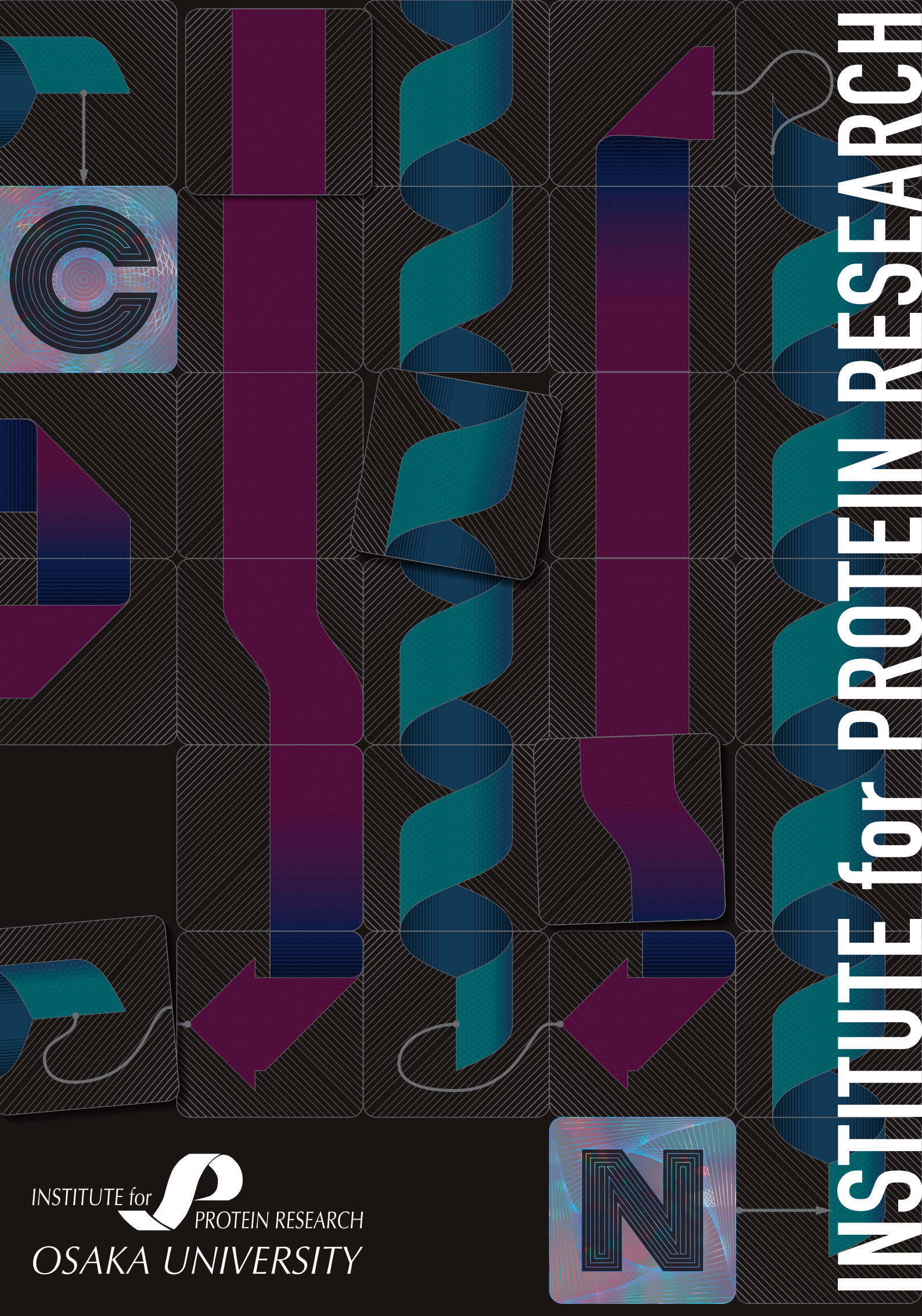


INSTITUTE for PROTEIN RESEARCH

OSAKA UNIVERSITY

Director Mariko Okada

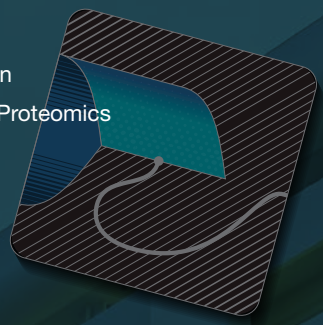
Protein research at Osaka University has long been active, and with the mission of elucidating the principles of biological activities through fundamental protein research, the Institute for Protein Research (IPR) was established as a Joint-use Research Organization in 1958. At the time of its establishment, IPR consisted of three divisions: Organic Chemistry, Physical Chemistry, and Protein Metabolism, and with the advance of technologies like molecular biology and computational science, IPR has expanded to cover a wide range of life science fields. In 2010, IPR was certified by MEXT as a Joint Usage / Research Center in recognition of its activities since its establishment. Up until now, through the domestic and international joint use of large facilities such as SPring-8 Beamline for Biological Macromolecular Assemblies, Cryo-electron microscopes, and NMR (Nuclear Magnetic Resonance) instruments, as well as through the operation of Protein Data Bank Japan (PDBj), IPR is dedicated to advancing protein research and encouraging the growth of research communities within and outside of Japan.

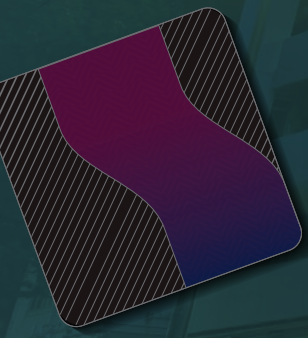
In recent years, there has been a significant focus on the new findings generated from the fusion of image analysis and deep learning technologies (such as cryo-electron microscopy and AlphaFold) with the protein structural information, or even the data itself. There is also a growing need for integrating information technology with genomic and other data to comprehend multi-level networks, from proteins to life. Given this situation, in October 2020, IPR set up the Division of Protein Network Biology and the Research Center for Next-Generation Protein Sciences to elucidate life phenomena based on protein-protein interactions. Furthermore, based on the activities of PDBj, IPR established the Advanced Data Science Center for Protein Research (ASPiRE) in October 2022 to promote data science as well as to create novel functional molecules. Under this structure, IPR is collaborating with related institutions worldwide to pioneer data-driven research on protein information and to encourage research and educational activities.

