Getting the best from your samples: On-line dehydration and diffraction cartography

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The weakly diffracting nature of protein crystals often leads to data of insufficient quality to answer the biological question being asked, either due to a failure to solve the structure or to other factors, such as insufficient resolution to accurately determine modes of ligand binding. Increasing the diffraction limit and quality by dehydration has been performed since the earliest days of crystallography. A new device has been developed to produce an air stream at the sample position allowing precise control of the relative humidity (RH) between 50 and 99% making dehydration experiments a practical way to improve the diffraction properties of some protein crystals.

Once an experiment has started selecting the most ordered part of a relatively large crystal or searching for small (<10 μm) crystals is often challenging and time consuming. Interfaces to assist with these screening methods will be presented. For the case where the diffraction quality of a relatively large crystal is probed using a mini beam the usefulness of mapping diffraction quality heterogeneity is considered.