Resource Summary Report

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Rhode Island INBRE Molecular Informatics Core Facility

RRID:SCR_017685
Type: Tool

Proper Citation

Rhode Island INBRE Molecular Informatics Core Facility (RRID:SCR_017685)

Resource Information

URL: https://web.uri.edu/riinbre/mic/

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Description: Core provides sequencing and bioinformatics support for INBRE and non-INBRE researchers. Provides data science services adjacent to traditional bioinformatics; access to computational and software resources for INBRE network institutions, particularly primarily undergraduate institutions; training for students and faculty in data science methods. Maintains professional network with other core and user facilities in Rhode Island and beyond to maximize resources available to our users.Utilizes novel technologies such as virtual/augmented reality for use in teaching and research.

Synonyms: Rhode Island INBRE Molecular Informatics, RI-INBRE Bioinformatics Core; RI Genomics and Sequencing Center

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

Keywords: Analysis, interpretation, nucleotide, amino acid, sequence, protein, domain, structure, service, 3D visualization, modeling, USEDit

Funding: NIGMS P20 GM103430

Availability: Open

Resource Name: Rhode Island INBRE Molecular Informatics Core Facility

Resource ID: SCR_017685

Alternate IDs: ABRF_3

Record Creation Time: 20220129T080336+0000

Record Last Update: 20250407T220417+0000

Ratings and Alerts

No rating or validation information has been found for Rhode Island INBRE Molecular Informatics Core Facility.

No alerts have been found for Rhode Island INBRE Molecular Informatics Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Hemme CL, et al. (2024) A cloud-based learning module for biomarker discovery. Briefings in bioinformatics, 25(Supplement_1).

Macaraeg A, et al. (2024) Genetic screen identifies cell wall enzyme is key for freshwater survival of Francisella tularensis. bioRxiv : the preprint server for biology.

Catlett D, et al. (2023) Temperature dependence of parasitoid infection and abundance of a diatom revealed by automated imaging and classification. Proceedings of the National Academy of Sciences of the United States of America, 120(28), e2303356120.

Trautmann HS, et al. (2023) Ribosome heterogeneity results in leader sequence-mediated regulation of protein synthesis in Francisella tularensis. Journal of bacteriology, 205(9), e0014023.

Crisalli AM, et al. (2023) Probing the Interactions of Perfluorocarboxylic Acids of Various Chain Lengths with Human Serum Albumin: Calorimetric and Spectroscopic Investigations. Chemical research in toxicology, 36(4), 703.

Trautmann HS, et al. (2022) A Ribosomal Protein Homolog Governs Gene Expression and Virulence in a Bacterial Pathogen. Journal of bacteriology, 204(10), e0026822.

Nadolny C, et al. (2021) Dysregulation and activities of ubiquitin specific peptidase 2b in the pathogenesis of hepatocellular carcinoma. American journal of cancer research, 11(10), 4746.

Hemme CL, et al. (2021) RI-INBRE: A Statewide NIH Program Grant to Improve Institutional Biomedical Research Capacity in Rhode Island. Rhode Island medical journal (2013), 104(2), 25.

Gallucci GM, et al. (2021) Adjunct Fenofibrate Up-regulates Bile Acid Glucuronidation and Improves Treatment Response For Patients With Cholestasis. Hepatology communications, 5(12), 2035.

Ghonem NS, et al. (2020) Fenofibrate Improves Liver Function and Reduces the Toxicity of the Bile Acid Pool in Patients With Primary Biliary Cholangitis and Primary Sclerosing Cholangitis Who Are Partial Responders to Ursodiol. Clinical pharmacology and therapeutics, 108(6), 1213.

Lowerre KM, et al. (2019) Bioinformatics Structural and Phylogenetic Characterization of Entamoeba histolytica Alcohol Dehydrogenase 2 (EhADH2). Bios, 90(1), 30.

Eid A, et al. (2018) Histone acetylation maps in aged mice developmentally exposed to lead: epigenetic drift and Alzheimer-related genes. Epigenomics, 10(5), 573.