Laboratory of Protein Crystallography

Institute for Protein Research

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Our laboratory analyzes the three-dimensional structure of protein complexes using protein crystallography and cryo-electron microscopy to understand biological functions based on the three-dimensional structure. We do not believe that we can understand all biological systems by analyzing the structure of purified proteins, but are trying to understand the basic reactions of life, such as "respiration," "photosynthesis," and "cellular motility". When we consider only those proteins in "bioenergetics," its function can be understood on the basis of the three-dimensional structure of complex proteins. A good example is the crystal structure of F1-ATPase (Nobel Prize in Chemistry 1998), which was analyzed as it were about to start rotating. In our laboratory, we have been working on "photosynthesis" and "molecular motors" with the keywords of "energy converting supramolecules".

Bioenergetics of photosynthetic, and related redox metabolic networks

By structurally analyzing the membrane protein complexes and related redox proteins in the energy transacting membranes, we aim to elucidate the dynamic regulation mechanisms of these functional biological membranes. Specifically, we are focusing on understanding the electron transfer mechanism around Photosystem I complexes through ferredoxin, the mechanism of cyclic electron flow around cytochrome b6f complex, and the mechanism of supramolecular complex formation that adapts to the light environment, based on the 3D structures of the supramolecular complexes. The structural study of photoacclimation is a part of international collaborations with Queen Mary University of London (UK), Ruhr University Bochum (Germany), and University of Münster (Germany).

High-resolution structural analysis of dynein, a huge molecular motor in the cell

Dynein is a microtubule-based motor protein, consisting of the identical heavy-chains with assorted light-, light intermediate- and intermediate chains. The motor activity is located in the heavy chain, whose molecular mass is more than 500kDa. Sequence analysis and electron microscopy reconstruction indicate that the microtubule-binding domain of dynein heavy chain is separated from the AAA core of the motor which contains the ATP hydrolysis sites, by an elongated stalk domain consisting of an anti-parallel coiled-coil structure. It was hypothesized that the dynein utilized small amounts of sliding displacement between the AAA core and the microtubule-binding head. However, the structural basis of how to slide the two long colied-coil helices in the opposite directions and couple the microtubule binding is still unknown. In order to address these questions, we are trying to crystallize the several recombinant proteins of the dynein stalk.

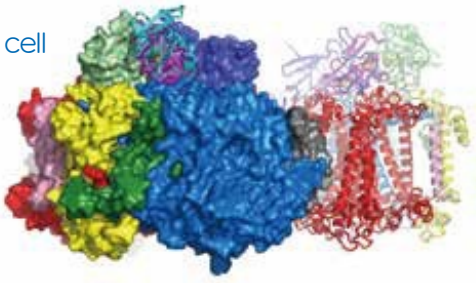

Figure 1. Crystal structure of Photosystem I complexed with the electron transfer protein ferredoxin (Nature Plants 2018)

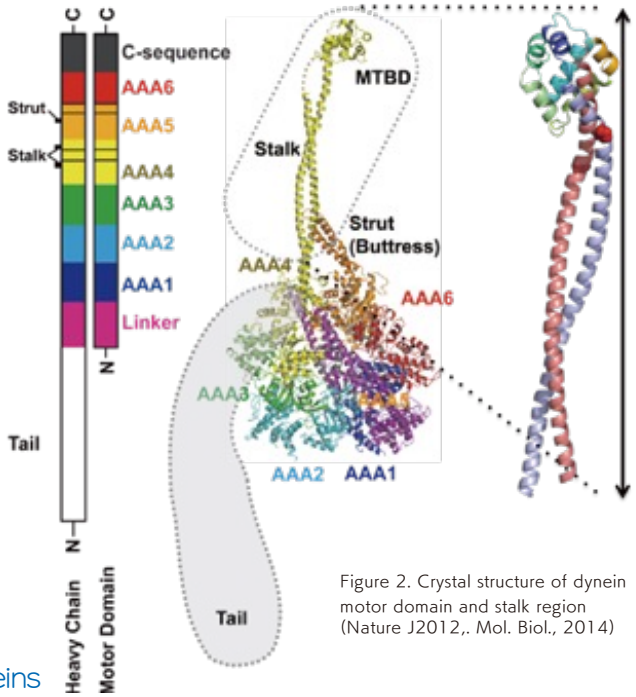

Figure 2. Crystal structure of dynein motor domain and stalk region (Nature J2012,. Mol. Biol., 2014)

High resolution and damage-free structure analysis of metalloproteins

Although there are many structural report of plant-type Ferredoxin at high resolution, it may be suggested that currently reported structures were time-averaged of partially reduced and oxidized Fds, which is crystallographically very difficult to be resolved. In order to elucidate the radiation-free structure of plant-type Fd crucial to understand the structural change of Fd upon reduction, further diffraction study of the plant-type Fd is necessarily needed.

This lab will not accept students in 2025

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