Protein structure and dynamics using X-ray free-electron lasers

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Protein crystallography using synchrotron radiation sources has had tremendous impact on biology, having yielded the structures of thousands of proteins and given detailed insight into their working mechanisms. However, the technique is limited by the requirement for macroscopic crystals, which can be difficult to obtain, as well as by the often severe radiation damage caused in diffraction experiments, in particular when using tiny crystals. To slow radiation damage, data collection is typically performed at cryogenic temperatures.

The femtosecond X-ray pulses provided by X-ray free-electron lasers (FELs) allow the acquisition of high resolution diffraction data from micron-sized macromolecular crystals at room temperature beyond the limitations of radiation damage imposed by conventional X-ray sources. Moreover, the short duration of the pulses enable time-resolved studies at the chemical time-scale of femtoseconds. The novel sources require new approaches for sample preparation, delivery, data collection and analysis. These approaches [1] as well as recent results obtained will be presented.

References

[1] - I. Schlichting, (2015) IUCrJ 2: 246-255. Serial femtosecond crystallography: the first five years.