Resource Summary Report

Generated by NIF on May 13, 2025

Cincinnati Children's Hospital Single Cell Genomics Core Facility

RRID:SCR_022653
Type: Tool

Proper Citation

Cincinnati Children's Hospital Single Cell Genomics Core Facility (RRID:SCR_022653)

Resource Information

URL: https://www.cincinnatichildrens.org/research/cores/single-cell-genomics

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Description: Core to perform expression level analysis of thousands of genes in parallel.Uses RNA-Seq assays from Tecan Genomics, Takara and Illumina for samples with limited amounts of starting RNA. Microarray technology utilizing the Affymetrix GeneChip platform is also available.

Abbreviations: SCGC

Synonyms: Cincinnati Children's Hospital Single Cell Genomics Core, Single Cell Genomics Core

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

Keywords: USEDit, ABRF, expression level analysis, genes in parallel

Funding:

Availability: open

Resource Name: Cincinnati Children's Hospital Single Cell Genomics Core Facility

Resource ID: SCR_022653

Alternate IDs: ABRF_1495

Alternate URLs: https://coremarketplace.org/?FacilityID=1495&citation=1

Record Creation Time: 20220805T050153+0000

Record Last Update: 20250513T062303+0000

Ratings and Alerts

No rating or validation information has been found for Cincinnati Children's Hospital Single Cell Genomics Core Facility.

No alerts have been found for Cincinnati Children's Hospital Single Cell Genomics Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Krishnan JM, et al. (2024) Effect of fentanyl on HIV expression in peripheral blood mononuclear cells. Frontiers in microbiology, 15, 1463441.

Waggoner S, et al. (2024) KLF2 determines the susceptibility of T cells to immunoregulatory NK cells. Research square.

Stepanchick E, et al. (2024) DDX41 haploinsufficiency causes inefficient hematopoiesis under stress and cooperates with p53 mutations to cause hematologic malignancy. Leukemia, 38(8), 1787.

Al Reza H, et al. (2024) Self-Assembled Generation of Multi-zonal Liver Organoids from Human Pluripotent Stem Cells. bioRxiv : the preprint server for biology.

He H, et al. (2024) PRDM3/16 regulate chromatin accessibility required for NKX2-1 mediated alveolar epithelial differentiation and function. Nature communications, 15(1), 8112.

Wayman JA, et al. (2024) Accessible chromatin maps of inflammatory bowel disease intestine nominate cell-type mediators of genetic disease risk. bioRxiv : the preprint server for biology.

Dao L, et al. (2024) Modeling blood-brain barrier formation and cerebral cavernous malformations in human PSC-derived organoids. Cell stem cell, 31(6), 818.

Shi T, et al. (2023) Single-cell transcriptomic analysis of renal allograft rejection reveals insights into intragraft TCR clonality. The Journal of clinical investigation, 133(14).

Khorki ME, et al. (2023) Prior viral infection primes cross-reactive CD8+ T cells that respond to mouse heart allografts. Frontiers in immunology, 14, 1287546.

He H, et al. (2023) PRDM3/16 Regulate Chromatin Accessibility Required for NKX2-1 Mediated Alveolar Epithelial Differentiation and Function. bioRxiv : the preprint server for biology.

Shi T, et al. (2023) Single cell transcriptomic analysis of renal allograft rejection reveals novel insights into intragraft TCR clonality. bioRxiv : the preprint server for biology.

Shanmuganad S, et al. (2023) Subset-specific and temporal control of effector and memory CD4+ T cell survival. bioRxiv : the preprint server for biology.

Múnera JO, et al. (2023) Development of functional resident macrophages in human pluripotent stem cell-derived colonic organoids and human fetal colon. Cell stem cell, 30(11), 1434.