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A Crystallization Platform Enabling Automated *in situ* Diffraction Screening. Rouven Bingel-Erlenmeyer[a], Vincent Olieric[a], Meitian Wang[a], Clemens Schulze-Briese[a]. [a]*Swiss Light Source, Paul Scherrer Institut,CH-5232 Villigen, Switzerland.*
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The structural genomics era has promoted high throughput methods in the crystal structure determination process. However, generating macromolecular crystals suitable for structure solution remains a time consuming iterative process. Initial crystallization hits yielding low resolution data have to be evaluated in the X-ray beam before the crystallization conditions are further optimized. In order to shorten the time for this loop the Swiss Light Source has built a crystallization facility which is directly interfaced with the superbend magnet protein crystallography beamline X06DA. This unique configuration allows users to request and evaluate crystallization experiments using nano-dispensing robots and automated imaging systems. Moreover, it will enable to screen initial crystals *in situ* in the X-ray beam for their diffraction behaviour in an automated manner. Therefore, the novel layout designed by the Swiss Light Source gives users a rapid feedback on the diffraction limit, anisotropy, cell parameters, and mosaicity of their crystals. It also aids to prioritize subsequent optimization steps which could be carried out at the Swiss Light Source crystallization facility. We will present first results on the crystallization platform and the *in situ* diffraction screening. In addition, a perspective on the ongoing activities is given.

Keywords: protein crystallization; automation; in situ diffraction

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Latest Developments of *in situ* Dynamic Light Scattering and Imaging to Analyze, Score and Optimize the Crystallization Process. Arne Meyer[b], Dierk Hilterhaus[a], Karsten Dierks[a], Christian Betzel[b]. [a]*Dierks & Partner Systemtechnik, Hamburg-Germany.* [b]*University of Hamburg, Department of Chemistry, Hamburg-Germany.*
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In the field of protein crystallization several fully automated instruments are available to support the search for crystallization conditions of macromolecules. Nevertheless, to find optimal growth conditions remains a bottleneck. Therefore we have designed and constructed a so far unique hardware combination, which supports the identification of suitable crystallization conditions and can control the crystallization process in the desired direction. One applied method and technique is dynamic light scattering (DLS), which has already many applications, but which we have found useful for detection of aggregation and nucleation in droplets. The other is the use of combined white/UV illumination for microscopic determination of whether crystal-like objects are biomolecular and identification of crystals in crystallisation set ups. The outcome is an advanced instrumentation, which combines a imaging and dynamic light scattering (DLS) system for routine measurements in drops in standard multi-well plates used in protein crystallization as well as geltube crystallisation experiments and crystallization experiments kept under oil, allowing a systematic optimization of the crystallization process. Furthermore the system is most suitable for upscaling crystallization conditions obtained in nanodrops prepared by crystallization robots towards higher volumes yielding more X-ray suitable crystals. The system was tested with several standard proteins and found to be of high value for rapid identification of good crystallization conditions. A relationship between the rate of protein-aggregate-size increase and the probability of crystal formation was observed and results will be presented accordingly. All together the newly designed hardware has several advantages: no additional pipetting is necessary to perform measurements; the crystallisations process can be monitored online in situ, without interruption; measurements can be taken from even small volumes. This new DLS technique has been adapted to an automated CCD-camera-based plate-screening system (Spectro-Imager 501) allowing monitoring and evaluation of the entire process of crystallisation in an automated way. The data obtained provide information to understand in detail the process of crystal growth. Finally we will also describe in detail a method to support the identification of protein crystals, exploiting the fact that most proteins and other biomolecules fluoresce when illuminated with UV light. The Spectro-Imager 501® is a completely new instrumental design incorporating all of the techniques described above in one device. Images taken from various droplets/set ups will be presented along with corresponding DLS measurements

Keywords: crystallogenesis; crystal growth kinetics; image analysis