

Do Initial Models Matter?

- Not normally, but be careful with:
 - Particles with a lot of motion/heterogeneity
 - Particles with strong preferred orientation
 - Particles with insufficient contrast (bad data)
- If you don't know the quaternary structure, you should always use tilt-validation.
- Ribosomes refine from anything
- GroEL actually one of the hardest cases

Per-Particle SSNR

Image Evaluation

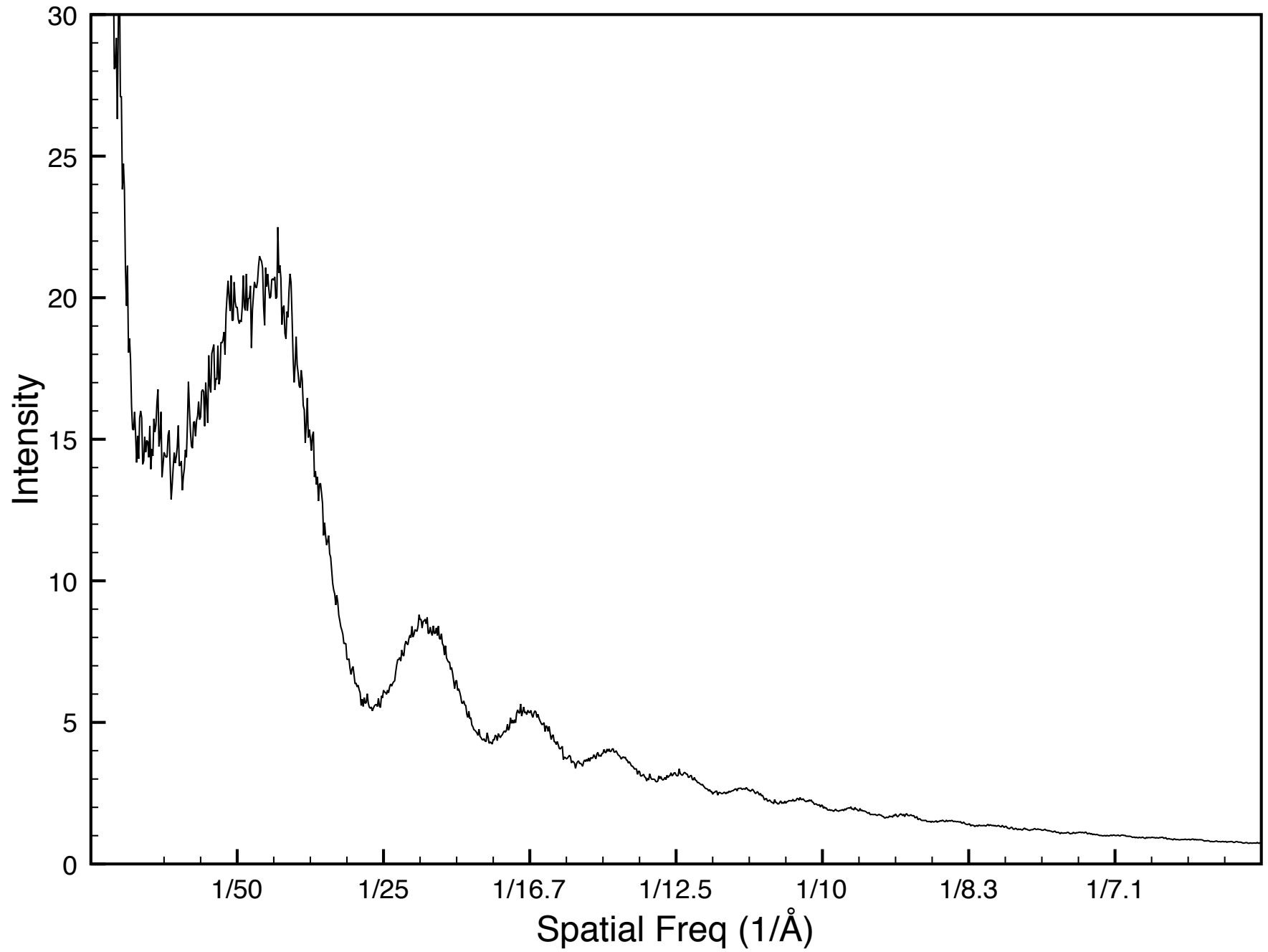
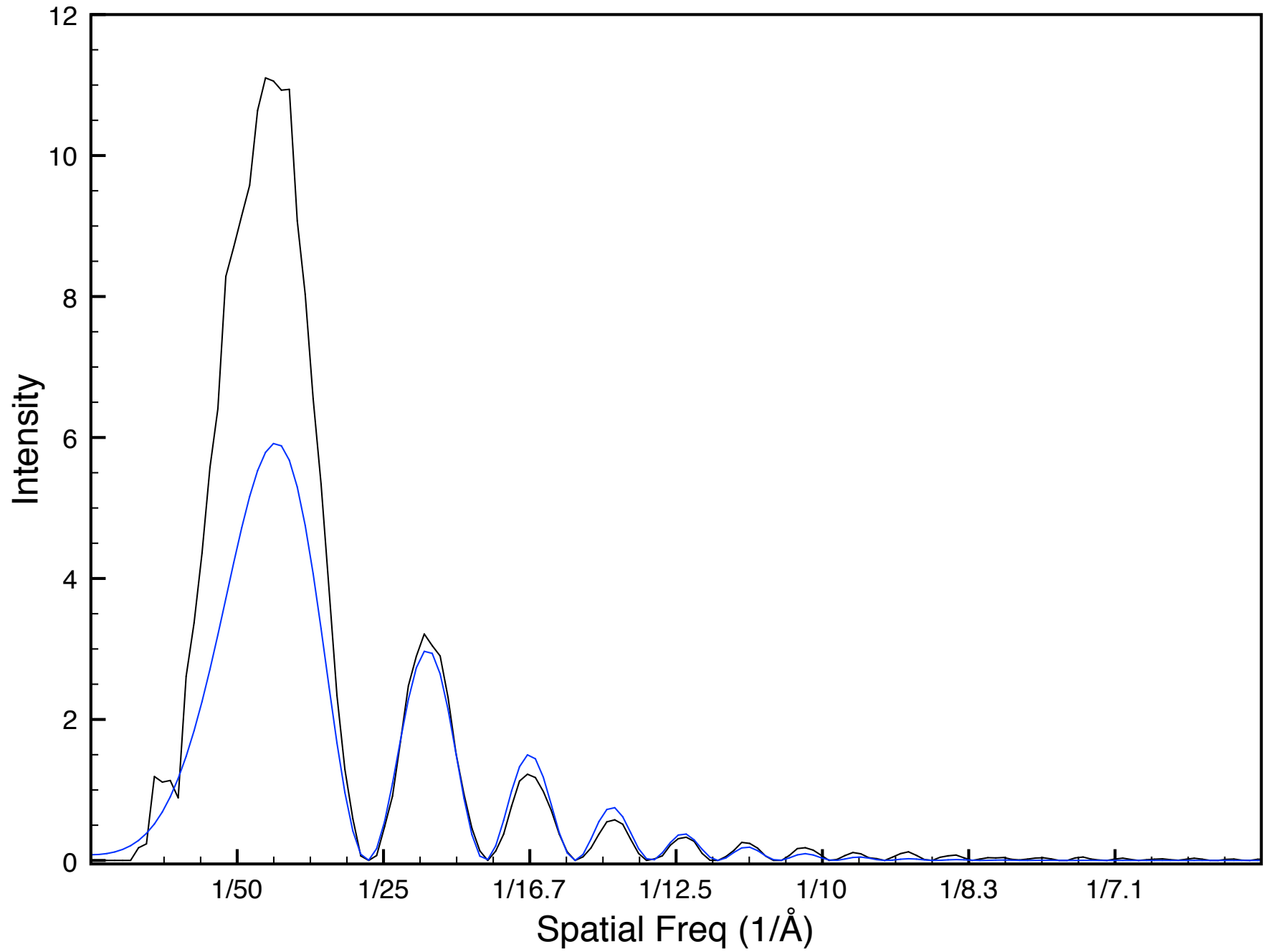
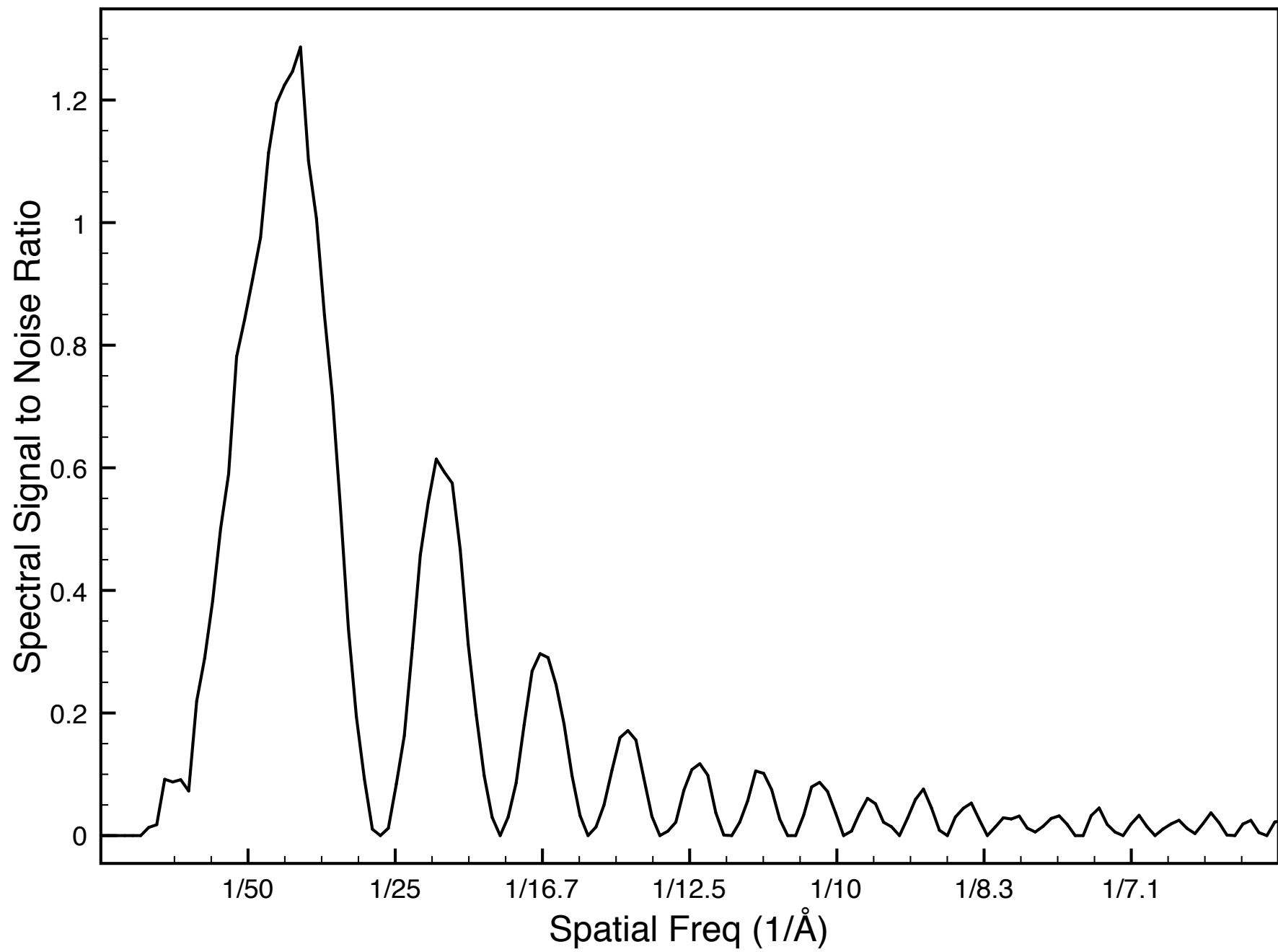
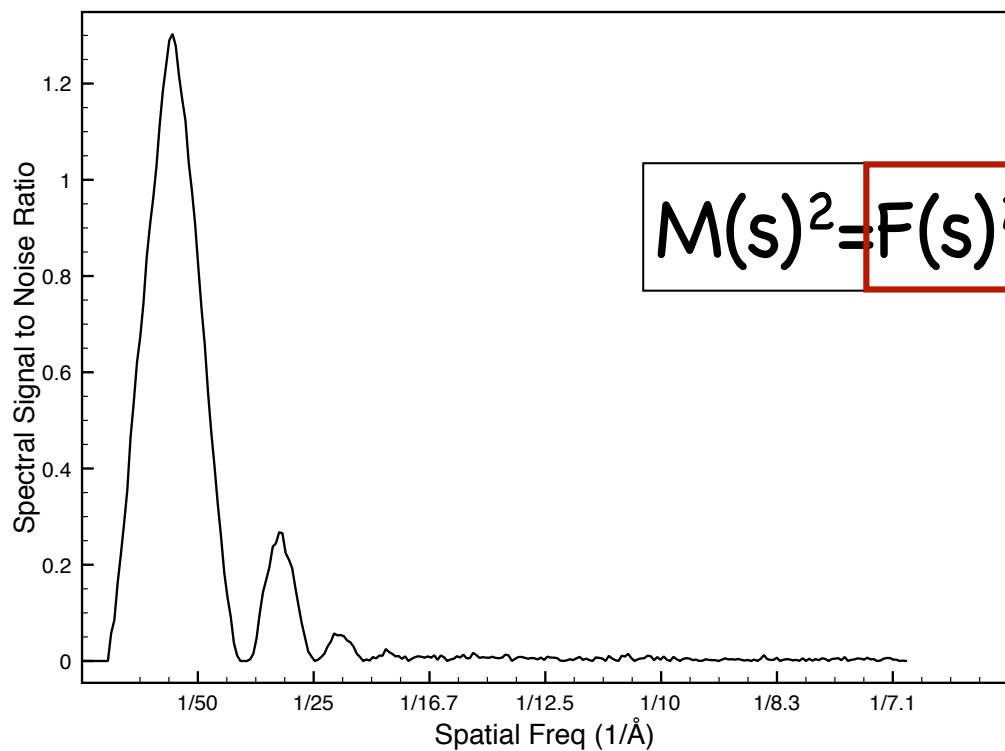
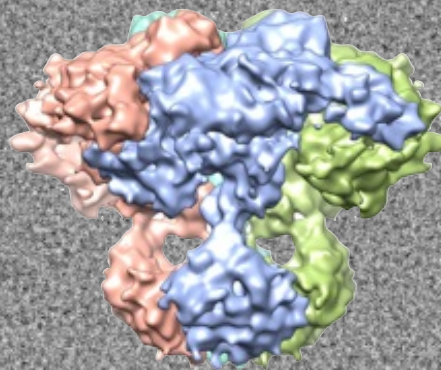
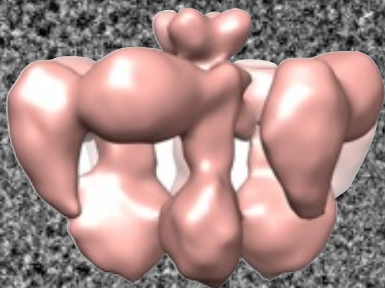


