Crystallization strategy when no crystals are obtained in the initial screening

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Protein crystallography is an indispensable tool in the pharmaceutical and biochemical sciences. Refinements of the protein crystallography beam lines and their integrated programs for crystal structure analysis allow us to perform automatic or semi-automatic structural determinations using well-diffracted crystals. However, the production of well-diffracted crystals is still a bottleneck, even when using crystallization robots and common screening kits. The process of protein crystallization does not follow a standardized, routine protocol, except in the case that good crystals are obtained at an initial crystallization screening. In the more frequent case that no crystals or only poor crystals appear at the initial screening, there is no general consensus regarding the next step. Nonetheless, even in the absence of well-diffracted crystals at an initial screening, it is still possible to optimize the crystallization conditions based on the accumulated data from a wide range of protein-crystallization attempts. The more such crystallization data are available, the more appropriate and efficient optimization will be possible, since the crystallization conditions differ for each protein. Therefore, at our laboratories, we are currently trying to accumulate many experiences of protein crystallization and crystal quality improvement of poor crystals through collaboration with not only academia but also with pharmaceutical companies. Here, we present our strategy for the efficient generation of good quality crystals and the successful application of our crystal quality improvement method to histone chaperone TAF-Ibeta, the CagA oncoprotein from Helicobacter pylori and GTP sensor PI5P4Kbeta. We believe that our strategy will be applicable to other proteins as well.

Recent Publications


Biography

Miki Senda has completed her PhD from Nagaoka University of Technology in 2008. She is an Assistant Professor of Structural Biology Research Center in High Energy Accelerator Research Organization (KEK). She has several collaborations in which she has worked as an expert of protein crystallization and crystal quality improvement. She received Oxford Cryosystems Low Temperature Prize at the 63rd Annual meeting of the American Crystallographic Association (ACA) in 2013.