

## Poster Presentation

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### *Joint neutron/Xray cryocrystallography: developments for cryocooling experiments*

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Cryo-cooling of protein crystals is not often used in neutron crystallography. However cryo-temperatures are used to block the reaction processes at specific intermediate stages, and this has been widely used in X-ray studies (1); (2). In order to develop this area for joint neutron/X-ray applications, trypsin was chosen as a suitable system for which its interaction with the substrate succinyl-Ala-Ala-Pro-Arg-p-nitro-aniline could be studied (3). Here the neutron developments were carried out in parallel with complementary X-ray techniques, and also using in crystallo UV-visible and Raman spectroscopy. Various strategies for doing this have been tested. The installation of an N<sub>2</sub>-gas-cryostream system on the D19 single crystal diffractometer at the Institut Laue Langevin (ILL) and the development of a new carboloop mounting system, has opened new avenues to perform cryo-cooling experiments using a neutron source. Preliminary data collection carried out at the ILL and at the European Synchrotron Radiation Facility (ESRF), have confirmed the feasibility of the approach. A full description of the experimental procedures and results will be presented. As part of this a new carboloop mounting system has been developed that is suitable for both X-ray and neutron data collection. These mounts resolve the problems of activation and hydrogen incoherent scattering in neutron experiments We describe the use of these and their advantages over conventional X-ray mounting systems - including compatibility with standard magnetic goniometer heads and resistance to cryogenic temperatures.

[1] Garman, E. F. & Schneider, T. R. (1997). *J. Appl. Crystallogr.* 30, 211–237, [2] Moffat, K. & Henderson, R. (1995). *Curr. Opin. Struct. Biol.* 5, 656–663, [3] Radisky, E. S., Lee, J. M., Lu, C.-J. K., & Koshland, D. E. (2006). *Proc. Natl. Acad. Sci. U. S. A.* 103, 6835–6840

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