IPR, based on its strength of protein structural science, is expanding the scope of its research into the functional analysis of proteins, development of protein synthesis and design technology, protein information science and in-silico drug discovery. We sincerely appreciate your continued support and guidance.

Organization

- Director
  - Faculty Meeting
  - Administrative Council
  - Panel on Joint Usage / Research
  - Research Divisions
    - Division of Protein Chemistry
      - Laboratory for Protein Organic Chemistry
      - Laboratory for Nanobiology
      - Laboratory for Protein Synthesis and Expression
      - Laboratory for Protein Profiling and Functional Proteomics
      - Laboratory for Physical Biology
    - Division of Protein Structural Biology
      - Laboratory for Molecular Biophysics
      - Laboratory for Protein Crystallography
      - Laboratory for CryoEM Structural Biology
      - Laboratory for Supramolecular Crystallography
    - Division of Integrated Protein Functions
      - Laboratory for Molecular and Developmental Biology
      - Laboratory for Genome and Chromosome Functions
      - Laboratory for Advanced Brain Functions
      - Laboratory for Organelle Biology
    - Division of Protein Network Biology
      - Laboratory for Cell Systems
      - Laboratory for Computational Biology
      - Laboratory for Infection Systems
  - Special Research Facilities
    - Research Center for Next-Generation Protein Sciences
      - Laboratory for Ultra-High Magnetic Field NMR Spectroscopy
      - Laboratory for Synchrotron Radiation Research
      - Laboratory for High Resolution Cryo-EM
      - Laboratory for Biomolecular Analysis
      - Open Space Laboratory for Advanced Protein Science
    - Advanced Data Science Center for Protein Research
      - Laboratory for Protein Design
      - Laboratory for Biomolecular Modeling and Dynamics
      - Laboratory of Protein Databases
      - Laboratory for Protein Network
      - Laboratory for Drug Discovery Informatics
  - Division of Donated Fund Research
    - Division for Matrixome Research and Application
  - Technology Division
  - Administration
    - General Affairs Section
    - Accounting Section
      - Project Team of Joint Usage / Research Center
    - Research Support Section
  - Office of Research Strategy and Promotion
  - Public Relations Office
  - Library
  - IPR Alumni Office



