

## Macromolecular crystallography in situ data collection strategies at a second-generation synchrotron

In situ macromolecular crystallography is a technique used in structural biology to determine the three-dimensional structure of biomolecules without the need for subsequent handling or modification of the crystals that are operated in their native environment. Exposing macromolecular objects to strong X-ray radiation causes significant damage that has a noticeable impact on the quality and accuracy of the data that can be collected on the crystals under study. Among the diverse approaches applied to minimize the effects of radiation damage, exposing the crystals to low-intensity X-ray beams and short exposure times assists in elongating the life of the exposed samples. The combination of both strategies is especially efficient when using high-speed reading detectors, more widely used at macromolecular crystallography beamlines. The second and third-generation synchrotrons mainly differ in the method that is used for producing and providing the X-ray photons used for the experiments. Although second-generation synchrotrons are still used and offer high-quality X-ray beams, they remain restricted in terms of brightness, coherence, and beam tunability. In the current presentation, we aim to highlight how macromolecular crystallography beamlines at second-generation synchrotrons could be optimized for the industrial development of in situ protein crystallography experiments.

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