Visiting Professors

Visiting Professor
ITOH, Shinobu *(from Osaka University)*

Dioxygen Activation Mechanism by Copper Proteins and Their Models

The structure and reactivity of copper/active-oxygen complexes have attracted much interest during the past decades because of their potential relevance to biological systems and numerous copper-catalyzed oxidation reactions. In our laboratory, we have been studying the reactivity of several types of copper/active-oxygen species such as mononuclear and dinuclear copper(II)-peroxo and copper(III)-oxo complexes in order to evaluate the catalytic mechanism of copper oxygenases and to develop efficient oxidation catalysts for organic synthesis.

Visiting Associate Professor
HASEGAWA, Miki *(from Aoyama Gakuin University)*

Development of Lanthanide Complexes with Novel Optical Properties by the Coordination Chemistry

The 4f-electrons of the lanthanides, which are the key to developing functional molecules such as molecular magnets and emissive compounds, are shielded by the 5d and 6s orbitals. The interrelation of molecular design and functionality has not been established yet, because the electronic structure of f-elements is more complicated than that of d-block ions. Coordination chemistry is useful in this context. For instance, we succeeded in manipulating the ff-emission selectively by tuning the energy state of the ligand with some substituents. In addition, molecular arrangements on ultra-thin films have been used to induce polarized optical behavior. These approaches are based on our concepts to develop high-efficient optical materials under a scientific strategy. The ff-transitions of lanthanide complexes can be observed easily, but the underlying theory is not sufficient yet. We are ambitious to control the optical functionality of lanthanide ions with the help of coordination chemistry.

Visiting Associate Professor
TAKAHASHI, Satoshi *(from Osaka University)*

Dynamics of Protein Folding by Single Molecule and Ensemble Techniques

Protein is a linear macromolecule that has a unique property to fold to a specific three-dimensional structure from fully unfolded conformations. We are interested in the physical principles that connect the unfolded and the folded conformations of proteins. To detect fast kinetic processes involved in protein folding, we use rapid mixing device for the time resolved observation of average protein structures. To observe heterogeneity and dynamic fluctuations, we use single molecule observation systems. Based on the ensemble measurements on several proteins using small angle X-ray scattering and circular dichroism spectroscopy, we proposed “collapse and search” mechanism of protein folding. The recent application of single molecule fluorescence measurements clarified a relatively slow conformational dynamics in the unfolded state. We are hoping to obtain important information required for the protein structure prediction and design through the further examination of protein folding dynamics.