**Poster Presentation**

**MS22.P32**

## *Visualisation of membrane protein crystals using X-ray imaging*

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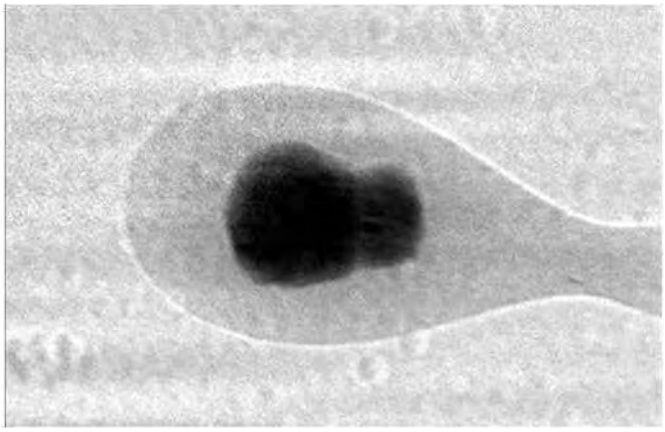
The focus in macromolecular crystallography is moving towards even more challenging target proteins that often crystallise on much smaller scales and are frequently mounted in opaque or highly refractive materials.[1,2] It is therefore essential that X-ray beamline technology develops in parallel to accommodate such difficult samples. In this poster the use of X-ray microradiography and microtomography is reported as a tool for crystal visualisation, location and characterization on the macromolecular crystallography beamlines at the Diamond Light Source. The technique is particularly useful for microcrystals, and crystals mounted in opaque materials such as lipidic cubic phase. X-ray diffraction raster scanning can be used in combination with radiography to allow informed decision-making at the beamline prior to diffraction data collection. It is demonstrated that the X-ray dose required for a full tomography measurement is similar to a diffraction grid scan. However, for sample location and shape estimation alone, just a few radiographic projections may be required; hence reducing the dose the crystals will be exposed to prior to the diffraction data collection.[3]

***[1]*** *J. A. Lyons., D. Aragao, O. Slattery, et al. Nature, 2012, 487, 514-518.,* ***[2]*** *A. S. Doré, N. Robertson, J. C. Errey, et al. Structure, 2011, 19, 1283-1293.,* ***[3]*** *A. J. Warren, W. Armour, D. Axford, et al. Acta Cryst., 2013, D69, 1252-1259.*



**Keywords:** X-ray microtomography, Macromolecular crystallography, Membrane proteins