

Resource Summary Report

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Pennsylvania State University Huck Institutes Genomics Research Incubator Core Facility

RRID:SCR_024530

Type: Tool

Proper Citation

Pennsylvania State University Huck Institutes Genomics Research Incubator Core Facility (RRID:SCR_024530)

Resource Information

URL: <https://www.huck.psu.edu/about/collaborative-ventures/genomics-research-incubator/about-the-genomics-research-incubator>

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Description: Provides access to highly specialized and custom genomics and epigenomics assays that Genomics Core Facility does not currently support. Examples include ATAC sequencing; RUN sequencing; Tag sequencing; Chromatin immunoprecipitation; Custom assays. Offers hands-on experiences and training for researchers in genomic technologies, methodologies, and instrumentation.

Abbreviations: GRI

Synonyms: Pennsylvania State University Huck Institutes Genomics Research Incubator

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

Keywords: ABRF, Tag sequencing, sequencing library preparation, library quality control analysis, library quantification, sequencing run planning and set up,

Resource Name: Pennsylvania State University Huck Institutes Genomics Research Incubator Core Facility

Resource ID: SCR_024530

Alternate IDs: ABRF_2513

Alternate URLs: <https://coremarketplace.org/?FacilityID=2513&citation=1>,
https://coremarketplace.org/RRID:SCR_024530?citation=1

Record Creation Time: 20231003T050246+0000

Record Last Update: 20260808T043014+0000

Ratings and Alerts

No rating or validation information has been found for Pennsylvania State University Huck Institutes Genomics Research Incubator Core Facility.

No alerts have been found for Pennsylvania State University Huck Institutes Genomics Research Incubator Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

James DQ, et al. (2026) Optimized ChIP-exo for mammalian cells and patterned sequencing flow cells. G3 (Bethesda, Md.), 16(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.

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.

Knox G, et al. (2026) Oncofetal RNA-binding proteins of IGF2BP family suppress IRF-3 and NF-κB dependent transcription downstream of cytosolic RNA sensors. bioRxiv : the preprint server for biology.

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.

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.

Foley L, et al. (2026) Core-shell commensal biocapsules for in situ gut microbiome engineering. Bioactive materials, 65, 796.

- Kulkarni SD, et al. (2026) CCR4-NOT is required for suppressing pervasive transcription and retrotransposable elements. *The Journal of biological chemistry*, 302(8), 113289.
- Traxler EA, et al. (2026) An optimized CRISPR-Cas12a genome-wide screen reveals PTPA phosphatase pathway in fetal hemoglobin silencing. *Blood*, 147(17), 1999.
- Liu P, et al. (2026) STING agonist protects against exacerbation of schistosome egg-induced immunopathology. *PLoS pathogens*, 22(7), e1014394.
- Koo H, et al. (2025) A synthetic gut microbiota provides an understanding of the maintenance and functional impact of phage. *mBio*, 16(12), e0234125.
- 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*.
- Wang X, et al. (2025) Single-stranded DNA-binding proteins are essential components of the architectural LDB1 protein complex. *Molecular cell*, 85(16), 3074.
- 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*.
- Kulkarni S, et al. (2024) Human CCR4-NOT globally regulates gene expression and is a novel silencer of retrotransposon activation. *bioRxiv : the preprint server for biology*.