3 Genomics Research & Technology Hub

GRT HUB

UCI 趙 Chao Family Comprehensive Cancer Center

LEADERSHIP & MISSION +

Suzanne Sandmeyer, PhD
Director

Remi Buisson, PhD
Assistant Director

Melanie Oakes, PhD
Manager, Tech Ops

Jenny Wu, PhD
Director, Bioinformatics

Ivan Chang, PhD
Bioinformatics Engineer

GRT Hub puts emerging nucleic acid technologies into the hands of investigators and enables bioinformatics analysis through consultation, training and collaboration

- Provides guidance and education throughout the entire experimental process, including design, analysis and publication
- Provides in-house staff with professional expertise in genome wide molecular technologies
- Bioinformatics Consulting Service for experimental design and data analysis staffed with PhD-level scientists experienced in bioinformatics

SERVICES, TECHNOLOGIES & EQUIPMENT +

- **INSEIllumina iScan beadarray**: linkage analysis, copy number variants, epigenetics
- **Illumina NovaSeq X Plus**: whole human genomes, deep sc sequencing
- **PacBio Revio**: whole genome seq, structural variants, scRNA isoforms
- **BioNano-Saphyr 2**: long-range optical mapping; structural variants
- **Library preparation**: single cell, multi-omic, HiFi, Me-seq, etc
- **NanoString nCounter**: digital quantification of known nucleic acid targets
- **10X Genomics ChromiumX**: scRNA-seq; scATAC-seq; multiome; VD(J) typing

- **Parse Biosciences**: split-seq; reduced cost for 100,000-1 M cells
- **Mission Bio Tapestri**: scDNA and protein typing tumor lineage mapping; CNV
- **Bruker Isoplexis**: monitoring single cell secreted proteins, e.g. cytokines
- **Digital PCR:** Bio-Rad ddPCR, ThermoFisher Quantstudio Q
- **Nanostring GeoMx and 10x Visium**: spatial transcriptomics on fixed or fresh
- **Data visualization portals:** Publicly accessible web interactive dashboards enabling visual exploration of processed data
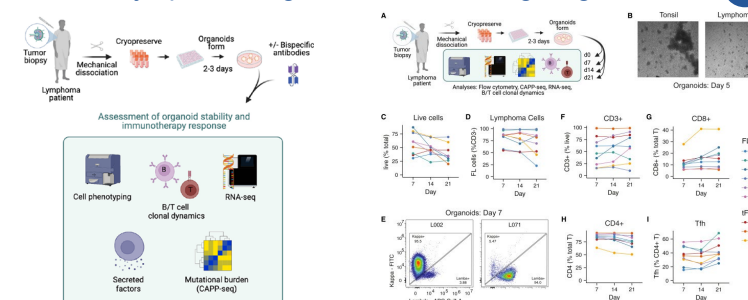
RESEARCH HIGHLIGHTS

APOBEC3 cytidine deaminases shape tumor responses +
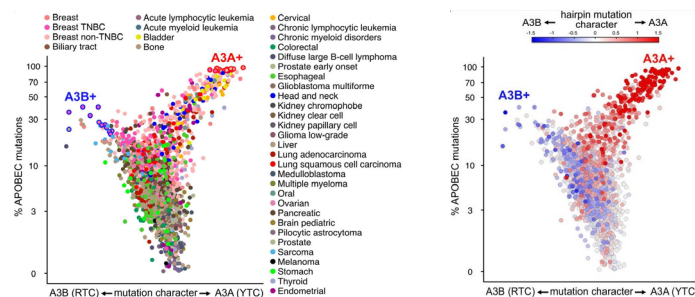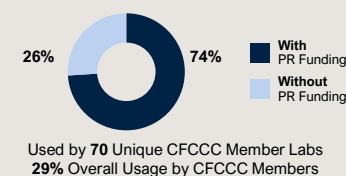

Cytidine deaminase activity at specific loci is linked +
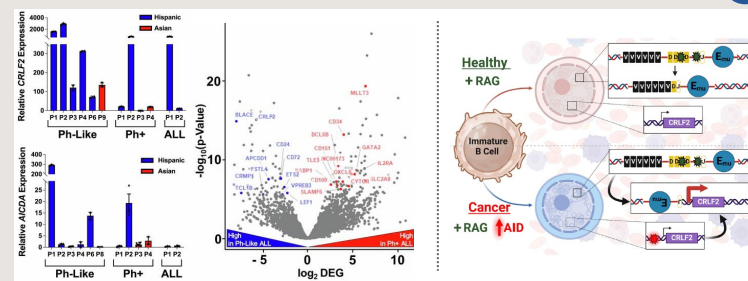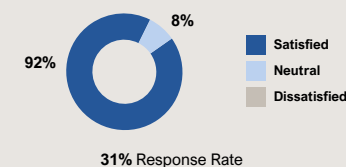

A human lymphoma organoid model for targeting tumors +

IMPACT & KEY METRICS CY2024 +

CFCCC MEMBER UTILIZATION

26% With PR Funding
74% Without PR Funding

Used by **70** Unique CFCCC Member Labs
29% Overall Usage by CFCCC Members

CFCCC USER SATISFACTION

92% Satisfied
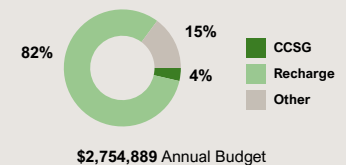8% Neutral / Dissatisfied

31% Response Rate

$11.6M Supported CFCCC Members Receive 22 New Cancer-relevant Grants (Total Direct Costs)

20 Support Led to New Cancer-Relevant Publications **(35%)** in IF ≥ 10 Journals)

BASE SR FUNDING

82% Recharge
15% CCSG
4% Other

$2,754,889 Annual Budget

TRAINING +

Outreach Event	Qty	Attendees
Hub Presentations	9	15-25
Workshops	4	10-15
Tech Seminar	14	20-30
Seminar Series	4	15-20
Symposium	1	95
Tours	9	1-20

[UPCOMING] Genetics, Biomedical Computing and Genomics Seminar Series, "Navigating NIH's New Security Requirements" Friday 05/07/2025 10:00 to 11:00 a.m. (PST) Event Details