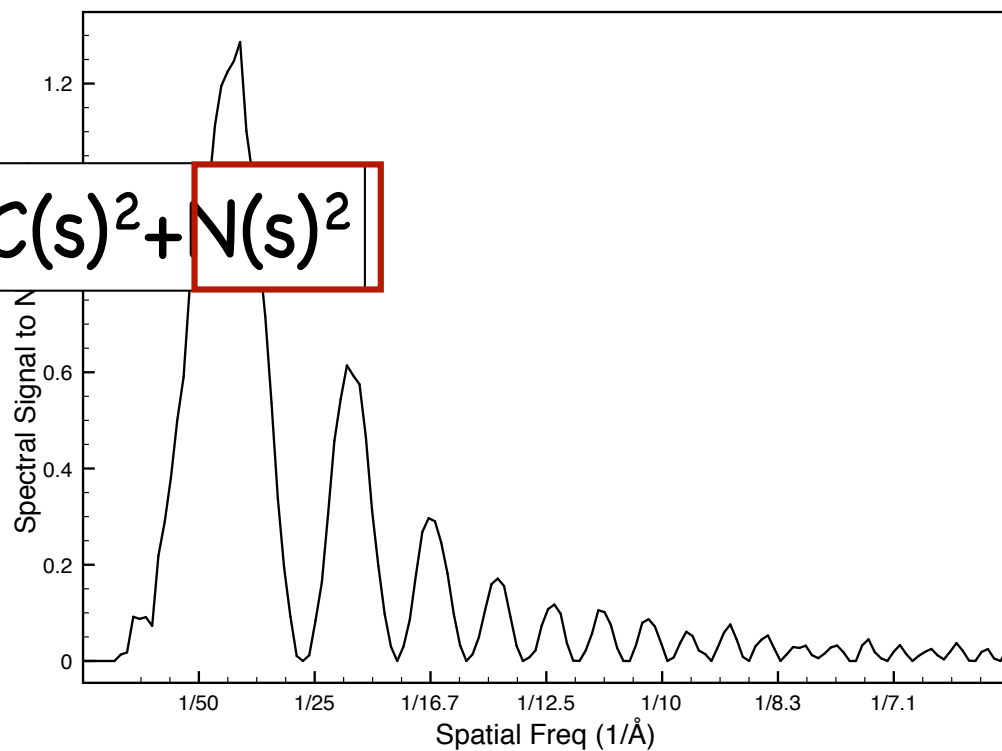
Image Evaluation



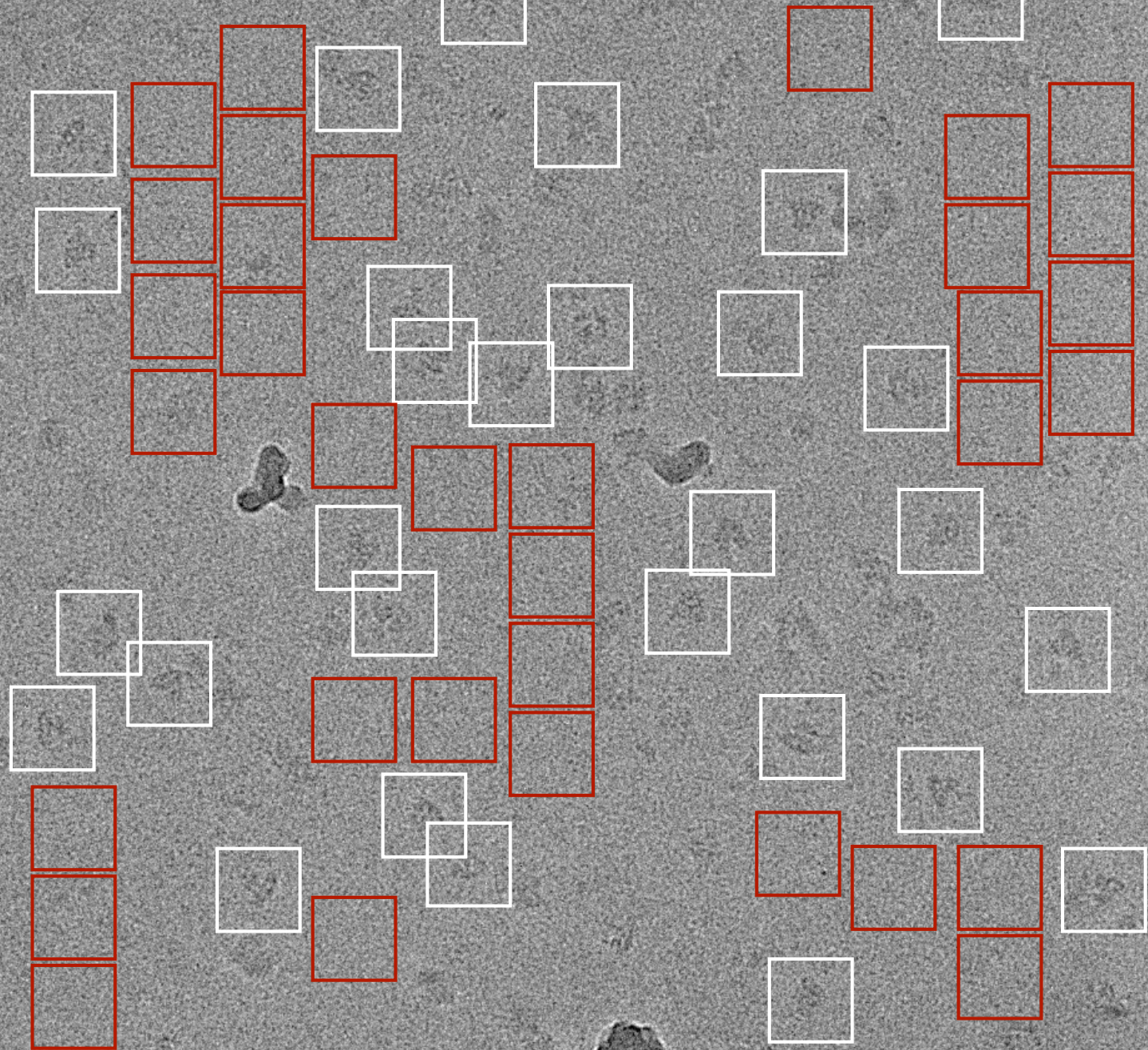




$$M(s)^2 = F(s)^2 C(s)^2 + N(s)^2$$



Particles Rather than Regions



Density Problems

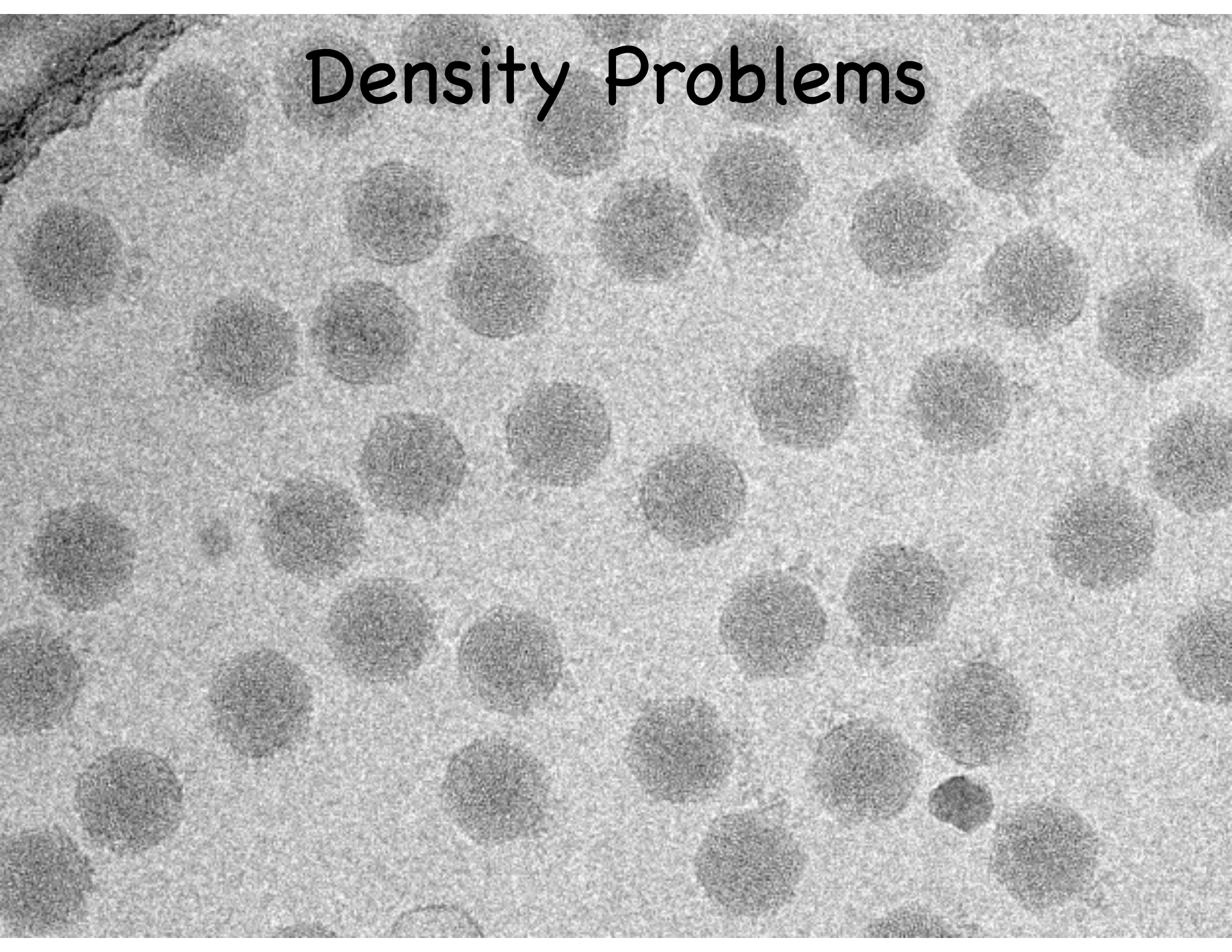
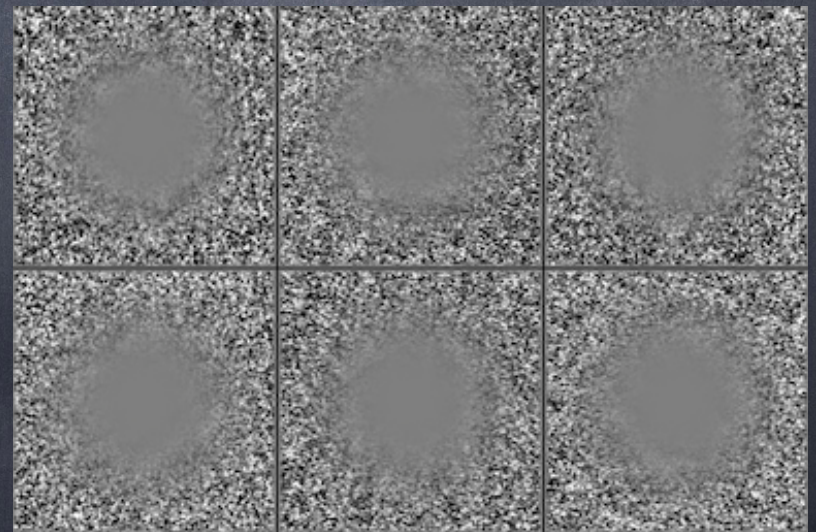
