# Comprehensive strategy for quick determination of protein structures

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A special advantage of protein crystallography is quick determination of target proteins for biological science and high-throughput structure determination of a large number of protein-compound complexes for pharmaceutical science. To achieve the quick structure determination, utilization of well-experienced protein crystallization technique and the latest approach of structure determination are crucial. We developed a standard protocol to obtain well-diffracted crystals through a lot of projects. At the first step, our integrated crystallization robot is useful for the initial crystallization screening. If crystals appeared at several conditions, we evaluate their crystal quality and choose relatively good crystals based on the snapshot images using X-ray. When obtained crystals have insufficient quality, cryoprotectant screening is effective to improve the crystal quality in many cases. Qualities of various crystals have been improved using our strategy when original crystals were of poor quality (1, 2, 3, 4). MR-native SAD method is quite useful for quick structure determination with semi-automatic model building program. Diffraction data collection using lower energy X-ray like 1.9 Å or 2.7 Å wavelength is essential for measurement of an anomalous signal from sulfur atoms (5). Here we show several examples of crystal structure determination using MR-native SAD method. In some cases, MR-native SAD method easily gave high quality model without manual model building despite MR method gave poor model which was too difficult to fix problems by manually. References 1. Hayashi et al., (2017) Cell Reports 20, 2876. 2. Senda et al., (2016) Crystal growth & Design 16, 1565. 3. Sumita et al., (2016) Molecular Cell 61, 1. 4. Hayashi et al., (2012) Cell Host Microbe 12, 20. 5. Liebschner et al., (2016) Acta Crystallogr. D 72, 728.