In meso in situ serial crystallography (IMISX) of soluble and membrane proteins using automatic data correction program at macromolecular crystallography synchrotron beamlines

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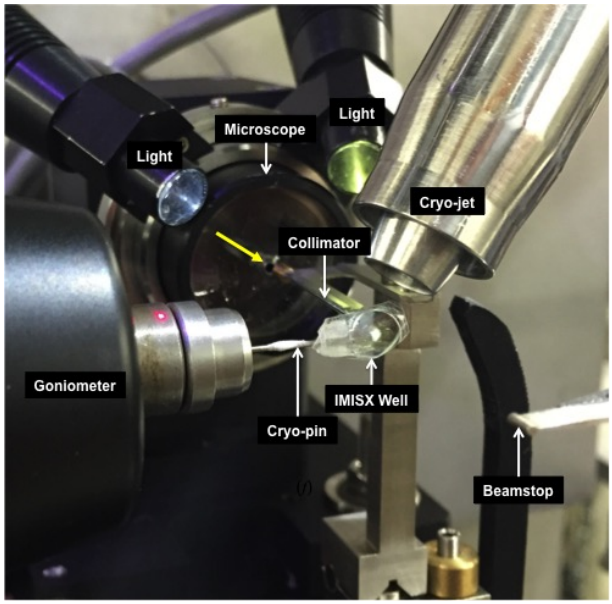
The growing number of membrane protein entries in the Protein Data Bank (PDB) indicates the importance of membrane protein structure for scientific research. Lipid cubic phase (LCP) provides a native-like environment for growing crystals of membrane protein, and resulted in crystals with better packing and resolution [1]. To date, the PDB includes 481 records with 141 unique structures attributed to the LCP method. However, the glass plates designed for crystallization trial of LCP crystals are challenging to harvest crystals from. In response to this challenge, we developed the IMISX method, which employs a thin plastic windowed plate for *in situ* data collection [2, 3]. With the method, hundreds of tiny crystals in LCP can be collected *in situ* in a serial and high-throughput manner at beamline X06SA at the Swiss Light Source by using the variable beam size, fast detector, and dedicated data collection software [4]. The method has been validated with a wide range of membrane proteins including GPCR and applied to solve a *De Novo* structure [2, 3, 5]. The IMISX method works with inexpensive materials and can be adopted at most macromolecular crystallography synchrotron beamlines.



Experimental setup for IMISXcryo data collection at 100 K

References

[1] Caffrey, M., and Cherezov, V. (2009) Nat. Protoc. 4:706-731.

[2] Huang, C.-Y. *et al.,* (2015) Acta Cryst. D71, 1238-1256.

[3] Huang, C.-Y. *et al.,* (2016) Acta Cryst. D72, 93-112.

[4] Wojdyla, J. A. *et al.,* (2018) J. Synchrotron Rad. 25: 293-303.

[5] Ghachi *et al.,* (2018) Nat. Commun. Accepted.