Using Microfluidic as a Tool for Biological Macromolecular Serial Crystallography on a Synchrotron Beamline : Proxima-1

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Abstract

Example of bibliographic citations : [1],[2],[3]

One of the major evolution in recent macromolecular crystallography experiments lies in the implementation of serial crystallography, originally developed for hard x-ray Free-Electron Lasers (FELs), and later adapted to synchrotron sources. These new approaches, allow to further expand the spectre and possibilities in crystallography. The techniques validated to date bring successful results, yet suffer from the requirement of extensive amounts of sample crystals and recorded images to start structure analysis; potentially, this also requires long beamtime shifts at x-ray FELs. At various synchrotron sources including SOLEIL, serial crystallography was adapted by using microfluidic chips[1] to handle batches of macromolecular crystals and expose those to the synchrotron beam. These new developments allow acquiring diffraction data over several degrees *per* crystal, permitting to drop consequently the number of crystals required for acquiring a complete data set. In addition of facilitating a better control during serial crystallography experiments, microfluidic chips provide with the possibility of mastering the crystal environment, the injection of ligands, or even opens access to diffraction experiments on biologically hazardous molecules. Moreover, the trapping method employed within the microfluidic chips facilitates bypassing most of the chemical issues currently occurring when handling and preparing macromolecular crystals for diffraction experiments.

The presentation will highlight the results of microfluidic induced macromolecular serial crystallography at synchrotron SOLEIL. Using specific patterns inspired from an experiment by Lyubimov[2], macromolecular crystals or macromolecular crystal containing cells are trapped at known and precise positions within a microfluidic chip. The chip can then be handled and oriented using an adapted 3D-printed frame placed on the goniometer at PROXIMA-1[3] beamline. Our initial results illustrated here were obtained using an *in house* device; complete data could be acquired with high redundancy prior to solving the structure of a reference protein sample.

References

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