

Resource Summary Report

Generated by ASWG on Aug 3, 2026

University of Texas at Austin Genomic Sequencing and Analysis Core Facility

RRID:SCR_021713

Type: Tool

Proper Citation

University of Texas at Austin Genomic Sequencing and Analysis Core Facility
(RRID:SCR_021713)

Resource Information

URL: <https://wikis.utexas.edu/display/GSAF/Home+Page>

Proper Citation: University of Texas at Austin Genomic Sequencing and Analysis Core Facility (RRID:SCR_021713)

Description: Full service sequencing core that provides both Sanger and Next Generation Sequencing services, in addition to library prep and quality check services, open access to equipment and training. Works directly with the bioinformatics core who can provide assist in any of your analysis needs to data storage solutions.

Abbreviations: GSAF

Synonyms: The University of Texas at Austin Genomic Sequencing and Analysis Facility, Genomic Sequencing and Analysis Facility

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

Keywords: USEDit, ABRF, sequencing core, Sanger Sequencing service, Next Generation Sequencing service, library preparation, quality check service

Resource Name: University of Texas at Austin Genomic Sequencing and Analysis Core Facility

Resource ID: SCR_021713

Alternate IDs: ABRF_1209

Alternate URLs: <https://coremarketplace.org/?FacilityID=1209>

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260801T191247+0000

Ratings and Alerts

No rating or validation information has been found for University of Texas at Austin Genomic Sequencing and Analysis Core Facility.

No alerts have been found for University of Texas at Austin Genomic Sequencing and Analysis Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 54 mentions in open access literature.

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

Kalkunte N, et al. (2026) Development of low-cost electrical stimulation device to promote hiPSC-CM differentiation and functionality. *APL bioengineering*, 10(1), 016101.

Ince LM, et al. (2026) Time-restricted feeding rescues sociability deficits and reduces neuroinflammation in aged mice. *Neurobiology of aging*, 159, 1.

Park J, et al. (2025) Molecular features of the serological IgG repertoire elicited by egg-based, cell-based, or recombinant haemagglutinin-based seasonal influenza vaccines: a comparative, prospective, observational cohort study. *The Lancet. Microbe*, 6(2), 100935.

Gardner AL, et al. (2025) Mapping cell-cell fusion at single-cell resolution. *bioRxiv : the preprint server for biology*.

Kolling FW, et al. (2025) Multi-site Assessment of Methods for Cell Preservation Upstream of Single Cell RNA Sequencing. *bioRxiv : the preprint server for biology*.

Morgan D, et al. (2025) Lineage Tracing Reveals Clone-Specific Responses to Doxorubicin in Triple-Negative Breast Cancer. *bioRxiv : the preprint server for biology*.

Sohn S, et al. (2025) Cell Barcoding Reveals Lineage-dependent Outcomes in hiPSC Cardiac Differentiation. *bioRxiv : the preprint server for biology*.

Nice CC, et al. (2025) Extensive Admixture Among Karst-Obligate Salamanders Reveals Evidence of Recent Divergence and Gene Exchange Through Aquifers. *Ecology and evolution*, 15(1), e70785.

Ruan M, et al. (2025) Cytoplasmic localization of PUS7 facilitates a pseudouridine-dependent enhancement of cellular stress tolerance. *bioRxiv : the preprint server for biology*.

Larsen B, et al. (2025) Donor Age Impairs Vasculogenic Potential of hiPSC-Derived Endothelial Progenitors. *bioRxiv : the preprint server for biology*.

Parker JK, et al. (2025) Antibacterial microcins are ubiquitous and functionally diverse across bacterial communities. *Nature communications*, 16(1), 6048.

McDaniel JR, et al. (2025) Repertoire, function, and structure of serological antibodies induced by the R21/Matrix-M malaria vaccine. *The Journal of experimental medicine*, 222(10).

Galland LM, et al. (2025) Geography and Environment Shape Spatial Genetic Variation and Predict Climate Maladaptation Across Isolated and Disjunct Populations of *Pinus muricata*. *Molecular ecology*, e17638.

Hebert LS, et al. (2025) Gene discovery and expression analysis of the B cell receptor repertoire in the domestic ferret model. *Vaccine*, 64, 127725.

Park J, et al. (2025) Broadly neutralizing antibodies targeting pandemic GII.4 variants or seven GII genotypes of human norovirus. *Science translational medicine*, 17(788), eads8214.

Warden AS, et al. (2025) Elevated brain manganese induces motor disease by upregulating the kynurenine pathway of tryptophan metabolism. *Proceedings of the National Academy of Sciences of the United States of America*, 122(16), e2423628122.

Gordillo Sierra AR, et al. (2025) Developing a *Yarrowia lipolytica* platform for conversion of mannitol-containing waste streams. *Bioresource technology*, 437, 133161.

Bazzi SA, et al. (2025) Alcohol induces concentration-dependent transcriptomic changes in oligodendrocytes. *Addiction biology*, 30(2), e70012.

Woolley PR, et al. (2024) Regulation of transcription patterns, poly(ADP-ribose), and RNA-DNA hybrids by the ATM protein kinase. *Cell reports*, 43(3), 113896.

Arasappan D, et al. (2024) Brain transcriptomic signatures for mood disorders and suicide phenotypes: an anterior insula and subgenual ACC network postmortem study. *bioRxiv* : the preprint server for biology.