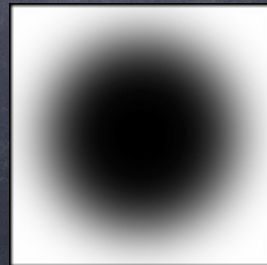
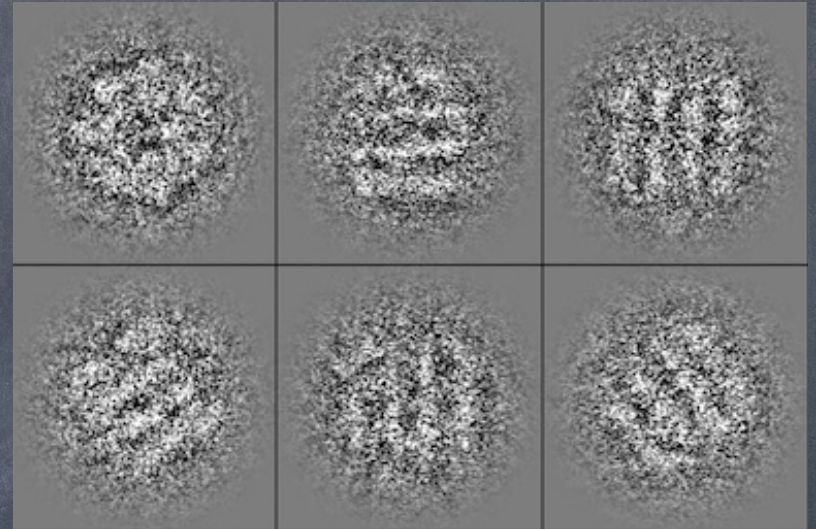
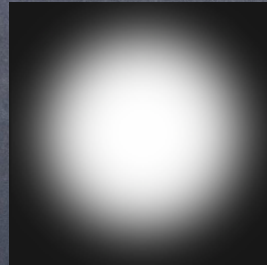
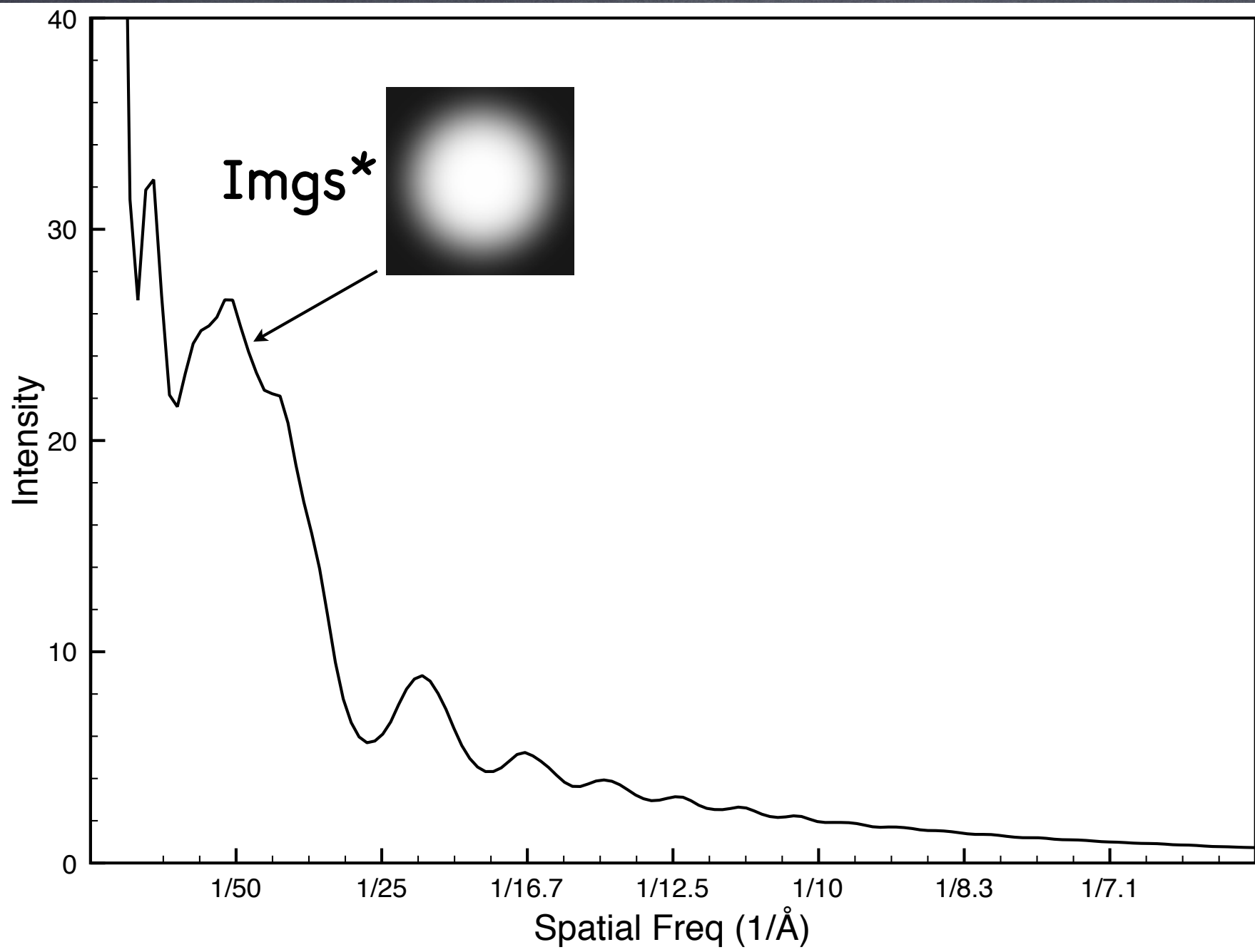
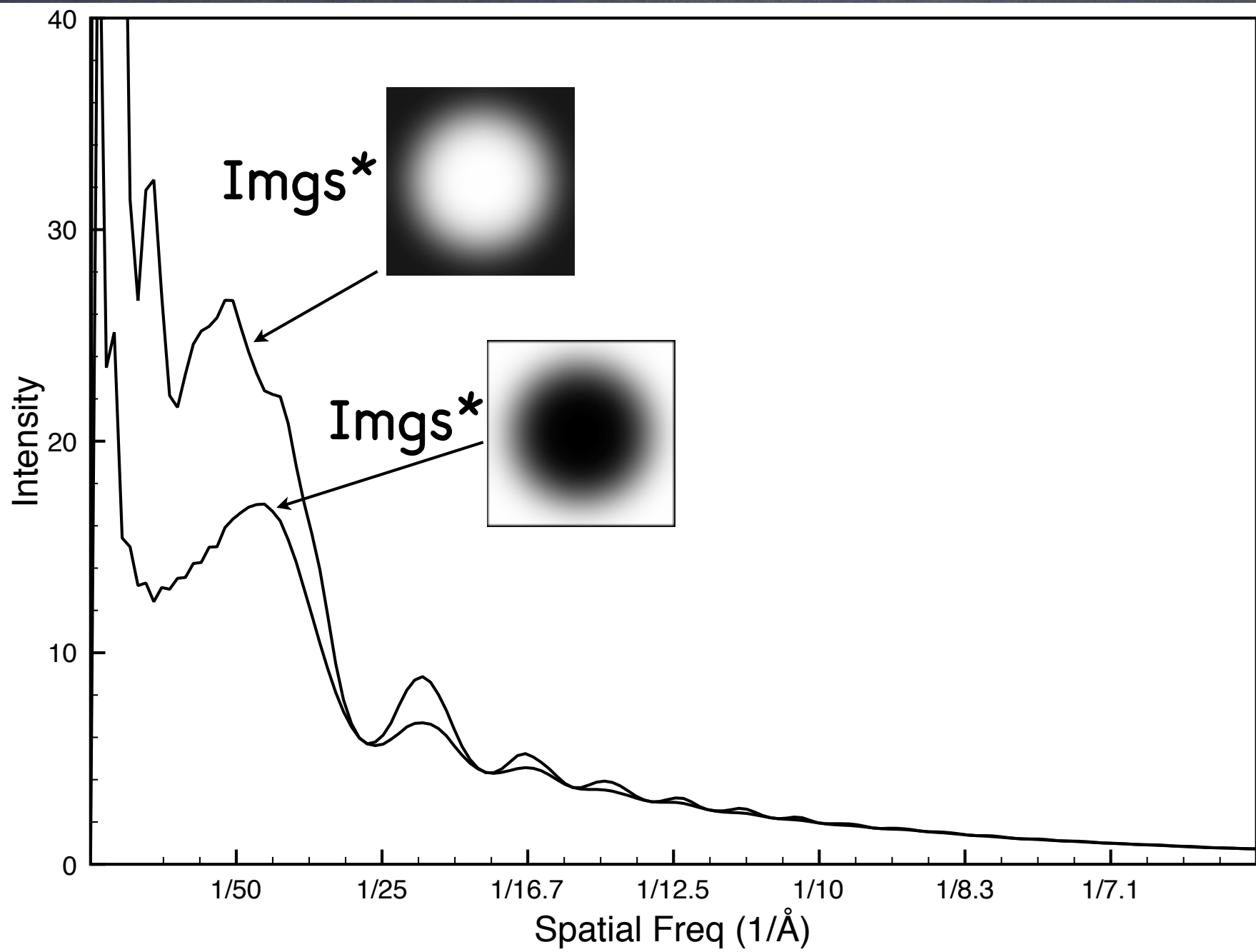
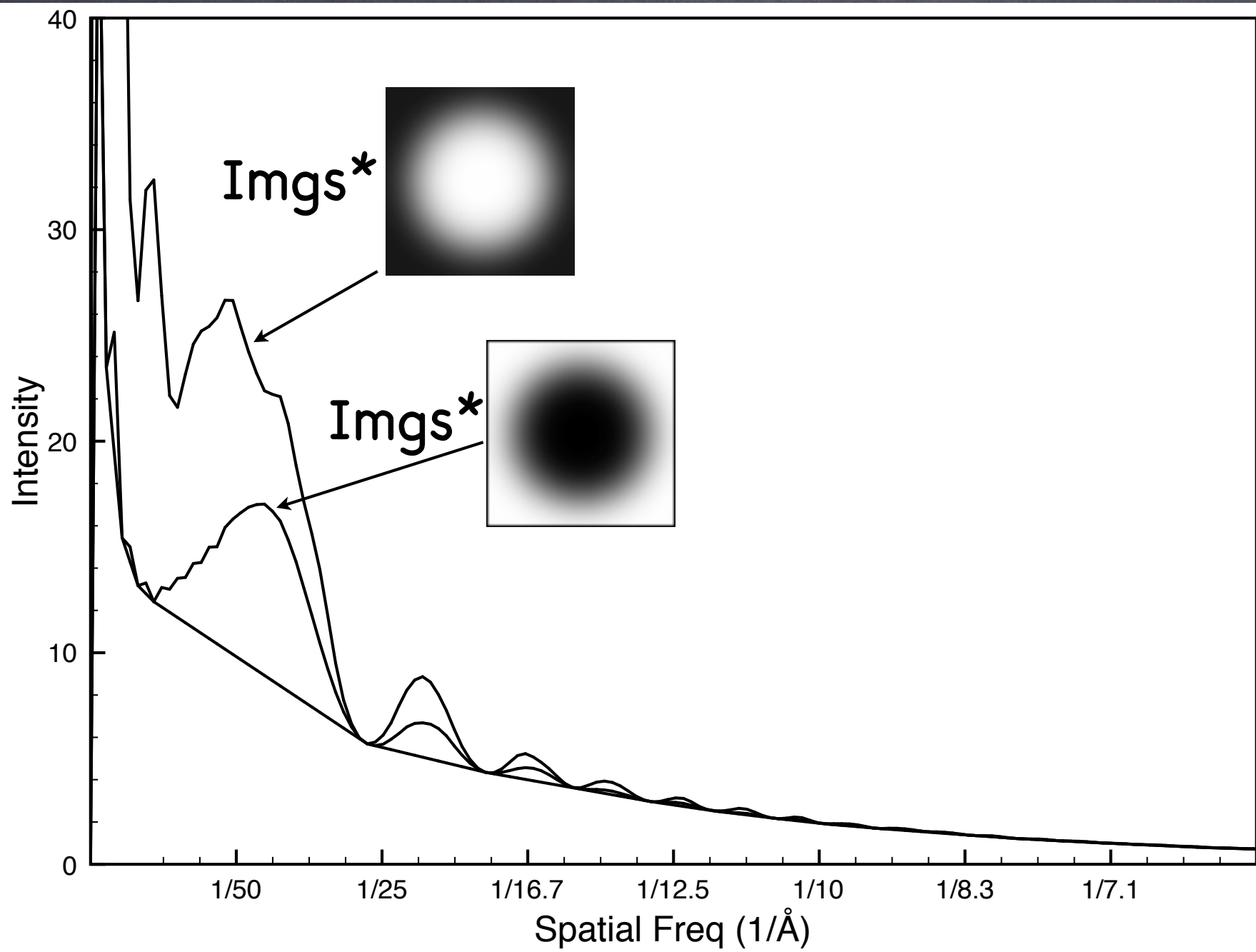


