

The Upgrade Programme for the Structural Biology Beamlines at the ESRF

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Structural Biology is faced nowadays to tackle more and more challenging projects, for example large macromolecular assemblies or more complex membrane proteins. Crystals from such complex systems often show considerable inter- and intra- crystal variability with respect to diffraction quality. Sample evaluation of dozens to thousands of crystals prior to data collection will thus become even more crucial as it is today as will data collection facilities optimised for the collection of diffraction data at longer wavelengths or from crystals that are very small and/or diffract to low resolution (i.e. $d_{\min} > 5 \text{ \AA}$).

The Upgrade Programme for the Structural Biology beam lines of the European Synchrotron Radiation Facility (ESRF; <http://www.esrf.fr/AboutUs/Upgrade>) will develop a unique resource, based on 2nd generation automation, designed to maximise the success rate for macromolecular crystallography (MX) experiments. The hub of this resource will be a sample evaluation and sorting facility, *MASSIF*. Macromolecular crystals that have been tested to be most suitable for diffraction data collection will be distributed from this hub to upgraded MX data collection beamlines that also form an integral part of the ESRF's upgrade plans.

The ESRF's Structural Biology Group's upgrade plans will be presented, with particular emphasis on a refurbished ID29 which will be optimised to enable diffraction data collection from crystals of macromolecules using x-rays of lower energies ($E = 5 \text{ keV}$, $\lambda = 2.5 \text{ \AA}$). Recent successes in the solution of a macromolecular crystal structure exploiting only the small anomalous signal from sulphur atoms innate to protein amino acid sequences will be also be described.