Resource Summary Report

Generated by NIF on Apr 18, 2025

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: access service resource, service resource, core facility

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

Funding:

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

Record Last Update: 20250418T055550+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 47 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

McGrath-Blaser SE, et al. (2024) Invasibility of a North American soil ecosystem to amphibian-killing fungal pathogens. Proceedings. Biological sciences, 291(2021), 20232658.

Markee A, et al. (2024) De Novo Long-Read Genome Assembly and Annotation of the Luna Moth (Actias luna) Fully Resolves Repeat-Rich Silk Genes. Genome biology and evolution, 16(7).

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

Zhou M, et al. (2024) Light has a principal role in the Arabidopsis transcriptomic response to the spaceflight environment. NPJ microgravity, 10(1), 82.

Poulos MG, et al. (2024) Complementary and Inducible creERT2 Mouse Models for Functional Evaluation of Endothelial Cell Subtypes in the Bone Marrow. Stem cell reviews and reports.

Ketchum RN, et al. (2024) Rapid speciation in the holopelagic ctenophore Mnemiopsis following glacial recession. bioRxiv : the preprint server for biology.

Viggars MR, et al. (2024) Skeletal muscle BMAL1 is necessary for transcriptional adaptation of local and peripheral tissues in response to endurance exercise training. Molecular metabolism, 86, 101980.

Gutierrez-Monreal MA, et al. (2024) Targeted Bmal1 restoration in muscle prolongs lifespan with systemic health effects in aging model. JCI insight, 9(22).

Poole B, et al. (2024) Sirtuin3 promotes the degradation of hepatic Z alpha-1 antitrypsin through lipophagy. Hepatology communications, 8(2).

Atanasova KR, et al. (2024) Epigenetic small-molecule screen for inhibition and reversal of acinar ductal metaplasia in mouse pancreatic organoids. Frontiers in pharmacology, 15, 1335246.

Al-Awadhi FH, et al. (2024) Isolation and Characterization of the Cyanobacterial Macrolide Glycoside Moorenaside, an Anti-Inflammatory Analogue of Aurisides Targeting the Keap1/Nrf2 Pathway. Journal of natural products, 87(10), 2355.

Lin C-Y, et al. (2024) An insect virus differentially alters gene expression among life stages of an insect vector and enhances bacterial phytopathogen transmission. Journal of virology, e0163024.

Lefler FW, et al. (2024) Microbial Community Response to Granular Peroxide-Based Algaecide Treatment of a Cyanobacterial Harmful Algal Bloom in Lake Okeechobee, Florida (USA). Toxins, 16(5).

Febres VJ, et al. (2024) Dissection of transcriptional events in graft incompatible reactions of "Bearss" lemon (Citrus limon) and "Valencia" sweet orange (C. sinensis) on a novel citrandarin (C. reticulata × Poncirus trifoliata) rootstock. Frontiers in plant science, 15, 1421734.

Zhou M, et al. (2024) Single-molecule long-read methylation profiling reveals regional DNA methylation regulated by Elongator Complex Subunit 2 in Arabidopsis roots experiencing spaceflight. Biology direct, 19(1), 33.

Murray KO, et al. (2024) Exertional heat stroke causes long-term skeletal muscle epigenetic reprogramming, altered gene expression, and impaired satellite cell function in mice. American journal of physiology. Regulatory, integrative and comparative physiology, 326(2), R160.

Barbosa M, et al. (2024) Macrophyte coverage drives microbial community structure and interactions in a shallow sub-tropical lake. The Science of the total environment, 923, 171414.

Marini S, et al. (2024) Oral Cannabidiol Treatment Is Associated with an Anti-Inflammatory Gene Expression Signature in Myeloid Cells of People Living with HIV. Cannabis and cannabinoid research.