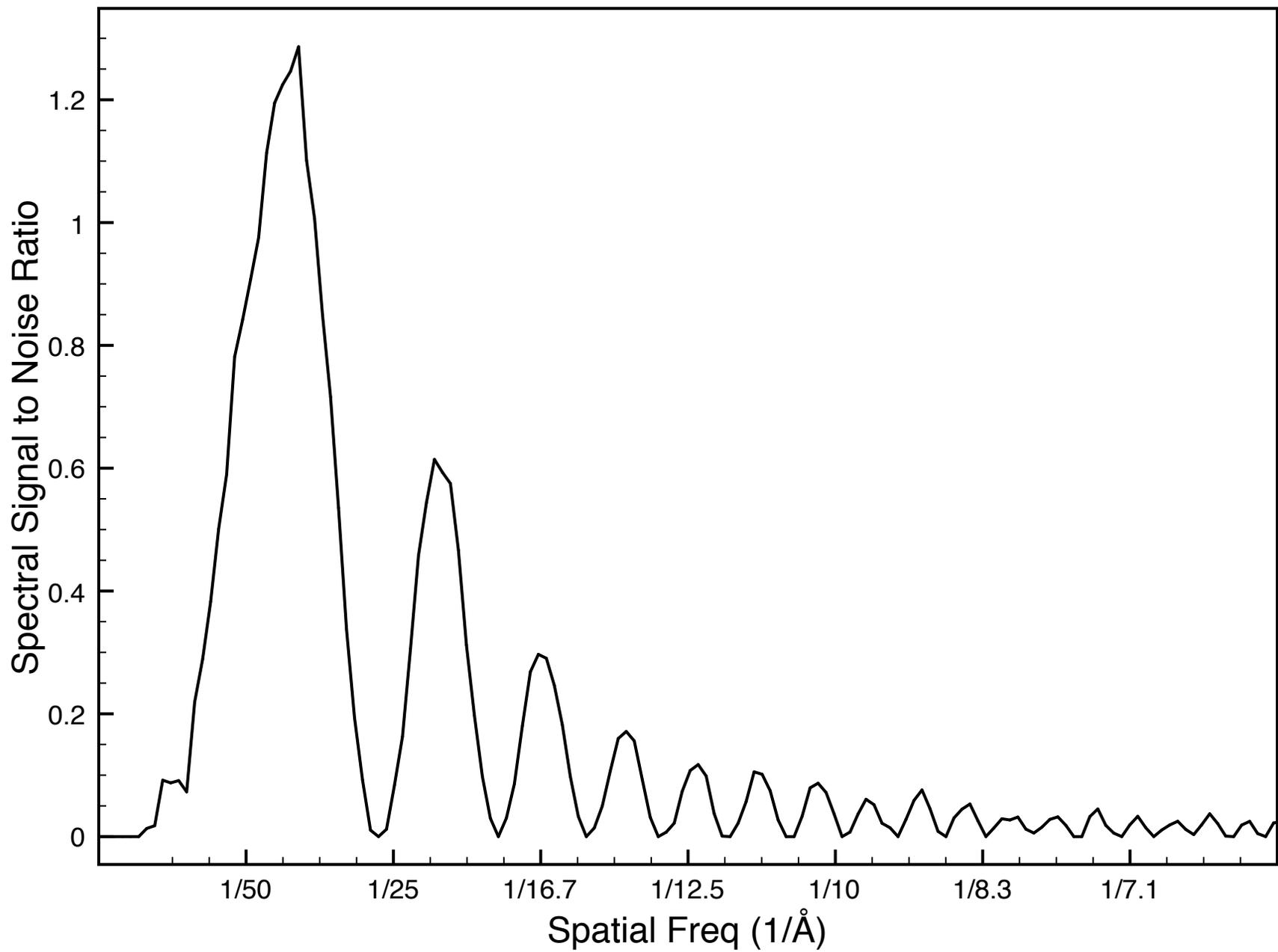
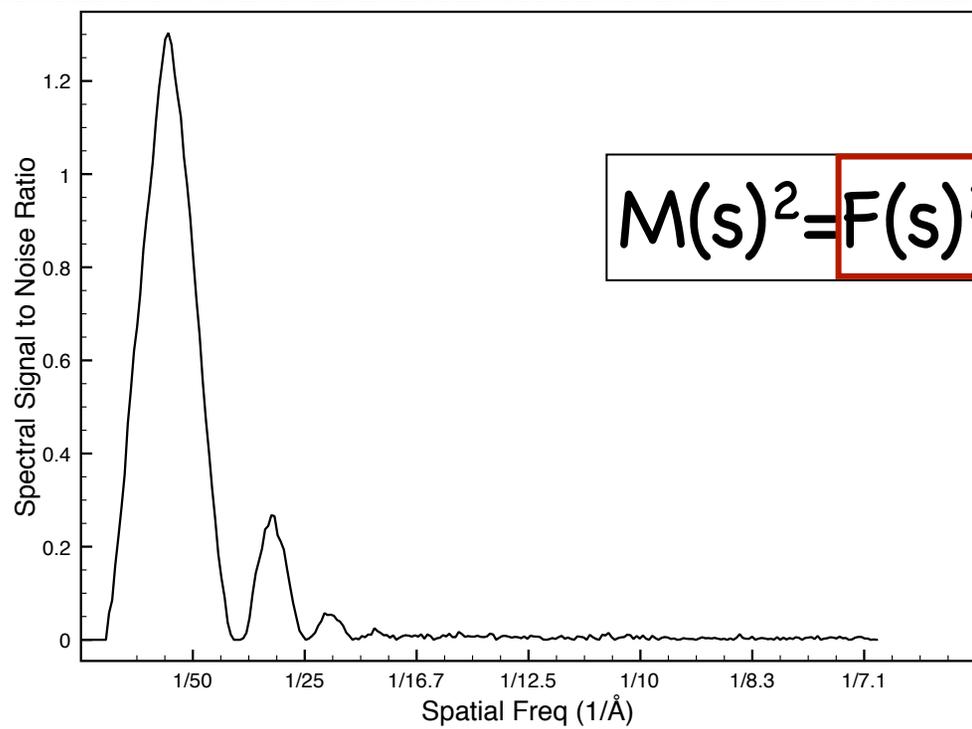
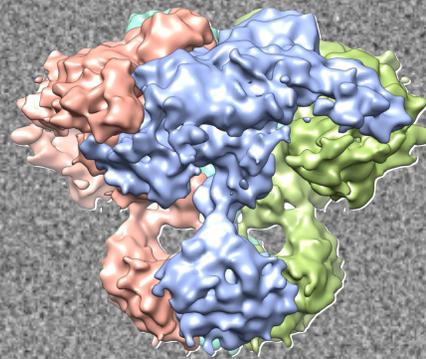
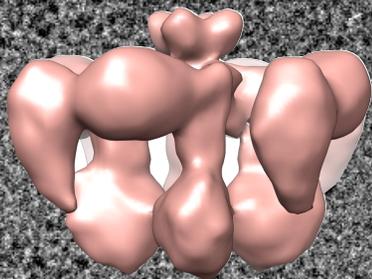


