手法としての構造生物学から、
視点としての構造生物学へ

■研究概要
構造生物学とはタンパク質を代表とする生体大分子の
立体構造を原子レベルの精度で決定し、機能発現のメカニズムを
解明する学問分野である。解析に際しては、
多くの生物試料は円形や四角形、その中に書
かれた文字のように、LIGANDを用いた照合解析で解明す
ることがある。すなわち、その根拠のほとんどは電気
信号の発信と受信に依存している。これに対し、
タンパク質の分子（リガンド）は、これらを正確に、
微妙なコントロールされた温度、反応を規約する物質を
物語と化学の言葉で表わすことができる。

■Research Projects
The structural biology is a special field of biology con-
cerned with the molecular structure of biological mac-
romolecules and the molecular basis of their functions. If
we were to speak out without a fear of being mistak-
en, most of biological phenomena could be described
as a picture card show containing gene symbols
in colorful graphical objects, and these pictures
relies almost entirely on the hands visualized in gel
electrophoresis images. In contrast, some people
including us desire to understand the biological phys-
ics, such as rigorous specificity of the recognition
of target molecules (ligands) and highly efficient enzy-
matic reactions, at atomic levels as if the molecules
were real objects.

The proteins are amino acid sequences stored as
information in genomic DNAs of which structures and
functions have been highly sophisticated through evo-
lution of life. We are determining the three dimensional
structures of molecular machines that were created
and optimized by Nature. We expect that we will find a
ravel mechanism beyond our imagination, and Nature
always respond to our expectations.

Our structural biology is characterized as follows: we
use an ingenious combination of X-ray crystallography,
nuclear magnetic resonance (NMR) spectroscopy, and
single particle analysis and tomography using clyreelec-
tron microscopy. These methods are complemented by
expertise in the fields of protein expression and purifi-
cation, and analyses of protein-ligand interactions with
various physicochemical techniques.

Our target biological systems include (1) Mitochon-
drial protein import system; (2) Oxidative phosphory-
lation that catalyzes glycogenolysis on asparagine residues
in protein; (3) Proteins involved in DNA replication,
repair, and recombination; (4) Proteins involved in
cytochrome remodeling and clathrin-mediated endocy-
tosis.
We are promoting structure determinations of
protein-protein complexes and supramolecular protein
complexes under the concept of ‘structure at work.’

■Major Recent Publications:
1. Sela S. S. Shatya, S. Srivastava A et al. Crystal Contact-Free Conformation of an Intrinsically
Flexible Loop in Protein Crystal, Tom21 as the Case Study. Biochim. Biophys. Acta Gen. Subj. 1864:
129418. 2020.
2. Hanawa-Suetsugu K., Irie Y., Fuchita M. Ab. et al. Phagocytosis is mediated by multidimensional
3. Fujimori T., Minob T. A., Elnayed K. M et al. The lathobiotic nuclease S1X exists in an equilibrium
4. Kose H. "Multiple partial recognitions in dynamic equilib-
rium" in the binding sites of proteins form the cellular
basis of promiscuous recognition of structur-
5. Mayanagi Y., Ishige S., Shirai T. et al. Direct visualization of DNA binding post repli-