

Resource Summary Report

Generated by T1D on Jul 30, 2026

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, service resource, core facility

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: 20260729T044451+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 71 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

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.

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

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

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.

Yadav N, et al. (2025) Synergistic activity of simvastatin and irinotecan chemotherapy against glioblastoma converges on TGF-?? signaling. Journal of neuro-oncology, 174(3), 621.

Zengeler KE, et al. (2025) Inflammasome signaling in astrocytes modulates hippocampal plasticity. *Immunity*, 58(6), 1519.

Achakkagari S, et al. (2025) Better together: Subgenomes for allotetraploid potato wild relative *Solanum acaule* Bitt. reveal origins in Petota Clade 3 and 4. *The plant genome*, 18(3), e70095.

Aragon JW, et al. (2025) Emergence of endothelial subtypes and role of cell cycle control in arterial-venous specification during embryonic vascular development. *Cell reports*, 44(10), 116368.

Bartosik AR, et al. (2025) Loss of DHX36/G4R1, a G4 resolvase, drives genome instability and regulates innate immune gene expression in cancer cells. *Nucleic acids research*, 53(12).

Su Z, et al. (2025) Regulation of epigenetics and chromosome structure by human ORC2. *Cell reports*, 44(6), 115816.

Phillips E, et al. (2025) Malformin C preferentially kills glioblastoma stem-like cells via concerted induction of proteotoxic stress and autophagic flux blockade. *Molecular oncology*, 19(3), 785.

Beshr G, et al. (2025) A fucose-binding superlectin from *Enterobacter cloacae* with high Lewis and ABO blood group antigen specificity. *The Journal of biological chemistry*, 301(2), 108151.

Nash WT, et al. (2025) Neuroimmune Regulation for Acute Kidney Injury Therapy: Insights Along the Path From Bench to Bedside. *Seminars in nephrology*, 151674.

Tajammal A, et al. (2025) BLADE-R: streamlined RNA extraction for molecular diagnostics and high-throughput applications. *bioRxiv : the preprint server for biology*.

Barnes RW, et al. (2025) LAG3⁺ CD8⁺ T cell subset drives HR⁺/HER2⁻ breast cancer reduction in bispecific antibody armed activated T cell therapy. *Journal of immunology* (Baltimore, Md. : 1950).

Garcia Diaz J, et al. (2025) Zika virus induces monocyte recruitment in the immunocompetent adult brain driving chronic inflammation. *Frontiers in immunology*, 16, 1597776.

Daboin C, et al. (2025) Mechanical maturation of human dermal fibroblast-laden microporous annealed particle scaffolds during long-term in vitro culture. *Acta biomaterialia*, 207, 353.

Abebayehu D, et al. (2024) A Thy-1-negative immunofibroblast population emerges as a key determinant of fibrotic outcomes to biomaterials. *Science advances*, 10(24), eadf2675.