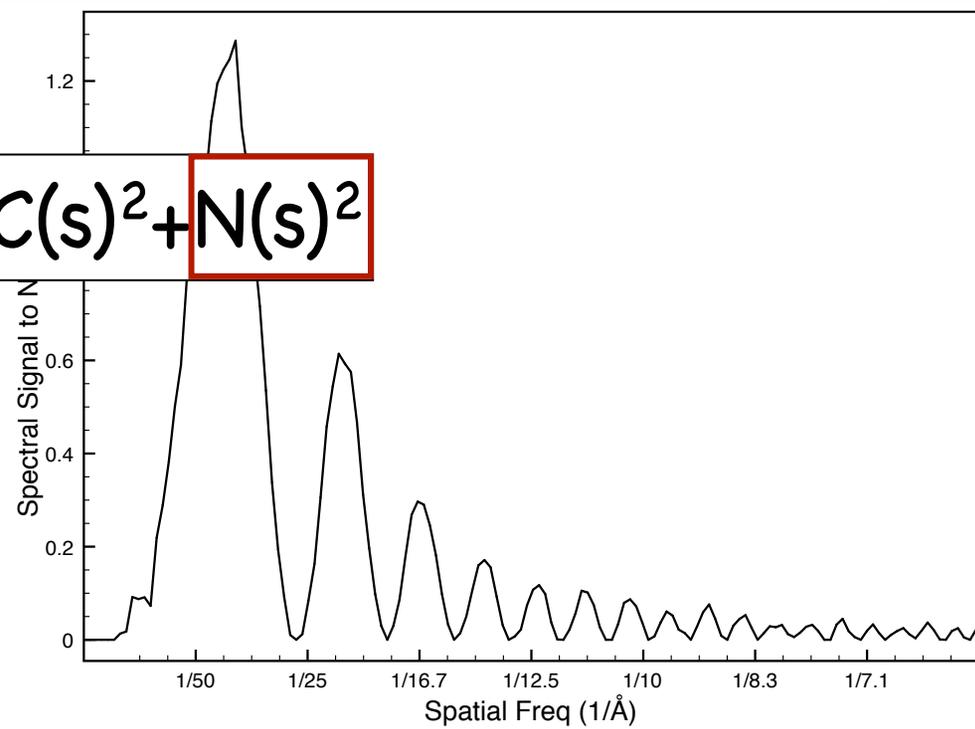
Image Evaluation



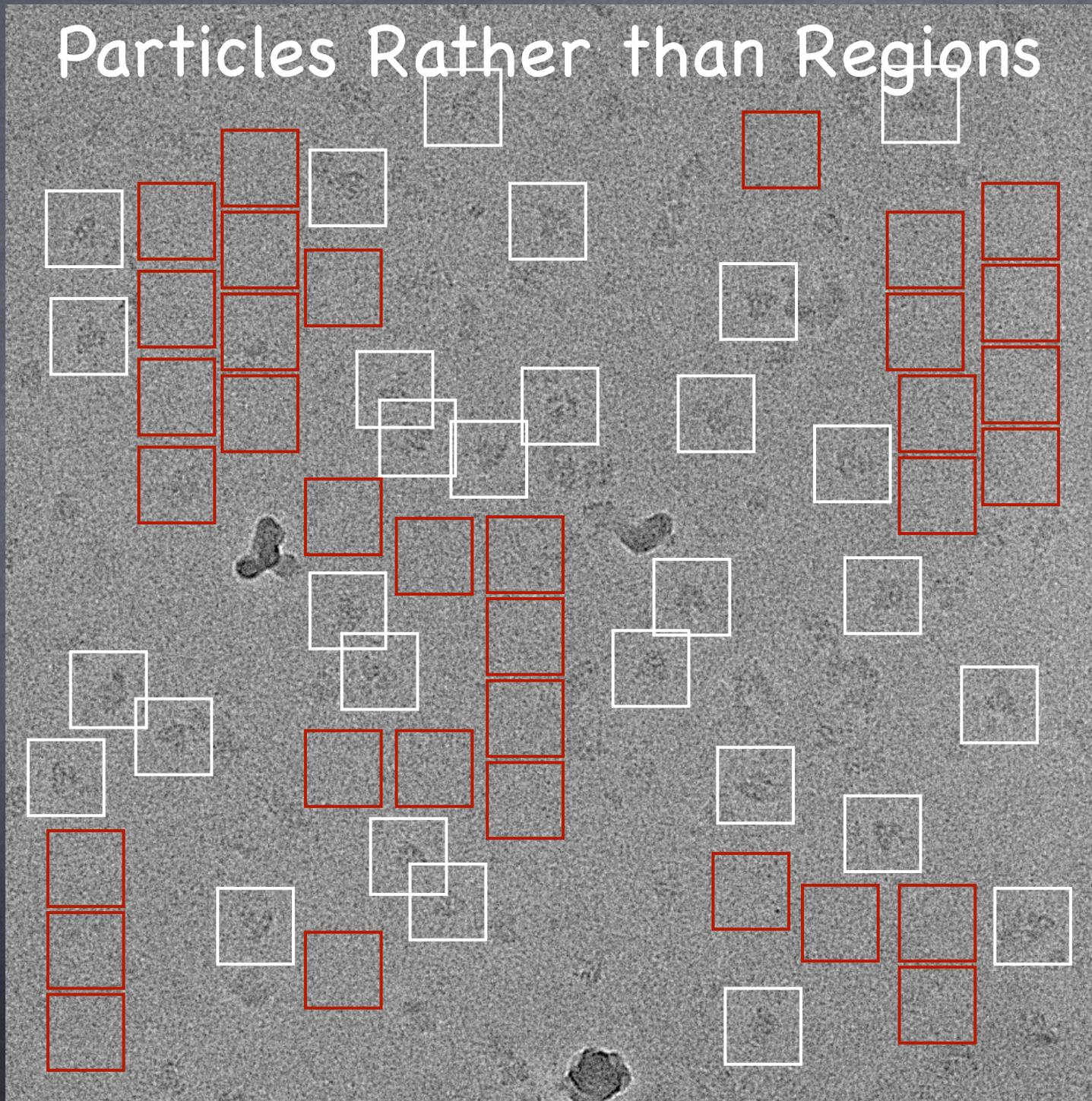




$$M(s)^2 = F(s)^2 C(s)^2 + N(s)^2$$



Particles Rather than Regions



Density Problems

