

The next generation of MX sample evaluation

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It is very common for crystals of large biological macromolecules, even when obtained under notionally identical conditions, to show considerable variation in the quality of their diffraction. This is almost certainly the result of the intrinsic physical properties of the systems being studied. Current data collection trends at the ESRF MX beam-lines show clearly that automation has led to a fundamental change in the way that MX data are collected. With the introduction of the automatic sample changer (SC3) at the ESRF MX beam-lines in 2005, a dramatic increase in the number of samples that were tested for diffraction quality before any full data collections were carried out was observed.

While there is already a high level of automation of sample handling on the ESRF MX beam-lines it is clear that there is a huge demand to increase the speed and capacity available. This can be achieved by improving the automation of the sample evaluation process through both software and hardware developments. The ESRF is seeking to address the needs of the MX community in the next decade by UPBL10 (MASSIF). This facility will have at its core three beam-lines optimised for highly automated high-throughput sample evaluation.