

Resource Summary Report

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Cornell University BRC Epigenomics Core Facility

RRID:SCR_021287

Type: Tool

Proper Citation

Cornell University BRC Epigenomics Core Facility (RRID:SCR_021287)

Resource Information

URL: <https://www.biotech.cornell.edu/core-facilities-brc/facilities/epigenomics-facility>

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Description: Provides service that maps protein DNA interactions genome wide, tracks experimental metadata, and implements quality controlled data processing and research based analysis pipelines. Provides epigenomic and bioinformatic research resources and services that include sample preparation services and data generation. Open source platforms enable and reinforce FAIR data practices. Core is able to receive and process cell and tissue samples for various diagnostic epigenetic assays.

Synonyms: CU Epigenomics Core Facility, Cornell University Epigenomics Core Facility

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

Keywords: USEDit, ABRF

Funding: NIH ;
NSF

Resource Name: Cornell University BRC Epigenomics Core Facility

Resource ID: SCR_021287

Alternate IDs: ABRF_1185

Alternate URLs: <https://coremarketplace.org/?FacilityID=1185>

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260821T194153+0000

Ratings and Alerts

No rating or validation information has been found for Cornell University BRC Epigenomics Core Facility.

No alerts have been found for Cornell University BRC Epigenomics 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 [dkNET](#) .

Chen H, et al. (2026) Genome-wide rotational and translational phasing of nucleosomes with human transcription factors. *Molecular cell*, 86(14), 2722.

Rogers JV, et al. (2025) Kar4 acts as a Ste12 regulator in *Saccharomyces cerevisiae*, promoting Ste12 binding to a specific DNA motif genome-wide. *bioRxiv : the preprint server for biology*.

Gafur J, et al. (2025) Adversarial attack of sequence-free enhancer prediction identifies chromatin architecture. *Bioinformatics (Oxford, England)*, 41(7).

Ranjan A, et al. (2025) Histone acetylation readers Bdf1 and Yaf9 direct SWR1 remodeler to +1 nucleosome. *Science advances*, 11(32), eadt2002.

Mathew VS, et al. (2025) Protein structure prediction and design for high-throughput computing. *bioRxiv : the preprint server for biology*.

Gonsales Spindola D, et al. (2025) Endothelial cells retain inflammatory memory through chromatin remodeling in a two-hit model of infection-induced inflammation. *American journal of physiology. Cell physiology*, 329(6), C1994.

Hwang SY, et al. (2025) Leveraging BRG1 Driven Ferroptosis Resistance to Overcome Treatment Resistance. *bioRxiv : the preprint server for biology*.

Lang OW, et al. (2023) GenoPipe: identifying the genotype of origin within (epi)genomic datasets. *Nucleic acids research*, 51(22), 12054.

Lang O, et al. (2023) GenoPipe: identifying the genotype of origin within (epi)genomic datasets. *bioRxiv : the preprint server for biology*.

van Breugel ME, et al. (2023) Locus-specific proteome decoding reveals Fpt1 as a chromatin-associated negative regulator of RNA polymerase III assembly. *Molecular cell*, 83(23), 4205.

Mittal C, et al. (2022) An integrated SAGA and TFIID PIC assembly pathway selective for poised and induced promoters. *Genes & development*, 36(17-18), 985.

Sun Q, et al. (2022) STENCIL: A web templating engine for visualizing and sharing life science datasets. PLoS computational biology, 18(2), e1009859.