Genetics, Biomedical Computing and Genomics Seminar

[UPCOMING] Workshop on Statistics and Machine Learning in Genomics – Presented by the GRT Hub Tuesday 05/18/2025 Sprague Hall, Room 105 Event Details
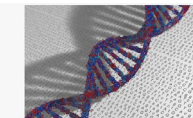
FUTURE PLANS

- Expand shared personnel model for bioinformatics support
- Innovate in spatial multi-omics
- Increase workshop emphasis for statistical and AI empowered approaches
- Expand clinician relevant support services
- Sustainability planning

Internal Advisory Committee

David Fruman, PhD
Associate Director
Basic Science, CFCCC

Anthony Long, PhD
Professor
Ecology & Evolutionary Biology

Moyra Smith, MD, PhD
Professor
Human Genetics & Pediatrics

Xiaohui Xie, PhD
Professor
Computer Science

Klemens Hertel, PhD
Professor and Chair
Microbiology & Molecular
Genetics

Daniel Mercola, MD, PhD
Professor
Pathology & Laboratory Medicine

Robert Spitale, PhD
Professor
Pharmaceutical Sciences

Kyoko Yokomori, PhD
Professor
Biological Chemistry

Jill Kay, MS
Director, Research Policy
UCI Office of Research

Ali Mortazavi, PhD
Professor
Developmental & Cell Biology

Leslie Thompson, PhD
Professor and Chair
Neurobiology & Behavior

Al LaSpada, MD, PhD (Chair)
Professor, Chair & Assoc. Dean
Pathology & Laboratory Medicine

Nicholas Pannunzio, PhD
Assistant Professor
Medicine & Biological Chemistry

Craig Walsh, PhD
Professor & Assoc. Dean
Molecular Biology & Biochemistry

Wei Li, PhD
Professor
Biological Chemistry

Maksim Plikus, PhD
Professor
Developmental & Cell Biology

Marian Waterman, PhD
Associate Director
Shared Resources, CFCCC

FREQUENCY
Quarterly

FUNCTION
Advises regarding purchases, symposia, services, and grant applications

AUTHORITY
Advisory

MAIN

Services, Technologies & Equipment

https://genomics.uci.edu

Services, Technologies & Equipment

https://genomics.uci.edu

Epigenome

Iscan: methylome, CNV

Lineage Tracing

Tapestri

Secretome

SC Cytokines: IsoSpark

Digital PCR

Absolute Q

Spatial Transcriptomics

Probe based

Vizgen MERSCOPE Ultra

Primer based

10X Genomics Xenium

Sequencing: RNA, DNA, multi-omics

Short read

Long read

NovaSeq X
Plus 30X
human genome

Revio
30X
human genome;
single cell isoform

NEXT

Services, Technologies & Equipment

https://genomics.uci.edu
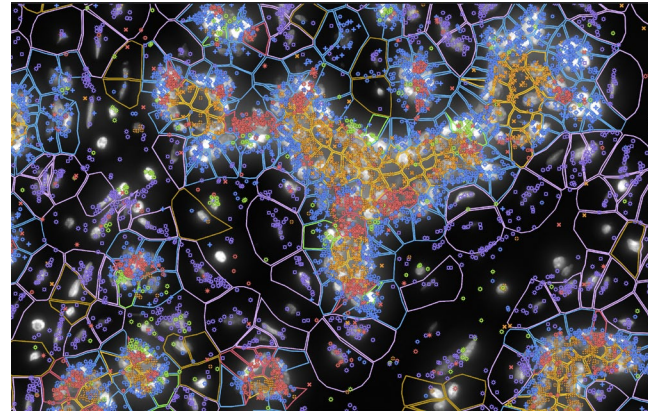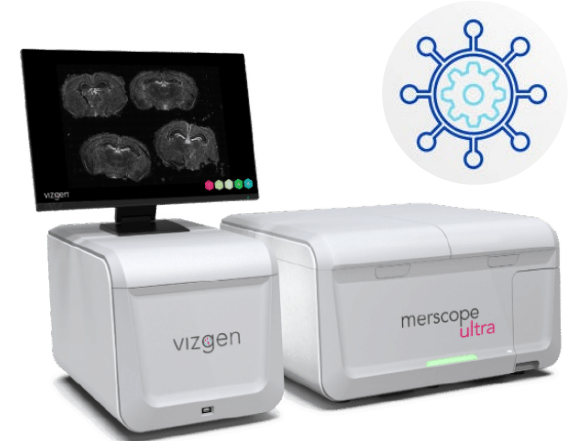
Sub-Cellular Spatial: FFPE & FF

Xenium:
Segmentation staining;
5000 probes;
Post analysis proteomics

Kessenbrock/Lawson
Breast Tissue by Xenium

Stellaromics Pyxa
3D spatial
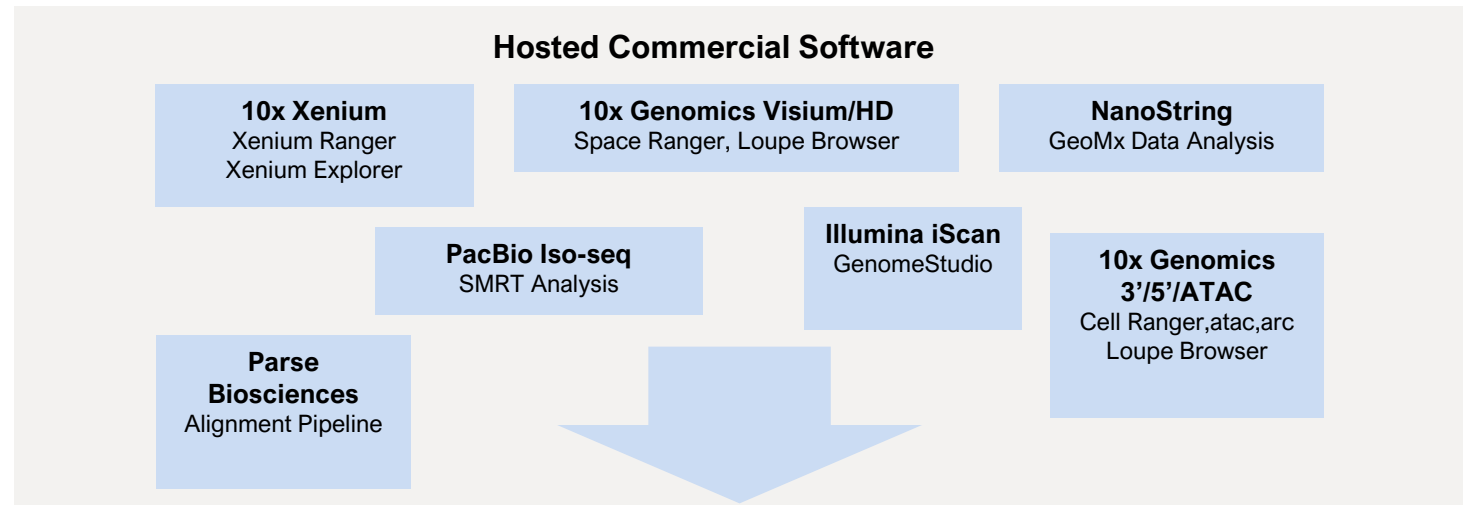*UCI Early Access*