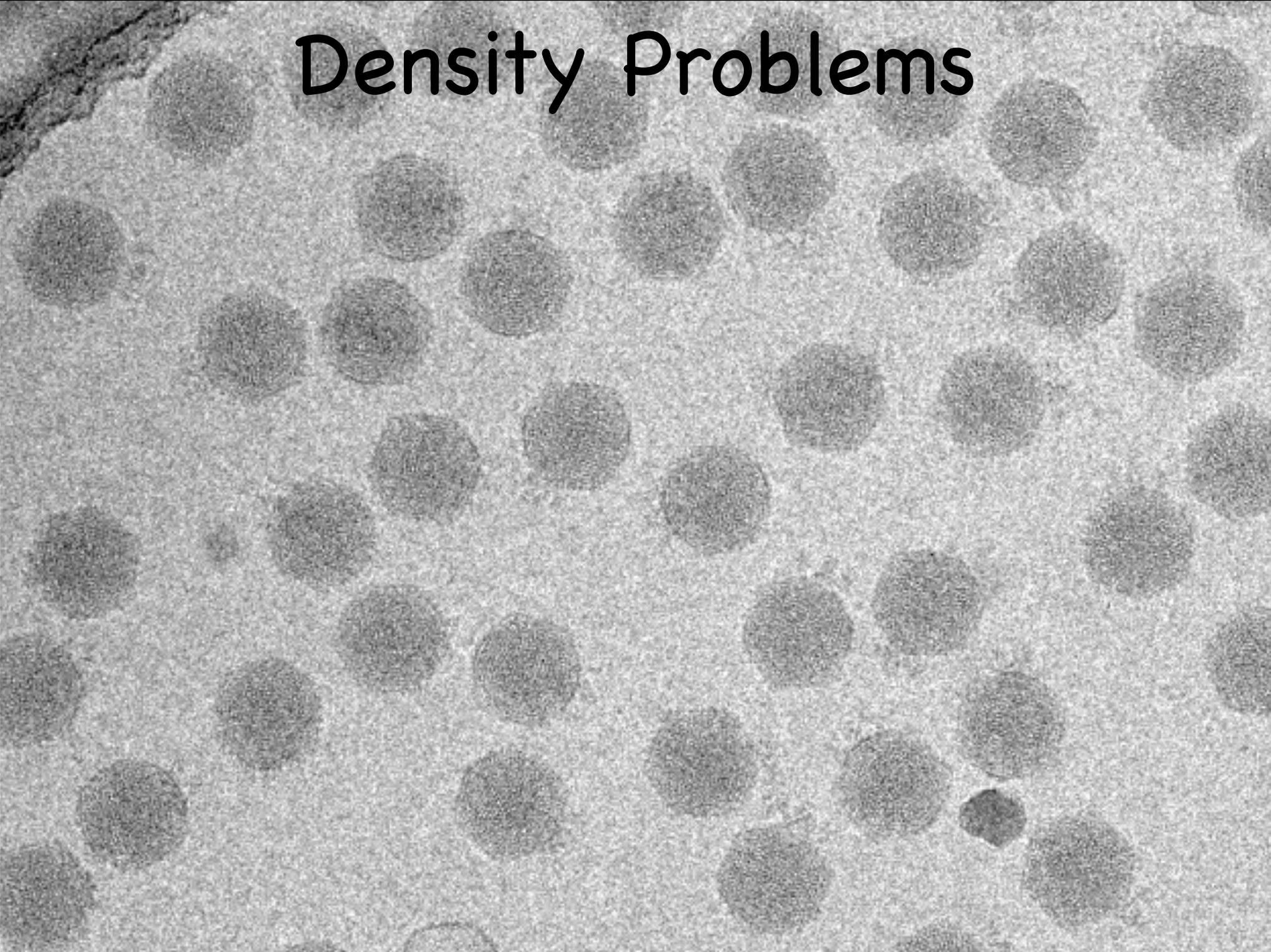
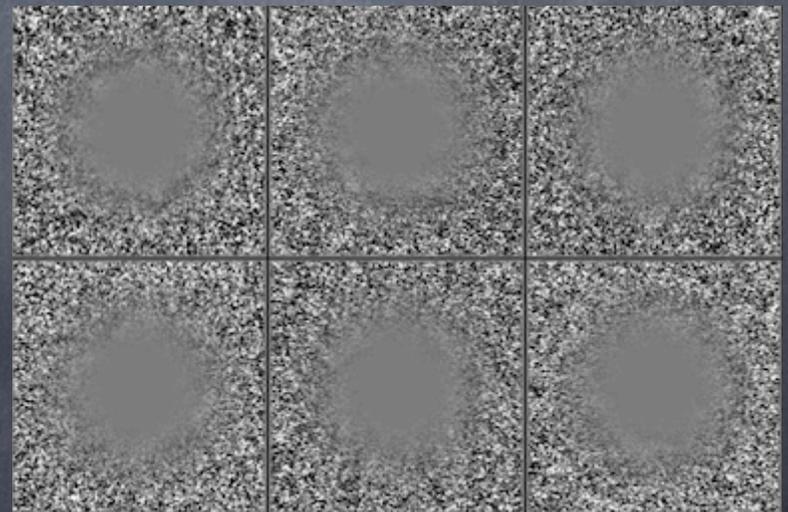
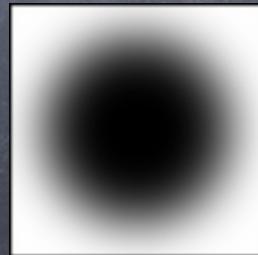
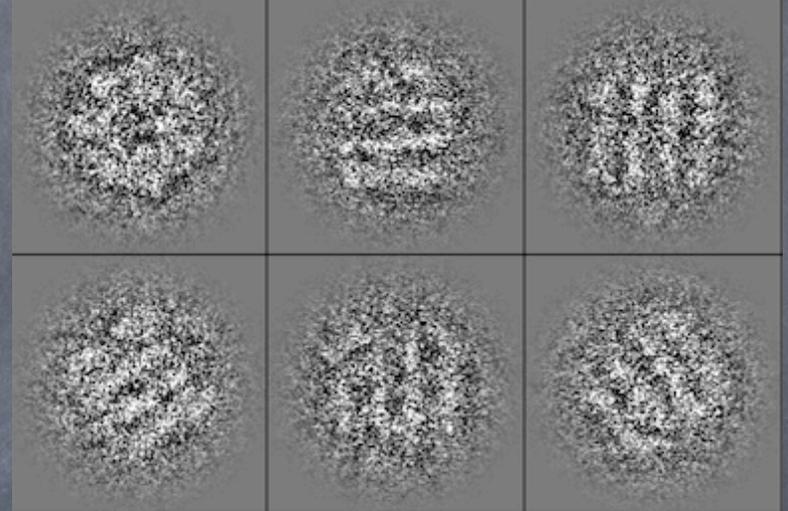
