# **Resource Summary Report**

Generated by <u>NIF</u> on May 20, 2025

# **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

**Proper Citation:** Cornell University BRC Epigenomics Core Facility (RRID:SCR\_021287)

**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: core facility, service resource, access 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

#### **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 4 mentions in open access literature.

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

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

van Breugel ME, et al. (2023) Locus-specific proteome decoding reveals Fpt1 as a chromatinassociated 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.