

# Resource Summary Report

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

RRID:SCR\_023645

Type: Tool

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### Proper Citation

Pennsylvania State University Huck Institutes of the Life Sciences Genomics Core Facility (RRID:SCR\_023645)

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### 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 Sciences Genomics Core Facility, PennState Huck Institutes of the Life Sciences Genomics Core Facility, HUC-Genomics, PennState UHC Genomics Core Facility, Huck Institutes Genomics Core Facility

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

**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,

**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

## 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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 26 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Locatelli NS, et al. (2025) Genomes of the Caribbean reef-building corals *Colpophyllia natans*, *Dendrogyra cylindrus*, and *Siderastrea siderea*. *G3* (Bethesda, Md.), 15(4).

Chan K, et al. (2025) Genome Instability Precedes Viral Integration in Human Papillomavirus-Transformed Tonsillar Keratinocytes. *Molecular cancer research : MCR*, 23(2), 119.

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.

Kulkarni S, et al. (2025) Auxin-induced depletion of human CCR4-NOT subunits reveals opposing functions of CNOT1 and CNOT4 in mRNA metabolism. *The Journal of biological chemistry*, 301(12), 110862.

Akinniyi OT, et al. (2025) Degradation factor 1, Def1, regulates mRNA translation and decay through Ccr4-Not-dependent ubiquitylation of the ribosome. *bioRxiv : the preprint server for biology*.

Lawrence SS, et al. (2025) Interferon- $\gamma$ /Janus Kinase 1/STAT1 Signaling Represses Forkhead Box A1 and Drives a Basal Transcriptional State in Muscle-Invasive Bladder Cancer. *The American journal of pathology*, 195(5), 1013.

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

Gontu A, et al. (2025) Pasteurized Milk Serves as a Passive Surveillance Tool for Highly Pathogenic Avian Influenza Virus in Dairy Cattle. *Viruses*, 17(10).

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

Bresnahan ST, et al. (2025) Intragenomic conflict associated with extreme phenotypic plasticity in queen-worker caste determination in honey bees (*Apis mellifera*). *Genome biology*, 26(1), 171.

Ortigas-Vasquez A, et al. (2025) High-Fidelity Long-Read Sequencing of an Avian Herpesvirus Reveals Extensive Intrapopulation Diversity in Tandem Repeat Regions. *bioRxiv* : the preprint server for biology.

Ortigas-Vasquez A, et al. (2025) High-fidelity long-read sequencing of an avian herpesvirus reveals extensive intrapopulation diversity in tandem repeat regions. *PLoS pathogens*, 21(8), e1013435.

Vanek A, et al. (2025) miRScore: A rapid and precise microRNA validation tool. *PLoS computational biology*, 21(11), e1013663.

Sieg J, et al. (2025) Comparative analysis of single-stranded and non-canonical DNA formation in human and other ape cells with telomere-to-telomere genomes. *bioRxiv* : the preprint server for biology.

Akinniyi OT, et al. (2025) The DNA damage response and RNA Polymerase II regulator Def1 has posttranscriptional functions in the cytoplasm. *bioRxiv* : the preprint server for biology.

McKinley LN, et al. (2025) CHiTA: A scarless high-throughput pipeline for characterization of ribozymes. *Methods (San Diego, Calif.)*, 234, 120.

Guiltinan MJ, et al. (2025) Reduced Susceptibility to *Phytophthora* in Non-Transgenic Cacao Progeny Through CRISPR-Cas9 Mediated TcNPR3 Mutagenesis. *Plant biotechnology journal*.

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.

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. *Nucleic acids research*, 52(22), 14133.