

## MS03-P12 | ALL-IN-ONE SAMPLE HOLDER FOR MACROMOLECULAR CRYSTALLOGRAPHY

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Various types of sample holders have been developed and are widely used in protein X-ray crystallography [1, 2].

Collection of diffraction data from a single protein crystal involves a number of manual handling step, including crystal fishing, cryo protection and mounting onto an individual sample holder. Numerous enhancements have been done in order to improve many handling steps, including *in-situ screening* to characterize well-diffracting crystals [3, 4].

We have developed a novel type of sample holder, which acts as an all-in-one platform. As a replacement of commonly used cover slips, it supports all steps in the workflow from crystal setup to data collection without any direct crystal handling. Further, crystal manipulation is realized in-place and does not require any handling steps of individual crystals.

Diffraction data collection can be carried out at both, ambient and cryogenic temperature. Additionally, the sample holder is compatible with the SPINE standard format and can therefore be used with automatic sample mounting robots. Finally, with using the new type of sample holder, the number of crystals / dewar can be drastically increased.

The patent pending sample holder can be used on both, 22- and 18-millimeter standard 24-well plates. Auxiliary tools support a straightforward workflow, using the novel sample holder with a minimized chance of damaging sensitive crystalline material.

[1] Papp, G. *et al.* doi:10.1107/S2059798317013742

[2] Pflugrath, J.W. doi:10.1107/S2053230X15008304

[3] le Maire, A. *et al.* doi:10.1107/S0907444911023249

[4] Soliman, A.S.M. *et al.* doi:10.1107/S090744491101883X