

September 13th, 2018

Call for Urgent Joint Research with Researchers  
in Hokkaido Eastern Iburi Earthquake Disaster Area

We would like to offer our sincere sympathy to the people living in Hokkaido hit by the earthquake.

All of the staff at our institute are wishing for earliest relief and restoration on the affected areas and will try to provide the best possible support. We understand that universities and research institutes in Hokkaido were severely damaged and have a lot of trouble with their research activities. National Institute of Genetics will provide an opportunity for the researchers and students who are suffering from the disaster to continue their research in our institute for a certain period of time. Our Inter-University Collaboration Committee is inviting proposal for the “Urgent Joint Research” as follows.

**“Urgent Joint Research”**

We offer research opportunity for those who have difficulty in conducting research due to damage to their laboratories. If you are interested in this program, please refer to the list of our faculty members and their research outlines shown below and contact a member whose research is most closely related to your own. If you have any trouble finding your host partner, please contact Research Promotion Team at [kyodo-mail@nig.ac.jp](mailto:kyodo-mail@nig.ac.jp)

**1. How to apply**

Please download an application form from the link below and submit it in Word format to the address below.

Application Form for Urgent Joint Research ([Word](#)) / ([PDF](#))

【Send your application to】 [kyodo-mail@nig.ac.jp](mailto:kyodo-mail@nig.ac.jp) (Research Promotion Team)

**2. Application**

Beginning from today, you can submit your application to our office. Screening will be held immediately and the result will be informed by e-mail.

**3. Expenses**

Up to five hundred thousand yen will be provided per project. It can be used for research, living and travel. Travel cost should be decided based on our regulations.

**4. Research Term**

Up to 3 months, in principle.

**5. Report**

Research report should be submitted within 30 days after finishing the research.

Report Form ([Word](#))

【Contact/Inquiry】

Research Organization of Information and System

National Institute of Genetics

Research Promotion Team

1111 Yata, Mishima, Shizuoka-ken, 411-8540

Phone: 055-981-6728

E-mail: [kyodo-mail@nig.ac.jp](mailto:kyodo-mail@nig.ac.jp)

Isao Katsura

Director-General, National Institute of Genetics

Research Organization of Information and Systems

Inter-University Research Institute Corporation

## Research outline

※An extension number follows our standard phone number (055-981, or +81-55-981).

(Updated: September 1<sup>st</sup>,2018)

Department	Division	Faculty	Ext.	Research outline
Molecular Genetics	Molecular Cell Engineering	KANEMAKI, Masato / Professor	5830	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.
		NATSUME, Toyooki / Assistant Professor	5866	
Cell Genetics	Microbial Genetics	ARAKI, Hiroyuki / Professor	6754	Genetic and biochemical approach to elucidate molecular mechanism and regulation of eukaryotic DNA replication and checkpoint control using budding yeast
	Symbiosis and Cell Evolution	MIYAGISHIMA, Shin-ya / Professor FUJIWARA, Takayuki / Assistant Professor	9411 9414	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.
Developmental Genetics	Neurogenetics	IWASATO, Takuji / Professor NAKAGAWA, Naoki / Assistant Professor	6773 6777	We are studying molecular and cellular mechanisms of neuronal circuit development in the mammals, using mouse genetics and other related methods.
	Molecular and Developmental Biology	KAWAKAMI, Koichi / Professor ASAKAWA, Kazuhide / Assistant Professor MUTO, Akira / Assistant Professor	6740 6739 6739	Genetic studies on development, morphogenesis and behaviors by using a model vertebrate zebrafish.
Population Genetics	Population Genetics	SAITOU, Naruya / Professor JINAM, Timothy / Assistant Professor	6790 6787	We study evolution of genes and genomes, in particular human evolution. We also develop methods for study of genome evolution.
	Evolutionary Genetics	AKASHI, Hiroshi / Professor MATSUMOTO, Tomotaka / Assistant Professor	6793 5820	Mechanisms of genome evolution. Especially weak selection and biosynthetic constraints.
	Ecological Genetics	KITANO, Jun / Professor ISHIKAWA, Asano / Assistant Professor	9415 9416	We use threespine stickleback fishes to investigate the genetic and molecular mechanisms underlying adaptation and speciation.

