Structural biology using synchrotron radiation and cryo-electron microscopy

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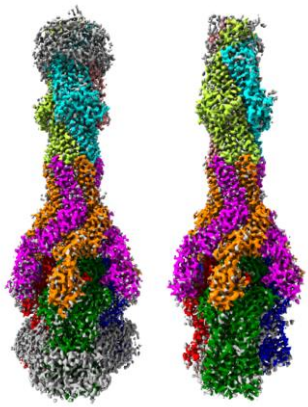
Abstract

X-ray crystallography and cryo-electron microscopy are two major tools for structure determination of biological macromolecules. High-brilliant X-ray source, synchrotron radiation, and state-of-the-art cryo-electron microscopy enable us to determine high-resolution structures of biological molecules. The Institute for Protein Research (IPR) of Osaka University is operating a synchrotron radiation beamline for biological macromolecular assemblies at SPring-8, and we offer beamtime to the researchers outside of the institute as one of the main facilities of the Joint Usage and Research Center for Proteins. The IPR also offers joint use of the top-end cryo-electron microscopy (Titan Krios, Themo Fisher Scientific).

The MexAB–OprM efflux pump of *Pseudomonas aeruginosa* is central to multidrug resistance of this organism, which infects immunocompromised hospital patients. The MexA, MexB, and OprM subunits were assumed to function as the membrane fusion protein, the body of transporter, and the outer membrane channel protein, respectively. MexAB–OprM belongs to the Resistance–Nodulation–Division (RND) family and consists of total of twelve protein components of three different proteins: six copies of MexA, three copies of MexB and three copies of OprM. To understand the molecular mechanism of complex formation and substrate recognition of MexAB-OprM from the atomic structure, we performed the structural analysis of each component of MexAB–OprM, MexA[1)] and OprM[2)], by X-ray crystallography and MexAB–OprM in both drug absence or presence state by cryo-electron microscopy and single-particle analysis[3)].



Structure of MexAB-OprM

Key words: Synchrotron Radiation, Cryo-electron Microscopy, Multi-drug efflux pump

References

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