

**Public call for collaborative research and research meeting for FY 2024**  
**The Medical Institute of Bioregulation, Kyushu University,**  
**(Start of the public call: December 2023)**

Having been recognized as a Joint Usage/Research Center for the Multi-Stratified Host Defense System since April 1, 2010, the Medical Institute of Bioregulation (MIB) , Kyushu University has been promoting collaborative research with researchers involved in host-defense studies.

We publicly call for research proposals for fiscal year 2024.

**1. Research Categories for which a Call for Proposals is Organized**

A. Collaborative research

(1) Instrument usage type project:

Research project using the multi-stratified levels of research facility infrastructure and the technology of this institute. Research expenses are distributed to cover the instrument usage fee, travel expenses and so on.

(2) Collaborative research type project:

Research project aiming at clarifying the host-defense system using the knowledge about host defense accumulated in this institute. Only travel and accommodation expenses are granted.

B. Research meetings

Meetings focusing on information exchange and presentation of research results among researchers involved in host-defense studies, or meetings for planning collaborative research among such researchers.

**2. Research Field**

We call for collaborative research proposals on the following four research fields. The available facilities and research support service for each field are listed (Attachment). For information on facilitators, please see the following link (Laboratory List):

[https://www.bioreg.kyushu-u.ac.jp/mib/labo\\_list\\_e.html](https://www.bioreg.kyushu-u.ac.jp/mib/labo_list_e.html)

(1) Nucleic Acid Omics (Genomics, Epigenomics, Transcriptomics, Informatics Analysis, Spatial Omics)  
Genomics:

We provide services of massive detection of genomic variations. We accept collaborative researches such as large-scale genome sequencing using NovaSeq or HiSeq. We also accept mid-to-small scale researches such as exome sequencing of disease pedigrees and Amlicon-seq of biomes using MiSeq. Furthermore, starting from fiscal year 2024, we will support the determination of structural polymorphism in model organisms such as humans and mice, sequence acquisition for non-model organisms, and metagenomic sequencing using the PacBio Sequel IIe long-read sequencer, which provides high accuracy and longer reads compared to the short-read NovaSeq.

#### Epigenomics:

We plan to perform collaborative research on epigenetic modifications, such as DNA methylation and histone modifications, which are important for the maintenance of function and homeostasis of living tissues. For example, using our cutting-edge technology applicable to a limited amount of DNA, we are able to reveal the genome-wide distribution pattern of DNA methylation at single-base resolution. Such studies will provide a comprehensive understanding of epigenetics and contribute to the progress of biosciences related to health and diseases.

#### Transcriptomics:

We accept proposals for collaborative studies on understanding cell homeostasis and its deficiency appearing as abnormal development, tumorigenesis, and ageing using transcriptome quantification and/or epigenome regulation. Single Cell transcriptomics has enabled elucidation of the phenotype of an individual not only by identifying the cells responsible for the phenotype but also by understanding the cell dynamics reconstructed from capturing cell population. Applicants are encouraged to apply these comprehensive analyses for humans or other model/non-model organisms with appropriate statistical analyses.

#### Information Analysis Infrastructure:

We have established an information analysis system primarily for sequence information related to genomics. This system can be utilized for the analysis of information primarily obtained from collaborative research projects.

#### Spatial Omics:

We conduct collaborative research involving spatial multi-omics analysis in cell and tissue samples using methods such as Photoisolation chemistry, which enables transcriptome analysis in any given tissue region or intracellular area, as well as sequential immunostaining and sequential RNA/DNA-FISH methods. These methods allow for the quantification of the localization of numerous molecules while preserving the spatial arrangement of molecules within cells or the spatial arrangement of cells within tissues.

## (2) Proteomics and Metabolomics

Proteomics is a comprehensive analytical method for proteins that employs mass spectrometry. Proteomics approach makes it possible to obtain information on expression levels, post-translational modifications, and even interactions between many general proteins. By adopting this kind of comprehensive analytical method, it is possible to gain a deeper understanding of life processes and promote researches more efficiently than conventional techniques allow.