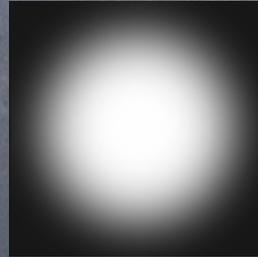
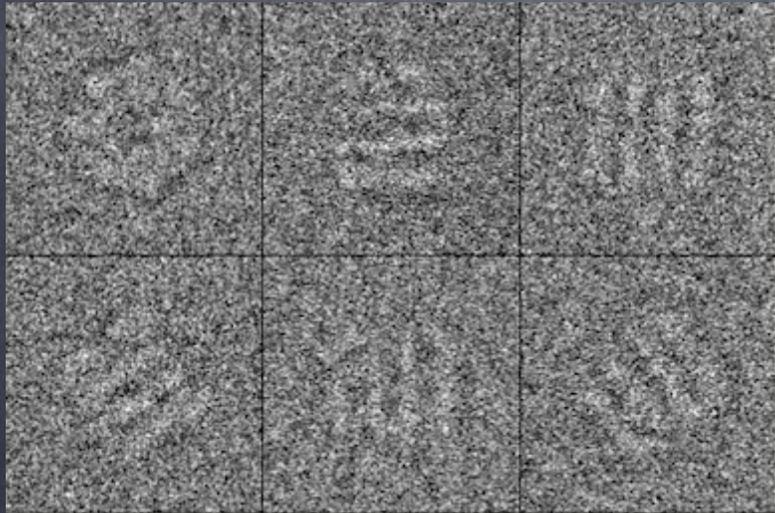
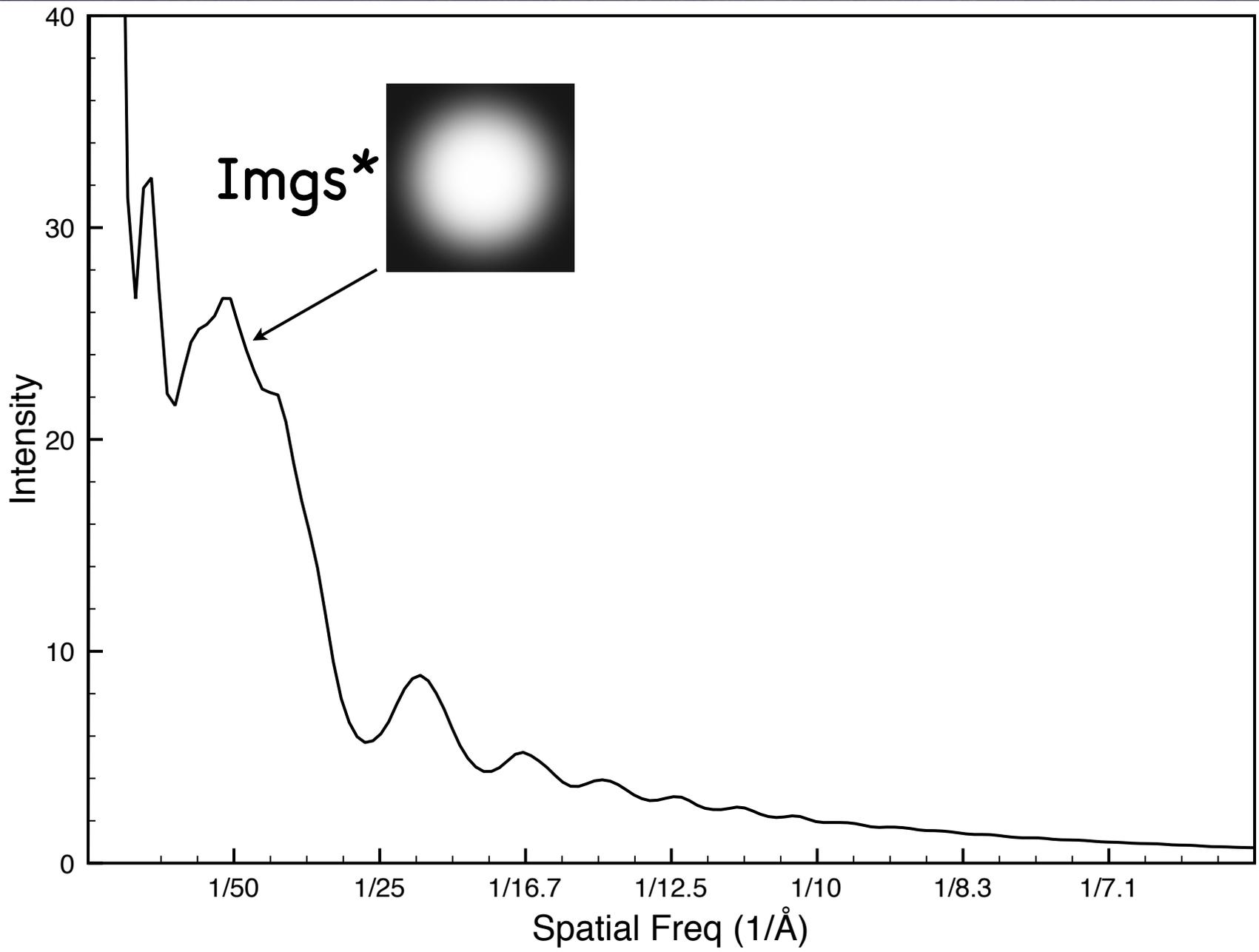
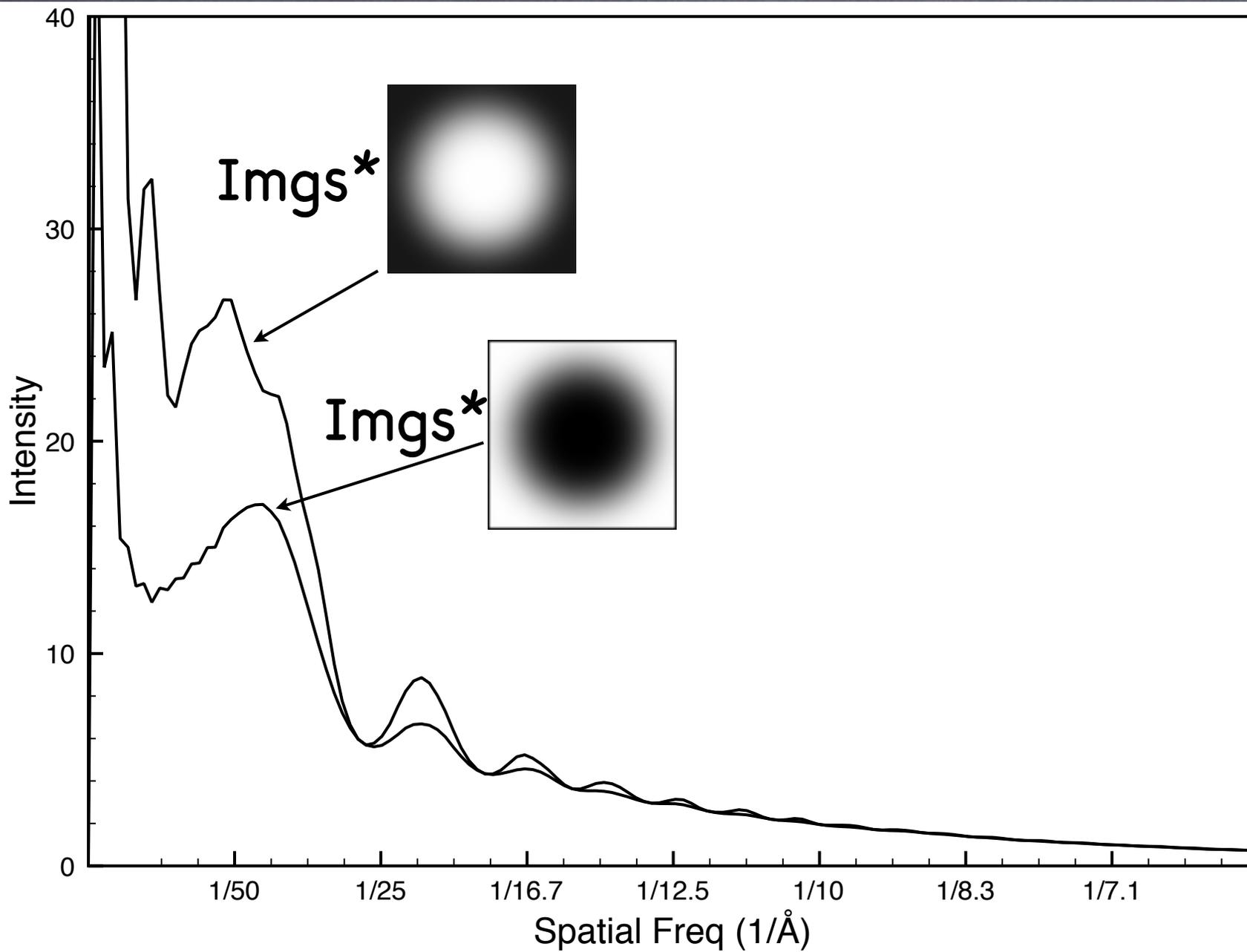
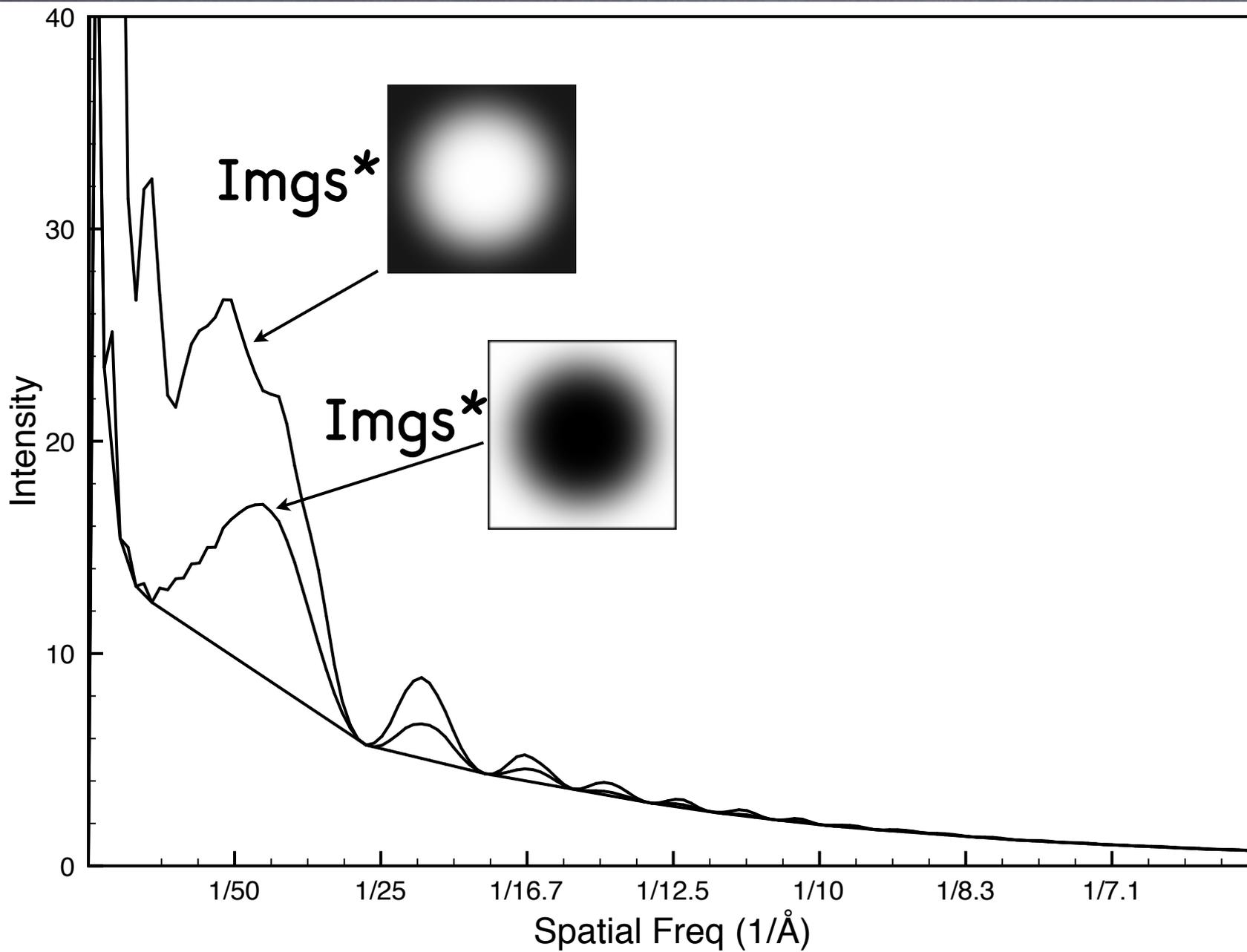


