Attachment

Available Facilities

1.Genome Science (including Genomics, Epigenomics, Transcriptomics, and Infomatics Analysis)

1) DNA sequencing analysis using next generation sequencers.

Fig.1 Next Generation Sequencers

The Medical Research Center for High Depth Omics possesses short-read-type next generation sequencers, mainly Illumina instruments, including Illumina NovaSeq6000, HiSeq2500, HiSeq1500, and MiSeq, which are beneficial for super parallel analysis in single cell transcriptomics or epigenomics (ATACSeq, ChILSeq) adding to regular genome/transcriptome analysis. We are flexible to accept proposals of various other studies that require the use of NGS upon request.

2) DNA sequencing Analysis with Third-Generation Sequencers

Fig.2 Third-Generation Sequencer

The Medical Research Center Initiative for High Depth Omics has introduced the PacBio Sequel IIe. This sequencer is capable of reading much longer sequences (14kb to 18kb) with high precision compared to next-generation sequencers (Long Read-Seq). It can be used for determining structural polymorphisms in model organisms such as humans and mice, enhancing genomic sequence determination in non-model organisms, sequencing metagenomes, and IsoSeq analysis.

3） Infrastructure System Usage for Information Analysis of 1) and 2)

The analysis of information from next-generation and third-generation sequencers requires the use of various bioinformatics tools. Our institute has established an information analysis system that can be utilized for the analysis of sequence-centered information obtained from 1) and 2)

○Inquiries about available instruments and technology

*Please add “kyushu-u.ac.jp” to each email address.

Division	Facilitator	E-mail Address	Remarks
Genomics	Hiroki Shibata (Associate Professor)	hshibata@gen.	Whole Genome Seq, Exome-Seq, Amplicon-Seq
Transcriptomics	Yasuyuki Ohkawa (Professor)	yohkawa@bioreg.	ChIP/ChILSeq, scRNA/ATAC-Seq
Biomedical Information Analysis	Masao Nagasaki (professor)	nagasaki@bioreg.	Utilization of Information Analysis Infrastructure,

2. Spatial Omics（including spatial transcriptomics, Spatial proteomics, and Spatial metabolomics）

The Medical Research Center Initiative for High Depth Omics is equipped with the necessary microscopy systems and other infrastructure to conduct spatial multi-omics analyses. These include spatial transcriptome analysis using the Photoisolation Chemistry (PIC) method, proteome and metabolome analysis through sequential immunostaining, and spatial multi-omics analysis in cellular and tissue samples using sequential RNA/DNA-FISH techniques.

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Division	Facilitator	E-mail Address	Remarks
Transcriptomics	Yasuyuki Ohkawa (Professor)	yohkawa@bioreg.	PIC, sequential immunostaining, and sequential RNA-FISH
Biomedical Information Analysis	Masao Nagasaki (professor)	nagasaki@bioreg.	Informatic analysis
Gene Expression Dynamics	Hiroshi Ochiai (Professor)	ochiai@bioreg	Sequential RNA/DNA -FISH

3. Structural Biology

1) Single particle analysis using cryo-electron microscopy and negative staining method

- FEI Tecnai G3 Polara (300 kV transmission electron microscope)
  Cryo measurements at liquid nitrogen temperature,
  Tomography including STEM tomography, STEM(HAADF),
  4K x 4K CCD (UltraScan4000, GATAN),
  Energy filter (GIF BioQuantum K3, GATAN with 24 Mega-Pixel CCD)
- FEI Tecnai20 (200 kV transmission electron microscope)
  Tomography, 2K x 2K CCD (Eagle 2k, FEI)

Fig. 1Cryoelectron microscope
(Tecnai Polara)

2) Automatic setting-up devices for crystallization screening

- Search under 96 different crystallization conditions using a total of 25 μl protein solution (0.2 μl per drop).

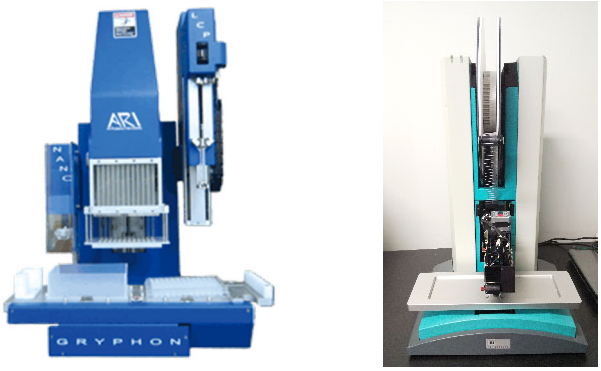

Fig. 2 (left) Crystal Gryphon LCP Setting-up Device (Art Robbins Instruments)
(right)Mosquito (SPT Labtech)

3) Circular Dichroic Polarimeter (CD)
-JASCO J-820

*1) The conditions or quantities of protein samples required for successful measurements may vary depending on the type of analysis or research aim. Please contact the facilitator beforehand to inquire whether the experiment is feasible or not.

*2) Preliminary experiments such as protein crystallization, determination of lattice constant, and electron microscopic observation, are not necessary. －However, discussion about the sample preparation and condition with the facilitator is desirable.

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Division	Facilitator	E-mail Address	Remarks
Trans-Scale Structural Life Science	Kenji Inaba (Professor)	kenji.inaba@bioreg.	

4. Embryonic and Genetic Engineering

We can provide the following technological support regarding developmental engineering experiments: ES injection into blastocysts, DNA injection (including Crispr/Cas9) into fertilized eggs, in vitro fertilization/preparation of frozen fertilized eggs, etc.

Fig. Electroporator (left) and Micromanipulator System (right)

Service	Reception	Comments
ES cell injection	1 to 2 days p.w. (Tue, Wed, Thu, Fri)	Use of C57BL/6J mice
DNA injection	1 to 2 days p.w. (Tue, Thu)	Use of C57BL/6J mice
Preparation of frozen fertilized egg	Arbitrary	Embryo freezing via in vitro fertilization (IVF); cleaning of mice
Bringing in frozen fertilized egg	Arbitrary	Thawing/transplantation of frozen embryo from other institutions; aim of transfer
Carrying out/thawing frozen fertilized egg	Arbitrary	Thawing/transplantation of frozen embryo, transporting frozen embryo
Preparation of frozen sperm	Arbitrary	Preparation and preservation of frozen sperm

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○Inquiries about available instruments and technology

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Division	Facilitator	E-mail Address	Remarks
Immunology and Genomic Biology	Yoshihiro Baba (Professor)	babay@bioreg.	