Metabolomics, exhaustive analysis of metabolites, has been applied in various fields as precise phenotypic characterization by means multi-component profiling. However, since the targeted metabolites are widely ranging from low- to high-molecular weight, technology used for simultaneous multi-component analysis has become critical concern. Selection of suitable technology is essential to effectively conduct metabolome analysis. Our laboratory has strong

knowledge background and is equipped with numerous sophisticated technologies for high-resolution metabolomics research.

### (3) Structural Biology

We plan to conduct collaborative research for the elucidation of molecular mechanisms of proteins functions using structural biology technologies, such as cryo-electron microscopy (cryo-EM) and X-ray crystallography.

The necessity of determination of biomacromolecule structures is now widely recognized, based on the fact that this approach often leads to deep understanding of how proteins work to fulfill their functions and enables drug design that specifically controls protein functions. It is to be noted that cryo-EM analysis sometimes allows structure determination of proteins that are hard to achieve by X-ray crystallography, such as membrane proteins and biomacromolecule complexes.

### (4) Embryonic and Genetic Engineering

We plan to conduct collaborative research on the elucidation of host-defense mechanism at an individual level by developmental engineering methods using mice, and the development of new therapies for diseases caused by the breakdown of the host-defense mechanism. Generation of genetically engineered mice by developmental engineering includes the production of knockout, knock-in, and transgenic mice from fertilized eggs and ES cells. We also actively introduce genome editing technology based on the CRISPR/Cas9 system.

## 3. Eligibility for Applicants

Researchers belong to universities, national or public institutions, or equivalent institutions

## 4. Period of Research

From April 1, 2024 to March 31, 2025

## 5. How to Apply

Please fill out the application form and send it to the address (see 11. Contact below) by post or e-mail. You MUST discuss the details of the collaboration with the facilitator of the MIB, before sending your completed application form.

The application form is downloadable at: [https://www.bioreg.kyushu-u.ac.jp/mib/activities\\_collabo\\_e.html](https://www.bioreg.kyushu-u.ac.jp/mib/activities_collabo_e.html)

### Required Documents:

- A. Collaborative research : application form 1
- B. Research meeting : application form 2

### Application deadline:

February 26, 2024

\* Each research group is not allowed to apply two or more collaborative research projects per year, and the same application title must not be used more than 2 years.

\*We may accept your application even after the application deadline. Please contact the facilitator of the MIB or the contact person (see “11. Contact” below) in advance. In case that we stop accepting applications, we will notify in the MIB HP.

## 6. Screening Results

Once the review committee has made a decision to either accept or reject the application, applicants will be informed of the result as soon as possible.

## 7. Report of the Research Results

Please submit a report describing the progress and results of the research once the study has been completed. If you are going to publish a paper based on the results of the study, please acknowledge the facilities of our institute that you have used. The sentence is as follows:

*“This work was partly performed in the Cooperative Research Project Program of the Medical Institute of Bioregulation, Kyushu University.”*

In addition, please submit a copy of the reprint of the paper.

## 8. Research Expenses

Research expenses are allocated on the basis of screening results.

### A. Collaborative research

A maximum budget of 500,000 yen, as travel and accommodation expenses, is provided. Travel expenses can be provided to research collaborators as well within the budget. In the case of instrument usage type project, research expenses are distributed as well. However, they can only cover the service fees of the institute, and cannot be allocated to personal consumable supplies and materials.

### B. Research meetings

The meeting, travel, and accommodation expenses are granted.

International academic meetings: up to 1,500,000 yen

The other meetings: up to 500,000 yen

## 9. Handling of Intellectual Properties

Intellectual properties are handled in accordance with the Intellectual Property Handling Rules of Kyushu University.

## 10. Others

(1) MIB is not responsible for any injuries or accidents during collaborative research / research meeting.

(2) By laws and ordinances, you **MUST** receive an appropriate education and training or an ethical approval from either internal or external committee to meet the required ethical standards, for researches that contain genetic modifications and animal experiments, ethical issues such as human genomic information and materials, or other restricted activities.

## **11. Contact**

Akira Nagashima (contact person)

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