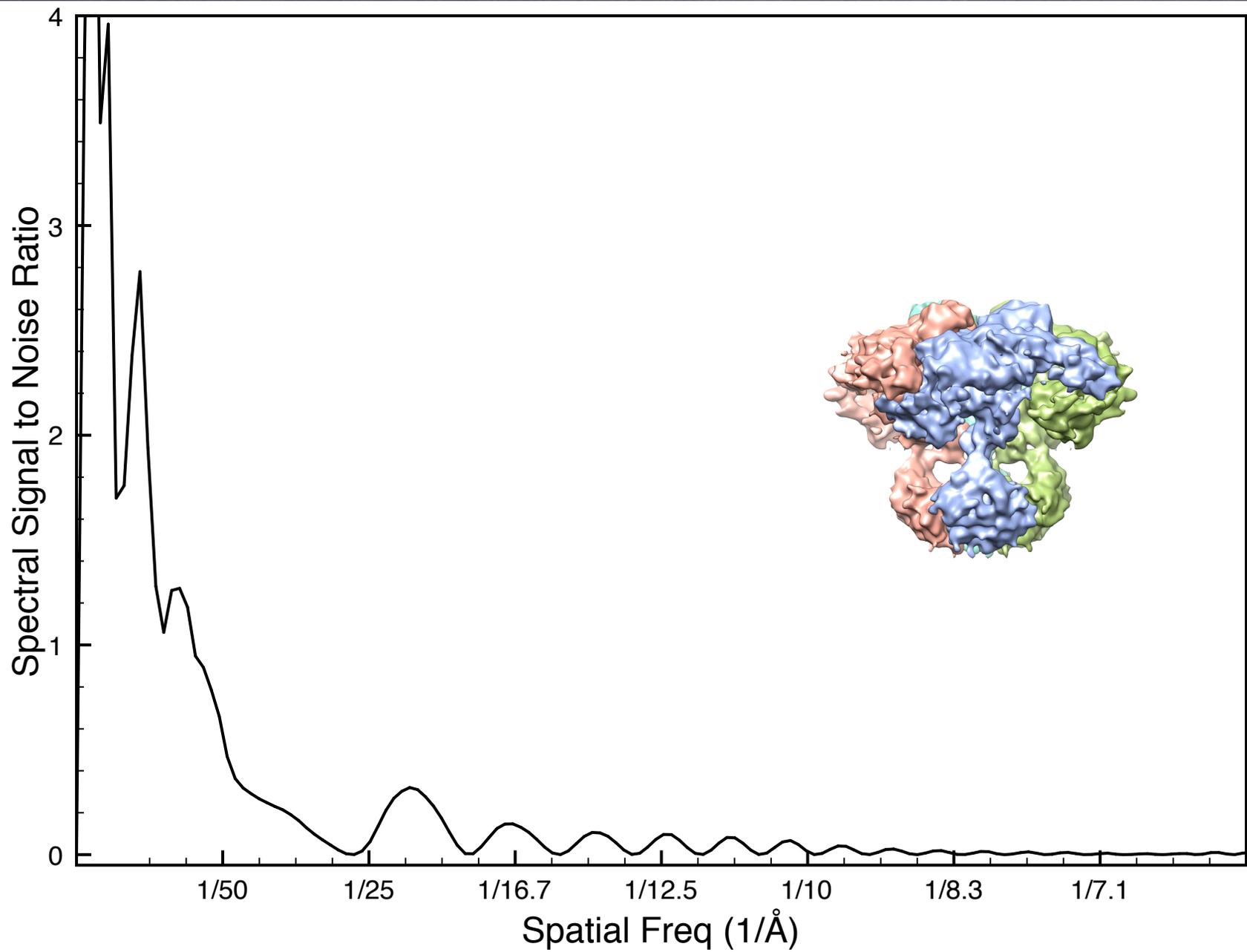
Image Evaluation

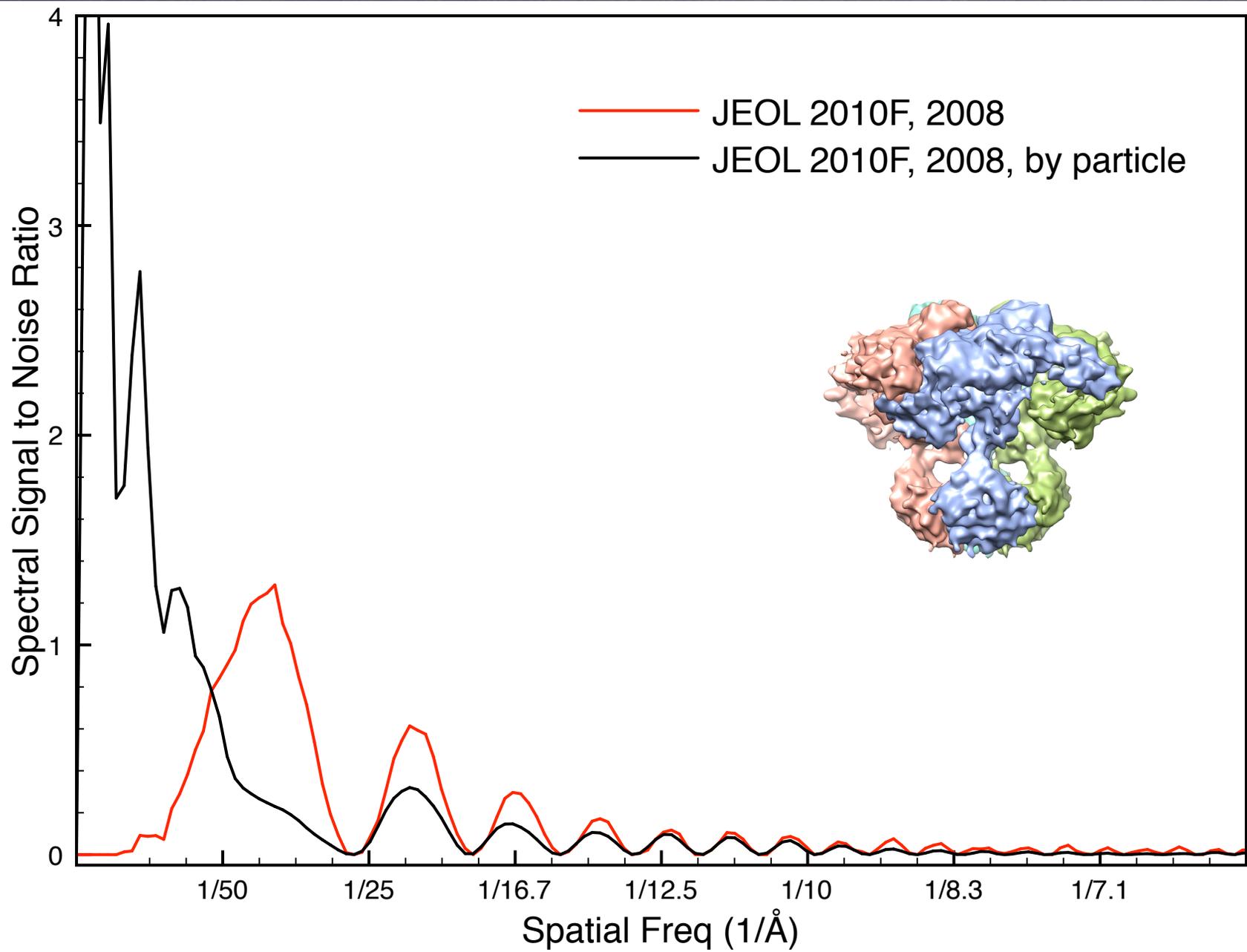


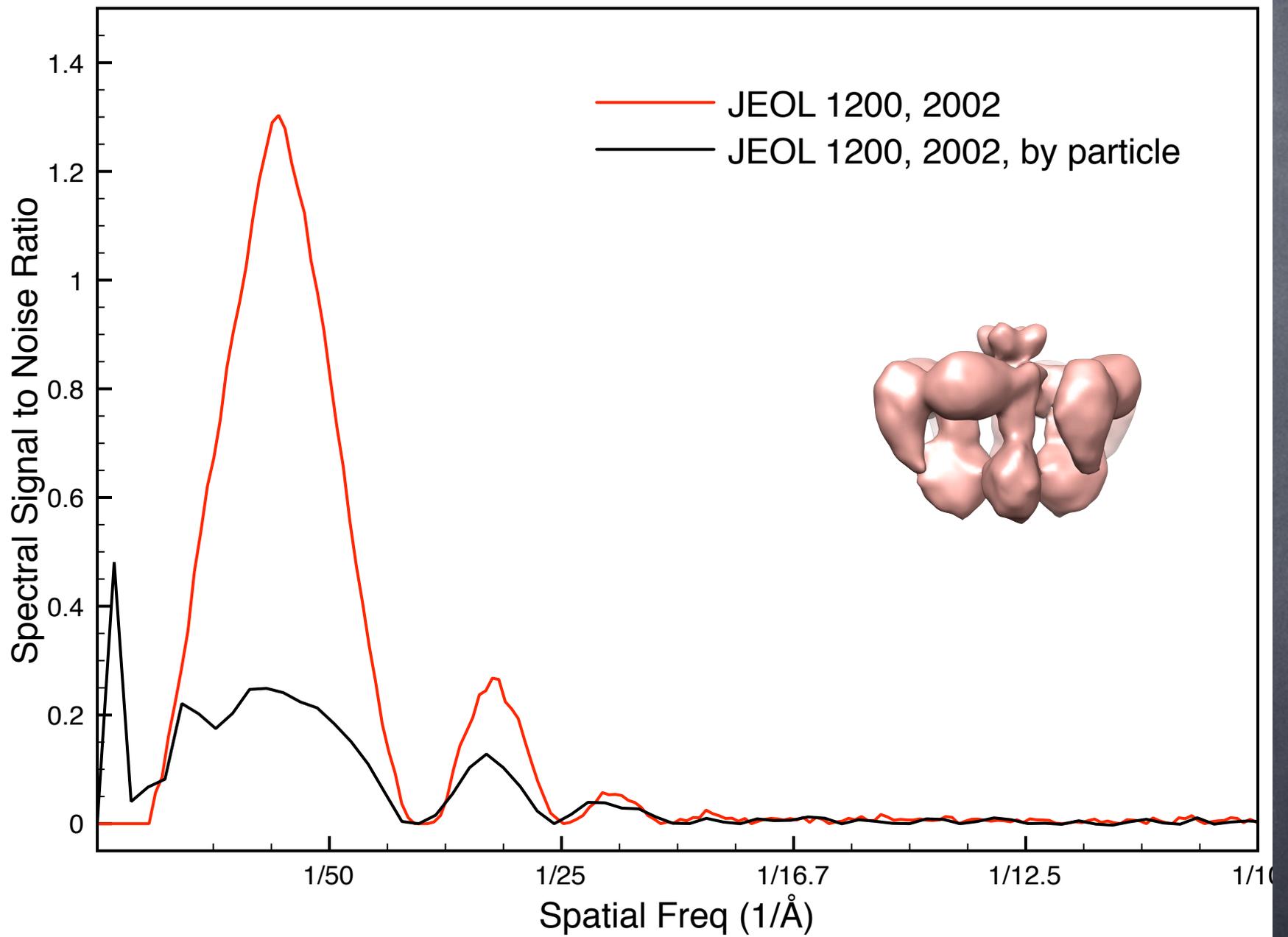


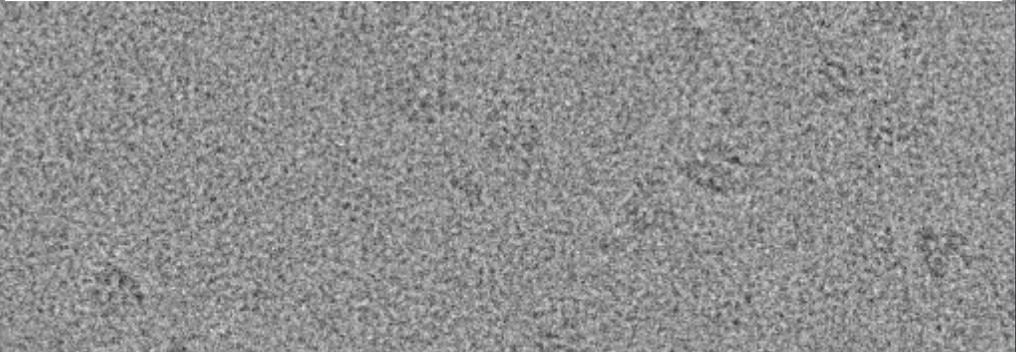