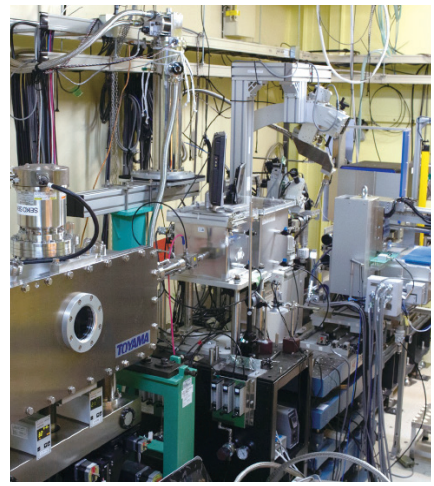


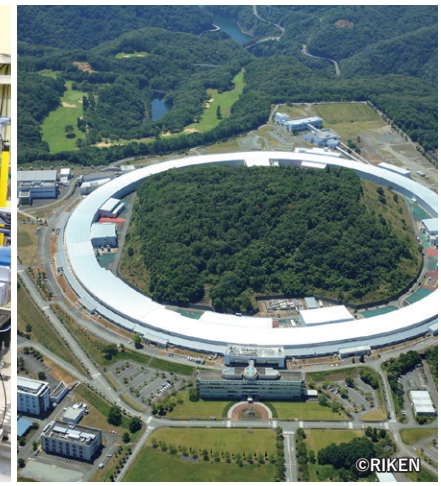
Joint use of large facilities

The Institute for Protein Research (IPR) was established in 1958 as a Joint-use Research Organization attached to Osaka University. Since its establishment, IPR has actively collaborated with numerous domestic and international researchers, and in recognition of its activities, IPR was certified as a Joint Usage / Research Center in April 2010 by the Ministry of Education, Culture, Sport, Science and Technology (MEXT) of Japan. As one of the main activities of the Joint Usage / Research Center, IPR offers large facilities for protein and life sciences, including SPring-8 synchrotron radiation beamline (IPR beamline, BL44XU), high-magnetic field solution and solid-state NMR machines, and state-of-the-art cryo-electron microscopes. In addition to these large facilities, IPR also operates PDBj (Protein Data Bank Japan) as one of the members of the Worldwide Protein Data Bank (wwPDB) organization that manages the PDB archives, the most important and successful database on protein structures. IPR is committed to contributing to the future of life sciences.

Beamline for Macromolecular Assemblies

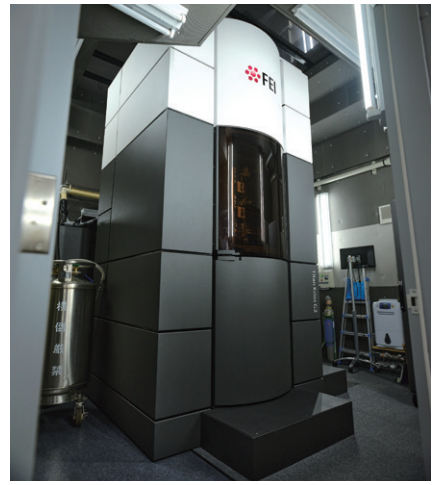
SPring-8 is the largest synchrotron radiation facility in the world. It produces a high brilliance X-ray beam suitable for data collection of biological macromolecules. IPR installed a contract beamline named "Beamline for Macromolecular Assemblies (BL44XU)" at SPring-8. This beamline is designed for high-precision diffraction data measurements from large biological macromolecular assemblies and is used for advanced research by researchers worldwide.

