# Call for Research Proposals

# Structural Analysis Application for FY 2026

At the Institute for Protein Research, University of Osaka, we are pleased to announce the following call for joint research proposals in structural analysis.

## 1. Overview of the Joint Structural Analysis Research Call

This program unifies four previously independent joint research programs—Beamline for Structural Analysis of Biomacromolecular Complexes, Ultra-High Magnetic Field Nuclear Magnetic Resonance (NMR), Cryo-Electron Microscopy (cryoEM), and Microcrystal Electron Diffraction (MicroED) —which were offered separately until fiscal year 2025. In addition to allowing structural analysis using a single technique, this unified program provides the opportunity for correlative structural analysis\* using multiple methods. It also accommodates proposals in cases where the most suitable technique has not yet been clearly identified.

It is also possible to promote collaborative use with other institutions under the frameworks of Coalition of Universities for Research Excellence Programs: the "M³-Structural Science Platform" (<a href="https://www.multi3.jp/">https://www.multi3.jp/</a>) and the "Frontier of Spin Life Sciences" (<a href="https://www.nips.ac.jp/spinl/">https://www.nips.ac.jp/spinl/</a>).

\*Correlative structural analysis is an integrative approach that combines four structural biology techniques, X-ray crystallography, NMR, cryo-EM, and MicroED, to elucidate the structures of various biomolecules and complexes across multiple levels. Through hybrid analytical methods, data from these experimental techniques can be combined, making it possible to address challenges that are difficult to resolve with a single method. Some cases may include samples that are hard to crystallize, microcrystals, or biomolecules which undergo dynamic structural changes. Our goal is to provide the tools to not only characterize static molecular structures but to analyze dynamic structural changes and molecular interactions that are important for biological function, thereby contributing to advances in drug discovery and life sciences.

#### We encourage applications for the following categories.

In the application form, please select one or more techniques as appropriate. For the *Sample-Specific Approach*, experts at IPR will determine the most suitable method.

## **OBeamline for Structural Analysis of Biomacromolecular Complexes**

The beamline (SPring-8 BL44XU) is specially designed for data collection of biological macromolecular assembly crystals, such as protein complexes, protein–nucleic acid complexes, and viruses. It uses an undulator as a light source. More details regarding the beamline:

https://www.protein.osaka-u.ac.jp/rcsfp/supracryst/en/research/beamline/

- Applications for the X-ray crystallography of large biological macromolecular assemblies are welcome
- Preliminary crystallographic experiments are not necessarily required
- Applicants are encouraged to have commenced sample preparation or preliminary crystallization experiments at the time of application

Person-in-charge: Genji Kurisu

# OUltra-High Magnetic Field NMR Instrumentation

IPR is equipped with a highly sensitive and high-resolution NMR spectrometers at 950 MHz, enabling solution experiments across a wide range of resonance frequencies. The facility supports structure, dynamics, and interaction analysis of biological macromolecules, including protein complexes, as well as small compounds, with unparalleled spectral resolution and sensitivity.

More details regarding NMR instruments:

https://www.protein.osaka-u.ac.jp/rcsfp/apc/nmr/equipment.html

 Applicants are encouraged to have commenced sample preparation or preliminary studies for NMR measurement at the time of application

Person-in-charge: Yohei Miyanoiri

# **OCryo-Electron Microscopy**

To promote structural biology of proteins, the institute has installed two high-performance cryo-electron microscopes equipped with direct electron detectors, Titan Krios with K3 camera and Talos Arctica with FlaconIII. These allow for high-resolution structure determination via single-particle analysis and electron tomography of macromolecule complexes and vitrified tissue sections. More details regarding cryo-EM facility: <a href="https://www.protein.osaka-u.ac.jp/cryoem/cryoem.html">https://www.protein.osaka-u.ac.jp/cryoem/cryoem.html</a>

- Applicants are encouraged to have commenced sample preparation suitable for EM observation and to have conducted some preliminary studies (especially preliminary EM observations)
- Applications without preliminary data may still be considered depending on the proposal content

# Person-in-charge: Takayuki Kato

## **OMicroED**

MicroED (Microcrystal Electron Diffraction: Rotation method for the electron diffraction) is a crystallographic technique to collect diffraction images from thin (< 1µm) 3D crystals in a powdery sample. Even when traditional X-ray experiments yield only powder diffraction, MicroED may still provide high-quality diffraction patterns from single crystal(s) and solve the structure of complex natural products or synthetic organic materials. IPR has implemented an automatic data acquisition system capable of analyzing samples of polymorph mixtures or samples where the quantity of good crystals is low. For more details regarding the setup, equipment and examples: <a href="https://github.com/GKLabIPR/MicroED/wiki">https://github.com/GKLabIPR/MicroED/wiki</a>.