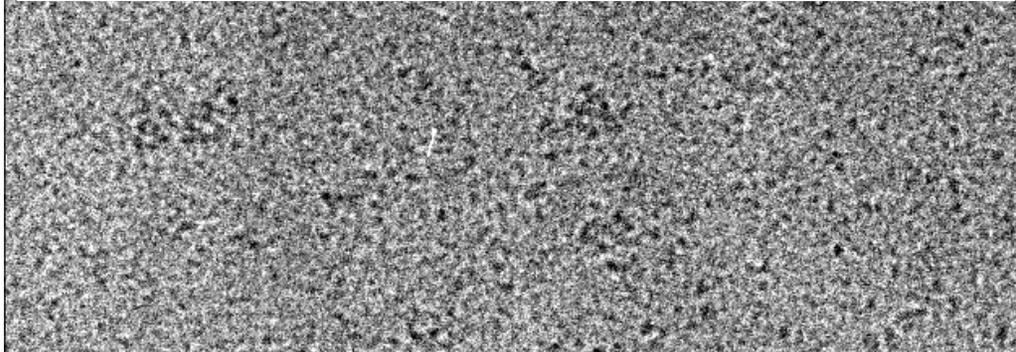
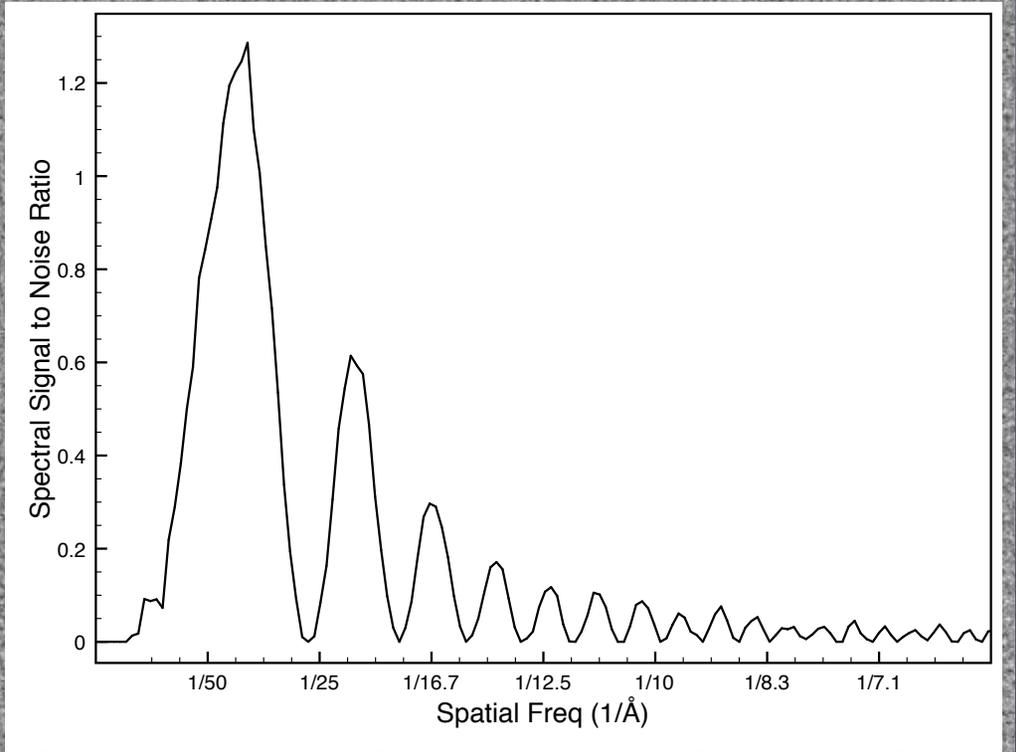
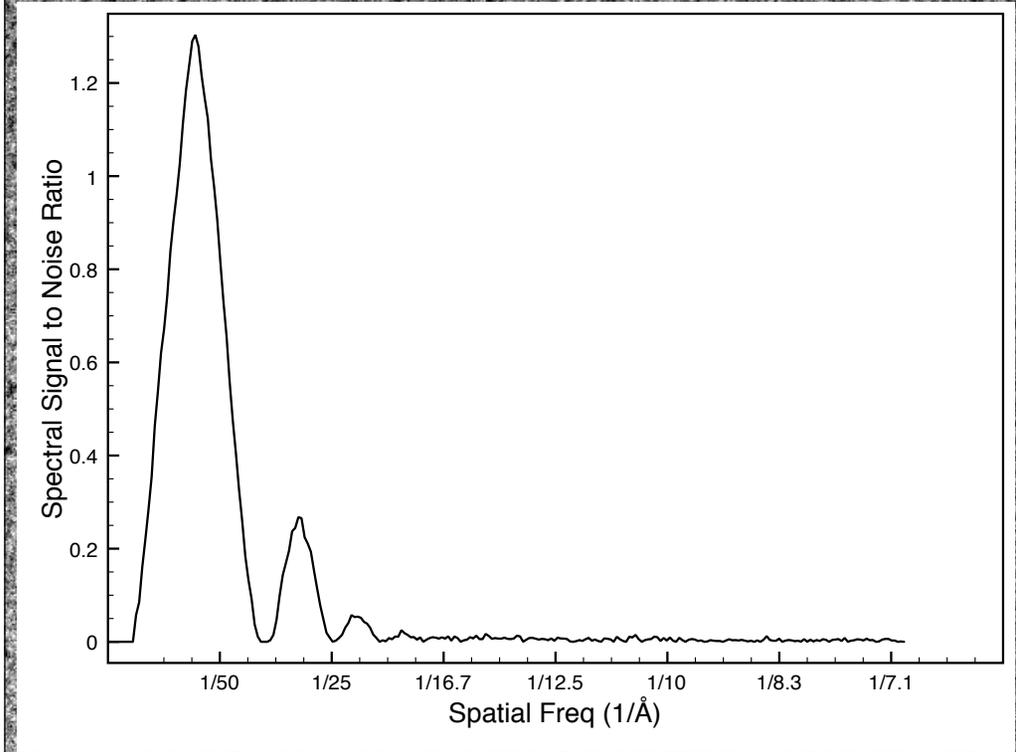
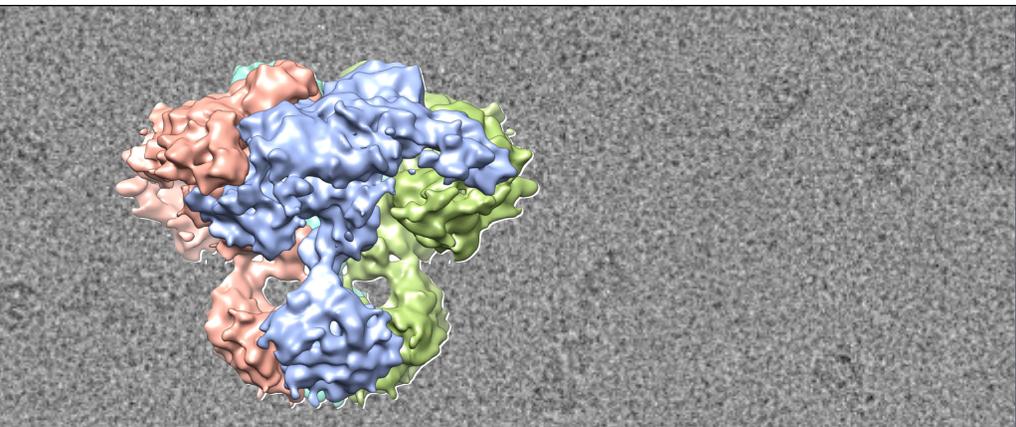
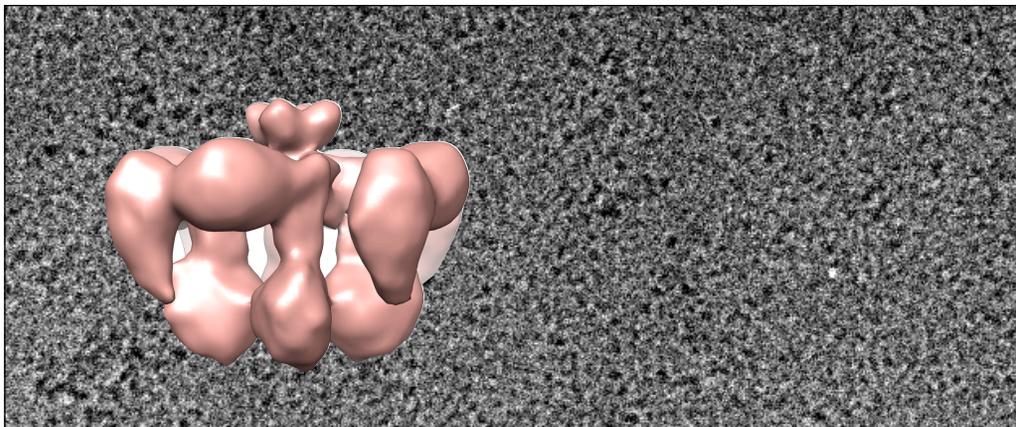


