

INSTITUTE FOR INTEGRATIVE GENOME BIOLOGY (IIGB)

Instrumentation Facilities



The Institute for Integrative Genome Biology (IIGB) is a nucleus for interdisciplinary research to overcome the academic barriers to train a new generation of scientists and to combine innovative tools in genome biology, chemistry, computer sciences, and engineering to unravel the real world of biology. To arrive at this goal, IIGB exploits and provides access and services to cutting-edge technologies through the following Core Facilities: Bioinformatics, Genomics, Metabolomics, and Proteomics.

BIOINFORMATICS CORE

The Bioinformatics Core provides services and hands-on training for computational data analysis and convenient access to the NGS data sequenced at UCR, data analysis, and programming expertise. The Bioinformatics Core provides project-specific consultation on experimental design and data analysis, development of novel analysis pipelines and workflow with special skills in the areas of genomics (e.g., Whole Genome- and Exome-seq), transcriptomics (e.g., RNA-seq, small RNA-seq, Ribo-seq), epigenomics (e.g., Methyl-seq, ATAC-seq), and systems biology. The Bioinformatics Core maintains over 800 open source bioinformatics software packages for NGS analysis, comparative genomics, data mining, statistics, molecular modeling, cheminformatics, evolutionary biology, and all common programming environments.

GENOMICS CORE

The Genomics Core Facility supports the campus research enterprise with tools for handling applications in genome, transcriptome, epigenome, microbiome, single cell and spatial omics, and many other exciting investigations in biotechnology. The Genomics Core houses three Illumina sequencing platforms, MiSeq, NextSeq 500, and a most updated NextSeq 2000. The 3rd generation long reads sequencing services through PacBio Sequel II and Oxford Nanopore platforms, and several robotics-based handling instrumentations are also available at the Genomics Core.

METABOLOMICS CORE

Metabolomics is the most recent frontier in “Omics” science where through advanced instrumentation thousands of small molecules can be identified and quantified simultaneously from a single biological sample. The Metabolomics Core Facility is fully equipped with state-of-the-art liquid chromatography and mass spectrometers capable of investigating a wide range of small molecules in biological and physical systems. These instrumentation include: Waters Synapt G2-Si Q-TOF, Waters G2-XS Q-TOF, Waters TQ-XS triple quadrupole, and the Thermo Scientific ISQ 7000 GC-MS system. The Metabolomics Core also provides users analytical platforms in central carbon metabolism, natural product discovery, phytohormones, lipids, and many other molecular classes.



PROTEOMICS CORE

The Proteomics Core houses state-of-the-art mass spectrometers, such as Q-TOF (nano-ESI) and Q-STAR (MALDI), that permit unprecedented sensitivity and accuracy in identifying protein sequences and their abundance. These technologies permit the Proteomics Core to support researchers in understanding molecular details such as protein modifications and components of protein complexes. The Proteomics Core also has a variety of equipment specifically for sample preparation and processing. Workstations for data processing are also housed in the Proteomics Core.

IIGB RESEARCH IN ACTION IDENTIFYING COVID-19 VARIANTS IN THE COMMUNITY

Sequencing and genetic analysis of COVID-19 samples at UC Riverside is helping California state officials prepare for potential infection surges caused by new variants of the disease. Variants, like Delta or Omicron, can render COVID-19 vaccines or antibody treatments less effective, and they can also be spread more easily than the original strain of the virus. UCR's genetic data helps the California Department of Public Health detect variants and gives officials a real-time view of how they may be migrating through the state.