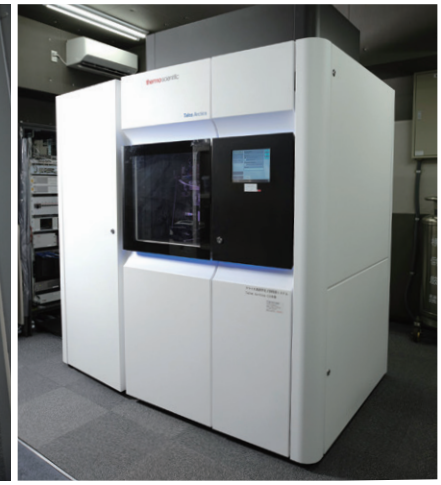




Cryo-electron Microscopes

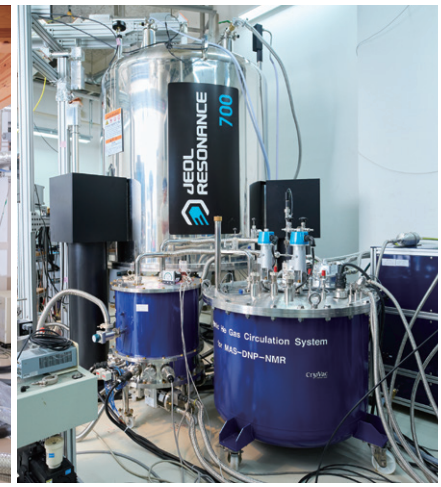
Cryo-electron microscopy is a type of electron microscopy that involves samples frozen in a vitreous ice and observed under nearly -190 degrees environment. In recent years, it has made significant progress, enabling atomic-level structural analysis of even non-crystallized biomolecules. As the base of cryo-electron microscopy facilities in Japan, IPR promotes world-leading research from the investigation of sample preparation methods to data acquisition, three-dimensional image analysis, and atomic model construction, to contribute to a wide range of research and technical support for industry and academia.





NMR (Nuclear Magnetic Resonance)

At IPR, a diverse range of NMR instruments, including the world's most high-sensitivity ultra-high field NMR device, is in operation. Through the maintenance and advancement of these NMR instruments, we are advancing the structural analysis of challenging targets, such as low-concentration proteins and high-molecular-weight protein complexes.

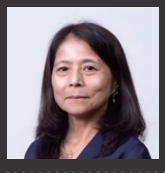


Division of Protein Chemistry

Hironobu Hojo | Organic chemistry / Chemical protein synthesis

Chemical synthesis of proteins and functional elucidation of their post-translational modifications

We have established an efficient method for the chemical synthesis of proteins, capable of introducing non-natural amino acids and post-translational modifications at arbitrary positions in the sequence. Using these chemically synthesized proteins, we are aiming to elucidate the function of protein modifications as well as to design new proteins and develop new drugs.



Yoshie Harada | Nanobiology

Measuring the environment of the nano region inside the cell to understand the fields where protein molecules work

Using fluorescent nanodiamonds and fluorescent polymeric thermometers, we analyze the relationship between intracellular local temperature and cellular functions, as well as elucidate the heat-sensing system of cells by local heating of cells. We are also working on a social implementation of drug discovery and regenerative medicine by using real-time imaging of bioactive proteins secreted from individual cells.

Junichi Takagi | Structural biology / Protein engineering

Elucidation of the structural mechanism of transmembrane signaling and development of novel biotherapeutics

Our research focuses on understanding cellular signal transduction mechainsm from the structural perspective, using techniques such as cryo-electron microscopy and X-ray crystallography. Furthermore, we combine our expertise in structural analysis and protein engineering to design proteins with novel functions, aiming at creating innovative biotherapeutics.

Toshifumi Takao | Protein mass spectrometry

Exploring the protein world by mass spectrometry

We have developed mass spectrometric methods for sensitive analysis of the primary structure and post-translational modifications of peptides and proteins, and software for accurate analysis of mass spectra, and are applying these methods to trace proteins obtained from living organisms. In addition, we are also applying these methods to the search for disease markers in body fluids.

Madoka Suzuki | Physical biology

Quantitative imaging and perturbation to understand the role of heat in biological systems

Cells respond to heat using proteins, but it is unclear how the proteins work, or whether the same mechanism responds to heat released by the cell itself. We use quantitative imaging and photothermal conversion to study the role of heat across the scales of biological systems at the molecular, cellular and organismal levels.

Division of Protein Structural Biology

Genji Kurisu | X-ray crystallography

Precise structural analysis of the protein to understand the system of biological reactions

We use X-ray crystallography together with NMR and Cryo-electron microscopy to analyze the working protein molecules and elucidate their structure-function relationship. Our goal is to understand the mechanism of controlled biological reactions in bioenergetics such as photosynthesis or dynein motors. In addition, we are also developing the method of neutron crystallography or MicroED for precise structural analysis of metal enzymes or bioactive compounds.

Takayuki Kato | Structural biology

Analyzing higher-order structure and function of biomacromolecules by Cryo-EM

We study superior functional mechanisms of living organisms, such as high energy conversion efficiency of molecular motors, by structural analysis using cryo-electron microscopy. We also develop technology for high-resolution analysis of protein structures and establish methods for analyzing thermal fluctuations of proteins using cryo-EM.

