Resource Summary Report

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University of California San Francisco Parnassus Flow Cytometry Core Facility

RRID:SCR_018206
Type: Tool

Proper Citation

University of California San Francisco Parnassus Flow Cytometry Core Facility (RRID:SCR_018206)

Resource Information

URL: https://flow.ucsf.edu/

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Description: Core assists investigators whose research requires molecular marker characterization of cells in suspension as well as isolation of cells based on those markers. Advanced cell sorting and cytometric analyses by Flow or Mass Cytometry are provided.

Abbreviations: PFCC

Synonyms: University of California San Francisco Diabetes Research Center Cytometry and Cell Sorting Core, , University of California San Francisco Diabetes Research Center Parnassus Flow Cytometry CoLab, UCSF Parnassus Flow CoLab

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

Keywords: Molecular marker, cell characterization, cell in suspension, cell isolation, cell sorting, flow cytometry, mass cytometry, cytometric analysis, core facility, ABRF

Funding: NIDDK P30DK063720

Availability: Restricted

Resource Name: University of California San Francisco Parnassus Flow Cytometry Core Facility

Resource ID: SCR_018206

Alternate IDs: ABRF_1007, SCR_015105

Alternate URLs: https://coremarketplace.org?FacilityID=1007

Record Creation Time: 20220129T080339+0000

Record Last Update: 20250519T205304+0000

Ratings and Alerts

No rating or validation information has been found for University of California San Francisco Parnassus Flow Cytometry Core Facility.

No alerts have been found for University of California San Francisco Parnassus Flow Cytometry Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 104 mentions in open access literature.

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

Berjis A, et al. (2024) Pretreatment with IL-15 and IL-18 rescues natural killer cells from granzyme B-mediated apoptosis after cryopreservation. Nature communications, 15(1), 3937.

Sytsma BJ, et al. (2024) Scalable intracellular delivery via microfluidic vortex shedding enhances the function of chimeric antigen receptor T-cells. bioRxiv : the preprint server for biology.

Ledergor G, et al. (2024) CD4+ CAR T-cell exhaustion associated with early relapse of multiple myeloma after BCMA CAR T-cell therapy. Blood advances, 8(13), 3562.

Leng K, et al. (2024) mTOR activation induces endolysosomal remodeling and nonclassical secretion of IL-32 via exosomes in inflammatory reactive astrocytes. Journal of neuroinflammation, 21(1), 198.

Mennillo E, et al. (2024) Single-cell and spatial multi-omics highlight effects of anti-integrin therapy across cellular compartments in ulcerative colitis. Nature communications, 15(1), 1493.

Alexander M, et al. (2024) A diet-dependent host metabolite shapes the gut microbiota to protect from autoimmunity. Cell reports, 43(11), 114891.

Berleant JD, et al. (2024) Scalable search of massively pooled nucleic acid samples enabled by a molecular database query language. medRxiv : the preprint server for health sciences.

Castillo JG, et al. (2024) A mass cytometry approach to track the evolution of T cell responses during infection and immunotherapy by paired T cell receptor repertoire and T cell differentiation state analysis. bioRxiv : the preprint server for biology.

Mowery CT, et al. (2024) Systematic decoding of cis gene regulation defines context-dependent control of the multi-gene costimulatory receptor locus in human T cells. Nature genetics, 56(6), 1156.

Luck C, et al. (2024) The Capicua C1 Domain Is Required for Full Activity of the CIC::DUX4 Fusion Oncoprotein. Cancer research communications, 4(12), 3099.

Sytsma BJ, et al. (2024) Scalable intracellular delivery via microfluidic vortex shedding enhances the function of chimeric antigen receptor T-cells. Research square.

Jowhar Z, et al. (2024) A ubiquitous GC content signature underlies multimodal mRNA regulation by DDX3X. Molecular systems biology, 20(3), 276.

Kuhn NF, et al. (2024) Localized in vivo gene editing of murine cancer-associated fibroblasts. bioRxiv : the preprint server for biology.

Caruso JA, et al. (2024) An adaptive Epithelial-Mesenchymal Transition Program Enables Basal Epithelial Cells to Bypass Stress-Induced Stasis and Contributes to Metaplastic Breast Cancer Progenitor State. Research square.

Kennedy DR, et al. (2024) Phosphorylation of HP1/Swi6 relieves competition with Suv39/Clr4 on nucleosomes and enables H3K9 trimethyl spreading. bioRxiv : the preprint server for biology.

Podolsky MJ, et al. (2024) Genome-wide screens identify SEL1L as an intracellular rheostat controlling collagen turnover. Nature communications, 15(1), 1531.

Cleary SJ, et al. (2024) IgG hexamers initiate complement-dependent acute lung injury. The Journal of clinical investigation, 134(11).

Ahanger SH, et al. (2024) Spatial 3D genome organization controls the activity of bivalent chromatin during human neurogenesis. bioRxiv : the preprint server for biology.

Wilkins KC, et al. (2024) A novel reporter for helicase activity in translation uncovers DDX3X

interactions. RNA (New York, N.Y.), 30(8), 1041.

Luck C, et al. (2024) The Capicua C1 Domain is Required for Full Activity of the CIC::DUX4 Fusion Oncoprotein. bioRxiv : the preprint server for biology.