

**The Guideline for Additional Application for 2023NIG-JOINT  
(Joint Research(A))  
National Institute of Genetics,  
Research Organization of Information and Systems**

**1. The Guidelines for Application**

(1) NIG-JOINT

National Institute of Genetics solicits joint research to be conducted between researchers from other universities or institutes and NIG faculties using NIG facilities and equipment on the proposed project. We are accepting additional applications for 2023 NIG-JOINT (A). As a general rule, travel expenses are provided to the researchers visiting NIG. NIG-JOINT projects should be conducted during the period of time from October 1<sup>st</sup>, 2023 to March 31<sup>st</sup>, 2024. Please note that for those who have already accepted as a research representative for other NIG-JOINT (A), (B) or (I) in FY2023, are not eligible to apply for this additional application.

NIG-JOINT (A)

- Eligible applicants are researchers affiliated with domestic or overseas universities or research institutes. Travel expenses required for the researchers to visit NIG conducting joint research are provided.
- Up to 100,000 JPY can be requested by an applicant.

**2. Applicants**

The applicants should be, as a general rule, researchers affiliated with universities, inter-university collaborative research institutes and independent administrative organizations in Japan or researchers affiliated with overseas universities or research institutes. Please note that graduate students are not eligible to apply, but they can be a member of joint researchers.

**3. Application**

The application must be completed via the online application system called “Joint Research On-line Integrated System (JROIS)”.

JROIS: <https://jrois2.rois.ac.jp/>

(Instructions for operating the application system can be downloaded from the above URL.) For more details regarding the online application system, please refer to the following NIG webpage (NIG-JOINT page).

<https://www.nig.ac.jp/nig/research-infrastructure-collaboration/nig-collaboration-grant>

(1) Before submitting the application, the applicant must consult closely with the prospective NIG representative regarding project subject, members, budget and other necessary matters. Research outlines of NIG researchers are described at the end of this application guideline.

(2) When applying for this program, please be sure to obtain approval from the head of your organization (or department). Submission of written approval is not required.

(3) Application form must be uploaded and submitted in PDF · DOCX · ZIP format to JROIS. The application form can be downloaded from the link below.

<https://www.nig.ac.jp/nig/research-infrastructure-collaboration/nig-collaboration-grant>

#### **4. Online Application Deadline**

Applications must be submitted no later than noon (12 PM JST) on Monday, July 31st, 2023.

**\*Your application will not be accepted under any circumstances if you don't submit it by the above deadline.**

#### **5. Selection**

The outcome of selection and amount of budget allocation are determined after screening by NIG committee and notified to the research representatives via e-mail by the end of around October 2023. Applications from those who have been adopted as research representatives in the past, regardless of whether it is a new or a continuous project, will be reviewed with an emphasis on the status of the past budget implementation.

Please also note that the allocation amounts may be reduced due to limited budget.

#### **6. Change of the Research Group**

(1) If there is a change in research representative's organization or position, the said researcher must change the registered information on the "Edit User" screen of JROIS website. If research representative's affiliation is changed, a written approval (fixed format) from new organization should be submitted. (No official seal or signature is required.)

(2) If there is a change in research representative, addition or removal of joint research members, or change in joint research member's organization or position, please submit an addition/change form (only in Japanese) through the NIG representative immediately.

(3) The NIG representative must submit the cancelation form in the event that the joint research is unable to be conducted due to unavoidable circumstances.

#### **7. Expenses Provided**

(1) The travel expenses are to be provided by NIG based on the rules of Research Organization of Information and Systems (ROIS). Because the expenses are allocated only to NIG, not to other organizations, they should be claimed through NIG representative. Accommodation fee for those who stay at our guest house will be 2,500JPY/night, and for those who stay at a hotel in the city will be 8,000JPY/night. (Outside researchers visiting NIG for attending meeting or conducting research are to stay at our guest house, whenever possible.) Please note that the travel expenses could not be fully provided if other business or private site visits are included in the entire trip.

(2) Research representatives are expected to spend the budget at an earlier stage. If you are unable to spend the full amount of the budget due to unavoidable reasons, please submit a statement of reasons (free format) and repay the unspent portion of the budget by the end of December. When it becomes obvious that the expenses are not used anymore, please contact the Research Promotion Team at that time.

