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Serial crystallography of a G-protein coupled receptor using polychromatic synchrotron radiation source

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Since the first successful serial crystallography (SX) experiment at synchrotron radiation sources, the popularity of this approach has continued to grow, showing that 3rd generation synchrotrons can be viable alternatives to scarce X-ray free electron laser sources. Synchrotron radiation flux may be increased about 100 times by a moderate increase in bandwidth ("pink beam" conditions) at some cost in data analysis complexity. Here, we report the first high-viscosity injector-based pink beam SX experiments. The structures of A_{2A} adenosine receptor (A_{2A}AR) and proteinase K (PK) were determined to 4.2Å and 1.8Å resolution using 24 and 4 consecutive 100 ps X-ray pulse exposures, respectively. Strong PK data were processed using existing Laue approaches, while weaker A_{2A}AR required an alternative data processing strategy. This demonstration of the feasibility presents new opportunities for the time-resolved experiments with micro-crystals to study structural changes in real-time at pink beam synchrotron beamlines worldwide.

Biography

Ming Yue Lee is an expert in macromolecular crystallography with focus on technology development and implementation in novel membrane protein crystallization and diffraction methods. He has made contributions in the field of GPCR structural biology in the forms of active participation and validation of serial femto-second crystallography using XFEL sources, as well as being involved in validation of delivery mechanisms for various cutting-edge diffraction experiments both at XFEL and synchrotron radiation sources. He is actively leading and driving the effort to develop and implement technology that can enhance and optimize serial crystallography at polychromatic synchrotron radiation sources. His current focus is building up a system approach to study membrane protein structure-function relationships between different components of the cellular membrane environment with an emphasis on spatial and temporal resolution of proteomic interactions.

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