Laboratory of CryoEM Structural Biology

Institute for Protein Research

Professor	Takayuki KATO	tkato @protein.osaka-u.ac.jp
Assistant Professor	Jun-ichi KISHIKAWA	kishi.jun @protein.osaka-u.ac.jp
Assistant Professor	Hiroko TAKASAKI	takahiro @protein.osaka-u.ac.jp

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

A protein is one long biopolymer consisting of 20 different amino acids joined by peptide bonds. According to a program called amino acid sequence, proteins spontaneously assume a fixed three-dimensional structure and act as sensors, motors, or other machines that can perform almost any function imaginable by humans. In order to elucidate how these nano-sized molecular machines adopt their three-dimensional structures and what mechanisms are responsible for their functions, we are performing structural analysis using cryo-electron emission microscopy (cryo-EM).

Analysis of the operating mechanism of molecular motors

Proteins flexibly and repeatedly undergo conformational changes in vivo to perform their functions. Flagellar motors and ATPases, which are rotating molecular motors, are examples of such proteins. In order to elucidate this mechanism, it is necessary to capture the conformational changes of these molecular motors while they are in motion. Cryo-EM allows us to take images of various structural states and visualize the motion by connecting them. In this way, the mechanism can be clarified from the structural analysis of the functional state.

Structural analysis of olfactory receptors

Humans are able to sense tens of thousands of odors through the use of some 400 different olfactory receptors. These olfactory receptors are seven transmembrane proteins belonging to the G protein-coupled receptor (GPCR) family. There are few examples of structural analysis of the binding of volatile odor molecules to these olfactory receptors, and most results are based on calculations of how odor molecules are recognized and bound. Therefore, cryo-EM is used to analyze the structure of the odor molecule binding state.

Development of cryo-electron microscopy and analysis methods

In the past, the low resolution of cryo-EMs made it impossible to construct atomic model molecules on their own. However, with the advent of new electron microscope cameras developed in the 20131990s, structures of large complexes and membrane proteins that could not be analyzed by other methods can now be analyzed at atomic resolution. As a result, cryo-EMs are now used first and foremost for proteins that would otherwise be difficult to crystallize. Despite the rapid development of cryo-EM, there are still many problems to be solved. It is still developing and still has a lot of potential. We are developing imaging and analysis methods to maximize their potential.

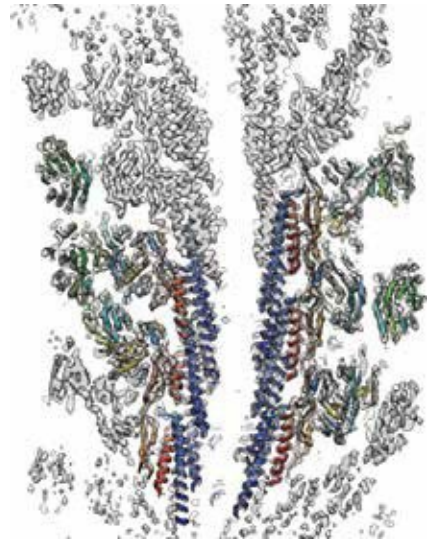

Fig. Structure of 1flagellar hook
The flagellum is in a bent state, and cryo-EM is the only technique that can analyze the structure of the flagellum in this bent state.

Fig. 2 Cryo-electron microscope owned by the Institute for Protein Research
The Institute for Protein Research has one of the world's best cryo-electron microscopes and one electron microscope for screening, providing a smooth environment for protein structure analysis.

It is a privilege to be a student to experience the joy of learning and discovery. Learn and play as much as you like.

Institute for Protein Research, Osaka University
3-2 Yamadaoka, Suita, Osaka 565-0871, Japan
TEL&FAX: +81-6-6105-6079

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