## 8. Submission of Research Report

The research representatives are required to fill in the "FOR MEXT Report (at the end of research)" on the Edit Application screen of JROIS by April 30th, 2024, and upload the research report in PDF·DOCX·ZIP format from the same screen for submission.

The research report form can be downloaded from the link below.

<https://www.nig.ac.jp/nig/research-infrastructure-collaboration/nig-collaboration-grant>

## 9. Publication of Research Result

You are requested to acknowledge NIG joint research as follows when results based on this research project are published, and submit a copy of papers together with the research report via JROIS.

NIG-JOINT (reference number)

\*Reference number 【serial number + category (A,B or I) + year】 , will be issued in the “acceptance notification” which will be sent to the successful applicant.

Example: (Successful applicant : Taro Iden, reference number : 1A2023)

“This work was supported by NIG-JOINT (1A2023) to T. Iden.”

## 10. Others

(1) NIG facilities and common equipment are available to be used for the joint research. Please refer to the following URL for the available common equipment.

<https://www.nig.ac.jp/nig/research-infrastructure-collaboration/common-equipment>

(2) If gene recombination and/or animal experiments are planned, NIG representatives are requested to submit an “experiment-on-gene recombination plan” and/or “experiment-on-animals plan” application form to the Research Promotion Team after acceptance of the application. As for animal experiments, researchers directly handle experimental animals are requested to apply for NIG qualification screening and undergo a training regardless of their affiliation. We strongly hope that all researchers comply with regulations and conduct the research properly.

(3) Researchers who handle radioisotope at NIG are requested to register as a radiation worker before starting to handle it.

(4) Outside researchers visiting NIG for conducting research are to stay at our guest house, whenever possible.

However, they can stay at a hotel in the city if the guest house is fully booked.

(5) Ownership of intellectual property rights created through joint research at NIG will be considered based on the regulations of ROIS employee invention.

(6) NIG assures that private information for this application should be used only for screening the proposal. Regarding the accepted proposal, the representative of the research, his/her institute and the research project title will be posted on NIG website and annual reports.

(7) As a general rule, NIG would not prepare the form of “business-trip request” for the joint research to simplify the procedures.

We sincerely ask outside researchers visiting NIG to follow appropriate business trip procedures according to the rules of their affiliated institute.

**【Contact】**

Department of Administration

Research Promotion Team, General Affairs and Project Section

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## Research Outline

(Updated: May 19th, 2023)

Department/Center	Laboratory	Faculty	Research outline
<b>Department of Informatics</b>	<b>Gene- Expression Analysis</b>	<b>OKUBO, Kousaku</b> / Professor	“How can we make use of data and information at our finger-tip in making smarter decisions in our own contexts?” Without solving this question, all analytical and descriptive efforts that digitalize the reality end up in vain. Our tentative answer/goal for this is to develop method to enhance “fluidity” and “utility”of medical knowledge among humans and machines.
	<b>Genetic Informatics</b>	<b>KAWAMOTO, Shoko</b> /Associate Professor	We are working on research and development of databases and information retrieval system for the national bio-resource project (NBRP).
	<b>Genome Evolution</b>	<b>KUROKAWA, Ken</b> / Professor <b>HIGASHI, Koichi</b> / Assistant Professor	We are interested in understanding about microbial genome evolution and microbial community dynamics, and we are currently reaching out in the following two major research directions: I. Facilitate the development of an integrated database “MicrobeDB.jp”, II. Microbial community dynamics.
	<b>Genome Diversity</b>	<b>MORI, Hiroshi</b> / Associate Professor	Our main research goal is to understand the relationships between the habitat of organisms and genome diversity. To facilitate the studies using comparative genomics and metagenomics, we are also developing various bioinformatics methodologies.
	<b>Biological Networks</b>	<b>ARITA, Masanori</b> / Professor <b>KOSHIMIZU, Shizuka</b> / Assistant Professor	Network analysis of metabolic pathways based on comprehensive identification and quantification of metabolites (metabolomics); Bioinformatics related to plant secondary metabolism and lipid metabolism
	<b>Genome Informatics</b>	<b>NAKAMURA, Yasukazu</b> / Professor <b>TANIZAWA, Yasuhiro</b> / Assistant Professor	Intelligent information technology for structural and functional annotations of large-scale nucleotide sequences.
<b>Department of Genomics and Evolutionary Biology</b>	<b>DNA Data Analysis</b>	<b>IKEO, Kazuho</b> / Associate Professor	Evolutionary study of genomic structure and gene expression pattern to elucidate the evolutionary mechanism of central nervous system and sensory organs. Evolutionary genomics analysis of various species. Metagenome analysis. Developing databases and computer software for biological research.