MERFISH Ultra
10,000 probes
3 cm * 3cm

NEXT

Services, Technologies & Equipment
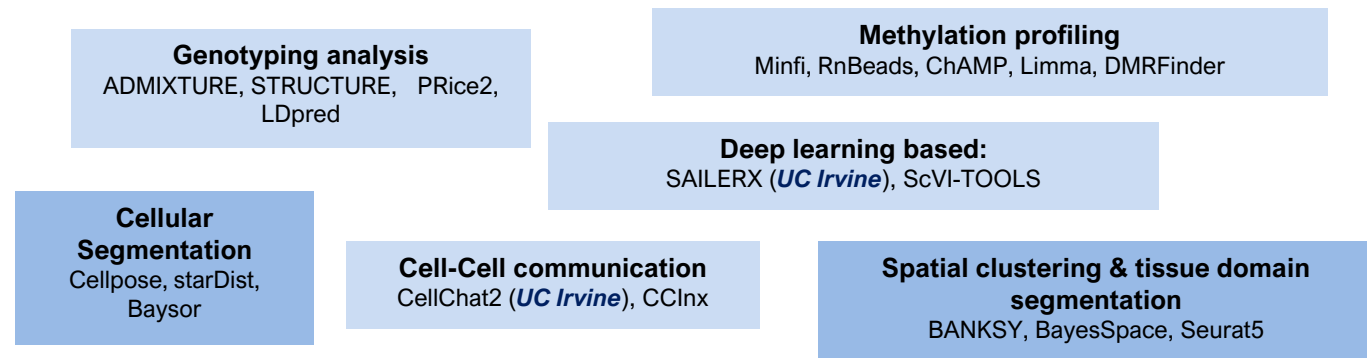
Analysis and Data Sharing

Jenny Wu, PhD

Director, Bioinformatics

Bioinformatics Applications, Workshops
Data Analysis

Hosted Commercial Software

10x Xenium
Xenium Ranger
Xenium Explorer

10x Genomics Visium/HD
Space Ranger, Loupe Browser

NanoString
GeoMx Data Analysis

PacBio Iso-seq
SMRT Analysis

Illumina iScan
GenomeStudio

10x Genomics 3'/5'/ATAC
Cell Ranger,atac,arc
Loupe Browser

Parse Biosciences
Alignment Pipeline

GRThub Curated Open Source Software for Pipeline Development

Genotyping analysis
ADMIXTURE, STRUCTURE,   PRice2, LDpred

Methylation profiling
Minfi, RnBeads, ChAMP, Limma, DMRFinder

Deep learning based:
SAILERX (*UC Irvine*), ScVI-TOOLS

Cellular Segmentation
Cellpose, starDist, Baysor

Cell-Cell communication
CellChat2 (*UC Irvine*), CCInx

Spatial clustering & tissue domain segmentation
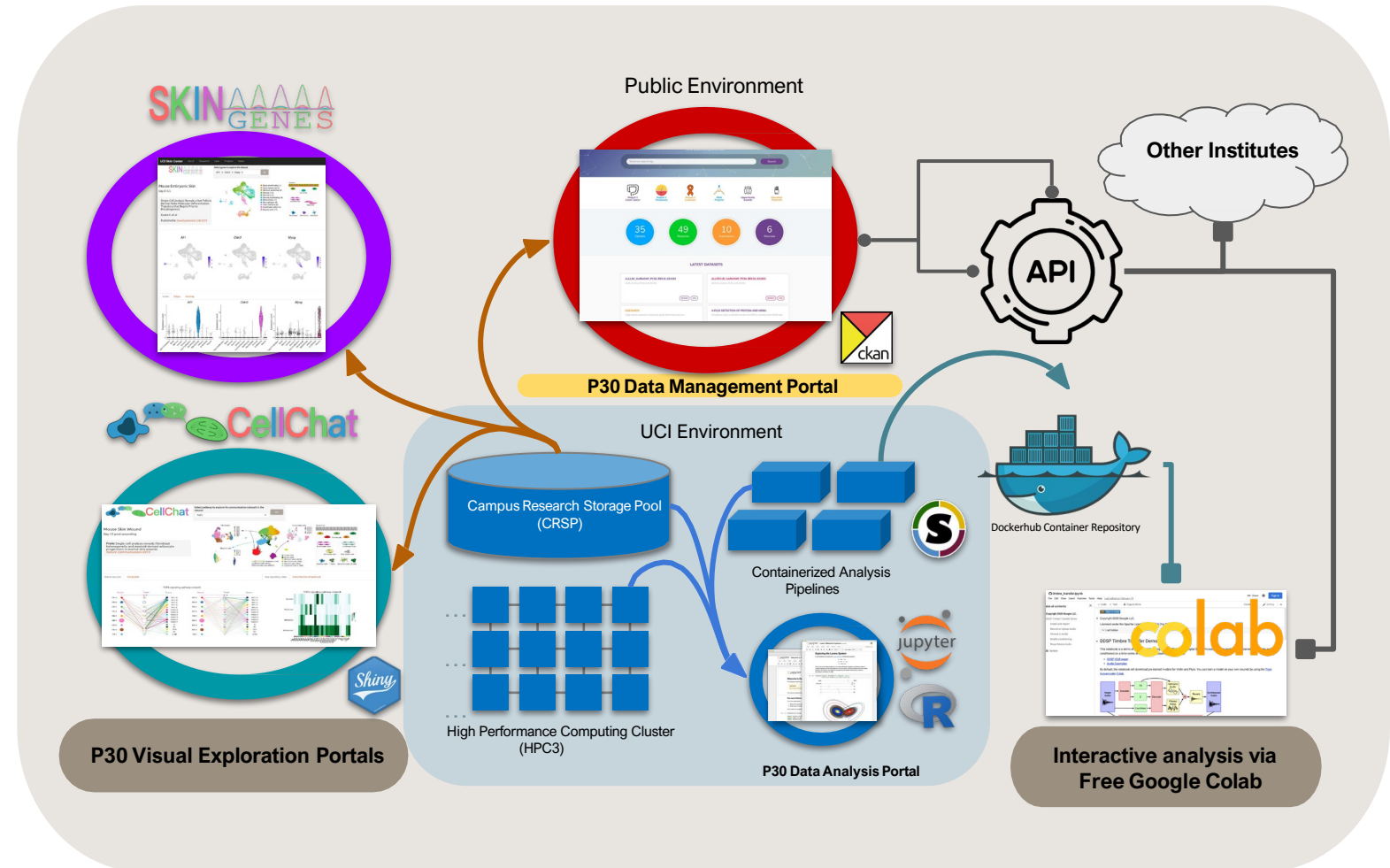BANKSY, BayesSpace, Seurat5

