

Resource Summary Report

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Virginia University School of Medicine Genome Analysis and Technology Core Facility

RRID:SCR_018883

Type: Tool

Proper Citation

Virginia University School of Medicine Genome Analysis and Technology Core Facility
(RRID:SCR_018883)

Resource Information

URL: <https://med.virginia.edu/gatc/>

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Description: Core offers instrumentation and expertise in all areas of bulk and single cell NGS genomics and transcriptomics, as well as training to access core shared instrumentations. Services include RNA Seq, CHIP Seq, ATAC Seq, Amplicon DNA Seq, 16S ribosomal gene sequencing, shot gun sequencing for small genomes and whole exome sequencing. 10X Genomics resources include single cell CNV, VDJ, and 3 or 5 RNA seq as well as linked reads. Core provides real time and droplet digital PCR services most suitable for targeted gene expression, SNP genotyping and CNV discovery.

Abbreviations: GATC

Synonyms: University of Virginia School of Medicine Genome Analysis and Technology Core Facility, UVA Genome Analysis and Technology Core, University of Virginia UVA Genome Analysis and Technology Core, Genome Analysis and Technology Core

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

Keywords: USEdit, genome analysis, NGS genomic, transcriptomics, RNA Seq, CHIP Seq, ATAC Seq, Amplicon DNA Seq, 16S ribosomal gene sequencing, shot gun sequencing, ABRF

Availability: Open

Resource Name: Virginia University School of Medicine Genome Analysis and Technology Core Facility

Resource ID: SCR_018883

Alternate IDs: ABRF_1024

Alternate URLs: <https://coremarketplace.org/?FacilityID=1024>

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260829T183319+0000

Ratings and Alerts

No rating or validation information has been found for Virginia University School of Medicine Genome Analysis and Technology Core Facility.

No alerts have been found for Virginia University School of Medicine Genome Analysis and Technology Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 86 mentions in open access literature.

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

Cwiek A, et al. (2026) Retinoic acid regulates fetoplacental vascularization via notch signaling and a SEMA3E/F-PLEXIND1 axis. *iScience*, 29(4), 115205.

Dunham N, et al. (2026) The LMO2-LDB1-TAL1 complex regulates transcription networks in acute myeloid leukemia. *Blood neoplasia*, 3(1), 100186.

Camacho LQ, et al. (2026) Systematic multivariate analysis of chromatin complex dependencies reveals Set1C/COMPASS as a melanoma-enriched epigenetic vulnerability. *bioRxiv : the preprint server for biology*.

Felton SM, et al. (2026) Enzyme-enhanced RNA isolation from biofilm-producing bacteria. *Microbiology spectrum*, 14(4), e0307725.

Kim DJ, et al. (2026) An epigenetic switch in vascular phenotype augments anti-tumor immunity. *Angiogenesis*, 29(3).

Wan Y, et al. (2026) Chromosome-scale assembly and annotation of *Phytophthora capsici* isolate BYA5. *Scientific data*, 13(1), 184.

Roosa CA, et al. (2026) Microporous annealed particle scaffolds avoid foreign body response by down regulating complement-fibroblast-macrophage signaling loop. *bioRxiv : the preprint server for biology*.

Uddin MJ, et al. (2026) CXCR3 ameliorates neutrophil-dependent disease severity in SARS-CoV-2 infection by regulating CD4+ T cell recruitment. *Frontiers in immunology*, 17, 1823264.

Wang X, et al. (2026) Systemic Cysteine Elevation Sustains T-Cell Activation to Potentiate PD-1 Blockade. *bioRxiv : the preprint server for biology*.

Islam MM, et al. (2026) Mucin-induced metabolic reprogramming in *Pseudomonas aeruginosa* clinical isolates. *mSystems*, 11(7), e0058026.

Neelamraju Y, et al. (2026) Elevated levels of TNF and its targets characterize better-risk older acute myeloid leukemia patients. *Leukemia*, 40(5), 1049.

Chavkin NW, et al. (2026) Regulation of endothelial cell chromatin availability and transcription factor activity during arterial-venous specification. *Development (Cambridge, England)*, 153(11).

Rodrigues-Jesus MJ, et al. (2026) Multi-strain *Clostridioides difficile* infection: Increased detection and clinical implications. *The Journal of infection*, 93(2), 106800.

Nicklow E, et al. (2025) Exploration of biomaterial-tissue integration in heterogeneous microporous annealed particle scaffolds in subcutaneous implants over 12 months. *Acta biomaterialia*, 196, 183.

Liu Y, et al. (2025) Co-Conservation of Synaptic Gene Expression and Circuitry in Collicular Neurons. *bioRxiv : the preprint server for biology*.

Fu Z, et al. (2025) Microglia modulate the cerebrovascular reactivity through ectonucleotidase CD39. *Nature communications*, 16(1), 956.

Barnes RW, et al. (2025) LAG3+ CD8+ T cell Subset Drives HR+/HER2- Breast Cancer Reduction in Bispecific Antibody Armed Activated T Cell Therapy. *bioRxiv : the preprint server for biology*.

Liu Y, et al. (2025) Co-Conservation of synaptic gene expression and circuitry in collicular neurons. *Nature communications*, 16(1), 9146.

Cwiek A, et al. (2025) Preterm birth increases susceptibility to hyperglycemia induced glomerular alterations in male mice. *Scientific reports*, 15(1), 18934.

Ho DV, et al. (2025) Ancestral Chromosome-Level Assemblies Reveal Posthybridization Genome Evolution in the New Mexico Whiptail Lizard (*Aspidoscelis neomexicanus*). *Genome biology and evolution*, 17(12).