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].

van den Ent F. et al., Structural and mutational analysis of the cell 
www2.mrc-lmb.cam.ac.uk/screens.html (Gorrec F., Hart P., 2007). 
Press.

Keywords: automation; screening; innovation

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X-ray Diffraction from Crystals in Crystallization 
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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 
aquisition 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