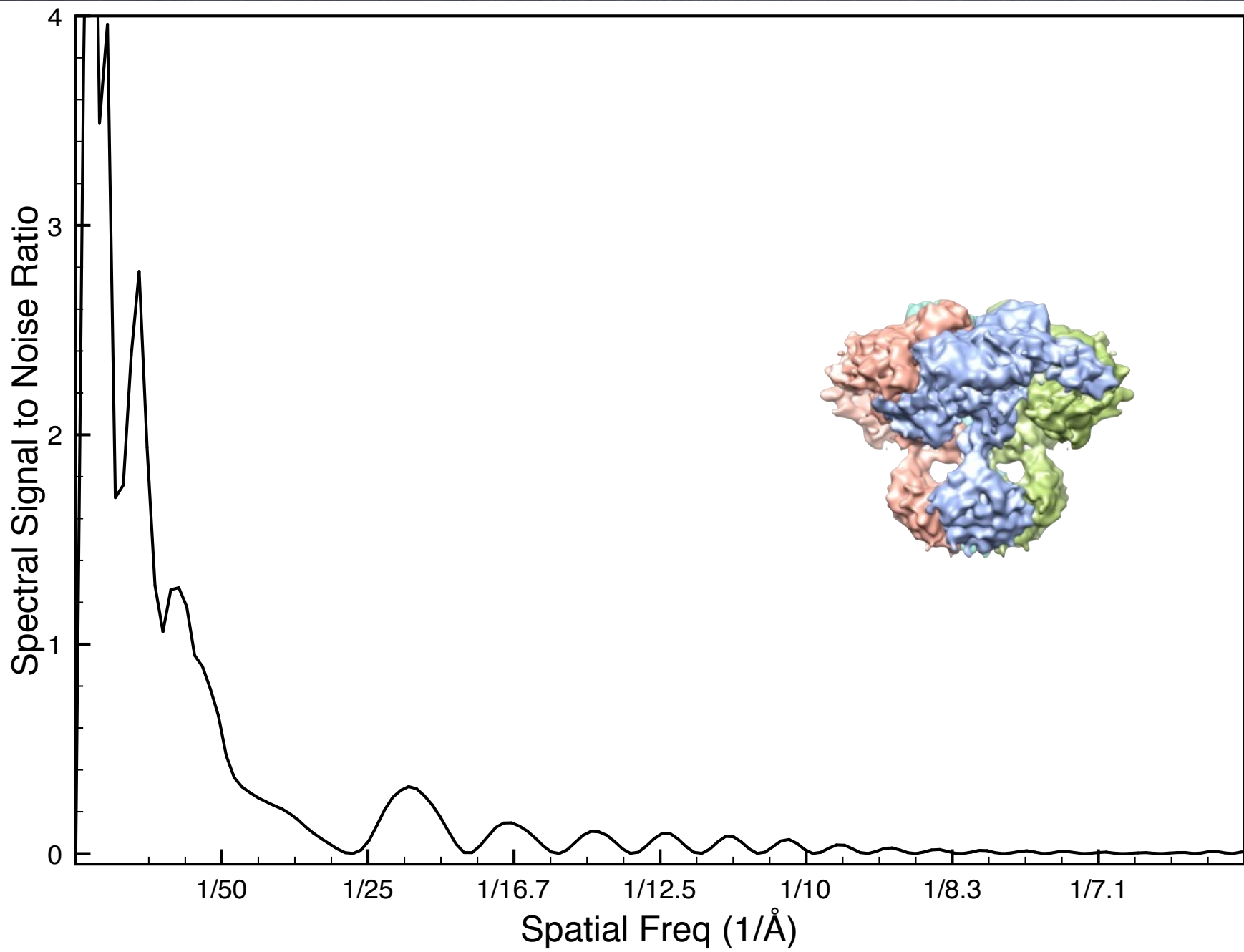
Image Evaluation

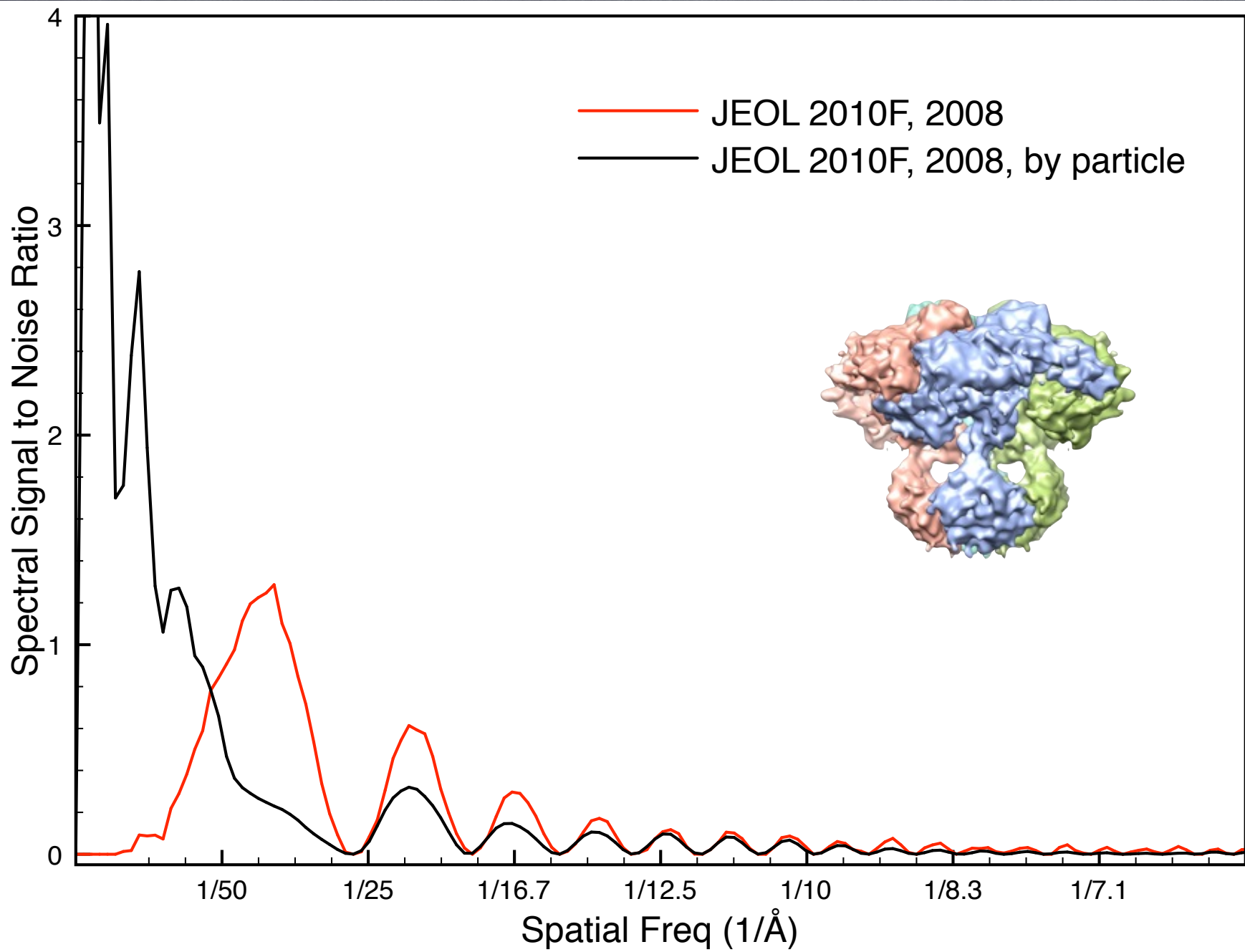


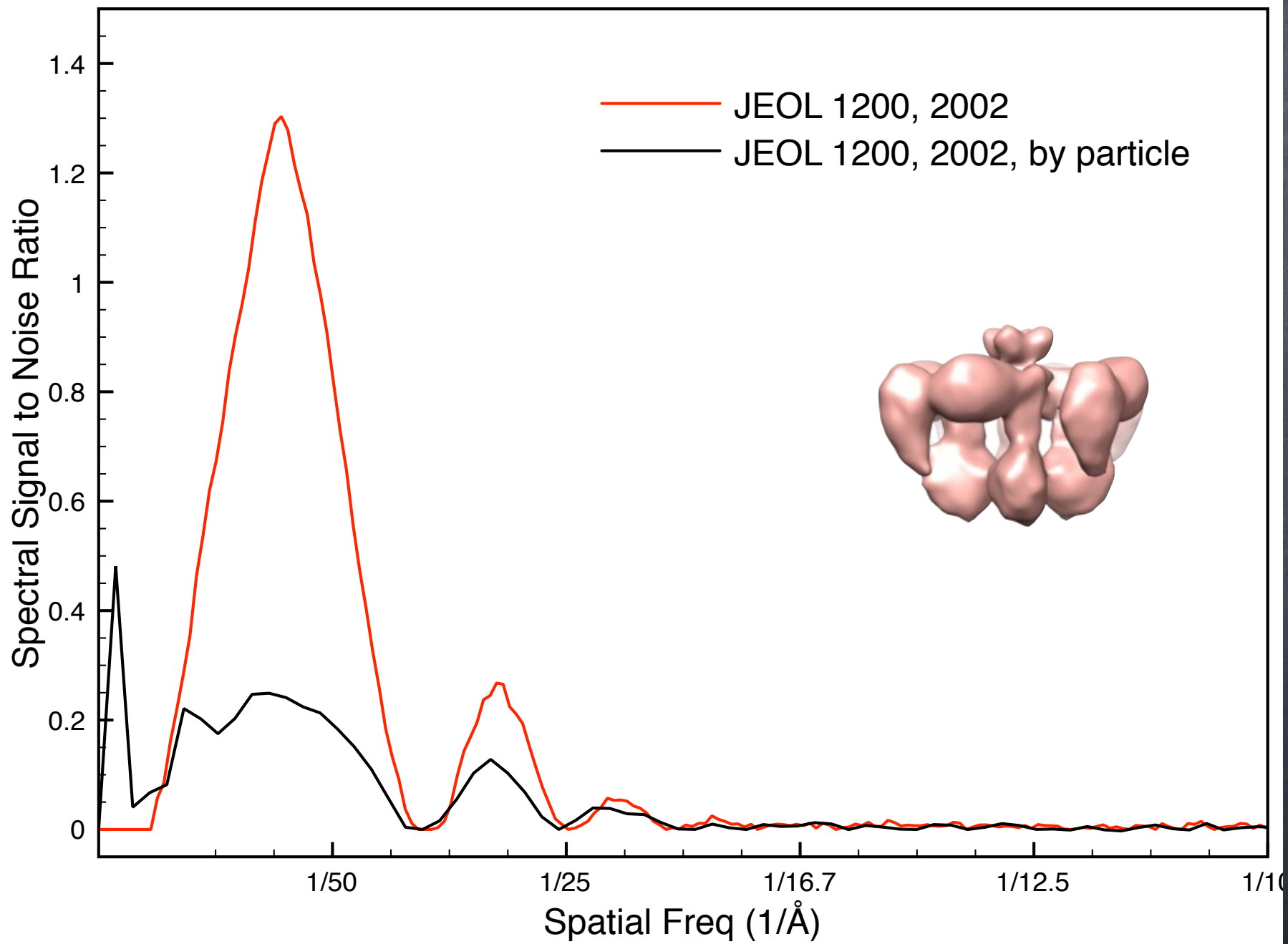


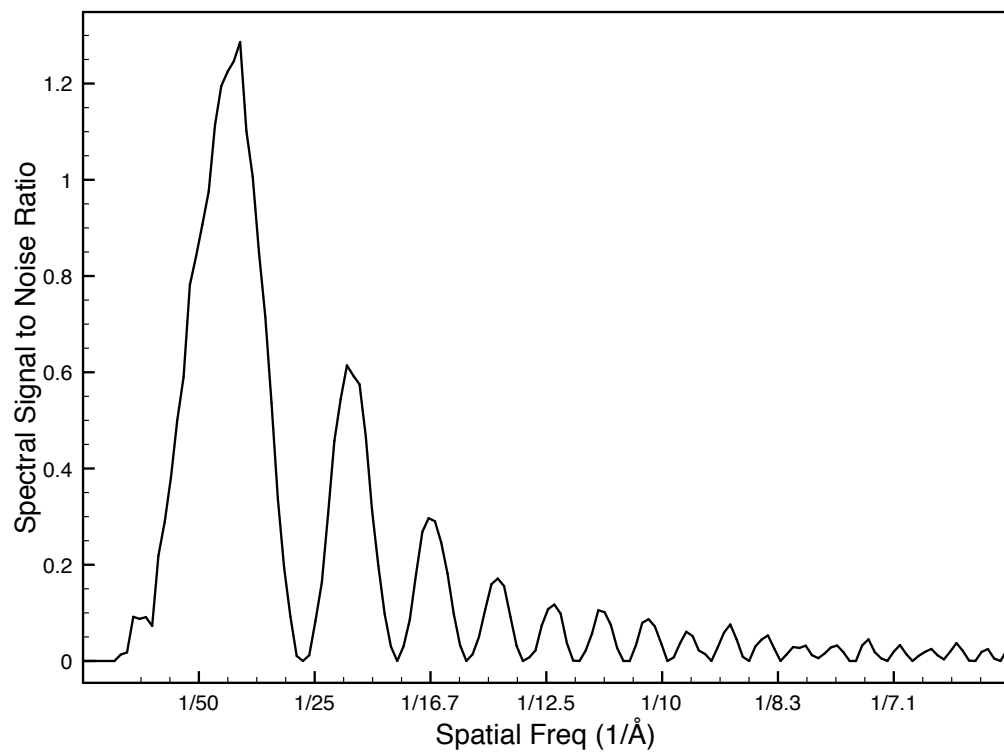
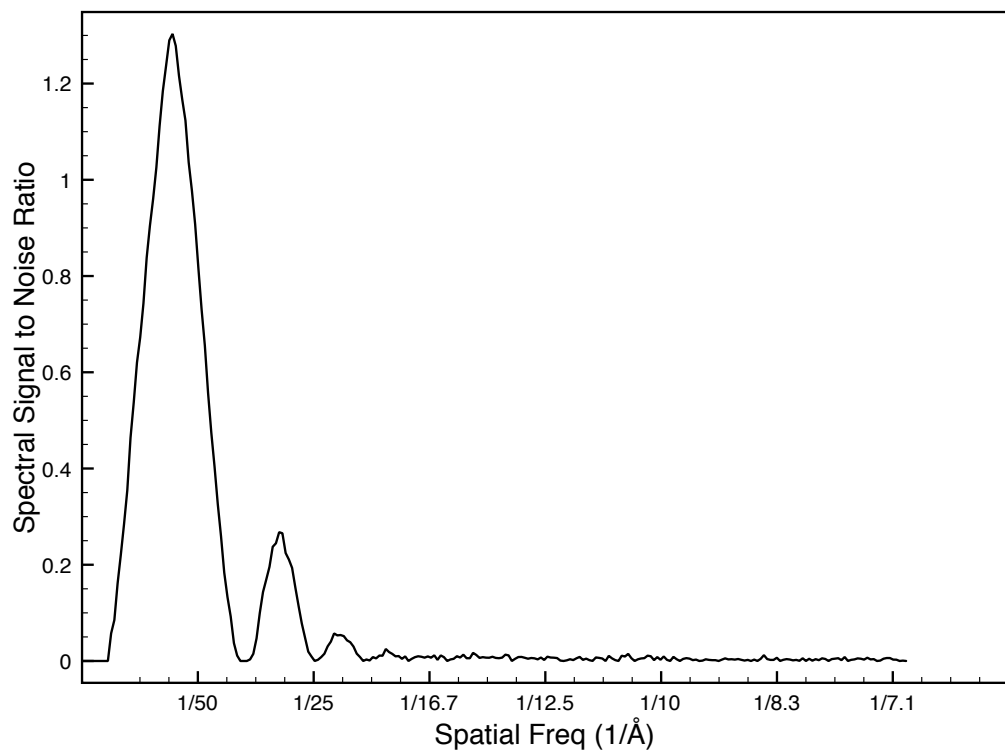
