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: access service resource, core facility, 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: 20260912T200405+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 90 mentions in open access literature.

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

Gershowitz E, et al. (2026) Transcriptional profiling of extraocular motor neurons reveals sim1a as a candidate strabismus-related gene. bioRxiv : the preprint server for biology.

Bertoli G, et al. (2026) Cardiomyocyte-Specific Plakophilin-2 Loss Is Sufficient to Induce Aging and Senescence of Nonmyocytes: Relevance to Arrhythmogenic Cardiomyopathy. Journal of the American Heart Association, 15(9), e047447.

Wang S, et al. (2026) Purinergic signaling promotes gliomagenesis through nuclear calcium transients. bioRxiv : the preprint server for biology.

Nakamura R, et al. (2026) YAP/TAZ inhibition refines TGF-? signaling to prevent laryngeal fibrosis. bioRxiv : the preprint server for biology.

Lizi?czyk AM, et al. (2026) APOE genotype differentially modulates prion pathology in a mouse model. Acta neuropathologica communications, 14(1), 29.

Meyer LN, et al. (2026) Integrin is required for basement membrane crossing and branching of an invading intracellular tube. Development (Cambridge, England), 153(1).

Cheng P, et al. (2026) PARP1 suppression drives ROS resistance in aneuploid cancer cells. Molecular cell, 86(9), 1742.

Blum JE, et al. (2026) Identification and characterization of dietary antigens in oral tolerance. Science immunology, 11(117), eaeb4684.

Arzu JL, et al. (2026) Associations of the gut microbiome and cardiometabolic risk in adolescence: the HOME study. BMC medical genomics, 19(1).

Santarossa CC, et al. (2026) LetA defines a structurally distinct transporter family. Nature, 651(8107), 1097.

Gartling G, et al. (2026) Preliminary Transcriptomic Effects of Lateralized RLN Denervation in Rat Vocal Fold. The Laryngoscope.

Subhan BS, et al. (2026) Duo-nano exosome encapsulating hydrogel boosts wound healing across xenogenic and allogenic models. Biomaterials, 329, 123975.

Manikas J, et al. (2026) RAB-35 regulates distinct steps of trogocytosis in the biting and bitten cell. bioRxiv : the preprint server for biology.

Ibrahim M, et al. (2026) NF1 Loss Remodels Tumor Niches for Immune Evasion. bioRxiv : the preprint server for biology.

Yamaguchi N, et al. (2026) ERBB4 deficiency promotes atrial myopathy underlying the atrial fibrillation substrate. medRxiv : the preprint server for health sciences.

Laue HE, et al. (2025) Early-life and concurrent predictors of the healthy adolescent microbiome in a cohort study. Genome medicine, 17(1), 50.

Newman AAC, et al. (2025) Ischemic Injury Drives Nascent Tumor Growth Via Accelerated Hematopoietic Aging. JACC. CardioOncology, 7(5), 559.

Fathi F, et al. (2025) Donor-reactive T cells and innate immune cells promote pig-to-human decedent xenograft rejection. Research square.

Fu L, et al. (2025) PRDM16-dependent antigen-presenting cells induce tolerance to gut antigens. Nature, 642(8068), 756.

Dannebaum R, et al. (2025) Digital PCR Assay Utilizing In-Droplet Methylation-Sensitive Digestion for Estimation of Fetal cfDNA From Plasma. Prenatal diagnosis, 45(4), 500.