

Resource Summary Report

Generated by [RRID](#) on Sep 10, 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: access service resource, core facility, 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: 20260905T133400+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 22 mentions in open access literature.

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

Popay TM, et al. (2026) Acute NIPBL depletion reveals in vivo dynamics of loop extrusion and its role in transcription activation. *Nature genetics*, 58(4), 869.

Revanna JS, et al. (2026) Impaired lipoprotein secretion by APOE4 leads to lysosomal and mitochondrial dysfunction in human microglia. *bioRxiv : the preprint server for biology*.

Lee TA, et al. (2026) Transient cell states encode positional information to direct asymmetric growth. *bioRxiv : the preprint server for biology*.

Chang L, et al. (2026) Single-cell Multiome Analysis of Chromatin State and Transcriptome in the Human Basal Ganglia. *bioRxiv : the preprint server for biology*.

Xie Y, et al. (2026) Single-Cell Atlas of Transcription and Chromatin States Reveals Regulatory Programs in the Human Brain. *bioRxiv : the preprint server for biology*.

Zeng Q, et al. (2026) Cell-type-specific transposon demethylation and TAD remodeling in aging mouse brain. *Cell*, 189(7), 2148.

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 γ t Structure and Dynamics. *bioRxiv : the preprint server for biology*.

Reina J, et al. (2025) LHPP expression in triple-negative breast cancer promotes tumor growth and metastasis by modulating the tumor microenvironment. *Proceedings of the National Academy of Sciences of the United States of America*, 122(49), e2505653122.

Lai CY, et al. (2025) Maternal Immune Activation Disrupts Epigenomic and Functional Maturation of Cortical Excitatory Neurons. *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*.

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

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.

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.