NEXT

Services, Technologies & Equipment

Analysis and Data Sharing

Ivan Chang, PhD

Bioinformatics Engineer

Portal Development

Seminars

Genetics, Biomedical Computing and Genomics Monthly Hub Seminar Series

Genetics, Biomedical Computing and Genomics Seminar Series – "Harnessing alternative polyadenylation and tandem repeat to understand the genetic basis of human diseases"

Friday 11/01/2024
10:00 to 11:00 a.m. (PST)
Zoom Only - This seminar will not be recorded.

Ya (Allen) Cui, PhD
Research Assistant Professor in the Wei Li lab
UCI Department of Biological Chemistry

Dr. Ya (Allen) Cui is a research assistant professor in Prof. Wei Li's lab in the Department of Biological Chemistry at the University of California Irvine. Dr. Cui will open his own lab early next year. Dr. Cui's research is focused on understanding the genetic association of tandem repeat (TR) and alternative polyadenylation (APA) association with complex traits and diseases, such as cancer, neurological, cardiovascular, and metabolic diseases. Dr. Cui will present his recently developed alternative polyadenylation transcriptome-wide association method (3'aTWAS) to identify APA-linked susceptibility risk genes (Nature Communications 2023) and an extremely exciting new research direction: TR-gnomAD, now known as TR-Atlas, a biobank-scale TR reference map for diverse ancestries (Cell 2024 and Nature Genetics accepted).
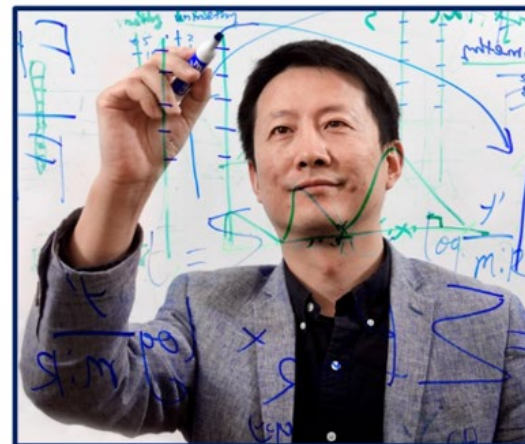
Genetics, Biomedical Computing and Genomics Monthly Seminar

Tuesday 06/04/2024
10:00 to 11:00 a.m. PST
Emerging Genetic Drivers of Human Diseases: A genome-wide spectrum of tandem repeat expansions in 338,963 humans

In this talk, Dr. Li will present an extremely exciting new research direction: the Tandem Repeat Genome Aggregation Database (UCI TR-gnomAD; *Cell* 2024). This groundbreaking project has positioned UCI as a leader in human and medical genetics. TR-gnomAD provides the first genetic reference maps for approximately 0.8 million Tandem Repeat (TR) expansions, such as the CAG expansion in Huntington's disease, across 340,000 humans. It revolutionizes TR-based disease-association studies, health disparity research, and clinical diagnostics. The international research and medical communities, including scientists, physicians, and genetic counselors, will heavily rely on TR-gnomAD for interpreting TR expansions in genetic diseases,

Genetics, Biomedical Computing and Genomics Monthly Meeting – "Translational Science at CFCCC-Opportunities for Collaboration and Clinical Trials", Farshid Dayyani, MD, PhD
Tuesday 05/07/2024
10:00 to 11:00 a.m. (PT)

Dr. Dayyani is a Professor of Clinical Medicine in the Division of Hematology/Oncology at University of California Irvine and board certified in Medical Oncology. He is also the Associate Director for Translational Science and the Medical Director of the Clinical Trials Unit at the Chao Family Comprehensive Cancer Center at UC Irvine.

Dr. Dayyani performs clinical and translational research in gastrointestinal and hepatobiliary carcinomas. He manages a wide portfolio of investigator initiated, NCI funded and industry sponsored clinical trials to develop novel treatment options and establish new biomarkers. He obtained his MD/PhD from LMU Munich, Germany, followed by a research fellowship and residency in internal medicine at Harvard Medical School, Boston. He then completed a combined clinical and research fellowship in medical oncology at the UT MD Anderson Cancer Center, Houston, TX. Dr. Dayyani also has industry experience as Global Clinical Lead for Oncology at Roche Diagnostics, Int. in Rotkreuz, Switzerland, prior to joining UC Irvine.