Atsushi Nakagawa | Synchrotron radiation protein crystallography

Structure determination of biological macromolecules using X-ray diffraction and cryo-electron microscopy

We aim to elucidate the detailed three-dimensional structures of biological supramolecular complexes, such as protein complexes and protein-nucleic acid complexes, at the atomic level using X-ray crystallography and cryo-EM in order to understand biological phenomena at the atomic level. We also develop methodologies for X-ray crystallography including the data collection system using the synchrotron radiaion beamline (BL44XU) at SPring-8.

Division of Integrated Protein Functions

Takahisa Furukawa | Developmental neurobiology / Visual science

Understanding central nervous system development from genes to neuronal function and human diseases

How does genetic information programmed in the genome lead to the development of diverse neurons? How does it relate to the formation of precise neural circuits and the neurophysiological functions of individuals? And how does it relate to the development of human diseases? We are tackling these questions by using the retina as a model system to explore the central nervous system (CNS) development and function with an integrated approach.

Akira Shinohara | Molecular biology

Studying the mechanisms of genome stability and instability in eukaryotes

We are conducting research employing molecular biology, biochemistry, and structural analysis to elucidate the molecular mechanisms of homologous recombination and DNA exchange. Our focus is particularly on dynamic changes in protein complexes involved in recombination. We aim to understand the mechanisms of genome stabilization and pathological conditions, such as the development of cancerous cells due to genome instability resulting from its breakdown, as well as miscarriages caused by aneuploidy formation in eggs, sperm, and other cells.

Takatoshi Hikida | Neuroscience / Psychiatry

Understanding molecular and circuit mechanisms in brain functions and mental disorders using model mice

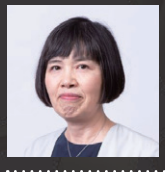
Our laboratory studies neural circuit mechanisms underlying various advanced brain functions, such as cognitive learning and decision-making behaviors, using molecular techniques for neural circuit-specific manipulation. We use several mouse models to reveal molecular pathologies of neuropsychiatric diseases. In particular, we focus on molecular mechanisms of gene-environment interaction in the pathogenesis of mental disorders. We also promote translational research for targeting mental disorders in collaboration with clinical departments and pharmaceutical companies.

Masato Nakai | Plant molecular cell biology

Analysis of molecular mechanisms of protein transport in chloroplasts and chloroplast biogenesis

We are investigating the process by which chloroplast proteins are synthesized outside the chloroplast and transported to the chloroplast, and the process by which the transported proteins are converted into functional molecules. By employing a wide variety of organisms ranging from algae to higher plants, we aim to elucidate molecular mechanisms and evolutions of chloroplast (plastid) biogenesis with techniques of biochemistry, genetics, and cell biology.

Division of Protein Network Biology



Mariko Okada | Systems biology

Understanding a cell, the smallest unit of life, as a dynamic integrated system of molecules

We develop methodologies for analyzing intracellular information using experiments and mathematical models and employ these methods to elucidate the regulatory rules of gene networks for cell and disease development. We are also working on the latest cell modeling methods and automated drug design, incorporating natural language processing and deep learning.

Kenji Mizuguchi | Computational biology

From the elucidation of biological mechanisms towards drug discovery applications using computational approaches

We are developing methods to predict protein structure, function, and interaction, while integrating a wide range of data and building databases, which provide a basis for linking molecular-level events and higher-order biological systems. We are also applying these databases and computational tools for specific problems in biological data analysis, and health and drug discovery research.

Yumiko Imai | Infection systems

Identification of higher-order-epigenetic modification machineries and development of potential novel therapeutics in severe virus infection

Our research is focused on understanding the molecular pathologies of viral infections and the networks involved in their severity through the integrated analysis of quantitative bioscientific data. We also apply genome synthesis and editing technologies in mouse models to develop novel drugs, diagnostics, and preemptive medicine.