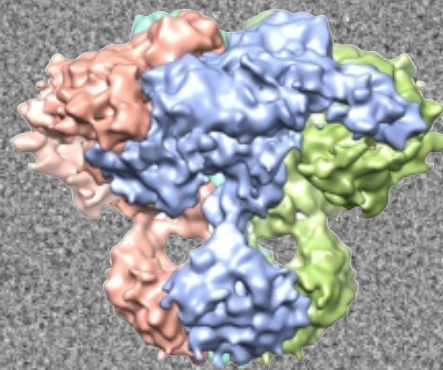
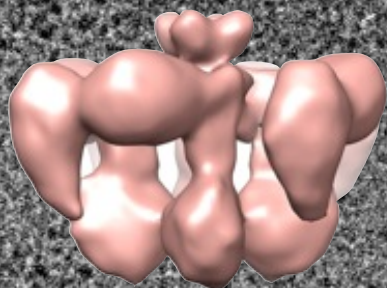


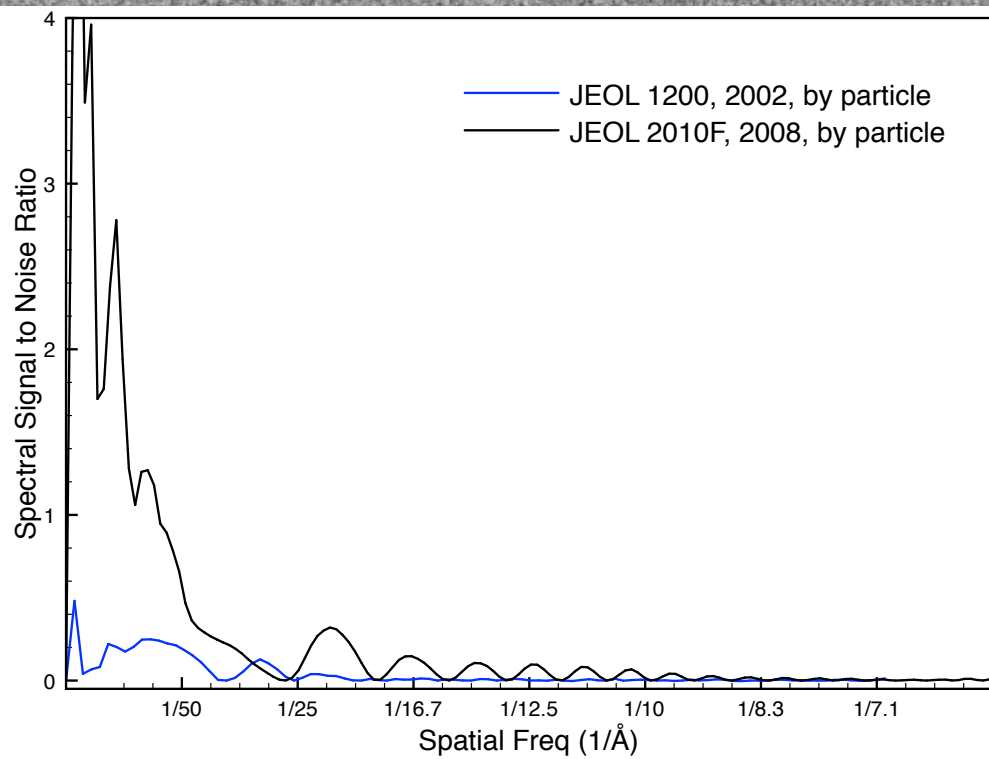
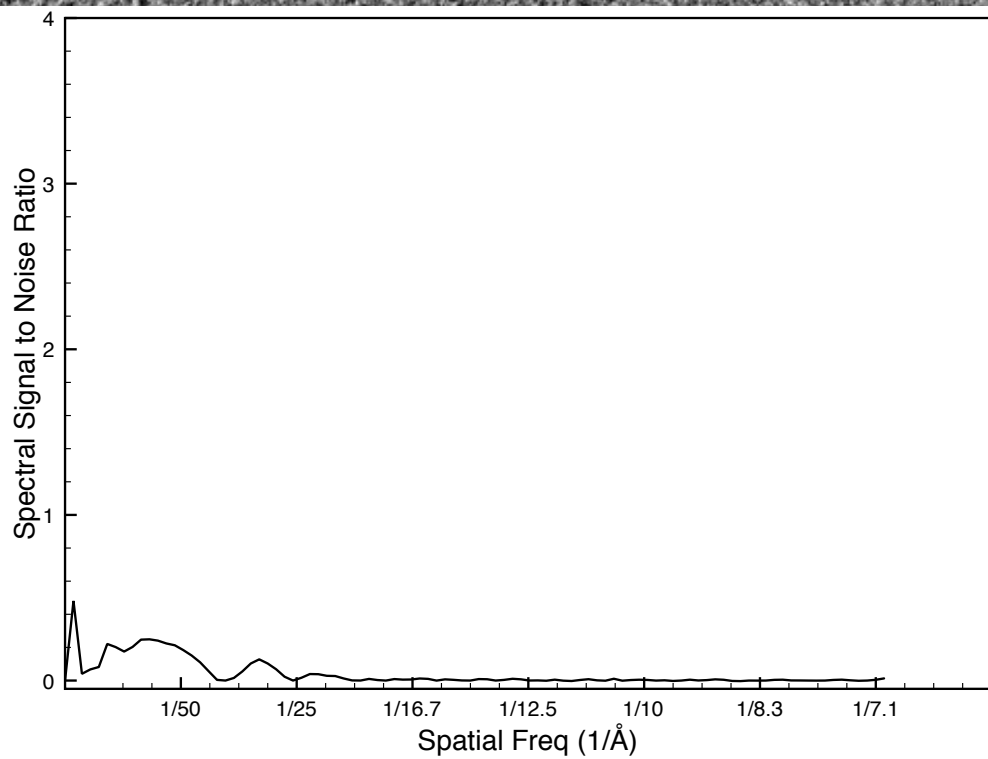
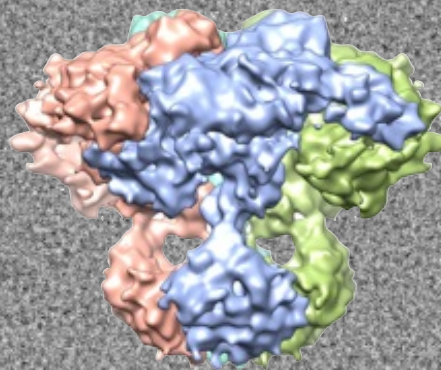
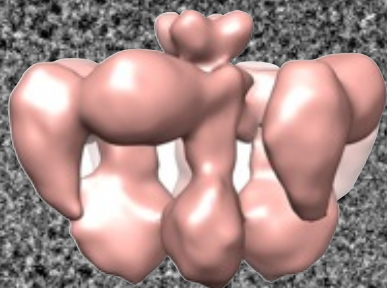


