

Resource Summary Report

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University of Florida ICBR NextGen DNA Sequencing Core Facility

RRID:SCR_019152

Type: Tool

Proper Citation

University of Florida ICBR NextGen DNA Sequencing Core Facility (RRID:SCR_019152)

Resource Information

URL: <https://biotech.ufl.edu/next-gen-dna/>

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Description: Core provides platforms including Illumina NextSeq500 and MiSeq, HiSeq3000 and Pacific Biosciences SEQUEL system. Offers free consultation in sequencing technologies including read length, error rate, predominant type of error, data output/run, speed, cost. Services include de novo sequencing of whole genomes, targeted sequencing, transcriptome sequencing, chromatin immunoprecipitation sequencing, methylation analysis and metagenomics.

Abbreviations: ICBR-NGS

Synonyms: UF ICBR NextGen DNA Sequencing, University of Florida UF ICBR NextGen DNA Sequencing

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

Keywords: USEdit, sequencing technologies, de novo sequencing, whole genomes, targeted sequencing, transcriptome sequencing, chromatin immunoprecipitation sequencing, methylation analysis, metagenomics, ABRF, ABRF

Resource Name: University of Florida ICBR NextGen DNA Sequencing Core Facility

Resource ID: SCR_019152

Alternate IDs: ABRF_650

Alternate URLs: <https://coremarketplace.org/?FacilityID=650>

Record Creation Time: 20220129T080343+0000

Ratings and Alerts

No rating or validation information has been found for University of Florida ICBR NextGen DNA Sequencing Core Facility.

No alerts have been found for University of Florida ICBR NextGen DNA Sequencing Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 67 mentions in open access literature.

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

Charles AM, et al. (2025) Sepsis Induces Age- and Sex-Specific Chromatin Remodeling in Myeloid-Derived Suppressor Cells. *bioRxiv : the preprint server for biology*.

Duran-Pinedo A, et al. (2025) Longitudinal host-microbiome dynamics of metatranscription identify hallmarks of progression in periodontitis. *Microbiome*, 13(1), 119.

Oshins R, et al. (2025) Alpha-1 antitrypsin modulates neutrophil phenotype and function: implications for inflammatory regulation. *Journal of leukocyte biology*, 117(6).

Sieber KR, et al. (2025) Caste- and environment-associated differential expression of olfactory receptors in pest ants. *Scientific reports*, 15(1), 31079.

Gurgel BCV, et al. (2025) Comprehensive analysis of transcriptome and pathway interactions in periodontitis. *Journal of applied oral science : revista FOB*, 33, e20250396.

Zhao N, et al. (2025) Genomic and functional characterization of a *Butyricicoccus porcorum* strain isolated from human gut microbiota. *mSystems*, 10(8), e0079025.

Kim HG, et al. (2025) Chromatin Remodeling and Transcriptional Silencing Define the Dynamic Innate Immune Response of Tissue Resident Macrophages After Burn Injury. *bioRxiv : the preprint server for biology*.

Laforest LC, et al. (2025) A chromosome-level *Mitragyna parvifolia* genome unveils spirooxindole alkaloid diversification and mitraphylline biosynthesis. *The Plant cell*, 37(9).

Geng P, et al. (2025) *Faecalibacterium prausnitzii* regulates carbohydrate metabolic functions of the gut microbiome in C57BL/6 mice. *Gut microbes*, 17(1), 2455503.

Seo D, et al. (2025) GLARE: discovering hidden patterns in spaceflight transcriptome using representation learning. *NPJ microgravity*, 11(1), 76.

Chitre S, et al. (2025) A defined bacterial consortium and spatial transcriptomics highlight the complex interaction between *Campylobacter jejuni* and the murine intestine. *bioRxiv* : the preprint server for biology.

Surphlis AC, et al. (2025) Characterizing the resistome of *Escherichia coli* isolated from farmed white-tailed deer (*Odocoileus virginianus*) in Florida, United States. *Frontiers in microbiology*, 16, 1681096.

Bogale M, et al. (2025) Development of Monoclonal Antibodies for Identifying Plant-Parasitic Nematodes. *Journal of nematology*, 57(1), 20250024.

Newsome RC, et al. (2025) Microbial-derived immunostimulatory small molecule augments anti-PD-1 therapy in lung cancer. *Cell reports. Medicine*, 102519.

Pan X, et al. (2025) Extracellular vesicle-mediated gene editing for the treatment of nonsyndromic progressive hearing loss in adult mice. *Science translational medicine*, 17(824), eadn3993.

Parafati M, et al. (2025) Tomatidine Attenuates Inflammatory Responses to Exercise-Like Stimulation in Donor-derived Skeletal Muscle Myobundles. *Medical research archives*, 13(4).

Scott KA, et al. (2025) Cardiometabolic and anxiogenic consequences of chronic social defeat stress in male mice. *Neurobiology of stress*, 38, 100752.

Skojec C, et al. (2024) Long read genome assembly of *Automeris io* (Lepidoptera: Saturniidae) an emerging model for the evolution of deimatic displays. *G3 (Bethesda, Md.)*, 14(3).

Kok HJ, et al. (2024) Transcriptomics reveals transient and dynamic muscle fibrosis and atrophy differences following spinal cord injury in rats. *Journal of cachexia, sarcopenia and muscle*, 15(4), 1309.

Duarte PM, et al. (2024) Distinctive genes and signaling pathways associated with type 2 diabetes-related periodontitis: Preliminary study. *PloS one*, 19(1), e0296925.