

Visiting Professors



Visiting Professor
SATO, Sota (*from The University of Tokyo*)

Integrated Molecular Structure Analysis Through Industry-Academia Collaboration

Elucidating molecular structures is crucial in various fields of molecular science, regardless of academia or industry. In addition to NMR and mass spectrometry, X-ray/electron diffraction is a powerful analytical technique that can directly determine atomic positions, enabling clear determination of three-dimensional structures. We are actively pursuing the “crystalline sponge method” as one of core technologies, which eliminates the need for the crystallization process and completes sample preparation by simply soaking the target molecules into crystalline sponge. Recently, we achieved to reduce sample amount into only 3 ng using small-wedge synchrotron crystallography method. Furthermore, we are building collaborative relationships with numerous companies to promote research aimed at creating new industries. Also, we have been dedicated to fostering future talent who will support the scientific community in Japan and the world. We organized mock lectures and research experiences for junior high and high school students in collaboration with corporate researchers, aiming to nurture the next generation of scientists.



Visiting Professor
HAYASHI, Kumiko (*from The University of Tokyo*)

Interdisciplinary Research on Motor Proteins

Motor proteins move and carry out their functions by using the energy obtained from the hydrolysis of adenosine triphosphate (ATP). Our group has conducted research on motor proteins such as F_1 -ATPase, a component of F_0F_1 -ATP synthase that produces ATP in cells, and the kinesin motor KIF1A, which is responsible for axonal transport in neurons. To study these systems, we employ single-molecule experiments, cellular experiments, and theoretical analyses based on extreme-value statistics and nonequilibrium statistical mechanics. These approaches have enabled physical measurements of motor proteins under nonequilibrium conditions, which had been difficult to achieve with equilibrium statistical mechanics. At present, through collaborations with the National Institute of Information and Communications Technology (NICT) and the Institute for Molecular Science (IMS), we are pursuing the development of high-precision force measurements of these motor proteins using DNA origami technology. In the future, we aim to elucidate the in-cell mechanisms of motor protein motility through the development of this approach.



Visiting Associate Professor
SATO, Shinichi (*from Tohoku University*)

Development of Protein Labeling Methods and Applications to Chemical Proteomics

Our research tackles the fundamental challenge of understanding protein behavior in living systems through the development of organic chemistry-based tools. To address questions such as post-translational modifications, protein–protein interactions, and protein conformational changes that are difficult to investigate using biological methods alone, we have established unique chemical methodologies including protein labeling techniques that function specifically in nanometer-scale spaces within living systems, methods for detecting changes in amino acid residue (Tyr, His) exposure on protein surfaces, and technologies for selectively labeling aggregated proteins. By combining these novel chemical approaches with rapidly advancing proteomics techniques using mass spectrometry—capable of simultaneously analyzing thousands to tens of thousands of proteins in a single experiment—we aim to advance our understanding of biological phenomena, develop new manipulation technologies, and contribute to drug discovery applications.