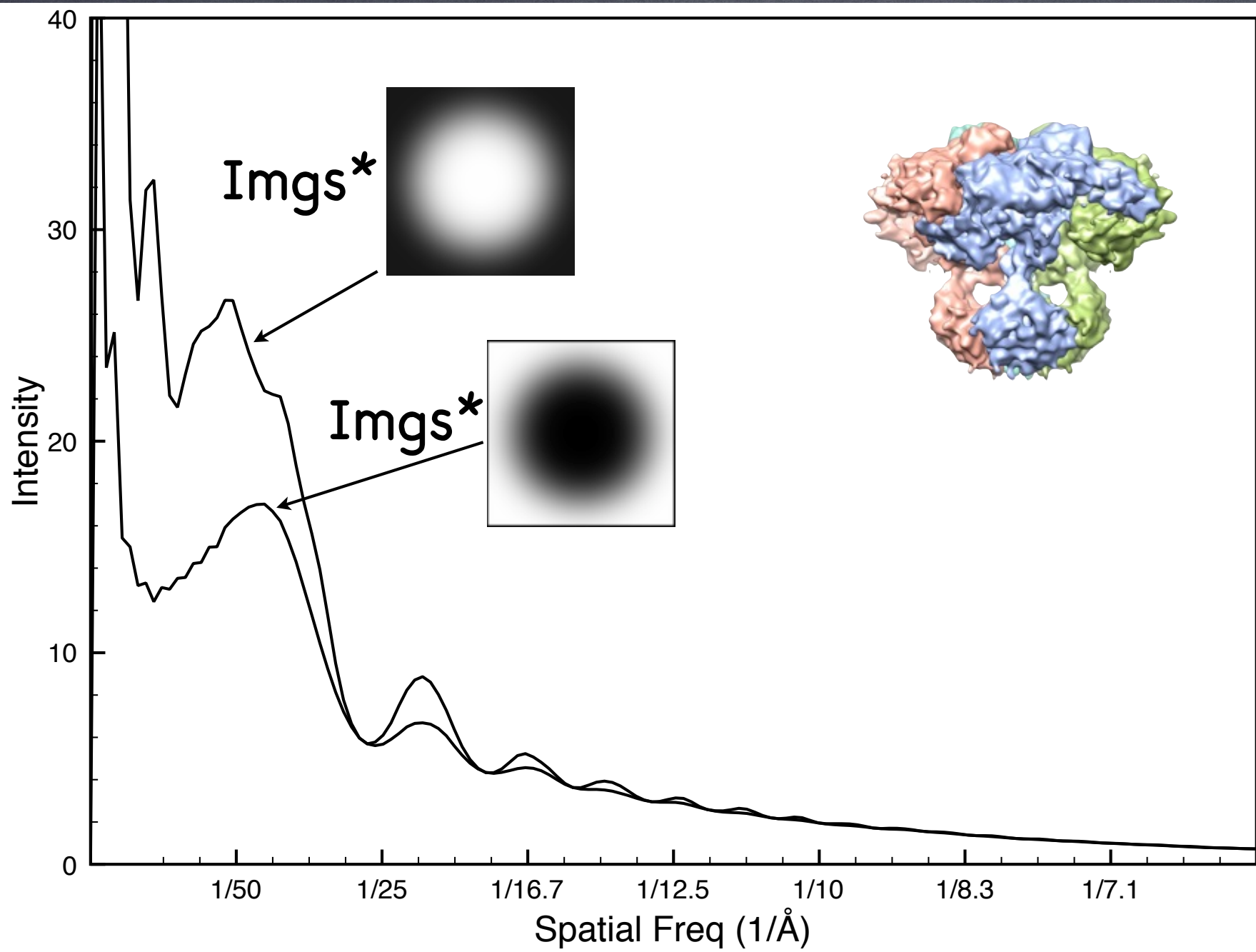




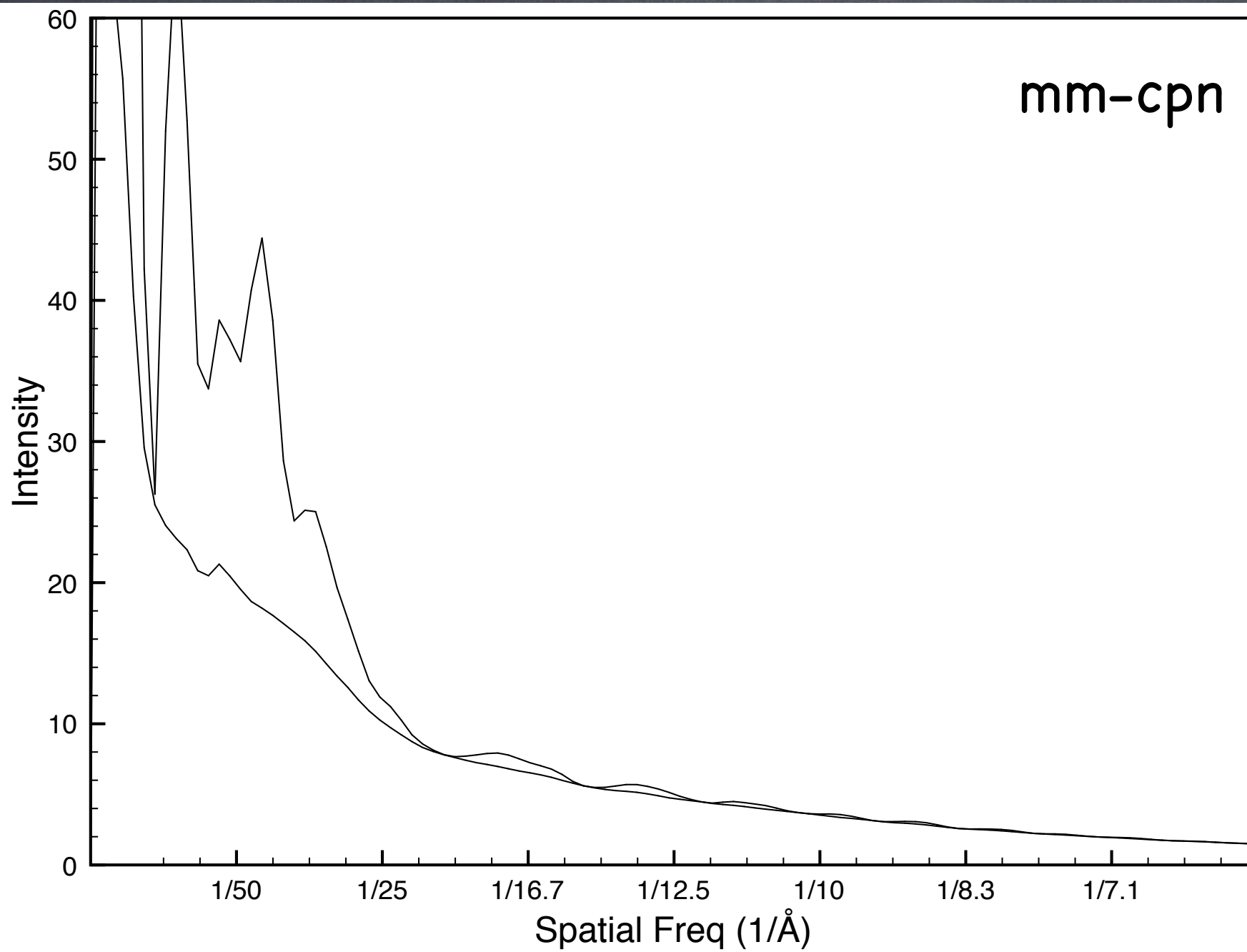




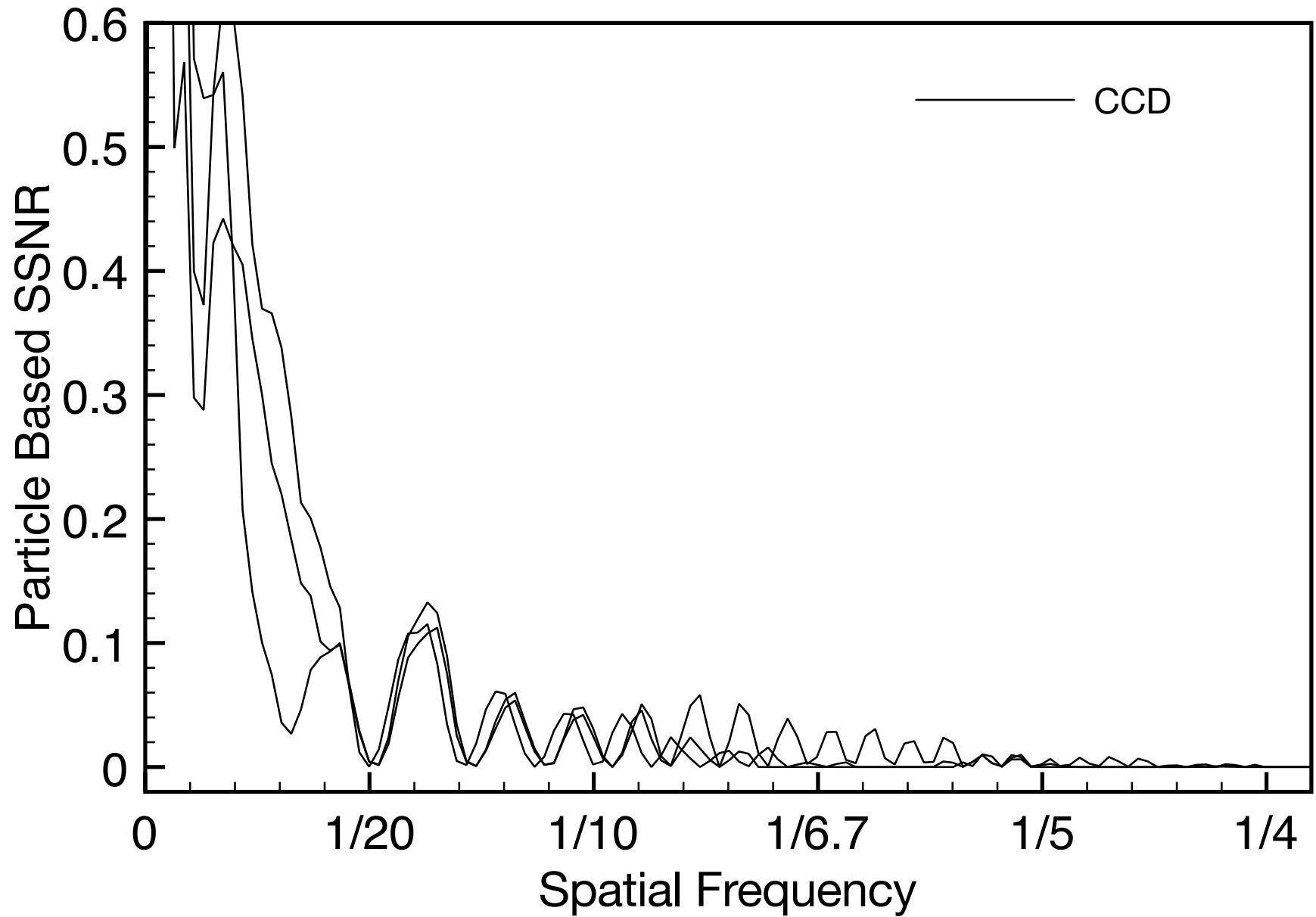




