Resource Summary Report

Generated by PRECISE-TBI on Aug 1, 2026

Salk Institute Flow Cytometry Core Facility

RRID:SCR_014839
Type: Tool

Proper Citation

Salk Institute Flow Cytometry Core Facility (RRID:SCR_014839)

Resource Information

URL: http://www.salk.edu/science/core-facilities/flow-cytometry/

Proper Citation: Salk Institute Flow Cytometry Core Facility (RRID:SCR_014839)

Description: Core facility dedicated to advancing research projects requiring cell sorting and/or analysis of cell populations by flow cytometry. The core offers training on and access to shared use instrumentation for analytical flow cytometry, services for fluorescence activated cell sorting (FACS) as well as technical consultation and support on experimental design, execution, and data analysis.

Synonyms: Salk Institute Flow Cytometry Core Facility (FACS)

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

Keywords: core facility, la jolla, flow cytometry, facs, fluorescent activated cell sorting,

Funding: Salk Institute Flow Cytometry Core Facility ;
NCI CCSG P30 014195

Resource Name: Salk Institute Flow Cytometry Core Facility

Resource ID: SCR_014839

Alternate IDs: ABRF_1643

Alternate URLs: https://coremarketplace.org/?FacilityID=1643&citation=1

Record Creation Time: 20220129T080322+0000

Record Last Update: 20260801T191208+0000

Ratings and Alerts

No rating or validation information has been found for Salk Institute Flow Cytometry Core Facility.

No alerts have been found for Salk Institute Flow Cytometry Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Esparza-Moltó PB, et al. (2025) ROS-dependent localization of glycolytic enzymes to mitochondria. Redox biology, 86, 103812.

Lorenzini MH, et al. (2025) Joint single-cell profiling of Cas9 edits and transcriptomes reveals widespread off-target events and effects on gene expression. bioRxiv : the preprint server for biology.

Strutzenberg TS, et al. (2025) Nucleosome Engagement Regulates ROR?t Structure and Dynamics. bioRxiv : the preprint server for biology.

Xu Z, et al. (2025) Scavenger Receptor CD36 in Tumor-Associated Macrophages Promotes Cancer Progression by Dampening Type-I IFN Signaling. Cancer research, 85(3), 462.

Labarta-Bajo L, et al. (2025) The antiviral Interferon pathway drives astrocyte aging and motor decline. bioRxiv : the preprint server for biology.

Miller CN, et al. (2025) A single-nuclei transcriptome census of the Arabidopsis maturing root identifies that MYB67 controls phellem cell maturation. Developmental cell, 60(9), 1377.

Ma S, et al. (2025) Nutrient-driven histone code determines exhausted CD8+ T cell fates. Science (New York, N.Y.), 387(6734), eadj3020.

Jaquish A, et al. (2025) Mammary intraepithelial lymphocytes and intestinal inputs shape T cell dynamics in lactogenesis. Nature immunology, 26(8), 1411.

Cochrane WG, et al. (2024) Cross-chiral exponential amplification of an RNA enzyme. Proceedings of the National Academy of Sciences of the United States of America, 121(44), e2413668121.

Vallmajo-Martin Q, et al. (2024) The molecular chronology of mammary epithelial cell fate switching. bioRxiv : the preprint server for biology.

Reina J, et al. (2024) LHPP expression in triple-negative breast cancer promotes tumor growth and metastasis by modulating the tumor microenvironment. bioRxiv : the preprint server for biology.

Labarta-Bajo L, et al. (2023) Protocol for the purification and transcriptomic analysis of mouse astrocytes using GFAT. STAR protocols, 4(4), 102599.

Zhou J, et al. (2023) Brain-wide correspondence of neuronal epigenomics and distant projections. Nature, 624(7991), 355.

Chen HV, et al. (2023) Deletion mapping of regulatory elements for GATA3 in T cells reveals a distal enhancer involved in allergic diseases. American journal of human genetics, 110(4), 703.