	<b>Plant Genetics</b>	<b>SATO, Yutaka</b> / Professor <b>NOSAKA (TAKAHASHI), Misuzu</b> / Assistant Professor	The goal of our research is to understand molecular mechanisms governing early processes of plant development using a series of rice embryogenesis defective mutants. Currently we are focusing on the mechanism of regulating the cell division pattern and plasticity in cellular differentiation in rice embryo.
	<b>Evolutionary Genetics</b>	<b>AKASHI, Hiroshi</b> / Professor	We infer mechanisms of genome evolution using population genetic and comparative genomic approaches. Current interests include global forces such as biosynthetic constraints that underlie weak selection.
	<b>Ecological Genetics</b>	<b>KITANO, Jun</b> / Professor <b>YAMASAKI, Yo</b> / Assistant Professor	We use threespine stickleback fishes to investigate the genetic and molecular mechanisms underlying adaptation and speciation.
	<b>Comparative Genomics</b>	<b>TOYODA, Atsushi</b> / Project Professor	We have been conducting advanced genomics research on the plasticity of genome structure and functions using most advanced genome technology such as New-Generation Sequencers.
	<b>Molecular Life History</b>	<b>KURAKU, Shigehiro</b> / Professor <b>KAWAGUCHI, Akane</b> / Assistant Professor	We focus on vertebrates and bridge molecular-level laboratory approaches and genome informatics, in order to document genome evolution and elucidate its mechanism.
<b>Department of Gene Function and Phenomics</b>	<b>Symbiosis and Cell Evolution</b>	<b>MIYAGISHIMA, Shin-ya</b> / Professor <b>FUJIWARA, Takayuki</b> / Assistant Professor	In order to understand endosymbiotic evolution of eukaryotes, we are studying coordinating mechanisms of eukaryotic cell and organelle/endosymbiont proliferation using algae, plants, and protists.
	<b>Model Fish Genetics</b>	<b>SAKAI, Noriyoshi</b> / Associate Professor	We establish reliable protocols for genetically modification of zebrafish using sperm, and analyze the molecular mechanisms of spermatogenesis and early development in zebrafish.
	<b>Systems Neuroscience</b>	<b>KUBO, Fumi</b> / Associate Professor	We study how visual information generates goal-directed behavior. We aim to understand the neural circuit mechanisms underlying this process using a combination of genetic, optic and behavioral approaches in zebrafish.

