Resource Summary Report

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Fred Hutchinson Cancer Center Flow Cytometry Core Facility

RRID:SCR_022613
Type: Tool

Proper Citation

Fred Hutchinson Cancer Center Flow Cytometry Core Facility (RRID:SCR_022613)

Resource Information

URL: https://www.fredhutch.org/en/research/shared-resources/core-facilities/flow-cytometry.html

Proper Citation: Fred Hutchinson Cancer Center Flow Cytometry Core Facility (RRID:SCR_022613)

Description: Includes services from sterile cell sorting for therapeutic applications to whole cell mass spectrometry, diagnostics and early stage clinical trials. Provides expertise from experimental design to data analysis and troubleshooting, therapeutic cell sorting. Supports isolation of cells for Phase 1 clinical trials of cellular immunotherapies.

Synonyms: Fred Hutchinson Cancer Center Flow Cytometry Shared Resource

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

Keywords: sterile cell sorting, whole cell mass spectrometry, diagnostics, early stage clinical trials, therapeutic cell sorting, Phase 1 clinical trials, cellular immunotherapies, ABRF, USEDit

Funding:

Availability: Open

Resource Name: Fred Hutchinson Cancer Center Flow Cytometry Core Facility

Resource ID: SCR_022613

Record Creation Time: 20220802T050144+0000

Record Last Update: 20250412T060511+0000

Ratings and Alerts

No rating or validation information has been found for Fred Hutchinson Cancer Center Flow Cytometry Core Facility.

No alerts have been found for Fred Hutchinson Cancer Center Flow Cytometry Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 20 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Scharffenberger SC, et al. (2024) Targeting RSV-neutralizing B cell receptors with anti-idiotypic antibodies. Cell reports, 43(10), 114811.

Carr CR, et al. (2024) Deep mutational scanning reveals functional constraints and antigenic variability of Lassa virus glycoprotein complex. bioRxiv : the preprint server for biology.

Aditham AK, et al. (2024) Deep mutational scanning of rabies glycoprotein defines mutational constraint and antibody-escape mutations. bioRxiv : the preprint server for biology.

Dadonaite B, et al. (2024) Spike deep mutational scanning helps predict success of SARS-CoV-2 clades. Nature, 631(8021), 617.

Belmont L, et al. (2024) Functional genomics screens reveal a role for TBC1D24 and SV2B in antibody-dependent enhancement of dengue virus infection. bioRxiv : the preprint server for biology.

Larsen BB, et al. (2024) Functional and antigenic landscape of the Nipah virus receptor binding protein. bioRxiv : the preprint server for biology.

Tischler JD, et al. (2024) FLIP(C1orf112)-FIGNL1 complex regulates RAD51 chromatin association to promote viability after replication stress. Nature communications, 15(1), 866.

Belmont L, et al. (2024) Functional genomics screens reveal a role for TBC1D24 and SV2B in antibody-dependent enhancement of dengue virus infection. Journal of virology, 98(11),

e0158224.

Simon S, et al. (2024) Sensitive bispecific chimeric T cell receptors for cancer therapy. Research square.

Cucinotta C, et al. (2024) Sir2 is required for the quiescence-specific condensed three-dimensional chromatin structure of rDNA. bioRxiv : the preprint server for biology.

Konecny AJ, et al. (2024) OMIP-102: 50-color phenotyping of the human immune system with in-depth assessment of T cells and dendritic cells. Cytometry. Part A : the journal of the International Society for Analytical Cytology, 105(6), 430.

Carr CR, et al. (2024) Deep mutational scanning reveals functional constraints and antibody-escape potential of Lassa virus glycoprotein complex. Immunity, 57(9), 2061.

Radford CE, et al. (2023) Mapping the neutralizing specificity of human anti-HIV serum by deep mutational scanning. bioRxiv : the preprint server for biology.

Radford CE, et al. (2023) Mapping the neutralizing specificity of human anti-HIV serum by deep mutational scanning. Cell host & microbe, 31(7), 1200.

Garcia NMG, et al. (2023) APOBEC3 activity promotes the survival and evolution of drug-tolerant persister cells during acquired resistance to EGFR inhibitors in lung cancer. bioRxiv : the preprint server for biology.

Hamm DC, et al. (2023) The transcription factor DUX4 orchestrates translational reprogramming by broadly suppressing translation efficiency and promoting expression of DUX4-induced mRNAs. PLoS biology, 21(9), e3002317.

Lubow J, et al. (2023) Single B cell transcriptomics identifies multiple isotypes of broadly neutralizing antibodies against flaviviruses. PLoS pathogens, 19(10), e1011722.

Konecny AJ, et al. (2023) 50-color phenotyping of the human immune system with in-depth assessment of T cells and dendritic cells. bioRxiv : the preprint server for biology.

Dadonaite B, et al. (2023) Full-spike deep mutational scanning helps predict the evolutionary success of SARS-CoV-2 clades. bioRxiv : the preprint server for biology.

Tischler JD, et al. (2023) RADIF(C1orf112)-FIGNL1 Complex Regulates RAD51 Chromatin Association to Promote Viability After Replication Stress. bioRxiv : the preprint server for biology.