Workshops
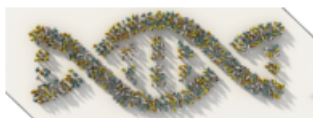
Spatial Transcriptomic Data Analysis with an Emphsis on 10x Genomics Visium Workshop

Tuesday 12/03/2024
9:00 a.m. to 1:00 p.m.
Sprague Hall, Room 207 - Registration Required

This workshop will introduce data analysis workflow with both sequencing- and imaging-based spatial transcriptomics platforms, using 10x Genomics Visium and Xenium as examples. The topics will include an overview of preprocessing and data visualization with both 10x Genomics proprietary software and the state-of-the-art open-source software. New topics such as Visium HD and Xenium 5k data analysis will be discussed including cellular niche and spatial differential analysis methods. A guided tour will be provided on how to run the latest visualization and data exploration tools to support spatial transcriptomics via command line and Jupyter Hub on HPC3. _Attendees are encouraged to bring their own project data for analysis and discussion._

Spatial Transcriptomic Data Analysis & Software

Tuesday 02/27/2024
8:00 a.m. to 12:00 p.m. - Light continental breakfast provided
Sprague Hall, Room 105

Genomics Research and Technology Hub (GRT Hub) Workshop

Required: Personal laptop (Mac or Windows) and HPC3 account

Instructors: Jenny Wu, PhD and Ivan Chang, PhD

This workshop introduces data analysis workflow with both sequencing and imaging based spatial transcriptomics platforms, using 10x Visium and Xenium as examples. The topics included an overview of data quality control, preprocessing and visualization, cellular segmentation etc. with 10x proprietary software and state of the art Open-source software. A guided tour was provided on how to run the latest visualization and data exploration tools to support spatial transcriptomics via both the command line and the Jupyterhub of HPC3.

10x Genomics Spatial Workshop Series – Three Sessions

Thursday 01/11/2024 – Wednesday 01/24/2024
Webinar

Because cells reside within microenvironments, their functions are influenced by the network cells surrounding them, sending and receiving messages. Spatially resolved biology, including whole transcriptomic and targeted in situ methods, allows scientists to build a more complete view of cellular function in a morphological context, representing a paradigm shift in the study of biological systems. Visium from 10x Genomics is a NGS-based spatial discovery platform that allows whole transcriptome profiling of tissues. The Xenium In Situ platform is an imaging-based solution that provides precise localization of thousands of RNA targets with subcellular resolution, offering true single cell spatial analysis. Insights from these spatial techniques can be combined with single cell data to bring greater resolution and enable a deeper understanding of gene expression patterns, helping researchers develop and refine hypotheses.

**January 11, 2024 – Visium**

January 18, 2024 – Xenium

January 24, 2024 – Visium Gene Expression

APOBEC3 cytidine deaminases shape tumor mutational responses

- APOBEC3A and APOBEC3B are major sources of mutations in cancer by catalyzing cytosine-to-uracil deamination

- APOBEC3A preferentially targets single-stranded DNAs, with an affinity for stem-loop secondary structures

- We found that APOBEC3B also selectively targets DNA stem-loop structures, and they are distinct from those subjected to deamination by APOBEC3A

- We developed Oligo-seq, an in vitro sequencing-based method to identify specific sequence contexts promoting APOBEC3A and APOBEC3B activity

- APOBEC3A and APOBEC3B deaminase activity is strongly regulated by sequences surrounding the targeted cytosine

- Importantly, we determined that APOBEC3B-induced mutations in hairpin-forming sequences within tumor genomes differ from the DNA stem-loop sequences mutated by APOBEC3A

- Our study provides evidence that APOBEC3A and APOBEC3B can generate distinct mutation landscapes in cancer genomes

APOBEC3B promotes mutations in hairpin-forming sequences in mouse and human tumors
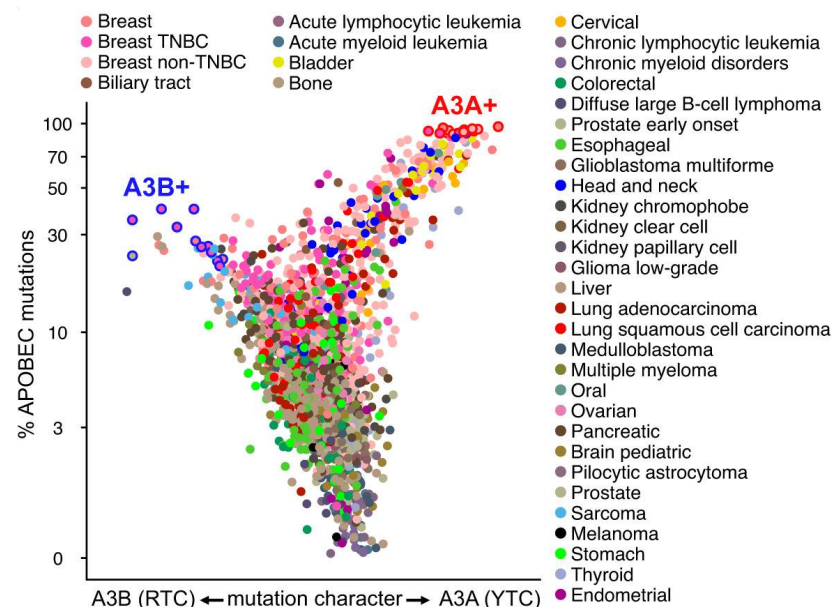
CATCHMENT AREA RELEVANCE

