

Resource Summary Report

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Wisconsin-Madison University Biotechnology Center DNA Sequencing Core Facility

RRID:SCR_017759

Type: Tool

Proper Citation

Wisconsin-Madison University Biotechnology Center DNA Sequencing Core Facility
(RRID:SCR_017759)

Resource Information

URL: <http://www.biotech.wisc.edu/facilities/dnaseq/home>

Proper Citation: Wisconsin-Madison University Biotechnology Center DNA Sequencing Core Facility (RRID:SCR_017759)

Description: Core provides sequencing resources. Service support for Illumina Next Generation and Sanger sequencing projects, from project design and sample preparation through downstream analysis. Provides DNA extraction, SNP genotyping, and fragment analysis services, and can facilitate custom projects upon request.

Synonyms: UWBC DNA Sequencing Facility

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

Keywords: Sequencing, next, generation, Sanger, design, sample, preparation, analysis, DNA, extraction, SNP, genotyping, service, core

Availability: Open

Resource Name: Wisconsin-Madison University Biotechnology Center DNA Sequencing Core Facility

Resource ID: SCR_017759

Alternate IDs: ABRF_294

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260912T200401+0000

Ratings and Alerts

No rating or validation information has been found for Wisconsin-Madison University Biotechnology Center DNA Sequencing Core Facility.

No alerts have been found for Wisconsin-Madison University Biotechnology Center DNA Sequencing Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 124 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Barnes KL, et al. (2026) Isolation, validation, and long-term culture of mouse ear fibroblasts. *Biology open*, 15(5).

Jiang N, et al. (2026) Deletion detection in SARS-CoV-2 genomes from COVID-19 patients: elimination of false positives. *Virus evolution*, 12(1), veag003.

Kerr CP, et al. (2026) Priming versus propagating: distinct immune effects of alpha-??versus beta-particle emitting radiopharmaceuticals when combined with immune checkpoint inhibition in mice. *Nature communications*, 17(1).

Yulfo-Soto GE, et al. (2026) First genome and transcription factor profile for *Asimina triloba*, a native North American fruit tree. *The plant genome*, 19(1), e70181.

Corban JE, et al. (2026) Systematic mapping of chromatin dysregulation driven by viral transcriptional regulators at scale. *bioRxiv : the preprint server for biology*.

Shen P, et al. (2026) RNAP-seq: in vitro genome-scale transcription reveals preferential RNA polymerase pausing on *Clostridioides difficile* antisense DNA. *bioRxiv : the preprint server for biology*.

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.

Kocik RA, et al. (2026) The importance of regulated resource reallocation during dynamic environmental shifts in yeast. *The EMBO journal*, 45(8), 2808.

Gin TE, et al. (2026) Pathogenic bacterial species and the microbiome of cat fleas (*Ctenocephalides felis*) inhabiting flea-infested homes. *PloS one*, 21(1), e0341824.

Kabra M, et al. (2026) Synonymous editing alters ion channel function, favoring prime editing for retinal disease correction. *International journal of biological sciences*, 22(9), 4670.

Enuh BM, et al. (2026) Metagenomes and metagenome-assembled genomes from a nutrient removal plant at Los Angeles County Sanitation Districts (LACSD) that transitioned from high to low dissolved oxygen. *Microbiology resource announcements*, 15(3), e0149425.

Melde R, et al. (2026) Meiotic double-strand DNA breaks and spontaneous mutation in *Drosophila melanogaster*. *G3 (Bethesda, Md.)*, 16(4).

Miller AH, et al. (2026) Inhibition of Cxcr4 chemokine receptor signaling improves habituation learning in a zebrafish model of neurofibromatosis. *Disease models & mechanisms*, 19(3).

Nickles GR, et al. (2026) Equipped for success: genomes and metabolomes of the European *Amanita muscaria* are conserved in its novel South African range. *The New phytologist*, 250(3), 1863.

Horianopoulos LC, et al. (2026) Convergent evolution of aerobic fermentation through divergent mechanisms acting on key shared glycolytic genes. *The EMBO journal*, 45(10), 3540.

Enuh BM, et al. (2026) Metagenomes and metagenome-assembled genomes from microbial communities in a biological nutrient removal plant operated at Hamptons Road Sanitation District (HRSD) with high and low dissolved oxygen conditions. *Microbiology resource announcements*, 15(6), e0149225.

Park SC, et al. (2026) Leaderless RiPPs expand the repertoire of fungal secondary metabolites. *Proceedings of the National Academy of Sciences of the United States of America*, 123(7), e2529748123.

Yuan NY, et al. (2026) Stimulus-Based ApoE Alzheimer's Disease Induction Model Using Microglia-Containing Brain Organoids for Drug Discovery. *Cells*, 15(14).

Xu Z, et al. (2026) An adaptable, self-organizing, single-cell morphology circuit optimizes suctorian predatory trap structure. *Current biology : CB*, 36(14), 3462.

Smith FM, et al. (2026) The paracrine factor myeloid derived growth factor regulates the inflammatory fate and motility of human induced pluripotent stem cell-derived neutrophils. *Journal of immunology (Baltimore, Md. : 1950)*, 215(2).