

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, access service resource, 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 87 mentions in open access literature.

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

Chopade A, et al. (2026) Shared biosynthetic architectures generate diverse β -amino polyketide residues in cyanobacterial peptides. *bioRxiv : the preprint server for biology*.

Chitre S, et al. (2026) *Campylobacter jejuni* infection impacts host-derived miRNAs targeting bacterial and host genes. *Microbiology spectrum*, 14(3), e0318425.

Collins JM, et al. (2026) Knockdown of RNA editing proteins reshapes the HepaRG transcriptome and pharmacogene expression. *Scientific reports*, 16(1).

Hong Y, et al. (2026) Herpesvirus-encoded lncRNA targets host splicing by interacting with splicing factors. *PLoS pathogens*, 22(3), e1014072.

Medina-Serpas MA, et al. (2026) Spatial transcriptomics from pancreas and local draining lymph node tissue reveals a lymphotoxin- β signature in human type 1 diabetes. *Cell reports*, 45(4), 117144.

Ali S, et al. (2026) Extracellular vesicle transcriptomic analysis to investigate muscle adaptation in microgravity. *iScience*, 29(6), 115838.

Foquet B, et al. (2026) Evolution of Highly Repetitive Silk Genes in the Luna Moth, *Actias luna*. *Genome biology and evolution*, 18(3).

Charles AM, et al. (2026) A murine model of sepsis induces age- and sex-specific chromatin remodeling in myeloid-derived suppressor cells. *Frontiers in immunology*, 17, 1750174.

Zhao N, et al. (2026) Multiomics-guided discovery of protective microbiome signatures in lupus-prone mice treated with *Faecalibacterium prausnitzii*. *Nature communications*, 17(1).

Ketchum RN, et al. (2026) Genomic signatures of speciation and adaptation in the ctenophore *Mnemiopsis*. *BMC biology*, 24(1).

Semel M, et al. (2026) Mitochondrial Permeability Transition in Skeletal Muscle Phenocopies Muscle Alterations seen in Cancer Cachexia and other Wasting Conditions. *bioRxiv : the preprint server for biology*.

Brant JO, et al. (2026) Divergent chromatin remodeling trajectories in CD66b + MDSCs distinguishes recovery from chronic critical illness after sepsis. *bioRxiv : the preprint server for biology*.

Maldonado MBC, et al. (2026) Alterations in gene expression and DNA methylation in the bovine blastocyst in response to choline supplementation during culture†. *Biology of reproduction*, 114(5), 1568.

Orosco C, et al. (2026) DNA-guided CRISPR-Cas12 for cellular RNA targeting. *Nature biotechnology*.

Kim HG, et al. (2026) Chromatin Remodeling and Transcriptional Silencing Define the Dynamic Innate Immune Response of Tissue Resident Macrophages After Burn Injury. *Shock (Augusta, Ga.)*, 65(3), 538.

Estellas C, et al. (2026) Synaptic plasticity in the perforant pathway drives inhibitory reorganization enhancing dentate gyrus functionality. *iScience*, 29(3), 114878.

Brummel BR, et al. (2026) Natural Products Inspired Scaffold Diversification Leads to Unnatural Molecular Warhead and Covalent Strategy to Modulating Protein Function through Electrophilic Bromine Transfer. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(42), e12849.

Adam EA, et al. (2026) Exploring Mechanisms of Calcific Tendonitis Using a Novel Turkey Model. *Journal of orthopaedic research : official publication of the Orthopaedic Research Society*, 44(1), e70136.

Chitre S, et al. (2025) A defined bacterial consortium and spatial transcriptomics highlight the complex interaction between *Campylobacter jejuni* and the murine intestine. *Gut microbes*, 17(1), 2600053.

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