Poster Presentation

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Detection of protein nanocrystals based on the reversibility of crystallization

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A prerequisite for conventional X-ray protein structure analysis is the growth of crystals with a sufficient size in the range of several µm. This is a time consuming and not always successful process, challenging especially when working with membrane proteins. The recently developed technique of femtosecond X-ray crystallography enables structure analysis of crystals with a size in the nm range, thus the process of growing large single crystals can be avoided. Moreover femtosecond X-ray nanocrystallography is a potential method to overcome the radiation damage problem and to perform time-resolved structure analysis (1, 2). Nanocrystals are too small to be detected with an optical microscope, hence crystal growth cannot be monitored with common methods used in crystallography. A powerful technique to screen for nanocrystals is Second Order Nonlinear Imaging of Chiral Crystals (SONICC). This method is based on the principle of second harmonic generation and detects noncentrosymmetric ordered crystals (3). However, the instrumentation is not generally accessible yet. In addition, proteins ordered in higher symmetry crystal classes do not necessarily lead to a positive SONICC signal. In this work, a new method is developed to screen for nanocrystals based on the reversibility of crystallization. We show that dilution experiments performed with a crystallization robot and monitored by a crystallization imaging system enable the distinction between precipitation comprised of nanocrystals and precipitation caused by aggregated protein.

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