

Resource Summary Report

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Stanford University Shared FACS Core Facility

RRID:SCR_017788

Type: Tool

Proper Citation

Stanford University Shared FACS Core Facility (RRID:SCR_017788)

Resource Information

URL: <http://facs.stanford.edu/>

Proper Citation: Stanford University Shared FACS Core Facility (RRID:SCR_017788)

Description: Provides flow cytometry instrumentation and expertise. Provides operator assisted analyzer and sorter use, as well as training and support for user instrument operation.

Synonyms: Stanford Shared FACS Facility

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

Keywords: Flow, cytometry, instrumentation, analysis, cell, sorting, training, service, core

Funding: NCRR S10 RR025518;
NCRR S10 RR027431;
NIH Office of the Director S10 OD016318;
Parker Institute for Cancer Immunotherapy

Availability: Open

Resource Name: Stanford University Shared FACS Core Facility

Resource ID: SCR_017788

Alternate IDs: ABRF_398

Record Creation Time: 20220129T080337+0000

Record Last Update: 20260819T044450+0000

Ratings and Alerts

No rating or validation information has been found for Stanford University Shared FACS Core Facility.

No alerts have been found for Stanford University Shared FACS Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Stiber A, et al. (2026) Dynamic, single-cell monitoring of CAR T cell identity and activation with Raman spectroscopy. *bioRxiv : the preprint server for biology*.

González-Suárez P, et al. (2026) Targets of SPEECHLESS and FAMA control guard cell division and expansion in the late stomatal lineage. *Development (Cambridge, England)*, 153(11).

Obenaus M, et al. (2026) T cell engagers control solid tumors through clonal replacement and IL2-driven effector differentiation of CD8 T cells. *bioRxiv : the preprint server for biology*.

Stanton M, et al. (2026) The ER membrane protein complex acts as a chaperone to promote the biogenesis of multi-bundle membrane proteins. *bioRxiv : the preprint server for biology*.

MacKenzie TMG, et al. (2026) In Depth Characterization of the Promoter Proximal Proteome of Single Copy Locus FOXP2. *Molecular & cellular proteomics : MCP*, 25(6), 101570.

Latarski AE, et al. (2026) Preformulated, Shelf-Stable, Dendritic Cell-Targeting Nanogel mRNA Vaccine Delivery Platform. *Bioconjugate chemistry*, 37(6), 1172.

Jiang H, et al. (2026) IL-9 as a naturally orthogonal cytokine with optimal JAK/STAT signaling for engineered T cell therapy. *Immunity*, 59(1), 177.

Belk JA, et al. (2026) Somatic mutations reveal the ontogeny of human microglia. *bioRxiv : the preprint server for biology*.

Chen Y, et al. (2026) Ribo-Tweezer: Rapid removal of ribosomal proteins reveals additional layers of post-transcriptional gene regulation. *Molecular cell*, 86(13), 2635.

Song YE, et al. (2026) Sustained Delivery of a Shingles Subunit Vaccine Overcomes Age-Related Declines in Humoral and Cellular Immunity Relative to Shingrix. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, e76481.

Lee S, et al. (2025) Pharmacologic stimulation of insulin granule acidification increases β -cell zinc content and augments β -cell-targeted drug delivery. *The Journal of biological chemistry*, 301(10), 110645.

Raposo CJ, et al. (2025) Functional memory T cells are derived from exhausted clones and expanded by checkpoint blockade. *bioRxiv : the preprint server for biology*.

Zhao H, et al. (2025) Elucidating the role of N-myristoylation in the excessive membrane localization of PD-L1 in hypoxic cancers and developing a novel NMT1 inhibitor for combination with immune checkpoint blockade therapy. *Journal of experimental & clinical cancer research : CR*, 44(1), 181.

Jiang H, et al. (2025) IL-9 as a naturally orthogonal cytokine with optimal JAK/STAT signaling for engineered T cell therapy. *bioRxiv : the preprint server for biology*.

Butler DSC, et al. (2025) Eosinophils enhance granuloma-mediated control of persistent *Salmonella* infection in mice. *Nature microbiology*, 10(12), 3176.

Schwartz CI, et al. (2025) Toward optimizing diversifying base editors for high-throughput mutational scanning studies. *Nucleic acids research*, 53(12).

Chen D, et al. (2025) Connectome-seq: High-throughput Mapping of Neuronal Connectivity at Single-Synapse Resolution via Barcode Sequencing. *bioRxiv : the preprint server for biology*.

Wang T, et al. (2025) Sensitive, direct detection of non-coding off-target base editor unwinding and editing in primary cells. *bioRxiv : the preprint server for biology*.

Naktang C, et al. (2025) Chromosome-level assemblies of two hexaploid bamboos, *Thyrsostachys oliveri* and *Thyrsostachys siamensis*, provide a foundation for functional and comparative genomics studies. *GigaScience*, 14.

Yamamoto Y, et al. (2025) Scaled multidimensional assays of variant effect identify sequence-function relationships in hypertrophic cardiomyopathy. *bioRxiv : the preprint server for biology*.