Research Center for Next-Generation Protein Sciences

Yohei Miyanoiri | Structural biology / Protein chemistry

Elucidating the structural dynamics of proteins by developing advanced solution NMR methods

Utilizing advanced stable isotope labeling techniques and nuclear magnetic resonance (NMR) methods, we comprehensively analyze the three-dimensional structure, dynamics, and interactions of proteins at atomic resolution. Our primary focus is on elucidating molecular mechanisms related to molecular motors and neurodegenerative diseases. Additionally, we are advancing drug discovery research through in-cell NMR measurements and the development of NMR measurement technology via joint usage and collaborative research.

Nobuaki Okumura | Biochemistry

Developing sequence-based methods for protein analysis and supporting protein research.

We perform biochemical analysis of proteins and peptides, in particular by mass spectrometry and protein sequencing. We develop methods for protein identification and quantification using these technologies and apply these to analysis of actual biological samples. We are also interested in peptide and protein metabolism.

Advanced Data Science Center for Protein Research

Nobuyasu Koga | Protein design

De novo design of protein molecules

The goal of our lab is to develop methodologies that enable us to create protein molecules customized to the desired function, using computational approaches based on physical chemistry and data science, along with biochemical experiments.

Sandhya Premnath Tiwari | Computational biology

Investigating the collective motions of proteins via computational modeling and simulations to understand their biological function

Our goal is to model the dynamic motions of biomolecules, mainly proteins, and explore their role in biological function. By integrating existing biophysical and structural data, we model biomolecular structure and dynamics using a variety of computational methods.

Division of Donated Fund Research

Kiyotoshi Sekiguchi | Biochemistry / Cell biology

Uncovering the mechanisms governing homeostasis and dynamics of multicellularity through cell-extracellular matrix interactions

Our long-term goal is to understand the molecular mechanisms that govern the morphogenetic interactions of cells with surrounding extracellular matrices. We are particularly interested in the role of basement membranes in embryonic development and tissue homeostasis with an emphasis on the molecular interactions of basement membrane proteins with their receptors on the cell surface and the resulting signaling events that regulate proliferation, differentiation, apoptosis, and motility of cells.

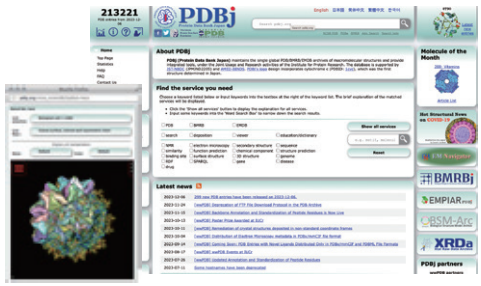
Development/Management of Databases

Protein Data Bank Japan (PDBj), an Asian data center of the worldwide Protein Data Bank (wwPDB), accepts biological macromolecular structures experimentally determined by crystallography, NMR spectroscopy or cryo-Electron Microscopy (cryo-EM) in Asia. PDBj processes and validates the deposited data by global standards and distributes them as the single global archive (pdbj.org). PDBj also processes and provides the cryo-EM map data as the Electron Microscopy Data Bank (EMDB), and curates the NMR experimental data as the Biological Magnetic Resonance Data Bank Japan (BMRBj) together with the BMRB center in the US.

PDBj

(Protein Data Bank Japan)

>> https://pdbj.org



BMRBj

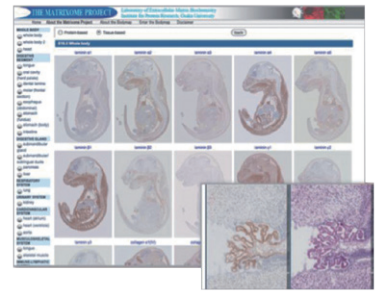
(Biological Magnetic Resonance Data Bank Japan)

>> https://bmrbj.pdbj.org/

Mouse Basement Membrane Bodymap

(Immunohistochemical database for basement membrane proteins)

