Introduction to "What can and can't we see"

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This introduction to the session will be a reminder of some of the changes with resolution that we probably all know about. At what resolution can we see holes in rings? When do the carbonyl groups fade into the backbone? When do nucleic acids shift from connected base pairs to connected density along the base-stacking direction? What feature visibilities differ between crystallography and cryo-EM? And a reminder that it's the local resolution/disorder that matters, not the overall resolution. The image shows two specific regions in T4 lysozyme, the only protein in the PDB with a deposited structure at 1A, 2Å, 3Å, and 4Å.

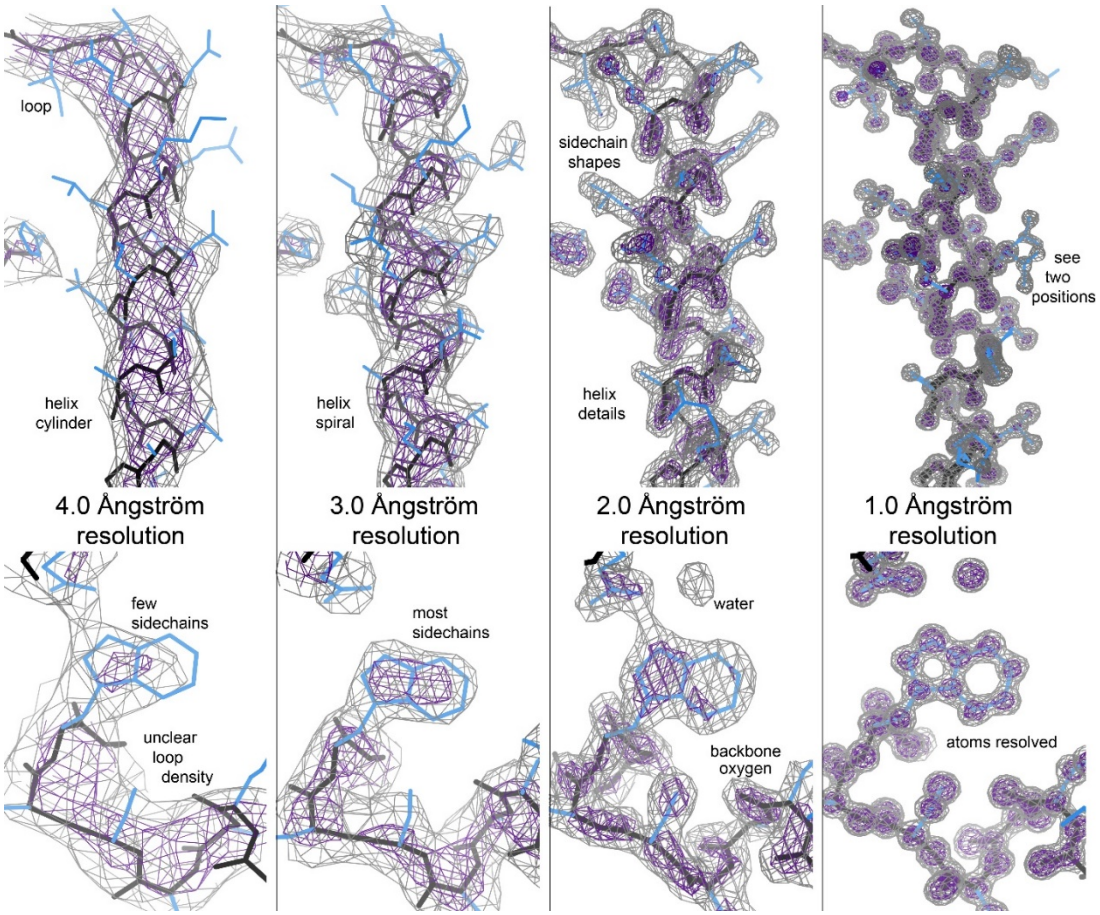

Figure 1