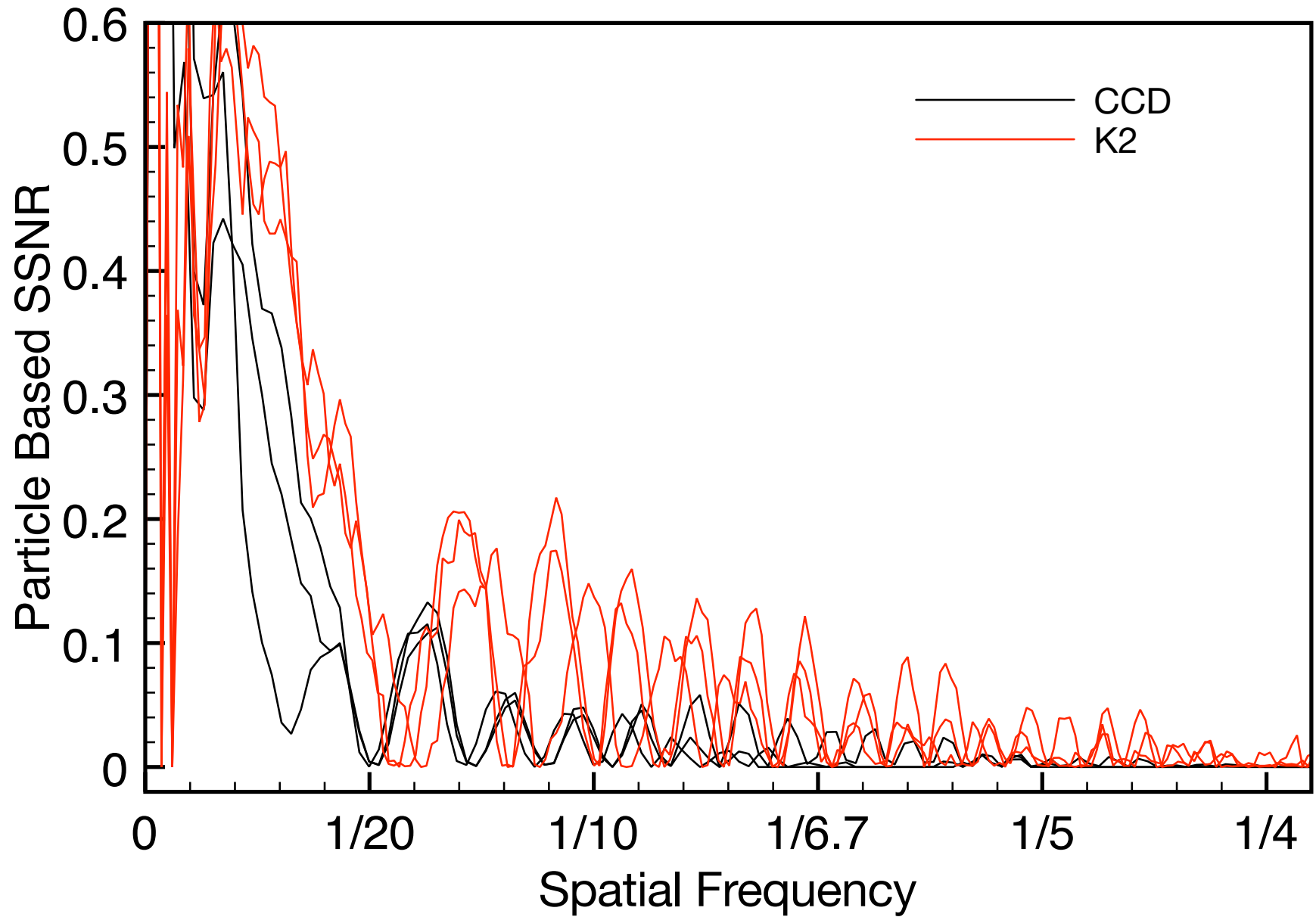
mm-cpn



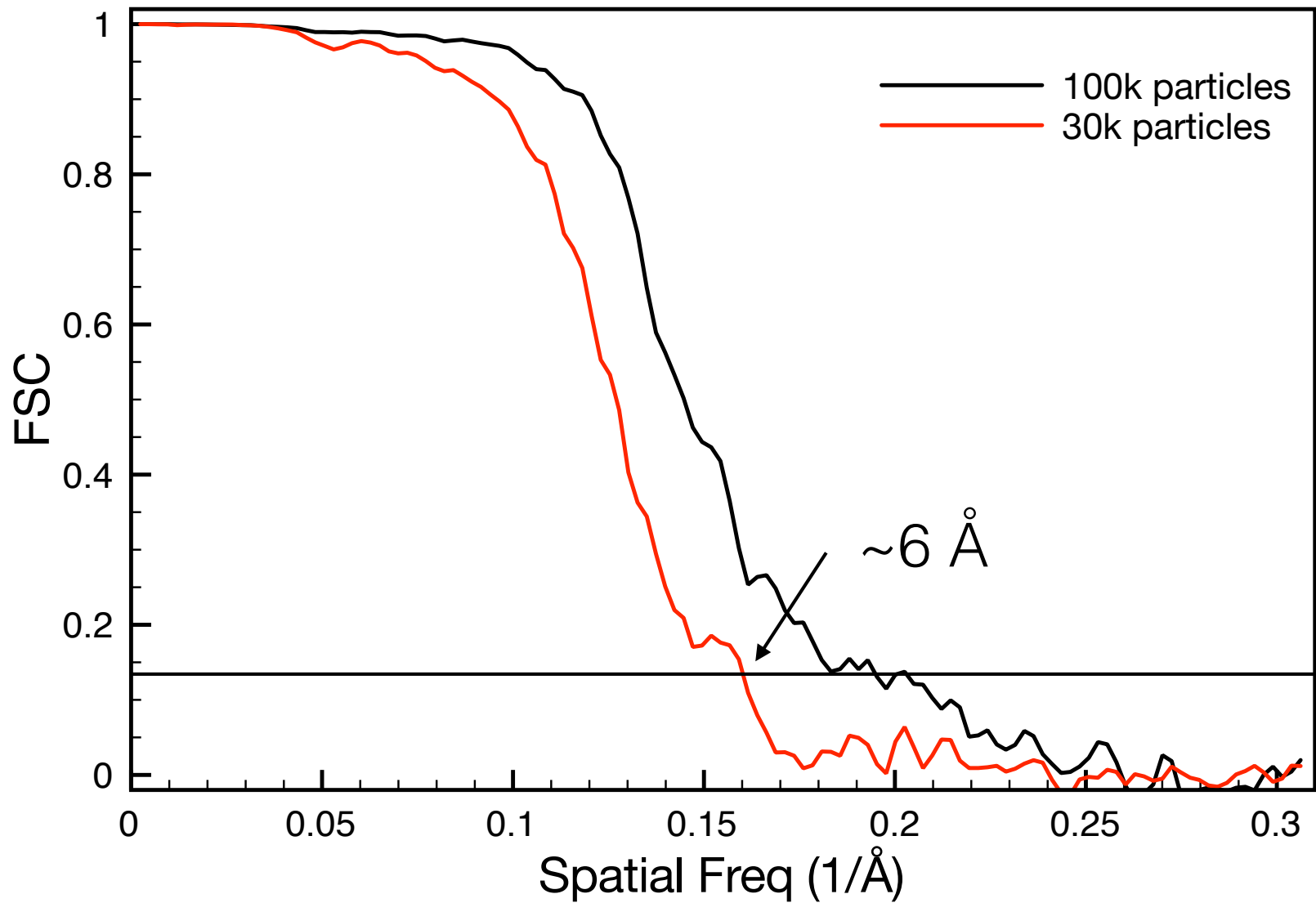
SSNR



SSNR



Particles



Gold Standard Refinement