- As the method is still under development, applicants must operate the electron microscope with a responsible IPR member.
- We recommend using synchrotron beam lines when the sample crystals are large enough (> a few micrometers).
- Preliminary analysis of samples such as single crystal X-ray diffraction or (P)XRD, is not required at the time of application. However, priority will be given to samples that are either unsuitable for traditional X-ray structure determination or have adequate crystallinity. Please provide any available data from X-ray experiments if applicable.

## Person-in-charge: Genji Kurisu

# **OSample-Specific Approach**

In the sample-specific approach, facility experts select the most suitable analysis method depending the desired information, as well as the properties and condition of the sample. To address challenges such as crystallization difficulty, molecular size, and dynamic behavior, the institute combines X-ray crystallography, NMR, cryo-EM, and MicroED technologies to conduct optimal structural analyses. Applicants do not need to have detailed knowledge of each method, as specialists will choose appropriate techniques and provide guidance regarding the analyses.

## Person-in-charge: P-CONCIERGE

#### 2. Eligibility

- Researchers affiliated with national, public, or private universities or institutions, or equivalent organizations in anywhere in the world.
- Proposals must be non-proprietary.

### 3. Research Preiod

From April 1, 2026 to March 31, 2027.

## 4. Application Procedure

[Required documents]

- 1. Application and Consent Form for Structural Analysis Program, FY2026
- 2. Consent Form for Research Collaborators Structural Analysis Program, FY2026
- 3. Pledge Form for Individual Engaged in Recombinant DNA Experiments (This is required only if an applicant is affiliated with institution other than IPR.)

Designated forms for items 1-3 are available at:

#### Submission Deadline Monday, December 1, 2025

Late submission may be considered in urgent cases. Please contact the office listed in Section 5 for details.

[Submission Address]

Project Team of Joint Usage / Research Center,

Institute for Protein Research, The University of Osaka.

E-mail: tanpakuken-kyoten@office.osaka-u.ac.jp

#### 5. Contact

Protein Research Help Desk "P-CONCIERGE"

E-mail: p-con@protein.osaka-u.ac.jp

#### 6. Review Result

The proposal will be reviewed by the Panel on Joint Usage/Research. Applicants will be informed of the results around mid-March 2026.

#### 7. Reports

## [Beamline for Structural Analysis of Biomacromolecular Complexes]

Users must submit an Experiment Summary Report within 60 days after the research term ends. They are also required to publish their research results in a peer-reviewed journal or in the SPring-8 Publications within three years after the end of the research term. When publishing an academic paper based on the results obtained through this program, users are required to:

- 1) clearly state that they used this beamline as shown in 8.
- 2) submit one reprint of the paper,
- 3) and register the paper in the SPring-8/SACLA Research Report Database.

# [NMR, Cryo-EM, MicroED and Sample-Specific Approach]

"Research Report" must be submitted within one month after the end of the research period. Of the documents submitted, the section titled "Summary of Research Results" (item (1) to (5), one page) will be published as is on the IPR website. The report format will be made available on the website at a later date.

#### 8. Publication of the results of this research in an academic papers

When the research results obtained this program are published as academic papers, please clearly state that the research has been conducted under this program with the following,

"This research was supported by the Joint Research Program in Structure Determination and Analysis Program at the Institute for Protein Research, The University of Osaka, Japan"

# 9. Others

- 1. If the proposal is accepted, the Principal Investigator will become a Collaborative Researcher of the Institute of Protein Research, the University of Osaka. Those who wish to receive travel expenses as a Collaborative Researcher should indicate this in the appropriate section of the application form. When applying from overseas, travel support may be limited. However, travel expenses can be covered by also applying to the International Collaborative Research program. It should be noted that travel expenses cannot be provided if the applicant is employed by the Institute for Protein Research.
- 1. Accommodation facility "Kasugaoka House" is available for Collaborative Researchers(https://www.osaka-u.ac.jp/ja/schools/facilities/BandB/kasugaoka\_house)
- 2. Graduate and undergraduate students may be included in the research team, provided that the academic supervisor approves (signature required on page 2 of the "Application Form for the Research Proposal for the Structural Analysis") and the students are enrolled in insurance such as "Personal Accident Insurance for Students Pursuing Education and Research".
- 3. If the academic supervisor who signed the "Application Form for the Research Proposal for the Structural Analysis" changes due to transfer or other reasons, approval from the new supervisor is required. Additionally, if any students are added after the initial application, their supervisor's approval is also required. In these cases, consult with the Project Team of Joint Usage / Research Center.