	<b>Plant Cytogenetics</b>	<b>NONOMURA, Ken-ichi</b> / Associate Professor <b>TSUDA, Katsutoshi</b> / Assistant Professor	We aim to elucidate the regulatory system of plant germ-cell development and chromosome kinetics, mainly using seed-sterile rice mutants.
	<b>Mammalian Neural Circuits</b>	<b>IWASATO, Takuji</b> / Professor <b>NAKAGAWA, Naoki</b> / Assistant Professor	We are studying molecular and cellular mechanisms of neuronal circuit development in the mammals, using mouse genetics and other related methods.
	<b>Multiscale Sensory Structure</b>	<b>YONEHARA, Keisuke</b> / Professor <b>MATSUMOTO, Akihiro</b> / Assistant Professor	We use mice and marmosets to understand the structure, function, development, disease, and environmental adaptation of visual neural circuits at multi-levels, including genes, neural circuit physiology, and behavior.
	<b>Multicellular Organization</b>	<b>SAWA, Hitoshi</b> / Professor <b>NEGISHI, Takefumi</b> / Assistant Professor	We are studying the mechanisms that produce a variety of cell types through asymmetric cell divisions using the nematode <i>C.elegans</i> .
	<b>Brain Function</b>	<b>HIRATA, Tatsumi</b> / Professor <b>KAWASAKI, Takahiko</b> / Assistant Professor <b>ZHU, Yan</b> / Assistant Professor	Development of the vertebrate nervous system with special focus on neuronal network formation.
	<b>Molecular and Developmental Biology</b>	<b>KAWAKAMI, Koichi</b> / Professor <b>ASAKAWA, Kazuhide</b> / Specially Appointed Associate Professor	Genetic studies on development, morphogenesis and behaviors by using a model vertebrate zebrafish.
	<b>Microbial Physiology</b>	<b>NIKI, Hironori</b> / Professor	We investigate higher order structure of chromosomes and their dynamics in yeast and bacteria through genetic and cell biological analysis.
	<b>Mouse Genomics Resource</b>	<b>KOIDE, Tsuyoshi</b> / Associate Professor	For understanding genetic basis of behavioral diversity, behavioral and genetic analyses are applied on a variety of mouse resources including wild-derived strains. We are developing genome editing methods in mice for analyzing function of genes.
<b>Department of Chromosome Science</b>	<b>Genome Dynamics</b>	<b>MAESHIMA, Kazuhiro</b> / Professor <b>IDE, Satoru</b> / Assistant Professor <b>HIBINO, Kayo</b> / Assistant Professor	Our research interest lies in determining how a long string of genomic DNA is three-dimensionally organized in living cells, and how the organized genome functions during cellular proliferation, differentiation, and development. We are using a novel combination of molecular cell biology and biophysics to elucidate 3D-organization and dynamics of human genome chromatin.

	<b>Cell Architecture</b>	<b>KIMURA, Akatsuki</b> / Professor <b>TORISAWA, Takayuki</b> / Assistant Professor	To understand the three-dimensional architecture of the cell and its dynamics, quantitative imaging and modeling approaches are employed. Specific targets of the research are size and shape of organelles, the mechanics of cytokinesis, and cytoplasmic streaming in the <i>C. elegans</i> embryo.
	<b>Chromosome Biochemistry</b>	<b>MURAYAMA, Yasuto</b> / Associate Professor <b>KUROKAWA, Yumiko</b> / Assistant Professor	We investigate molecular mechanism underlying regulation of chromosome organization and dynamics by recapitulating their biochemical reactions using purified proteins. We now especially focus on SMC complexes.
	<b>Physics and Cell Biology</b>	<b>SHIMAMOTO, Yuta</b> / Associate Professor <b>SAITO, Kei</b> / Assistant Professor	Our laboratory uses a combination of biophysics, biochemistry, cell biology, and materials science to study how the mitotic spindle properly assembles and segregates chromosomes in cell division.
	<b>Molecular Cell Engineering</b>	<b>KANEMAKI, Masato</b> / Professor	To understand DNA transactions in human cells, we generate conditional cells using the auxin-inducible degron technology for genetic and cytological analyses. We also develop new technologies for construction of mutant human cells.
	<b>Invertebrate Genetics</b>	<b>SAITO, Kuniaki</b> / Professor <b>MIYOSHI, Keita</b> / Assistant Professor	We investigate molecular mechanisms of Drosophila gene expression and repression through biochemical and genetic techniques. Especially, we are focusing on the small RNA pathways and chromatin regulation during germ cell development.
<b>Center for Frontier Research</b>	<b>Gene Quantity Biology</b>	<b>SASAKI, Mariko</b> / Associate Professor	We study molecular mechanisms underlying genomic changes in eukaryotic cells. We mainly use budding yeast and human cell cultures and analyze genomic changes that result in changes to DNA quantity, using genetic and molecular biology tools. We specialize in isolating Mbp-sized DNA and separating it by Pulsed-Field Gel Electrophoresis.
	<b>Theoretical Ecology and Evolution</b>	<b>YAMAMICHI, Masato</b> / Associate Professor	We combine mathematical models, microcosm experiments, and meta-analyses to investigate complex feedbacks between rapid evolution and ecological processes.
<b>Chemical and Radioisotope Management Unit</b>		<b>ANDACHI, Yoshiki</b> / Assistant Professor	We study microRNA-mediated post-transcriptional regulation in <i>C. elegans</i> using our original methods for the detection of microRNAs and target genes.