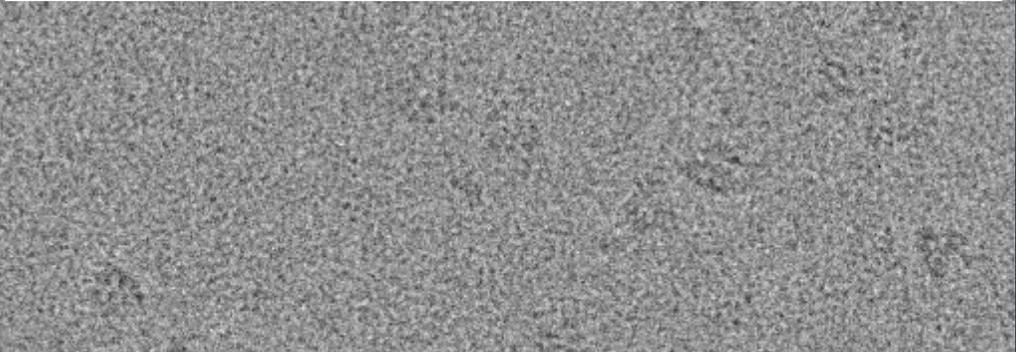
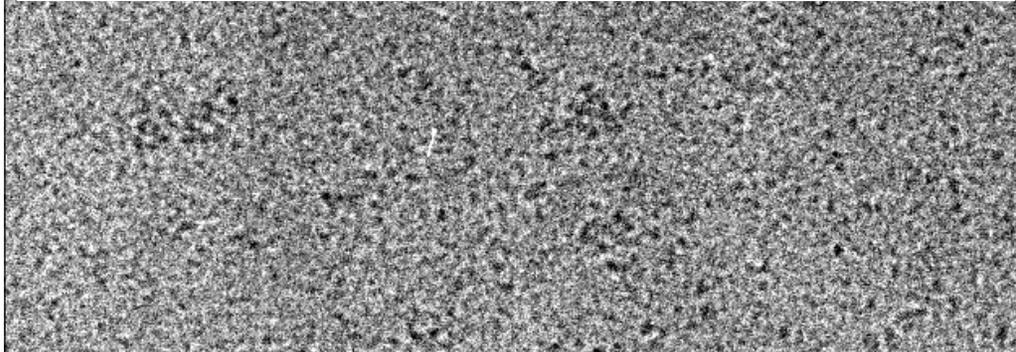
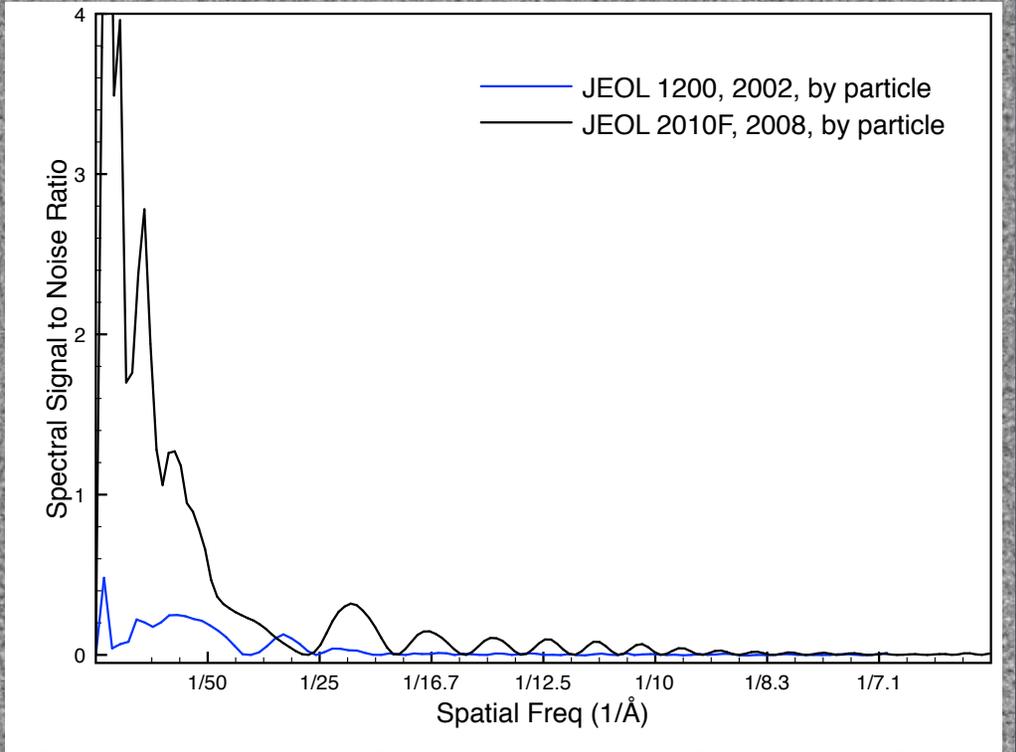
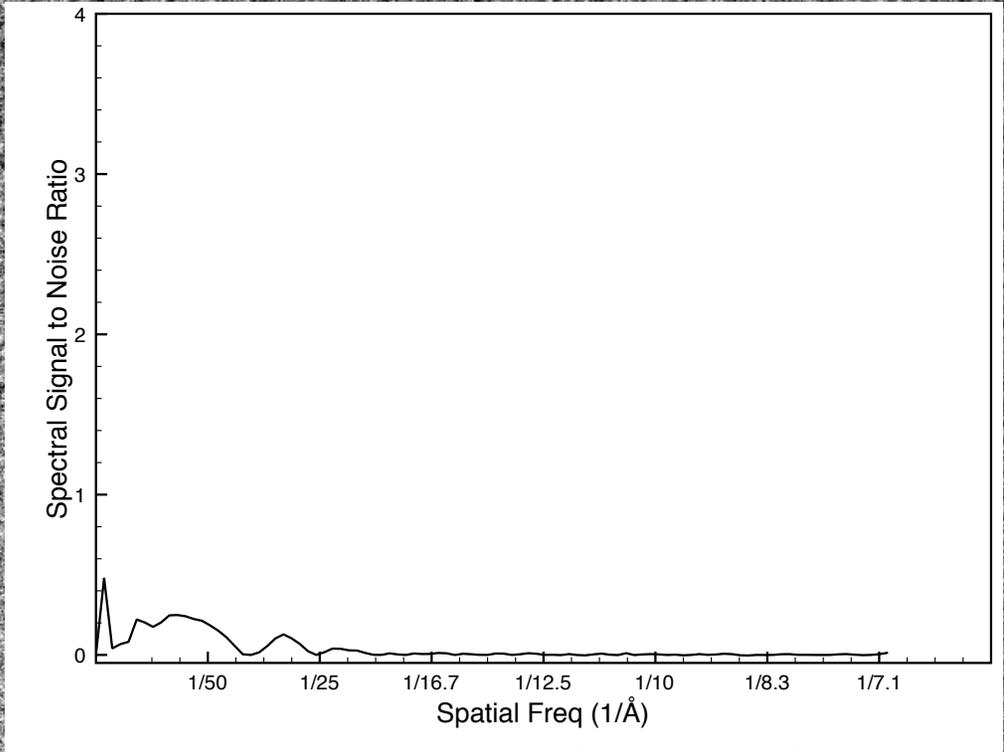
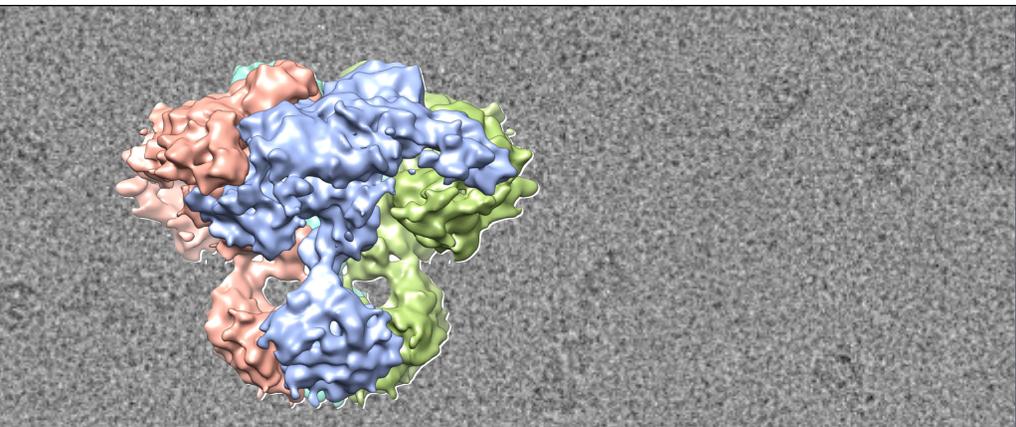
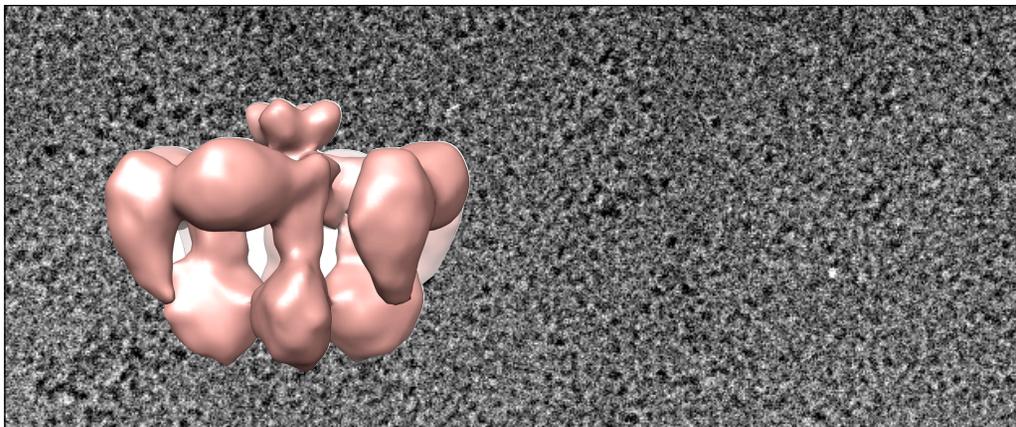




