Information from X-ray analysis - molecular recognition and conformational change - Yokohama City University Toshiyuki Shimizu

Precise information of ternary structures is most important output from X-ray analysis. In addition, the supramolecular structure enables us to determine the interaction precisely. These knowledge help us to understand the molecular recognition mechanism, which is most important theme imposed on Structural Biology. Also, it leads to a drug design. Here, we present knowledge based on the ternary structures we solved.

## 1) DNA recognition by proteins

DNA recognition by transcription factors is one of the most typical molecular recognition. Pap1, a fission yeast transcription factor, plays important roles in multidrug resistance and oxidative stress response. Pap1-DNA structure reveals that Pap1 recognizes DNA containing novel consensus sequence by Pap1-specific residues.

## 2) Conformational change by Metal ions

In many cases, metal ions affect the conformational change and activity. By solving the tertiary structures, roles of magnesium ion in Rho, one of small GTP binding proteins, and the structure of CBL2, EF-hand containing calcium sensor, will be discussed.