

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, service resource, core facility

Keywords: USEEdit, 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: 20260806T054710+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 26 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).

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.

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.

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

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.

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

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.

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.

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.

Sobh A, et al. (2024) NSD2 drives t(4;14) myeloma cell dependence on adenylate kinase 2 by diverting one-carbon metabolism to the epigenome. *Blood*, 144(3), 283.

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.

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*.

Parafati M, et al. (2023) Human skeletal muscle tissue chip autonomous payload reveals changes in fiber type and metabolic gene expression due to spaceflight. *NPJ microgravity*, 9(1), 77.

Morozov VM, et al. (2023) HIRA-mediated loading of histone variant H3.3 controls androgen-induced transcription by regulation of AR/BRD4 complex assembly at enhancers. *Nucleic acids research*, 51(19), 10194.

Ferl RJ, et al. (2023) Transcriptomic dynamics in the transition from ground to space are revealed by Virgin Galactic human-tended suborbital spaceflight. *NPJ microgravity*, 9(1), 95.

Dougherty MW, et al. (2023) The microbial genotoxin colibactin exacerbates mismatch repair mutations in colorectal tumors. *Neoplasia (New York, N.Y.)*, 43, 100918.

Morozov VM, et al. (2023) HIRA-mediated loading of histone variant H3.3 controls androgen-induced transcription by regulation of AR/BRD4 complex assembly at enhancers. *bioRxiv : the preprint server for biology*.