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

Funding:

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: 20250418T055550+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 19 mentions in open access literature.

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

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

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.

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.

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

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.

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.

Magalis BR, et al. (2022) Low-frequency variants in mildly symptomatic vaccine breakthrough infections presents a doubled-edged sword. Journal of medical virology, 94(7), 3192.

Nguyen LT, et al. (2022) A thermostable Cas12b from Brevibacillus leverages one-pot discrimination of SARS-CoV-2 variants of concern. EBioMedicine, 77, 103926.

Paul AL, et al. (2022) Plants grown in Apollo lunar regolith present stress-associated transcriptomes that inform prospects for lunar exploration. Communications biology, 5(1), 382.

Haveman NJ, et al. (2022) Utilizing the KSC Fixation Tube to Conduct Human-Tended Plant Biology Experiments on a Suborbital Spaceflight. Life (Basel, Switzerland), 12(11).

Rife Magalis B, et al. (2022) Severe Acute Respiratory Syndrome Coronavirus 2 Delta Vaccine Breakthrough Transmissibility in Alachua County, Florida. Clinical infectious diseases : an official publication of the Infectious Diseases Society of America, 75(9), 1618.

Paul AL, et al. (2021) Epigenomic Regulators Elongator Complex Subunit 2 and Methyltransferase 1 Differentially Condition the Spaceflight Response in Arabidopsis. Frontiers in plant science, 12, 691790.