

Resource Summary Report

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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: access service resource, core facility, 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: 20260905T133422+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 61 mentions in open access literature.

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

Kolling Iv FW, et al. (2026) Multisite Assessment of Methods for Cell Preservation Upstream of Single-Cell RNA Sequencing. Journal of biomolecular techniques : JBT, 37(2), 9.

Pike A, et al. (2026) Deep mutational scan of the pore of the cold-sensing TRPM8 channel. bioRxiv : the preprint server for biology.

Ruan M, et al. (2026) Cytoplasmic localization of pseudouridine synthase 7 facilitates a pseudouridine-dependent enhancement of cellular stress tolerance. Nature communications, 17(1).

Han J, et al. (2026) Persistently Increased Expression of PKMzeta and Unbiased Gene Expression Profiles Identify Hippocampal Molecular Traces of a Long-Term Active Place Avoidance Memory and "Shadow" Proteins. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(28), e21254.

Friske MM, et al. (2026) Repeated TLR7 activation induces cell type- and brain region-specific transcriptome changes in male mice. Scientific reports, 16(1).

Aceves V, et al. (2026) Genetic interaction between Adgrg6 and Sox9 reveals a feedforward mechanism for postnatal spinal stability. bioRxiv : the preprint server for biology.

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.

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

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.

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*.

Jost TA, et al. (2025) Deep learning identifies heterogeneous subpopulations in breast cancer cell lines. *npj biomedical innovations*, 2(1).

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.

Sohn S, et al. (2025) Cell Barcoding Reveals Lineage-dependent Outcomes in hiPSC Cardiac Differentiation. *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*.

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

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

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

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.