

Protein structure determination

Three things can happen depending on the relationship between the size of the object you're observing and the wavelength λ of the radiation you're using to observe it.

- if λ is significantly smaller than the size of the object, you get reflection, imaging
- if λ is significantly larger than the size of the object, you get no resolution
- if λ is close to the size of the object, you get diffraction

The take-away message about X-ray diffraction vs NMR is this.

- X-rays are the cheapest, easiest way to get Å-resolution radiation in the lab. Also, X-ray crystallography can handle very large proteins. However, you have to first crystalize your protein, and this may take a very long time—if you can even do it at all.
- NMR requires quite a bit of work, but you're pretty much guaranteed to get the data you want when all is said and done. However, there is a size limitation to the proteins you can analyze with NMR.