<b>Integrated Genetics</b>	<b>Human Genetics</b>	<b>INOUE, Ituro</b> / Professor <b>NAKAOKA, Hirofumi</b> / Assistant Professor	6795 6796	Medical genomic study using high-throughput sequencing data is a promising procedure to create an innovate healthcare system and open a new aspect of population genetics.
	<b>Agricultural Genetics</b>	<b>KAKUTANI, Tetsuji</b> / Professor <b>TARUTANI, Yoshiaki</b> / Assistant Professor <b>INAGAKI, Soichi</b> / Assistant Professor	6801 6807 6807	Control and function of epigenetic gene modifications in Arabidopsis.
	<b>Brain Function</b>	<b>HIRATA, Tatsumi</b> / Professor <b>KAWASAKI, Takahiko</b> / Assistant Professor <b>YAN, Zhu</b> / Assistant Professor	6721 6721 6721	Development of the vertebrate nervous system with special focus on neuronal network formation.
<b>Center for Frontier Research</b>	<b>Cell Dynamics and Organization</b>	<b>ODA, Yoshihisa</b> / Associate Professor	6800	To understand the mechanism underlying plant cell wall patterning, we study the dynamic behavior of cortical cytoskeletons and small GTPases in xylem cells.
	<b>Quantitative Mechanobiology</b>	<b>SHIMAMOTO, Yuta</b> / Associate Professor	6784	Our laboratory studies mechanisms of force-based regulation in the mitotic spindle and the cell nucleus. Using our expertise of controlled mechanical manipulation and high-resolution fluorescence imaging, the micro-mechanics of these intracellular structures, assembled in Xenopus egg extracts, are quantitatively analyzed.
	<b>Chromosome Biochemistry</b>	<b>MURAYAMA, Yasuto</b> / Associate Professor	6810	We investigate molecular mechanism underling regulation of chromosome organization and dynamics by recapitulating their biochemical reactions using purified proteins. We now especially focus on SMC complexes.
	<b>Systems Neuroscience</b>	<b>KUBO, Fumi</b> / Associate Professor	5828	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>Genetic Strains Research Center</b>	<b>Mammalian Genetics</b>	<b>SHIROISHI, Toshihiko</b> / Professor *To be retired on March 31 <sup>st</sup> ,2019 <b>TAKADA, Toyoyuki</b> / Assistant Professor	6818  6820	In order to understand genetic regulation of complex traits, such as morphogenesis and energy metabolism, we are conducting genetic analyses using mouse spontaneous mutants (variants) and genetically modified mutants.
	<b>Mammalian Development</b>	<b>SAGA, Yumiko</b> / Professor <b>KATO, Yuzuru</b> / Assistant Professor <b>AJIMA, Rieko</b> / Assistant Professor	6829 6832 6832	We study the early developmental events and the regulatory mechanisms during mouse embryogenesis through generation and analyses of gene-knockout and transgenic mice. We are especially interested in the organs derived from mesoderm (heart, lung, somite), and the germ cell system.
	<b>Mouse Genomics Resource</b>	<b>KOIDE, Tsuyoshi</b> / Associate Professor <b>TAKANAMI, Keiko</b> /Assistant Professor	5843 5845	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>Model Fish Genomics Resource</b>	<b>SAKAI, Noriyoshi</b> / Associate Professor <b>KAWASAKI, Toshihiro</b> / Assistant Professor	5848  5849	We establish reliable protocols for genetically modification of zebrafish using sperm, and analyze the molecular mechanisms of spermatogenesis and early development in zebrafish.
	<b>Plant Genetics</b>	<b>SATO, Yutaka,</b> / Professor <b>TAKAHASHI, Misuzu</b> / Assistant Professor <b>SUZUKI, Toshiya</b> / Assistant Professor	6808 6802 6803	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>Microbial Genetics</b>	<b>NIKI, Hironori</b> / Professor <b>AOKI, Keita</b> /Assistant Professor	6870 6827	We investigate higher order structure of chromosomes and their dynamics in yeast and bacteria through genetic and cell biological analysis.
	<b>Invertebrate Genetics</b>	<b>SAITO, Kuniaki</b> / Professor <b>KONDO, Shu</b> / Assistant Professor <b>MIYOSHI, Keita</b> / Assistant Professor	6823 6824 6824	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>Genetic Informatics</b>	<b>KAWAMOTO, Shoko</b> /Associate Professor	6885	We are working on research and development of databases and information retrieval system for the national bio-resource project(NBRP).

<b>Structural Biology Center</b>	<b>Biological Macromolecules</b>	<b>MAESHIMA, Kazuhiro</b> / Professor <b>IDE, Satoru</b> / Assistant Professor <b>HIBINO, Kayo</b> / Assistant Professor	6864 6878 6878	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	5854 5854	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>Multicellular Organization</b>	<b>SAWA, Hitoshi</b> / Professor	6845	We are studying the mechanisms that produce a variety of cell types through asymmetric cell divisions using the nematode <i>C.elegans</i> .
	<b>Gene Network</b>	<b>SUZUKI, Emiko</b> / Associate Professor	6812	Combinations of molecular genetics of Drosophila and high-resolution light and electron microscopy are employed to study functional implication of structural and molecular organization of cells.
<b>Center for Information Biology</b>	<b>DNA Data Analysis</b>	<b>IKEO, Kazuho</b> / Associate Professor	6851	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>Biological Networks</b>	<b>ARITA, Masanori</b> / Professor <b>KAWASHIMA, Takeshi</b> / Assistant Professor	9449 9449	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	6859	Intelligent information technology for structural and functional annotations of large-scale nucleotide sequences.
	<b>Research and Development of Biological Databases</b>	<b>TAKAGI, Toshihisa</b> / Professor *To be retired on March 31 <sup>st</sup> ,2019	5821	We are researching to apply distributed database technology and/or parallel-distributed computing technology to huge life science databases including DDBJ. Studies on analyzing biological data with using supercomputer.

	<b>Gene- Expression Analysis</b>	<b>OKUBO, Kousaku</b> / Professor	5838	“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>Comparative Genomics</b>	<b>TOYODA, Atsushi</b> / Project Professor	6788	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>Genome Evolution</b>	<b>KUROKAWA, Ken</b> / Professor <b>MORI, Hiroshi</b> / Assistant Professor	9437 9438	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>Experimental Farm</b>		<b>NONOMURA, Ken-ichi</b> / Associate Professor <b>TSUDA, Katsutoshi</b> / Assistant Professor	6872 6874	We aim to elucidate the regulatory system of plant germ-cell development and chromosome kinetics, mainly using seed-sterile rice mutants.
<b>Radioisotope Center</b>		<b>ANDACHI, Yoshiki</b> / Assistant Professor	6871	We study microRNA-mediated post-transcriptional regulation in <i>C. elegans</i> using our original methods for the detection of microRNAs and target genes.
<b>Center for Advanced Genomics</b>		<b>FUJIYAMA, Asao</b> / Project Professor <b>NOGUCHI, Hideki</b> / Project Professor	6788 9459	Development of new algorithms for <i>de novo</i> sequence assemblies, and analytical tools for comparative genomics employing massive data produced from next generation sequencers.