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Automated Analysis of Vapor Diffusion Crystallization Drops With an X-ray Beam on Beamline FIP-BM30A at the ESRF. J.-L. Ferrer, L. Jacquamet, J. Joly, M. Pirocchi, P. Charrault, J. Ohana, A. Bertoni, L. Apostol, R. Kahn, and F. Borel, IBS J.-P. Ebel CEA-CNRS-UJF, 41 rue Jules Horowitz, 38027 Grenoble Cedex 1, France.

Crystallogenesi, usually based on the vapor diffusion method, is currently considered one of the most difficult steps in macromolecular X-ray crystallography. Due to the increasing number of crystallization assays performed by protein crystallographers, several automated analysis methods are under development. Most of these methods are based on microscope images and shape recognition. We propose, on beamline FIP-BM30A at the ESRF^[1], an alternative method of identifying protein crystals, by directly exposing the crystallization drops to an X-ray beam^[2]. The resulting diffraction provides far more information than classical microscope images. Not only is the presence of diffracting crystals revealed, but also a first estimation of the space group, cell parameters, and mosaicity is obtained. In certain cases, it is also possible to collect enough data to verify the presence of a specific substrate or a heavy atom. All these steps are performed without the sometimes tedious necessity of removing crystals from their crystallization drop.

[1] Roth M. *et al.* (2002). *Acta Cryst.* **D58**, 805-814.

[2] L. Jacquamet *et al.* (2004). *Structure* **12**, 1219-1225.