Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 25, 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

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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: 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

Record Last Update: 20250525T032915+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 FDI Lab - SciCrunch.org.

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 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.