

Resource Summary Report

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Texas Advanced Computing Center

RRID:SCR_012530

Type: Tool

Proper Citation

Texas Advanced Computing Center (RRID:SCR_012530)

Resource Information

URL: <https://tacc.utexas.edu/>

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Description: Texas Advanced Computing Center (TACC) at The University of Texas at Austin is one of the leading centers of computational excellence in the United States. Located on the J.J. Pickle Research Campus, the center's mission is to enable discoveries that advance science and society through the application of advanced computing technologies. To fulfill this mission, TACC identifies, evaluates, deploys, and supports powerful computing, visualization, and storage systems and software. TACC staff help researchers and educators use these technologies effectively, and conduct research and development to make these technologies more powerful, more reliable, and easier to use. TACC staff also help encourage, educate, and train the next generation of researchers, empowering them to make discoveries that change the world.

Abbreviations: TACC

Synonyms: UT Austin Texas Advanced Computing Center (TACC), UT Austin Texas Advanced Computing Center, University of Texas at Austin Texas Advanced Computing Center, University of Texas at Austin Texas Advanced Computing Center (TACC)

Resource Type: data or information resource, organization portal, portal

Resource Name: Texas Advanced Computing Center

Resource ID: SCR_012530

Alternate IDs: SciEx_4326

Old URLs: <http://www.scienceexchange.com/facilities/texas-advanced-computing-center-tacc>

Record Creation Time: 20220129T080310+0000

Ratings and Alerts

No rating or validation information has been found for Texas Advanced Computing Center.

No alerts have been found for Texas Advanced Computing Center.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 101 mentions in open access literature.

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

Luo S, et al. (2026) High-Speed AFM Reveals Ligand-Dependent Supramolecular Switching of Human Phosphofructokinase-1. Research square.

Kurapati V, et al. (2026) Fused ensembles of dynamic-rupture earthquake simulations to accelerate Bayesian inference. GEM : international journal on geomathematics, 17(1), 8.

Hassan SA, et al. (2026) Minimal Computational Framework for Systematic Identification of Antimicrobial Targets. bioRxiv : the preprint server for biology.

Shen R, et al. (2026) EEPD1 evolved a unique DNA clamping dimer protecting reversed replication forks. Nucleic acids research, 54(5).

Bhuiyan SA, et al. (2026) Improving coastal water level estimation by merging nadir-only satellite altimetry data into a hydrodynamic model. Environmental monitoring and assessment, 198(4).

Paul S, et al. (2026) CX-5461 and doxorubicin activate a shared DNA damage-associated transcriptional response in human cardiomyocytes. G3 (Bethesda, Md.), 16(3).

Sharifitabar M, et al. (2025) ZiPo: A Deep Neural Network to De-Noise Single-Cell RNA Sequencing Data. IEEE transactions on computational biology and bioinformatics, 22(6), 2341.

Donahue MM, et al. (2025) CA2 neurons show abnormal responses to social stimuli in a rat model of Fragile X syndrome. bioRxiv : the preprint server for biology.

Matthews ER, et al. (2025) Anthracyclines induce global changes in cardiomyocyte chromatin accessibility that overlap with cardiovascular disease loci. bioRxiv : the preprint server for biology.

Goodwin HV, et al. (2025) PPI-ID: Streamlining protein-protein interaction prediction through domain and SLiM mapping. PLoS computational biology, 21(10), e1013062.

Jaczynska K, et al. (2025) A lever hypothesis for Synaptotagmin-1 action in neurotransmitter release. *Proceedings of the National Academy of Sciences of the United States of America*, 122(1), e2417941121.

Medvedev KE, et al. (2025) Leveraging AI to explore structural contexts of post-translational modifications in drug binding. *Journal of cheminformatics*, 17(1), 67.

Ji K, et al. (2025) Probing the anion binding promiscuity of the soluble nitrate sensor NreA from *Staphylococcus carnosus*. *Communications chemistry*, 8(1), 275.

Ramirez P, et al. (2025) Long-read sequencing reveals genomic and epigenomic variation in the dark genome of human Alzheimer's disease. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(11), e70852.

Kazempour S, et al. (2025) ZipAER: A compressive convolutional autoencoder for high-dimensional spatial omics data at subcellular resolution. *Research square*.

Hiremath KC, et al. (2025) Identifiability and model selection frameworks for models of high-grade glioma response to chemoradiation. *Philosophical transactions. Series A, Mathematical, physical, and engineering sciences*, 383(2293), 20240212.

Dehkordi SK, et al. (2025) Identification of markers for neurescence through transcriptomic profiling of postmortem human brains. *Research square*.

Giese TJ, et al. (2025) FE-ToolKit: A Versatile Software Suite for Analysis of High-Dimensional Free Energy Surfaces and Alchemical Free Energy Networks. *Journal of chemical information and modeling*, 65(11), 5273.

Matthews ER, et al. (2025) Anthracyclines induce global changes in cardiomyocyte chromatin accessibility that overlap with cardiovascular disease loci. *PLoS genetics*, 21(10), e1011900.

Ramirez P, et al. (2025) Long-read sequencing-based analyses of the adult *Drosophila* brain transcriptome in physiological and pathological settings. *BMC genomics*, 26(1), 913.