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A comprehensive strategy to obtain high quality crystals

Current X-ray sources of synchrotron radiation enable us to determine the crystal structures of proteins even if the crystals were diffracted only to medium or low resolution. However, high-resolution crystal structures are still required for the pharmaceutical and biochemical sciences. When obtained crystals were of poor quality and insufficient for crystal structure determination, post-crystallization treatment could improve the crystal quality. Our experiences of crystal structure analyses of histone chaperon TAF-Iβ, CagA oncoprotein from *Helicobacter pylori* and GTP sensor PI5P4Kβ showed that crystal soaking into cryoprotectants improved crystal-quality (1, 2 & 3). Of the three proteins, crystal qualities of CagA and PI5P4Kβ were significantly improved by using more than one cryoprotectant. This method, multi-step soaking method, improved not only the maximum resolution but also success rate of high resolution data collection. Reproducibility of the crystallization is another critical problem in determining crystal structure. Anaerobic crystallization and immediate observation method are effective to improve the reproducibility of the crystallization. We would like to report some examples of the crystallization and crystal quality improvement by our strategy.

Biography

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

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