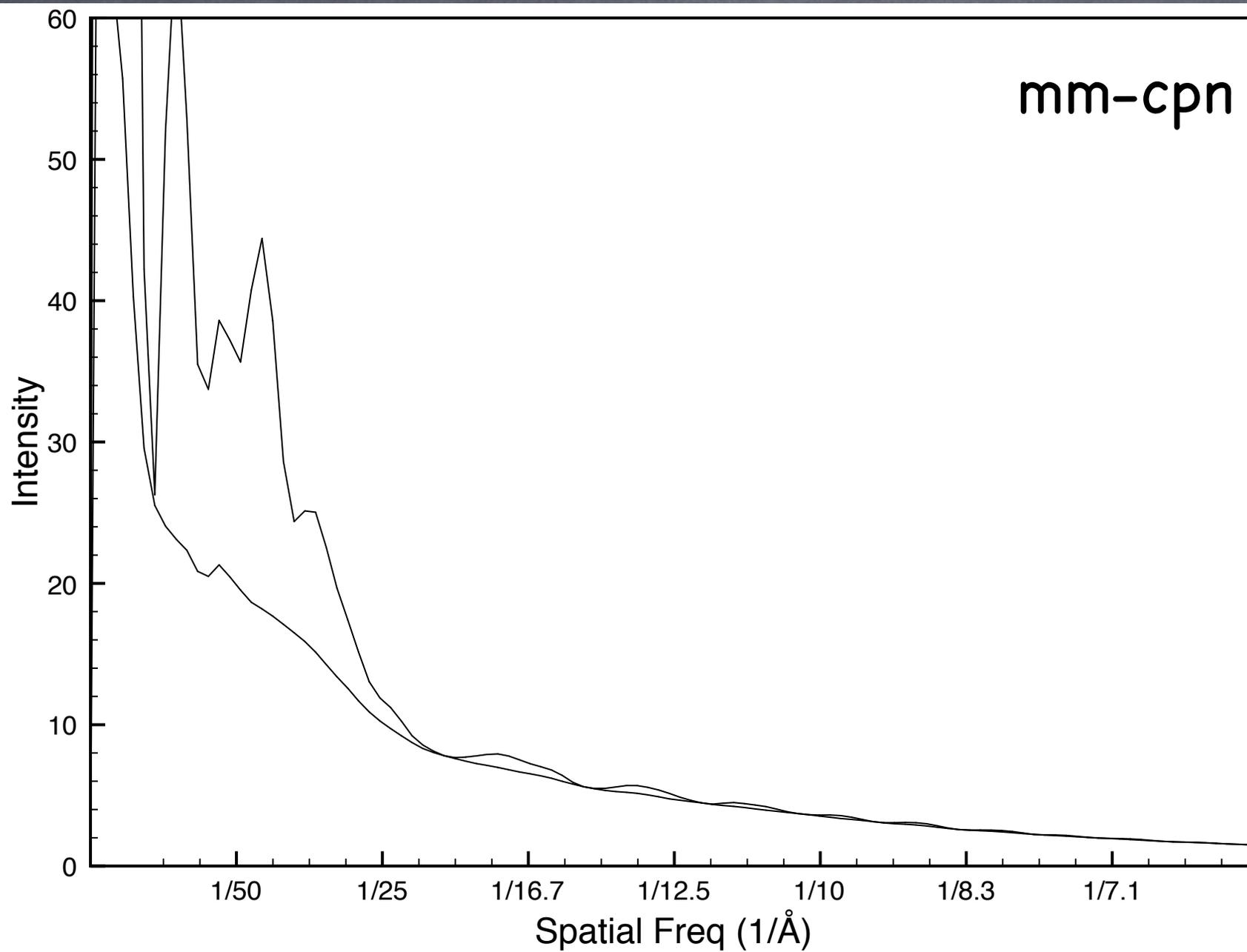








mm-cpn



Conclusions

- Gold Standard FSC
 - Less overinterpretation of data
 - It only makes resolutions worse when they are overestimated
- Tilt validation for low resolution/low symmetry
- SSNR analysis of particles for data evaluation

Questions ?