Investigators

Buisson, PhD

CFCCC Investments

SHARED RESOURCE

DOT	FUNDING	PROGRAMS
	2018	

IMPACT | First Discovery of the Sequence and Structural Specificity at sites of APOBEC3B-induced Mutations
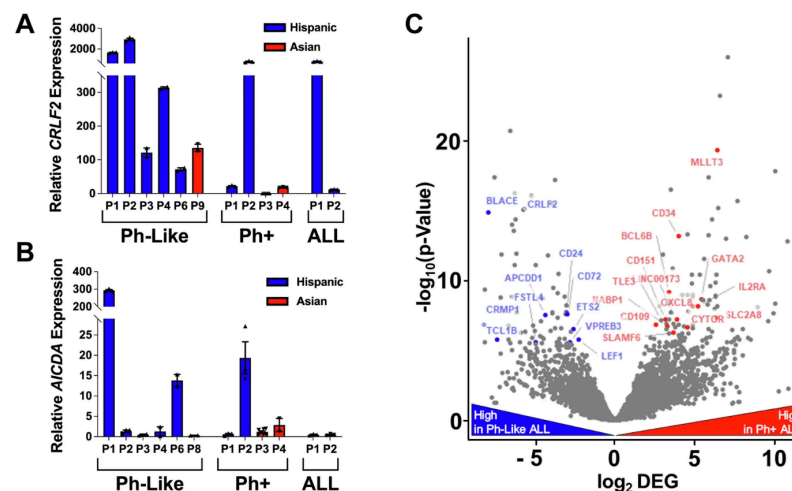
MAIN

Cytidine deaminase activity at specific loci is linked to cancer risk

A new assay identifies an important risk factor for Ph-like ALL

- Activation-induced cytidine deaminase (AID) is a B cell-specific mutator required for antibody diversification. It is also implicated in the etiology of several B cell malignancies

- Evaluating the AID-induced mutation load in patients at-risk for certain blood cancers is critical in assessing disease severity and treatment options

- We have developed a digital PCR (dPCR) assay that allows us to quantify mutations resulting from AID modification or DNA double-strand break (DSB) formation and repair at sites known to be prone to DSBs

- Implementation of this assay shows that increased AID levels in immature B cells increases genome instability at loci linked to chromosomal translocation formation

- This includes the CRLF2 locus that is often involved in translocations associated with a subtype of acute lymphoblastic leukemia (ALL) that disproportionately affects Hispanics, particularly those with Latin American ancestry

- Using dPCR, we characterize the CRLF2 locus in B cell-derived genomic

Fig. 4: Expression analysis on Ph-like, Ph-, and Ph+ ALL cohorts shows detection of variable *CRLF2* and AID expression levels in LA patients.

From: Increased AID results in mutations at the *CRLF2* locus implicated in Latin American ALL health disparities

IMPACT | AID levels are highly overexpressed and off-target activities at *CRLF2* are most prevalent during B cell maturation in Hispanics
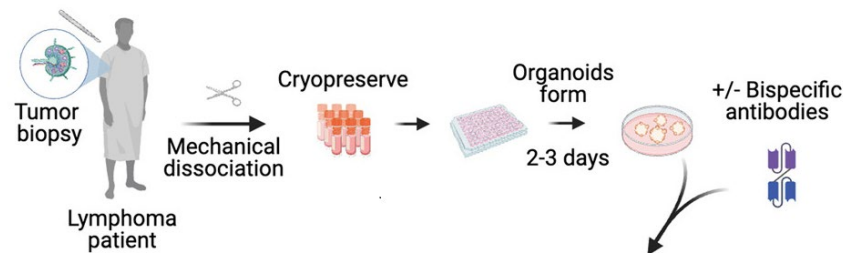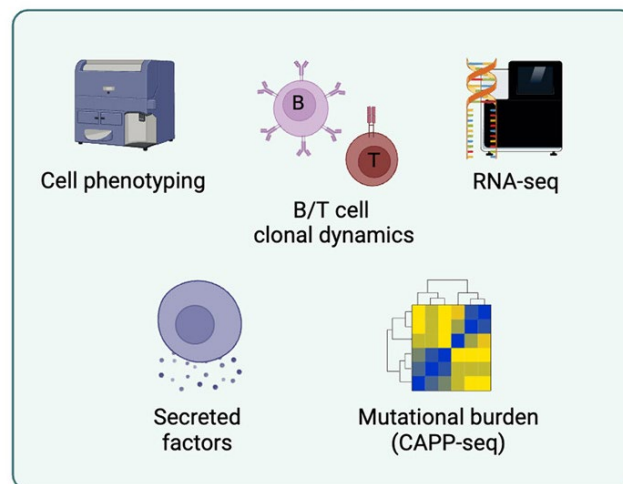
MAIN

A Robust Platform for Precision Medicine in Follicular Lymphoma

Patient-Specific Organoid Cultures

- Using primary follicular lymphoma tumor biopsies, Kastenschmidt et al. develop a patient-derived lymphoma organoid model demonstrating in vitro microenvironment stability over 3 weeks without exogenous cytokines

- Treated with bispecific immunotherapies, organoids recapitulated T cell-mediated lymphoma killing, allowing investigation of patient-specific microenvironment determinants of response

Tumor biopsy → Mechanical dissociation → Cryopreserve → Organoids form 2-3 days → +/- Bispecific antibodies

