MS03 Crystallization and biophysical characterization

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Successful sample preparation for serial crystallography at synchrotrons and XFELs

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The applications and potential advantages of serial crystallography, at both synchrotron and XFEL light sources, are growing. Despite advances in delivery methods, the sample volumes of micro-crystals required for serial crystallography, particularly time-resolved experiments, are still demanding. Batch crystallisation methods are the primary means in crystallographers toolbox to create these samples. However, the process to convert single crystals grown by vapour diffusion to large volumes (> 100 µL) of micro-crystalline slurry can be exceptionally challenging.

To try and ease the process, we have formulated a strategy to perform this translation. It is divided into three stages: (1) optimising crystal morphology, (2) transitioning to batch, and (3) scaling. Given the variation of protein crystallisation, we hope that this protocol can act as a useful framework when attempting the conversion from vapour diffusion to batch.

In this talk, I will explain how this process was developed and applied to model proteins. Then I will talk about some of the experiences, good and bad, we have had with user proteins at the SLS and SwissFEL. I will finish with a peak at some results from how this user crystals fared at the new SwissFEL endstation, Cristallina.