

liquid handling advances, new micro-plates and specialized gas-tight and strong-binding plate seal developments have enabled the adoption of automated procedures for seeding, for experiments under oil (with the MRC micro-batch plate) and for crystallization at high temperature (up to 50°C). A novel crystallization screen called Morpheus (commercialized by Molecular Dimensions) as also been developed recently [4].

[1] Stock D., Perisic O., Löwe J., Robotic nanolitre protein crystallisation at the LMB, *Prog. Biophys. Mol. Biol.*, **2005**. [2] van den Ent F. et al., Structural and mutational analysis of the cell division protein FtsQ, *Molecular Microbiology*, **2008**. [3] <http://www2.mrc-lmb.cam.ac.uk/screens.html> (Gorrec F., Hart P., **2007**). [4] Gorrec F., The Morpheus screen: putting pieces together, in Press.

Keywords: automation; screening; innovation

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X-ray Diffraction from Crystals in Crystallization Plates. Tadeusz Skarzynski. *Oxford Diffraction Ltd., Oxford Industrial Park, Yarnton, Oxfordshire, OX5 1QU, United Kingdom.*

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The PX Scanner is a unique instrument from Oxford Diffraction enabling the identification and characterization of protein crystals with X-rays, in-situ, in the crystallization plate. The PX Scanner addresses the bottleneck in high-throughput crystallization allowing a quantitative evaluation of the diffraction properties of crystals without having to manually extract crystals from the crystallization plate. Combining an optical imaging system with a powerful, micro-focus Cu X-ray source, highly sensitive CCD detector and intuitive software provides an essential laboratory resource for crystallographers involved in difficult structural biology projects.

The PX Scanner is now further enhanced with new software named CrystalEyes. CrystalEyes expands the functionality of the PX Scanner, utilizing new algorithms to improve the acquisition and quality of the optical and X-ray images. Furthermore, new database access capabilities allow the data to be easily output from the PX Scanner and integrated with a 'LIMS' style lab data management system.

We will show how the PX Scanner can be used as a powerful tool providing valuable feedback at all stages of macromolecule crystallization, including differentiating salt from protein crystals in initial screens, selecting the best crystals for synchrotron X-ray data collection, optimizing harvesting, cryo-protecting and soaking conditions, and determining crystal lattice parameters.

Keywords: crystallization of macromolecules; in-situ experiments; X-ray methods