

Resource Summary Report

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Cornell University BRC Bioinformatics Core Facility

RRID:SCR_021757

Type: Tool

Proper Citation

Cornell University BRC Bioinformatics Core Facility (RRID:SCR_021757)

Resource Information

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

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Description: Facility provides access to high performance computing environment, BioHPC, which includes both hosted hardware and shared machines. Provides consulting and collaborations for Bioinformatics analysis and workflows.

Synonyms: BRC Bioinformatics Facility

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

Keywords: USEDit, ABRF, bioinformatics, analysis, workflows

Resource Name: Cornell University BRC Bioinformatics Core Facility

Resource ID: SCR_021757

Alternate IDs: ABRF_109

Alternate URLs: <https://coremarketplace.org/?FacilityID=109>

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260905T133422+0000

Ratings and Alerts

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

No alerts have been found for Cornell University BRC Bioinformatics 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 [PRECISE-TBI](#) .

Hale CO, et al. (2026) Widespread turnover of a conserved cis-regulatory code across 589 grass species. *Molecular biology and evolution*, 43(1).

Reyes-Chavez B, et al. (2026) Carbohydrate utilization regulator reveals a noncanonical mechanism of nutrient differentiation. *bioRxiv : the preprint server for biology*.

Bai CK, et al. (2026) H3K9me3 controls epidermis morphogenesis by regulating RNA Pol II dynamics at developmental promoters and enhancers. *Nature communications*, 17(1).

Liu ZY, et al. (2025) GeneCAD: Plant Genome Annotation with a DNA Foundation Model. *bioRxiv : the preprint server for biology*.

West JD, et al. (2025) The quantitative impact of 3'UTRs on gene expression. *Nucleic acids research*, 53(12).

Oren E, et al. (2025) Grass Rhizome Proteomics Reveals Convergent Freezing-Tolerance Strategies. *bioRxiv : the preprint server for biology*.

Thomas GWC, et al. (2025) The Genomic Landscape, Causes, and Consequences of Extensive Phylogenomic Discordance in Murine Rodents. *Genome biology and evolution*, 17(2).

Stitzer MC, et al. (2025) Extensive genome evolution distinguishes maize within a stable tribe of grasses. *bioRxiv : the preprint server for biology*.

Hsu CH, et al. (2025) Therapy-Induced ECM Remodeling Creates a Transient Immune Barrier in Residual Melanoma. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, e08451.

Villwock SS, et al. (2025) Mediated pleiotropy drives the negative correlation of total carotenoid and dry matter contents in cassava (*Manihot esculenta*). *Genetics*, 231(2).

Gage JL, et al. (2024) Maize inbreds show allelic variation for diel transcription patterns. *bioRxiv : the preprint server for biology*.

An L, et al. (2024) Sexual dimorphism in melanocyte stem cell behavior reveals combinational therapeutic strategies for cutaneous repigmentation. *Nature communications*, 15(1), 796.

Wu Y, et al. (2023) Discovering dynamic plant enzyme complexes in yeast for novel alkaloid pathway identification from a medicinal plant kratom. *bioRxiv : the preprint server*

for biology.

An L, et al. (2023) Sexual dimorphism in melanocyte stem cell behavior reveals combinational therapeutic strategies for cutaneous repigmentation. *bioRxiv : the preprint server for biology*.

Loyola Irizarry HG, et al. (2023) Characterizing conjugative plasmids from an antibiotic-resistant dataset for use as broad-host delivery vectors. *Frontiers in microbiology*, 14, 1199640.

Thomas GWC, et al. (2023) The genomic landscape, causes, and consequences of extensive phylogenomic discordance in Old World mice and rats. *bioRxiv : the preprint server for biology*.

Wu Y, et al. (2023) Discovering Dynamic Plant Enzyme Complexes in Yeast for Kratom Alkaloid Pathway Identification. *Angewandte Chemie (International ed. in English)*, 62(38), e202307995.