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【704】 Serial femtosecond crystallography of two-dimensional protein crystals on solid supports: state of the art and perspectives

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Ultra-short, ultra-bright X-ray pulses from Free Electron Lasers are a viable tool for observing diffraction from two-dimensional (2D) crystals, unlike synchrotron-based data collection, extending the possibilities of structural determinations in membrane proteins.

Using serial diffraction frames from bacteriorhodopsin 2D crystals we extended the resolution limit of zero-tilt data to 4 Å (detector-limited) by summing equivalent portions of images, and developed a method to reconstruct diffraction intensities along Bragg lines, from which structural information can be gained.

Using these methods a data collection strategy (100'000 - 200'000 images at high tilt angles) allowing to detect structural changes in the length-scale of a few Å in a pump-probe configuration can be envisaged.

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