Poster Presentation

Optimizing Data Collection in the Home Lab

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Many of the projects currently under investigation in biological research labs focus on macromolecules that are difficult to crystallize such as: complexes, multi-domain and membrane proteins. Typically, crystallization trials can produce small, weakly diffracting crystals that may also have other challenging attributes. Recent hardware and software developments have improved in-house data quality on a wide range of samples. Small and highly focused x-ray beams allow one to select the best diffracting portion of a larger crystal and reduce background scatter for much smaller samples. Shutterless data collection helps to reduce instrument error resulting from shutter jitter and allows fine slicing of data runs without frame to frame dead time penalties while the practice of dealing with multiple, cracked or twinned crystals has improved greatly due to software enhancements. Results from in-house data collection including: shutterless operation, optimization of crystal orientation and collection parameters will be discussed.

Keywords: data collection, shutterless mode