



Data Analysis Service Request Form

Please fill out the request form.

1). Contact and Affiliation

Name of PI:
Designation:
Affiliation:
Department:
Email:
Phone:

2). Tell us about your data

What type of data you want to analyze?

- Whole genome sequencing (WGS)
- Whole exome sequencing (WES)
- RNA-sequencing (RNA-seq)
- Small RNA sequencing
- ChIP-seq
- 16S/Metagenomics
- Methylation array
- Microarray
- Molecular docking & simulation
- Others, please specify:

3). Tell us more about your experiment

Name of the organism

- Mammals: Human (), Mouse (), Rat (),
- Bacteria:
- Fungus:
- Virus:
- Others, please specify:

Reference genome version for human

- GRCh37
- GRCh38
- Others, please specify:

Sequencing platform

- Illumina
- Roche-454
- Ion Torrent
- PacBio
- ABI-Sanger
- Affymetrix
- Agilent
- EPIC BeadChips
- 450K BeadChips
- Other, please specify:

Required Information

- Raw data (e.g. fastq, .idat, .CEL etc.,)
- library preparation kit / BED file
- Number of samples:
- The estimated total file size of your dataset:
- Sample information (different groups/experimental conditions, if applicable).....
- Disease information:
- Sample type:

(e.g. culture, microbiome, environmental sample, single cells, cell line, tissue, etc.,)

Select the output that you would like to receive:

- Genome assembly & annotations
- Pan-genome
- Differentially expressed genes/transcripts/small-RNAs
- Transcriptome assembly
- Antibiotic resistance genes
- Single nucleotide variants /short variants
- Copy number variants
- Differentially methylated probes/genes
- Phylogenetic tree
- Drug targets and inhibitors
- Other, please specify:

Signature and stamp of PI

Signature and stamp of Faculty I/c

Job ID:

Date: