

Resource Summary Report

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University of California at San Diego Institute for Genomic Medicine Genomics Center Core Facility

RRID:SCR_022740

Type: Tool

Proper Citation

University of California at San Diego Institute for Genomic Medicine Genomics Center Core Facility (RRID:SCR_022740)

Resource Information

URL: <http://igm.ucsd.edu/genomics/>

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Description: Provides services including sequencing library preparation and sequencing on Illumina MiSeq and NovaSeq 6000 platforms. Supports single cell sequencing on 10X Genomics Chromium Controller. Provides Illumina Infinium Beadchips, which includes variety of whole genome genotyping arrays as well as Infinium MethylationEPIC BeadChip.

Synonyms: UCSD IGM Genomics Center

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

Keywords: USEEdit, ABRF, sequencing library preparation, sequencing, single cell sequencing, whole genome genotyping arrays

Funding: NCI P30CA023100;
NIDDK P30DK063491;
NIDDK P30DK120515;
NIH Office of the Director S10 OD026929

Resource Name: University of California at San Diego Institute for Genomic Medicine Genomics Center Core Facility

Resource ID: SCR_022740

Alternate IDs: ABRF_1025

Alternate URLs: <https://coremarketplace.org/?FacilityID=1025&citation=1>

Record Creation Time: 20220915T050143+0000

Record Last Update: 20260905T133429+0000

Ratings and Alerts

No rating or validation information has been found for University of California at San Diego Institute for Genomic Medicine Genomics Center Core Facility.

No alerts have been found for University of California at San Diego Institute for Genomic Medicine Genomics Center Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Hakim A, et al. (2026) A high-throughput, end-to-end pipeline for extracellular miRNA biomarker discovery from human biofluids. Cell reports methods, 101502.

Chang H, et al. (2025) Single-cell transcriptomics reveals immune remodeling of the murine lung microenvironment following chronic house dust mite exposure. Frontiers in immunology, 16, 1652539.