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Editorial

Serial X-ray Crystallography II

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Traditional macromolecular crystallography (MX) and recently spotlighted cryogenic electron microscopy (Cryo-EM) techniques have contributed greatly to the development of macromolecule structures and the related fields [1–7]. Although these methods are widely applied, they are limited by a cryogenic environment and radiation damage [8,9]. In this Special Issue, we covered a serial crystallography (SX) technique that overcomes the experimental limitations of MX and CryoEM. Because SX can determine the biological crystal structure at room temperature, it provides good biologically relevant information despite a molecular flexibility or fluctuation [10,11]. In addition, because the crystal sample is exposed only once to X-rays, it can provide accurate structural information by minimizing radiation damage [11]. Furthermore, pump–probe experiments using an optical laser and the liquid application method of the mix-and-inject concept are used to time-resolve the molecular substrate or inhibitor recognition process to provide an accurate reconstruction of the entire reaction mechanism and expand our knowledge [12–15].

Starting with serial femtosecond crystallography (SFX) using an X-ray free electron laser (XFEL) [11], the SX technique is widely applied to serial synchrotron crystallography (SSX) using synchrotron X-rays [16], which can aid in obtaining in-depth and accurate structural information. Although the SX experimental technique provides remarkable research results, it requires more effort than other methods in terms of the experimental aspects of the preparation of a crystal sample, the sample's delivery, and data processing [17–21]. Accordingly, studies that have contributed to the development of serial X-ray crystallography have been collected in this Special Issue. Herein, we briefly covered serial crystallography techniques [22], one review related to crystallization [23], and two research articles on SX [24,25].

Jang et al. reviewed general X-ray crystallography experiments for the crystallization, data collection, and structural determination [23]. In addition, various types of cryoprotectant solutions have been reviewed, along with the radiation damage and diffraction quality improvement [23]. This review aims to not only inform the reader regarding traditional protein crystallography experiments but also provides useful information for evaluating the sample's quality prior to SX applications.

Nam introduced a method to index the diffraction patterns obtained from multiple crystals using a serial crystallography program [24]. Owing to the nature of serial crystallography research, multiple crystals are exposed to X-rays during the sample delivery, resulting in a multicrystal diffraction pattern [17]. Programs have been developed to extract multicrystal diffraction patterns from these data [20] which can be used in macromolecular crystallography [24]. This approach contributes to lowering the boundary between MX and SX in data processing.

Kim and Nam reported experiments on serial crystallography using pink-beam X-rays in PLS-II [25]. Pink-beams not only have a higher flux than monochromatic beams but also provide more reflection information [26]. As a result, they have the advantage of reducing the amount of sample consumption and X-ray exposure time of the crystal sample [25,26]. Thus, pink-beam X-ray and various pump–probe experiments significantly contribute to the development of serial crystallography techniques and protein structure research.

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Overall, the contents covered in this Special Issue will contribute to the development of SX and MX.

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