

Resource Summary Report

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University of Hawaii at Manoa Cancer Center Genomics and Bioinformatics Shared Resource Core Facility

RRID:SCR_019085

Type: Tool

Proper Citation

University of Hawaii at Manoa Cancer Center Genomics and Bioinformatics Shared Resource Core Facility (RRID:SCR_019085)

Resource Information

URL: <https://www.uhcancercenter.org/research/shared-resources/genomics-and-bioinformatics>

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Description: Core offers central service that uses genomic technologies combined with expert data analysis. Provides genomic analyses and bioinformatics as well as technical and scientific consultation, collaboration and initial data interpretation to all UH faculty with priority given to Cancer Center members with federal funding for cancer related projects. Offers expertise in molecular biology, genetics, genomics and bioinformatics, and can provide project planning, advice, and troubleshooting at all phases of the project. Genomic analysis services include DNA/RNA isolation, plating, and quality analysis, custom genotyping, Real-Time qPCR-based gene expression, copy number and methylation assays, pyrosequencing, Affymetrix and Illumina microarray based assays, Next Generation Sequencing on NextSeq500, iSeq100, NanoString nCounter analysis.

Abbreviations: GBSR

Synonyms: UHCC Genomics and Bioinformatics Shared Resource, University of Hawaii at Manoa UHCC Genomics and Bioinformatics Shared Resource

Resource Type: access service resource, core facility, service resource

Keywords: USEdit, genomic technologies, data analysis, DNA/RNA isolation, plating, and quality analysis, custom genotyping, Real-Time qPCR-based gene expression, copy number and methylation assays, pyrosequencing, ABRF, ABRF

Funding: NCI P30 CA071789

Availability: Restricted

Resource Name: University of Hawaii at Manoa Cancer Center Genomics and Bioinformatics Shared Resource Core Facility

Resource ID: SCR_019085

Alternate IDs: ABRF_787

Alternate URLs: <https://coremarketplace.org/?FacilityID=787>

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260905T133418+0000

Ratings and Alerts

No rating or validation information has been found for University of Hawaii at Manoa Cancer Center Genomics and Bioinformatics Shared Resource Core Facility.

No alerts have been found for University of Hawaii at Manoa Cancer Center Genomics and Bioinformatics Shared Resource Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Kunihiro BP, et al. (2026) Gut microbiome signatures associate with DNA methylation-based biological aging. Scientific reports, 16(1).

Liu T, et al. (2026) The association of epigenetic age acceleration with internal smoking dose, risk of lung cancer, and all-cause mortality in cigarette smokers: the Multiethnic Cohort study. Clinical epigenetics, 18(1).

Du Y, et al. (2025) Multiomics analysis of umbilical cord hematopoietic stem cells from a multiethnic cohort of Hawaii reveals the intergenerational effect of maternal prepregnancy obesity and risks for cancers. GigaScience, 14.

Du Y, et al. (2024) Multi-omics Analysis of Umbilical Cord Hematopoietic Stem Cells from a Multi-ethnic Cohort of Hawaii Reveals the Transgenerational Effect of Maternal Pre-Pregnancy Obesity. medRxiv : the preprint server for health sciences.

Huang BZ, et al. (2024) Epigenome-wide association study of total nicotine equivalents in multiethnic current smokers from three prospective cohorts. American journal of human

genetics, 111(3), 456.

Kuwabara JT, et al. (2022) Regulation of extracellular matrix composition by fibroblasts during perinatal cardiac maturation. *Journal of molecular and cellular cardiology*, 169, 84.

Ma C, et al. (2021) Upregulated ethanolamine phospholipid synthesis via selenoprotein I is required for effective metabolic reprogramming during T cell activation. *Molecular metabolism*, 47, 101170.

Corley MJ, et al. (2021) Abrupt and altered cell-type specific DNA methylation profiles in blood during acute HIV infection persists despite prompt initiation of ART. *PLoS pathogens*, 17(8), e1009785.

Wang Z, et al. (2021) Genetic susceptibility to hepatocellular carcinoma in chromosome 22q13.31, findings of a genome-wide association study. *JGH open : an open access journal of gastroenterology and hepatology*, 5(12), 1363.