Massif-1 at MASSIF-1 and fragment based drug design Didier Nurizzo¹ ¹N/A nurizzo@esrf.fr

With the upgrade of EBS-ESRF storage ring, MASSIF-1 beamline entered a phase of refurbishment and upgrade. Since August 2020, it is equipped with a micro-diffractometer and mini-kappa. It is also fitted with an ESRF-FlexHCD sample changer taking up to 368 samples in Unipuck. The CrystalDirect harvester (CDh) for automatic harvesting of crystals is also installed since May 2021. These main improvements open new technical developments including plate screening and dehydration protocol to push forward macromolecular crystallography and elucidate challenging projects.

The beamline evolved in automatic data collection with the experience gained over 70,000 crystals collected since 2014. "User-free" data collection follows a well-established protocol in accordance with the decision-making workflow including automatic sample loading, optical and X-ray centring, crystal size measurement, crystallographic characterization, data collection strategy and data collection processing. We strengthen the quality of the services by adapting the beam diameter to match the best diffracting volume with the development of DOZOR software. The process is tracked on-line in the EXI database and data are retrieved via the web interface.

The CDh can deliver chemicals by diffusion from a solution to the top of the laser-generated aperture prior to crystal mounting. The automatic data processing is able to run molecular replacement based on the model declared in EXI. This development offers the option to provide the structure of the small molecules or even cocktail that have been soaked. The peaks in difference Fourier map are automatically fitted with the ligands. The automation from crystallisation/soaking up to structure solution opens with fragment based drug design a new era for structural biology in the field of health and medical science.