

Resource Summary Report

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University of Texas at Austin Biomedical Research Computing Core Facility

RRID:SCR_021979

Type: Tool

Proper Citation

University of Texas at Austin Biomedical Research Computing Core Facility
(RRID:SCR_021979)

Resource Information

URL: <https://research.utexas.edu/cbrs/cores/cbb/computing-resources/>

Proper Citation: University of Texas at Austin Biomedical Research Computing Core Facility (RRID:SCR_021979)

Description: Biomedical Research Computing Facility as core for Biomedical Research Support. Provides small, centrally managed compute clusters and storage, suitable for local, interactive computing, to biomedical research groups.

Abbreviations: BRCF

Synonyms: University of Texas at Austin UTA-Biomedical Research Computing Facility, UTA-Biomedical Research Computing Facility

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

Keywords: USEDit, ABRF, biomedical research computing

Resource Name: University of Texas at Austin Biomedical Research Computing Core Facility

Resource ID: SCR_021979

Alternate IDs: ABRF_1283

Alternate URLs: <https://coremarketplace.org/?FacilityID=1283>

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260919T195943+0000

Ratings and Alerts

No rating or validation information has been found for University of Texas at Austin Biomedical Research Computing Core Facility.

No alerts have been found for University of Texas at Austin Biomedical Research Computing Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Salazar G, et al. (2026) Identification of Novel Interacting Proteins of FUZ and GPR161. Proteomics, e70164.

Cox RM, et al. (2026) Agnostic material classification using differential de Bruijn graphs of DNA imprints. bioRxiv : the preprint server for biology.

Vieira LC, et al. (2025) Medium-sized protein language models perform well at transfer learning on realistic datasets. Scientific reports, 15(1), 21400.

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

Vieira LC, et al. (2025) Medium-sized protein language models perform well at transfer learning on realistic datasets. bioRxiv : the preprint server for biology.

Maguire C, et al. (2025) Dissecting clinical features of COVID-19 in a cohort of 21,312 acute care patients. Communications medicine, 5(1), 138.

Salazar G, et al. (2025) Identification of novel interacting proteins of FUZ and GPR161. bioRxiv : the preprint server for biology.

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

Feller AL, et al. (2025) Peptide-Aware Chemical Language Model Successfully Predicts Membrane Diffusion of Cyclic Peptides. Journal of chemical information and modeling, 65(2), 571.

Feller AL, et al. (2024) Peptide-specific chemical language model successfully predicts membrane diffusion of cyclic peptides. bioRxiv : the preprint server for biology.

Maguire C, et al. (2024) Molecular mimicry as a mechanism of viral immune evasion and autoimmunity. Nature communications, 15(1), 9403.

Maguire C, et al. (2024) Molecular Mimicry as a Mechanism of Viral Immune Evasion and Autoimmunity. *bioRxiv* : the preprint server for biology.

Zuniga A, et al. (2024) Extinction Training Suppresses Activity of Fear Memory Ensembles Across the Hippocampus and Alters Transcriptomes of Fear-Encoding Cells. *bioRxiv* : the preprint server for biology.

Maguire C, et al. (2023) Dissecting Clinical Features of COVID-19 in a Cohort of 21,312 Acute Care Patients. *medRxiv* : the preprint server for health sciences.

Ma CH, et al. (2023) The selfish yeast plasmid exploits a SWI/SNF-type chromatin remodeling complex for hitchhiking on chromosomes and ensuring high-fidelity propagation. *PLoS genetics*, 19(10), e1010986.

Wilder CS, et al. (2023) Enzymatic depletion of I-Met using an engineered human enzyme as a novel therapeutic strategy for melanoma. *Molecular carcinogenesis*, 62(10), 1531.

Bazzi SA, et al. (2023) Alcohol induces concentration-dependent transcriptomic changes in oligodendrocytes. *bioRxiv* : the preprint server for biology.

Siles N, et al. (2023) SARS-CoV-2 Humoral Immune Responses in Convalescent Individuals Over 12 Months Reveal Severity-Dependent Antibody Dynamics. *medRxiv* : the preprint server for health sciences.