# Resource Summary Report

Generated by ASWG on Sep 18, 2026

## 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:** access service resource, core facility, 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,

**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:** 20260912T200426+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 40 mentions in open access literature.

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


Ryu EP, et al. (2026) Integrative host transcriptomic and mucosal microbiome profiling reveals region-specific host-microbiome associations across the human intestine. bioRxiv : the preprint server for biology.

Guha S, et al. (2026) Mutations in legume genes that influence symbiosis create a complex selective landscape for rhizobial symbionts. The ISME journal, 20(1).

Akinniyi OT, et al. (2026) Degradation factor 1, Def1, regulates mRNA translation and decay through Ccr4-Not-dependent ubiquitylation of the ribosome. RNA (New York, N.Y.), 32(6), 930.

Okoye IC, et al. (2026) ATAD3 megadalton complex in Plasmodium falciparum is essential for mitochondrial and cellular viability. PLoS pathogens, 22(6), e1014317.

Akinniyi OT, et al. (2026) Gene expression analysis and proximity labeling reveal post-transcriptional functions of the yeast RNA polymerase II regulator Def1. The Journal of biological chemistry, 302(2), 111003.

Kenney SM, et al. (2026) Draft genomes of Salmonella Dublin from North Dakota State University veterinary diagnostic laboratory. Microbiology resource announcements, 15(4), e0063625.

Li Y, et al. (2026) Hi-C calibration by chemically induced chromosomal interactions. EMBO reports, 27(10), 2549.

Kulkarni S, et al. (2026) Human CCR4-NOT suppresses pervasive transcription and retrotransposable elements. bioRxiv : the preprint server for biology.

Ataie Z, et al. (2026) Cellular Snowballing: Cell Adhesion and Migration Drive the Self-Assembly of Cell-Microgel Biohybrid Spheroids. Advanced science (Weinheim, Baden-

Wurttemberg, Germany), 13(30), e11302.

Aththawala Gedara SVBD, et al. (2026) Membranes arrest the coarsening of mitochondrial condensates in human cells. Communications biology, 9(1).

Nien YC, et al. (2026) Trans-species microRNAs from the parasitic plant Cuscuta campestris specifically avoid loading onto self Argonautes. Nucleic acids research, 54(13).

Sha Z, et al. (2026) Coordination of cell organelles to promote metabolon formation. Proceedings of the National Academy of Sciences of the United States of America, 123(5), e2532504123.

Kulkarni SD, et al. (2026) CCR4-NOT is required for suppressing pervasive transcription and retrotransposable elements. The Journal of biological chemistry, 302(8), 113289.

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

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

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).

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

Lawrence SS, et al. (2025) Interferon-??/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.

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.

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.