Laboratory of Supermolecular Crystallography

Institute for Protein Research

Professor Atsushi NAKAGAWA atsushi @protein.osaka-u.ac.jp

Associate Professor Eiki YAMASHITA eiki@protein.osaka-u.ac.jp

URL: http://www.protein.osaka-u.ac.jp/rcsfp/supracryst/

There are various biological macromolecular assemblies consisting of proteins, nucleic acids, sugars, lipids, and other substances in living cells. These macromolecular assemblies play key roles in all living systems. Our laboratory works on structure determination of biological macromolecular assemblies, as well as proteins, which play important roles in biological systems, using X-ray crystallography and cryo-electron micrography. Development of tools for X-ray crystal structure determination of biological macromolecular assemblies, including synchrotron radiation beamtime at SPring-8, is also one of our main works.

Development of a method for structural analysis of biological macromolecular complexes

Crystals of biological macromolecular complexes are known to have larger lattice constants and much weaker diffraction intensities than ordinary protein crystals. Furthermore, many of them are easily damaged by X-ray irradiation. In order to measure the diffraction intensity data from such biological supramolecular complex crystals with high resolution and accuracy, we are operating a contract beamline, BL44XU, at SPring-8, a large synchrotron radiation facility. In addition, we are developing new X-ray crystallography methods, such as high-precision data acquisition methods and automatic structure refinement pipeline.

Structural analysis of biological macromolecular assemblies

Our laboratory aims to elucidate the molecular interactions and molecular recognition mechanisms that are important for understanding biological functions based on precise atomic structures. For this purpose, X-ray crystallography and cryo-electron micrography are used.

Major research targets include Rice dwarf virus with a molecular weight of 75 million, PfV, a virus-like particle that forms stable spherical particles even under high temperature conditions of over 90 ˚C, drug efflux complexes that play an important role in drug resistance in *Pseudomonas aeruginosa*, one of the bacteria causing hospital-acquired infections.

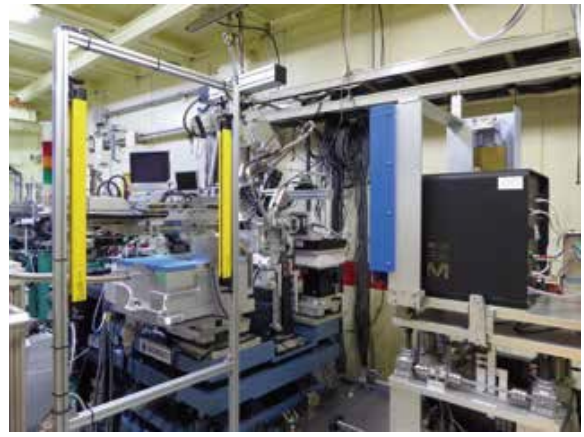

Figure 1: SPring-8's Biological Macromolecular Structure Beamlines

Structural analysis of proteins important for biological functions

Following the results of the Protein 3000 Project, which has been carried out for five years since FY2002, and the Targeted Proteins Research Program, which has been carried out for five years since FY2007, we aim to further develop these projects and conduct research aimed at understanding the structure and functions of proteins important for biological functions through the structural analysis of many proteins inside and outside of the university.

We are collaborating with laboratories. Major research targets include novel families of membrane potential sensor proteins, intracellular signaling protein complexes, and intercellular adhesion molecules.

Please keep in mind to acquire a broad perspective, not limited to your specialty.

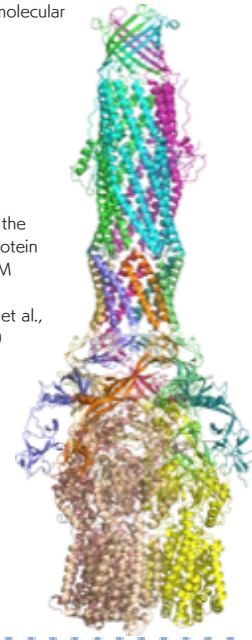

Figure 2: Structure of the foreign body efflux protein complex MexAB-OprM from Pseudomonas aeruginosa (Tsutsumi et al., *Nat. Commun.*, 2019)

Institute for Protein Research, Osaka University
3-2 Yamadaoka, Suita, Osaka 565-0871, Japan
TEL: +81-6-6105-8635
FAX : +81-6-6105-4313

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