Lymphoma patient

Assessment of organoid stability and immunotherapy response

Cell phenotyping — B/T cell clonal dynamics — RNA-seq
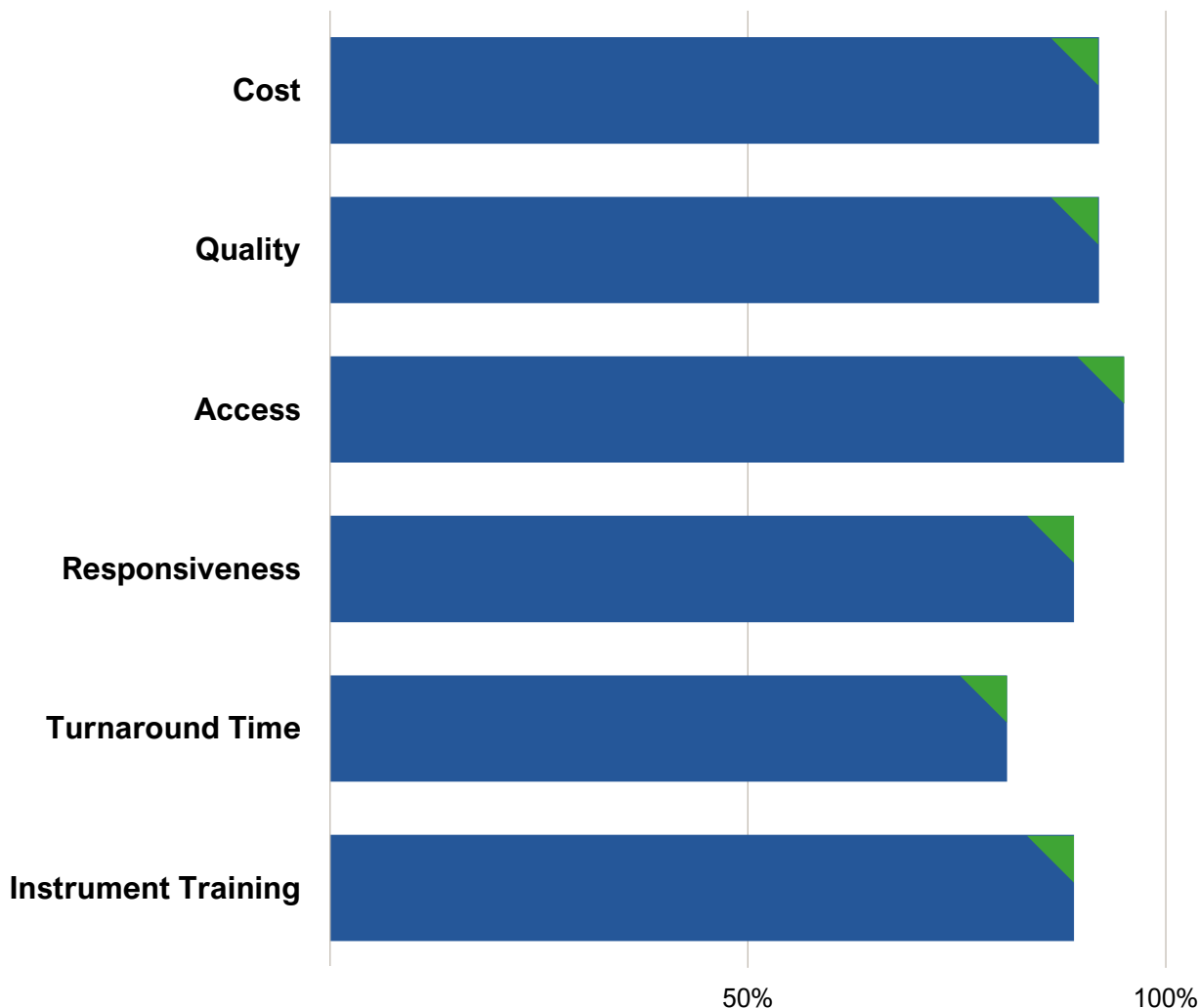
Secreted factors — Mutational burden (CAPP-seq)

IMPACT | New culture method enables real-time patient-derived lymphoma organoids for modeling, screening, microenvironment analysis, and treatment response

MAIN

2024 Annual Core Research Facilities Survey

● Excellent + Good (No scores below average received)   ◤ Improved since 2021

Chart (horizontal bars):

- Cost
- Quality
- Access
- Responsiveness
- Turnaround Time
- Instrument Training

X-axis: 50%   100%

SURVEY PROMOTION

UCI 趙Chao Family Comprehensive Cancer Center

Annual Shared Resources User Survey

Your feedback by May 10, 2024 is appreciated!

For the fourth year, the UCI School of Medicine and the UCI Chao Family Comprehensive Cancer Center are partnering on a survey regarding core research facilities in the School of Medicine.

Your answers are helpful and important; all responses will be factored in to optimize our School of Medicine and Chao Family Comprehensive Cancer Center research support structure. After answering a few basic questions, you will only be asked questions pertaining to the facilities and services used by you and the researchers under your supervision.

This survey is anonymous and your participation is highly encouraged. Thank you in advance for completing the survey!

