Resource Summary Report

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New York University School of Medicine Langone Health Genome Technology Center Core Facility

RRID:SCR_017929
Type: Tool

Proper Citation

New York University School of Medicine Langone Health Genome Technology Center Core Facility (RRID:SCR_017929)

Resource Information

URL: https://med.nyu.edu/research/scientific-cores-shared-resources/genome-technology-center

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Description: Core provides range of services related to genome, epigenome, and transcriptome analysis. Offers technologies including Illumina deep sequencing and sample preparation for variety of applications, including DNA and RNA sequencing (DNA- and RNA-seq), exome sequencing, targeted capture, chromatin immunoprecipitation sequencing (ChIP-seq), methylation sequencing (Methyl-seq), metagenomics, and many others;Automation of Illumina library and targeted capture preps, including 16S ribosomal RNA (rRNA) sequencing;Oxford Nanopore sequencing (long reads);Bio-Rad Droplet Digita polymerase chain reaction (PCR);Nanostring nCounter;Single-cell RNA- and DNA-seq using the C1 Auto Prep System from Fluidigm, and 10x Genomics Chromium System.Provides expertise on strategies to achieve research goals in any field related to genomics, and can tailor bioinformatics analysis to individual project. If you supply us with nucleic acids, we can perform every step required to help you achieve your desired results.

Abbreviations: NYU GTC, GTC

Synonyms: NYU Langone's Genome Technology Center, New York University School of Medicine Genome Technology Center, New York University School of Medicine Langone Health Genome Technology Center

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

Keywords: Genome, epigenome, transcriptome, analysis, deep, sequencing, sample, preparation, DNA, RNA, exome, rRNA, genomics, analysis, service, core, ABRF, USEDit

Funding: NIH Office of the Director S10 OD023423

Availability: Open

Resource Name: New York University School of Medicine Langone Health Genome Technology Center Core Facility

Resource ID: SCR_017929

Alternate IDs: ABRF_824, SciEx_41, SCR_012514

Alternate URLs: https://coremarketplace.org/?FacilityID=824&citation=1

Old URLs: http://www.scienceexchange.com/facilities/genome-technology-center-nyu

Record Creation Time: 20220129T080337+0000

Record Last Update: 20250517T060344+0000

Ratings and Alerts

No rating or validation information has been found for New York University School of Medicine Langone Health Genome Technology Center Core Facility.

No alerts have been found for New York University School of Medicine Langone Health Genome Technology Center Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 43 mentions in open access literature.

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

Assis BA, et al. (2025) Genomic signatures of adaptation in native lizards exposed to human-introduced fire ants. Nature communications, 16(1), 89.

Calderon A, et al. (2024) Chromatin accessibility and cell cycle progression are controlled by

the HDAC-associated Sin3B protein in murine hematopoietic stem cells. Epigenetics & chromatin, 17(1), 2.

Ulrich RJ, et al. (2024) Prophage-encoded methyltransferase drives adaptation of community-acquired methicillin-resistant Staphylococcus aureus. bioRxiv : the preprint server for biology.

Wang H, et al. (2024) Synergistic activation by Glass and Pointed promotes neuronal identity in the Drosophila eye disc. Nature communications, 15(1), 7091.

Fu L, et al. (2024) ROR?t-dependent antigen-presenting cells direct regulatory T cell-mediated tolerance to food antigen. bioRxiv : the preprint server for biology.

Wilson ML, et al. (2024) Rbpms2 promotes female fate upstream of the nutrient sensing Gator2 complex component Mios. Nature communications, 15(1), 5248.

Martin MF, et al. (2024) Distinct chikungunya virus polymerase palm subdomains contribute to virus replication and virion assembly. bioRxiv : the preprint server for biology.

Samper N, et al. (2024) Kir6.1, a component of an ATP-sensitive potassium channel, regulates natural killer cell development. Frontiers in immunology, 15, 1490250.

Blum JE, et al. (2024) Discovery and characterization of dietary antigens in oral tolerance. bioRxiv : the preprint server for biology.

Mays JC, et al. (2024) KaryoTap Enables Aneuploidy Detection in Thousands of Single Human Cells. bioRxiv : the preprint server for biology.

Mankiewicz Ledins P, et al. (2024) A deployable film method to enable replicable sampling of low-abundance environmental microbiomes. Scientific reports, 14(1), 23857.

Barcia Durán JG, et al. (2024) Immune checkpoint landscape of human atherosclerosis and influence of cardiometabolic factors. Nature cardiovascular research, 3(12), 1482.

Goehring L, et al. (2024) Dormant origin firing promotes head-on transcription-replication conflicts at transcription termination sites in response to BRCA2 deficiency. Nature communications, 15(1), 4716.

Li AH, et al. (2024) Transcriptome Analysis Reveals Anti-Cancer Effects of Isorhapontigenin (ISO) on Highly Invasive Human T24 Bladder Cancer Cells. International journal of molecular sciences, 25(3).

Samper N, et al. (2024) Kir6.1, a component of an ATP-sensitive potassium channel, regulates natural killer cell development. bioRxiv : the preprint server for biology.

Molenaars M, et al. (2024) Acute inhibition of iron-sulfur cluster biosynthesis disrupts metabolic flexibility in mice. bioRxiv : the preprint server for biology.

Goldberg GW, et al. (2024) Engineered transcription-associated Cas9 targeting in eukaryotic cells. Nature communications, 15(1), 10287.

Wilson ML, et al. (2024) Rbpms2 promotes female fate upstream of the nutrient sensing Gator2 complex component, Mios. bioRxiv : the preprint server for biology.

Zhou C, et al. (2024) Microbiota and metabolic adaptation shape Staphylococcus aureus virulence and antimicrobial resistance during intestinal colonization. bioRxiv : the preprint server for biology.

Marsman G, et al. (2024) Histone H1 kills MRSA. Cell reports, 43(11), 114969.