Resource Summary Report

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Pennsylvania State University Huck Institutes of the Life Sciences Genomics Core Facility

RRID:SCR_023645 Type: Tool

Proper Citation

Pennsylvania State University Huck Institutes of the Life Sciences Genomics Core Facility (RRID:SCR_023645)

Resource Information

URL: https://www.huck.psu.edu/core-facilities/genomics-core-facility

Proper Citation: Pennsylvania State University Huck Institutes of the Life Sciences Genomics Core Facility (RRID:SCR_023645)

Description: Genomics Core Facility provides services including Whole-genome and transcriptome sequencing of non-model organisms, Amplicon sequencing for metagenomic studies, Differential expression analysis of mRNA and miRNA, Degradome sequencing, ChIP and RIP sequencing.

Synonyms: PennState UHC Genomics, Huck Institutes of the Life Sciencies Genomics Core Facility, PennState Huck Institutes of the Life Sciencies Genomics Core Facility, HUC-Genomics, PennState UHC Genomics Core Facility, Huck Institutes Genomics Core Facility

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

Keywords: USEDit, ABRF, Whole-genome and transcriptome sequencing of non-model organisms, Amplicon sequencing for metagenomic studies, Differential expression analysis of mRNA and miRNA, Degradome sequencing, ChIP and RIP sequencing,

Funding:

Resource Name: Pennsylvania State University Huck Institutes of the Life Sciences Genomics Core Facility

Resource ID: SCR_023645

Alternate IDs: ABRF_1779

Alternate URLs: https://coremarketplace.org/?FacilityID=1779&citation=1

Record Creation Time: 20230602T050209+0000

Record Last Update: 20250503T061108+0000

Ratings and Alerts

No rating or validation information has been found for Pennsylvania State University Huck Institutes of the Life Sciences Genomics Core Facility.

No alerts have been found for Pennsylvania State University Huck Institutes of the Life Sciences Genomics Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>ASWG</u>.

Quinlan GM, et al. (2025) Leveraging Transcriptional Signatures of Diverse Stressors for Bumble Bee Conservation. Molecular ecology, 34(3), e17626.

Nichols RG, et al. (2025) Clade-specific long-read sequencing increases the accuracy and specificity of the gyrB phylogenetic marker gene. mSystems, 10(1), e0148024.

Rios KT, et al. (2025) Widespread release of translational repression across Plasmodium's host-to-vector transmission event. PLoS pathogens, 21(1), e1012823.

Rios KT, et al. (2024) Global Release of Translational Repression Across Plasmodium's Host-to-Vector Transmission Event. bioRxiv : the preprint server for biology.

Pearce DL, et al. (2024) Evaluation of DNA yield from various tissue and sampling sources for use in single nucleotide polymorphism panels. Scientific reports, 14(1), 11340.

Locatelli NS, et al. (2024) Genomes of the Caribbean reef-building corals Colpophyllia natans, Dendrogyra cylindrus, and Siderastrea siderea. bioRxiv : the preprint server for biology.

McKinley LN, et al. (2024) Direct testing of natural twister ribozymes from over a thousand

organisms reveals a broad tolerance for structural imperfections. Nucleic acids research, 52(22), 14133.

Locatelli NS, et al. (2024) Chromosome-level genome assemblies and genetic maps reveal heterochiasmy and macrosynteny in endangered Atlantic Acropora. BMC genomics, 25(1), 1119.

Seemiller LR, et al. (2024) Alcohol and fear conditioning produce strain-specific changes in the dorsal hippocampal transcriptome of adolescent C57BL/6J and DBA/2J mice. Alcohol, clinical & experimental research.

McKinley LN, et al. (2024) Direct testing of natural twister ribozymes from over a thousand organisms reveals a broad tolerance for structural imperfections. bioRxiv : the preprint server for biology.

Kulesza E, et al. (2024) The cacao gene atlas: a transcriptome developmental atlas reveals highly tissue-specific and dynamically-regulated gene networks in Theobroma cacao L. BMC plant biology, 24(1), 601.