Take Survey

Research Insider
UCI School of Medicine
Office of Research

2024 Core Facilities Survey

UCI School of Medicine and the UCI Chao Family Comprehensive Cancer Center are partnering on a survey regarding core research facilities in the School of Medicine. Your answers are helpful and important; all responses will be factored in to optimize our research support structure. After answering a few basic questions, you will only be asked questions pertaining to the facilities and services used by you and the researchers under your supervision. This survey is anonymous. For questions, contact Claire Brainard Draper. Please complete the survey by **May 10, 2024**.
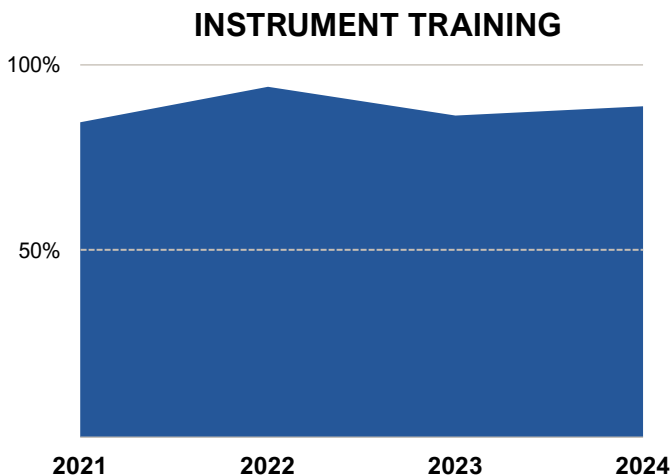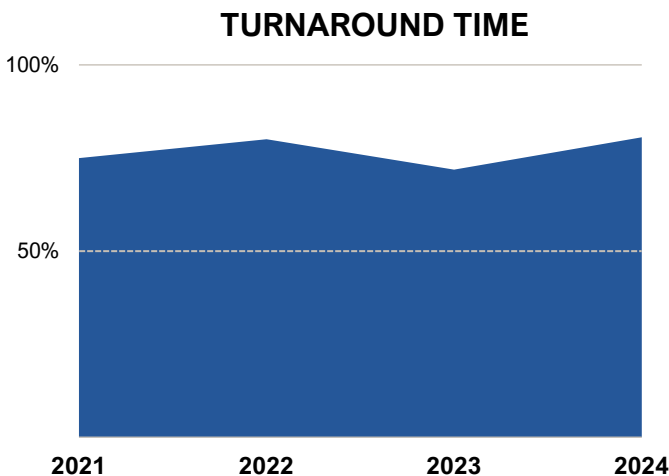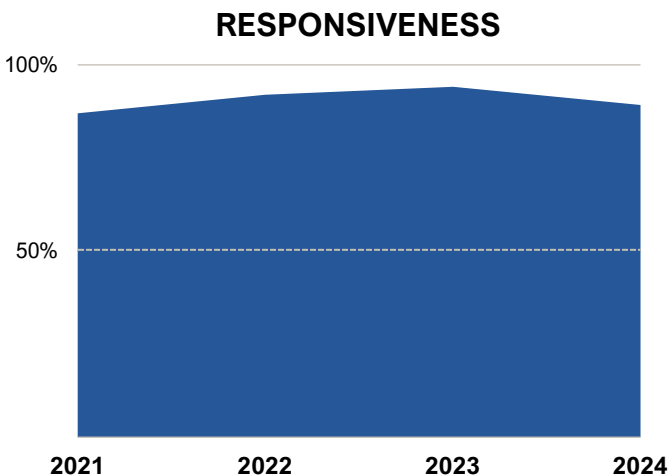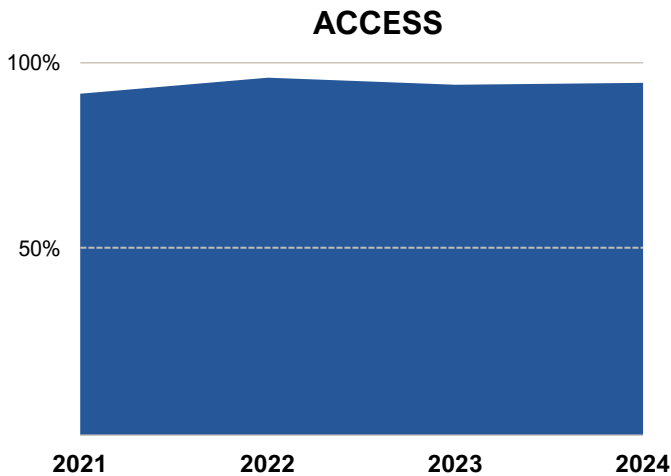
Complete Survey

NEXT

Annual Core Research Facilities Survey

Excellent + Good

COST

QUALITY

ACCESS

RESPONSIVENESS

TURNAROUND TIME

INSTRUMENT TRAINING
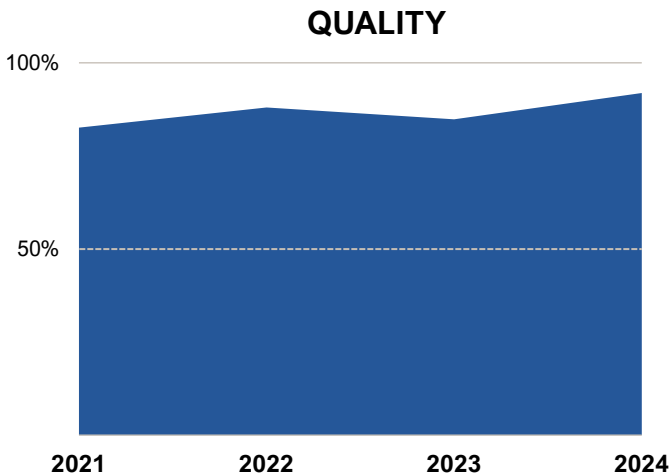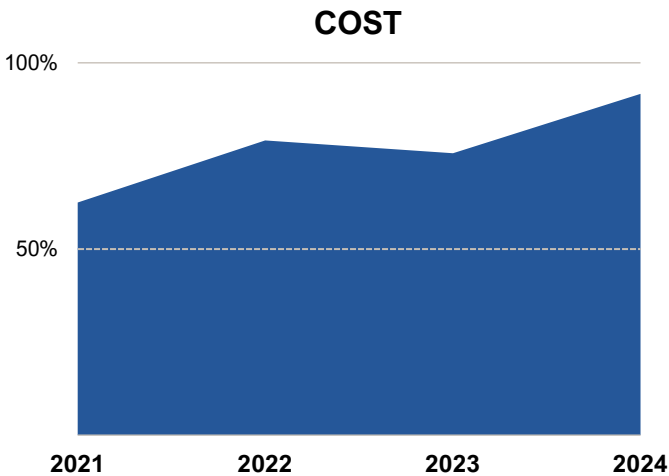
Selected 2024 Publications

CFCCC INVESTIGATOR(S)	PROGRAM	JOURNAL	YEAR
Nicholas Pannunzio, PhD; Marcus Seldin, PhD Ivan Marazzi, PhD; Francesco Marangoni, PhD Devon Lawson, PhD; Kai Kessenbrock, PhD Selma Masri, PhD	SPT	Nature Immunology	2024
Remi Buisson, PhD	SPT	Nature Communications	2024
Qing Nie, PhD; Arthur Lander, MD PhD Anand Ganesan, MD, PhD	SPT SPT BIDD	bioRxiv	2024
Oliver Eng, MD; Jennifer Valerin, MD; Sora Tanjasiri, DrPH; Marcus Seldin, PhD; Selma Masri, PhD; Angela Fleishman, MD, PhD; Nicholas Pannunzio, PhD	BIDD, SPT CC, SPT SPT, SPT SPT	Nature Communications	2024
Lisa Wagar, PhD	SPT	Cell Stem Cell	2024
Kai Kessenbrock, PhD Chris Hughes, PhD	SPT BIDD	Breast Cancer Research	2024
Angela Fleishman, MD, PhD Katrine Whiteson, PhD	SPT	Cancer Res Commun	2024
Selma Masri, PhD; Ivan Marazzi, PhD Remi Buisson, PhD	SPT	Nature Structure & Mol Bio	*in press* 2024