Resource Summary Report

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Stanford Genomics Service Center Core Facility

RRID:SCR_002050
Type: Tool

Proper Citation

Stanford Genomics Service Center Core Facility (RRID:SCR_002050)

Resource Information

URL: https://med.stanford.edu/sfgf.html

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Description: Stanford Genomics formerly Stanford Functional Genomics Facility provides services for high throughput sequencing, single cell assays, gene expression and genotyping studies utilizing microarray and real time PCR, and related services. High throughput sequencing (Illumina HiSeq 4000, NextSeq 500, MiSeq and MiniSeq), microarray gene expression and genotyping services (Affymetrix, Agilent and Illumina). Provides 24/7 access to instruments, equipment and software utilized within genomics field.

Abbreviations: SFGF,

Synonyms: Stanford Medicine Stanford Functional Genomics Facility, Stanford University Functional Genomics Core Facility, Stanford Functional Genomics Facility, Stanford Genomics, Stanford Genomics Service Center, Stanford School of Medicine Stanford Functional Genomics Facility

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

Keywords: ABRF, Stanford Genomics, genomics, high throughput sequencing, single cell assays, gene expression, genotyping, microarray, real time PCR,

Funding: NIAID ;
Comprehensive Cancer Center

Availability: Open

Resource Name: Stanford Genomics Service Center Core Facility

Resource ID: SCR_002050

Alternate IDs: SCR_008627, ABRF_200, nif-0000-31997, nif-0000-12246

Alternate URLs: https://coremarketplace.org/?FacilityID=200&citation=1

Old URLs: http://www.microarray.org/sfgf/

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Record Last Update: 20250501T080450+0000

Ratings and Alerts

No rating or validation information has been found for Stanford Genomics Service Center Core Facility.

No alerts have been found for Stanford Genomics Service Center Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Pham THM, et al. (2023) Single-cell profiling identifies ACE+ granuloma macrophages as a nonpermissive niche for intracellular bacteria during persistent Salmonella infection. Science advances, 9(1), eadd4333.

Hu J, et al. (2015) Gene Signatures Stratify Computed Tomography Screening Detected Lung Cancer in High-Risk Populations. EBioMedicine, 2(8), 831.

Xie H, et al. (2012) miR-205 expression promotes cell proliferation and migration of human cervical cancer cells. PloS one, 7(10), e46990.

Liu D, et al. (2010) Tumor necrosis factor receptor-associated protein 1(TRAP1) regulates genes involved in cell cycle and metastases. Cancer letters, 296(2), 194.

Granjon A, et al. (2009) The microRNA signature in response to insulin reveals its implication in the transcriptional action of insulin in human skeletal muscle and the role of a sterol regulatory element-binding protein-1c/myocyte enhancer factor 2C pathway. Diabetes, 58(11), 2555.

van Baarsen LG, et al. (2008) Pharmacogenomics of interferon-beta therapy in multiple sclerosis: baseline IFN signature determines pharmacological differences between patients. PloS one, 3(4), e1927.

Chan DA, et al. (2007) HIF gene expression in cancer therapy. Methods in enzymology, 435, 323.

Higgins JP, et al. (2007) Placental S100 (S100P) and GATA3: markers for transitional epithelium and urothelial carcinoma discovered by complementary DNA microarray. The American journal of surgical pathology, 31(5), 673.

Ekelund E, et al. (2006) Elevated expression and genetic association links the SOCS3 gene to atopic dermatitis. American journal of human genetics, 78(6), 1060.