

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

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>

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

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 Digital 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: service resource, access service resource, core facility

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: 20260804T043657+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 72 mentions in open access literature.

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

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

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

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

G??kbuget D, et al. (2025) KMT2C/KMT2D-dependent H3K4me1 mediates changes in DNA replication timing and origin activity during a cell fate transition. Cell reports, 44(2), 115272.

Ibrahim M, et al. (2025) NF1 Loss Promotes EGFR Activation and Confers Sensitivity to EGFR Inhibition in NF1-Mutant Melanoma. *Cancer research*, 85(17), 3348.

Son GY, et al. (2025) Loss of STIM1 and STIM2 in Salivary Glands Disrupts ANO1 Function but Does Not Induce Sjogren's Disease. *Function (Oxford, England)*, 6(1).

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.

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

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

Gong Z, et al. (2025) Schwann cell Lrp1 deletion drives trigeminal neuron sensitization and orofacial pain by modulating mitochondrial function and TRPV1/TRPA1 activity. *The journal of headache and pain*, 26(1), 290.

Tran PM, et al. (2025) Cell envelope maintenance by PhoP is essential for *Mycobacterium tuberculosis* methylglyoxal resistance. *Proceedings of the National Academy of Sciences of the United States of America*, 122(49), e2523024122.

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

Krishna Prasad GVR, et al. (2025) Macrophage-T cell interactions promote SLAMF1 expression for enhanced TB defense. *Nature communications*, 16(1), 6794.

Laskou M, et al. (2025) Platelets impair the resolution of inflammation in atherosclerotic plaques in insulin-resistant mice after lipid lowering. *JCI insight*, 10(21).

Zhang W, et al. (2025) Genome writing to dissect consequences of SVA retrotransposon disease X-Linked Dystonia Parkinsonism. *bioRxiv : the preprint server for biology*.

Santarossa CC, et al. (2025) LetA defines a structurally distinct transporter family involved in lipid trafficking. *bioRxiv : the preprint server for biology*.

Wang L, et al. (2025) CLNS1A regulates genome stability and cell cycle progression to control CD4 T cell function and autoimmunity. *Science immunology*, 10(108), eadq8860.

Bertoli G, et al. (2025) Cardiomyocyte-specific plakophilin-2 loss is sufficient to induce aging and senescence of nonmyocytes. Relevance to arrhythmogenic cardiomyopathy. *bioRxiv : the preprint server for biology*.

Maan H, et al. (2025) Sugar ABC transporter repertoires predict ecological dynamics in gut microbiome communities. *bioRxiv : the preprint server for biology*.

Park SY, et al. (2025) Transcriptomic analysis of Cr(VI)-induced changes in C2C12 cells during myogenic differentiation. *Journal of trace elements in medicine and biology : organ of the Society for Minerals and Trace Elements (GMS)*, 91, 127714.