Resource Summary Report

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University of Florida ICBR Bioinformatics Core Facility

RRID:SCR_019120
Type: Tool

Proper Citation

University of Florida ICBR Bioinformatics Core Facility (RRID:SCR_019120)

Resource Information

URL: http://www.biotech.ufl.edu/bioinformatics/

Proper Citation: University of Florida ICBR Bioinformatics Core Facility (RRID:SCR_019120)

Description: Core offers bioinformatics consulting and data analysis services to help researchers analyze and understand large data sets acquired from next generation sequencing and array based technologies.Bioinformatics staff members have extensive experience in bioinformatics, genomics, transcriptomics and translational informatics in plant, animal and microbial systems. Expertise includes big data analysis, statistical analysis, software development and high performance computing.

Synonyms: University of Florida UF ICBR Bioinformatics, UF ICBR Bioinformatics

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

Keywords: USEDit, bioinformatics consulting, bioinformatics data analysis services, statistical analysis, software development, high performance computing, ABRF, ABRF

Resource Name: University of Florida ICBR Bioinformatics Core Facility

Resource ID: SCR_019120

Alternate IDs: ABRF_645

Alternate URLs: https://coremarketplace.org/?FacilityID=645

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260912T200408+0000

Ratings and Alerts

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

No alerts have been found for University of Florida ICBR Bioinformatics Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 34 mentions in open access literature.

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

Tagliamonte MS, et al. (2026) CholeraSeq: a comprehensive genomic pipeline for cholera surveillance and near real-time outbreak investigation. Bioinformatics (Oxford, England), 42(1).

Canal R, et al. (2026) Enhanced Pro-Osteogenic Regulatory Modulation in Mesenchymal Stem Cells Derived from the Periosteum Under Simulated Microgravity. Cells, 15(11).

Rein B, et al. (2026) A Rapid Method for Accurately Determining Lipid Nanoparticle Size Using Nano-Flow Cytometry. Journal of biomolecular techniques : JBT, 37(2), 48.

Pant S, et al. (2026) Erdafitinib in Patients with FGFR-Altered Advanced or Metastatic Cholangiocarcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(6), 1136.

Mercado-Rodriguez C, et al. (2026) Defined bacterial consortium highlights the impact of intestinal bacteria on DNA methylation and tumorigenesis. Genome biology, 27(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.

Morris JG, et al. (2026) Molecular Epidemiology of Candidozyma auris Within a Case Cluster in North-Central Florida: Diverse Origins and Long-term Persistence of Strains. Open forum infectious diseases, 13(7), ofag379.

Cherabuddi K, et al. (2025) A Case Cluster of Aseptic Meningitis Associated With a Newly Identified Recombinant Echovirus 6/Coxsackievirus B1 Enterovirus. The Journal of infectious diseases, 232(3), e486.

Enriquez V, et al. (2025) Active Cryptococcus neoformans glucuronoxylomannan production prevents elimination of cryptococcal CNS infection in vivo. Journal of neuroinflammation, 22(1), 61.

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.

Paoli JE, et al. (2025) Virome and Microbiome of Florida Bats Illuminate Viral Co-Infections, Dietary Viral Signals, and Gut Microbiome Shifts. Microorganisms, 13(11).

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.

Dill MN, et al. (2025) Exploring the Unique Extracellular Matrix Composition of Acomys as a Potential Key to Resisting Fibrosis. ACS biomaterials science & engineering, 11(6), 3616.

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.

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.

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

Nasim S, et al. (2024) Multiple cell types including melanocytes contribute to elastogenesis in the developing murine aortic valve. Scientific reports, 14(1), 25481.

Scotti MM, et al. (2024) Spaceflight effects on human vascular smooth muscle cell phenotype and function. NPJ microgravity, 10(1), 41.

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.