>> http://dbarchive.biosciencedbc.jp/archive/matrixome/bm/home.html

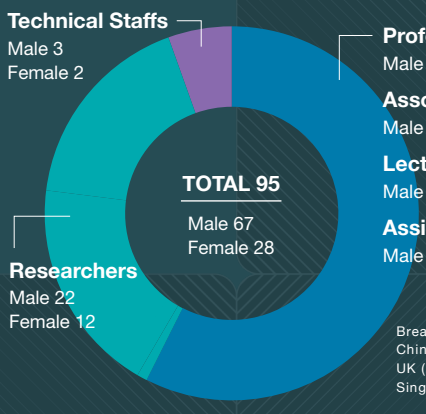


International Academic Exchanges

Country	Institution	Year of agreement
China	Human Proteome Project 2.0-Proteomics-Driven Precision Medicine (PDPM) and Westlake University	2022
Uruguay	Universidad de la República Uruguay	2022
Indonesia	Airlangga University	2020
Australia	The Australian National University	2020
Italy	Fondazione Istituto Italiano di Tecnologia	2018
Germany	Ruhr University Bochum(RUB)	2017
USA	University of Chicago	2017
India	Indian Institute of Science Education and Research(IISER) Thiruvananthapuram	2017
Ireland	University College Dublin	2017
India	Panjab University	2017
Taiwan	National Tsing Hua University	2015
USA	The State University of New Jersey, Rutgers	2015
Korea	Seoul National University	2015
China	Peking University	2014
India	Indian Institute of Chemical Biology	2009
Taiwan	National Synchrotron Radiation Research Center	2007
Cuba	Center for Genetic Engineering and Biotechnology	2003

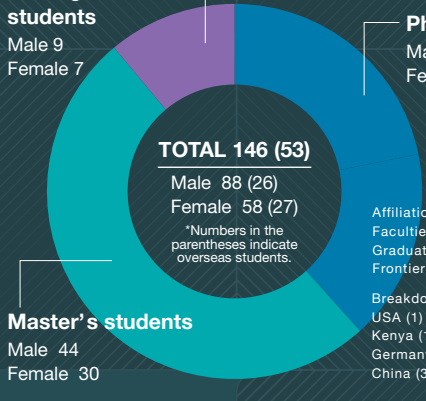
Key Facts

Faculty and staff members



Breakdown of foreign faculty and staff:
China (5) South Korea (1) Germany (1)
UK (1) Netherlands (1) Taiwan (1)
Singapore(1)

Students



Affiliation:
Faculties of Science, Medicine, Engineering
Graduate Schools of Science,
Frontier Biosciences, Medicine, Engineering

Breakdown of overseas students:
USA (1) India (1) Indonesia (4) Egypt (2)
Kenya (1) Sri Lanka (1) Thailand (3)
Germany (1) Fiji (1) Brazil (1) South Korea (5)
China (32)

Grants and Budgets

History

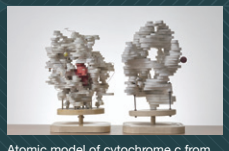
1956 Set up of a new laboratory in the Faculty of Science for organic chemical studies of proteins and amino acids (the predecessor of IPR) supervised by Prof. Shiro Akabori.


Faculty of Science

1958 IPR was established as a Joint-use Research Organization, composed of three divisions: Organic Chemistry, Physical Chemistry, and Protein Metabolism.

1962 IPR established the Peptide Center.

1972 The crystal structure of bonito heart ferrocytochrome c was determined by Prof. Kakudo of IPR for the first time in Japan.


Atomic model of cytochrome c from bonito heart

1978 IPR established the Crystallographic Research Center.

1988 IPR established the Research Center for Protein Engineering.

2000 The Protein Data Bank Japan (PDBj) started its operation.

2002 IPR established the Research Center for Structural and Functional Proteomics.

2004 IPR was transformed into a Research Institute of Japanese National Universities under the National University Corporation Law.

2010 IPR was certified as a Joint Usage / Research Center by MEXT.

2012 IPR established the Research Center for State-of-the-Art Functional Protein Analysis.

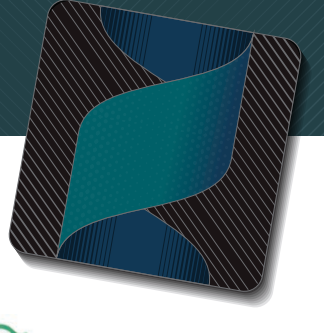
2016 IPR' s continued activity as a Joint Usage / Research Center was approved by MEXT.

2020 The atomic models of Cytochrome c and Taka-amylase were registered as Chemical Heritage authorized by the Chemical Society of Japan.

IPR established the Research Center for Next-Generation Protein Sciences.

2022 IPR' s continued activity as a Joint Usage / Research Center was approved by MEXT.

IPR established the Advanced Data Science Center for Protein Research.



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www.protein.osaka-u.ac.jp/en/


Official Mascot of IPR, Osaka Univ.
Tanpakun & Kimichan

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