

Structural biology: Biocrystallography and an appetizer for cryo-EM

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Building on general X-ray diffraction principles, this lecture introduces macromolecular crystallography as a route to structural biology and explains why synchrotron facilities are valuable for protein crystals. Large unit cells, high solvent content, disorder and radiation sensitivity impose constraints less severe in small-molecule crystallography. We will follow the workflow from crystal screening and data collection through structure solution, refinement and biological interpretation, emphasizing how intense, focused and tunable synchrotron beams enable weak, dose-limited measurements and anomalous-scattering experiments.

The phase problem will be presented as the main challenge of macromolecular structure determination. We will briefly contrast molecular replacement with experimental phasing approaches, including SAD, MAD and isomorphous/anomalous methods, and explain why wavelength tunability and beam stability matter. Differences in refinement and validation arising from disorder and limited resolution will be discussed, together with selected applications in structural biology.

The lecture concludes with a short appetizer on cryo-electron microscopy. Cryo-EM does not use synchrotron radiation, but its presence at synchrotron facilities reflects a shared dependence on large infrastructure, instrumentation, computing and open access in modern structural biology.