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Getting the Most Out of Your Synchrotron. Conn Mallett, Joseph D. Ferrara, Colin Acheson, Keith Crane, Angela Criswell, Pierre Le Magueres, Bret Simpson. *Rigaku Americas Corporation, 9009 New Trails Drive, The Woodlands, TX 773381, USA. Rigaku Europe, B6 Chaucer Business Park, Sevenoaks, Kent UK.*
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X-ray diffraction data collection at synchrotron beam lines is an essential tool for crystallographers to solve protein crystal structures. The characteristics of the X-ray beam: high intensity, low divergence, very small size, and tuneable wavelength are features required for anomalous diffraction phasing methods, high-resolution structure refinements and data collection on weak and difficult samples. In addition, the proliferation of synchrotron beam lines in many countries and the increased availability of beam time has made synchrotron facilities accessible to virtually every crystallographic laboratory in the world. To use the synchrotron most effectively, it is absolutely essential that crystallographers arrive prepared with samples whose quality and cryo-conditions have been previously tested and optimized at home. To address this, Rigaku has developed new instruments that will help researchers screen large numbers of samples in their own lab and recover those suitable for synchrotron data collection. In this work we will present:

The UV crystallization imaging systems from the Minstrel family, combining a UV light source with a visible light source in order to quickly detect protein crystals in crystallization drops and distinguish them from salt or detergent crystals.

The new ScreenMachine, a simple and self-contained X-ray diffractometer optimized for fast and easy screening of crystal candidates at home.

The automatic sample changer ACTOR, which can reliably mount and dismount a large number of samples without user intervention.

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