

Resource Summary Report

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Cornell University BRC Genomics Core Facility

RRID:SCR_021727

Type: Tool

Proper Citation

Cornell University BRC Genomics Core Facility (RRID:SCR_021727)

Resource Information

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

Proper Citation: Cornell University BRC Genomics Core Facility (RRID:SCR_021727)

Description: Full Service DNA Sequencing and Genotyping facility. Offers Sanger, Fragment Analysis, Illumina, RT and Digital PCR, Single Cell, large projects, sample/library prep and QC. Houses state of the art instruments for all your sequencing needs including, capillary DNA analysis, single cell applications, long read capabilities. We also provide many instruments that can be operated by you for sample preparation and quality control of all sample types.

Synonyms: Cornell University BRC Genomics Facility, BRC Genomics Facility

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

Keywords: USEEdit, ABRF, DNA Sequencing, Genotyping, capillary DNA analysis, single cell applications, long read capabilities

Availability: open

Resource Name: Cornell University BRC Genomics Core Facility

Resource ID: SCR_021727

Alternate IDs: ABRF_74

Alternate URLs: <https://coremarketplace.org/?FacilityID=74>,
<http://www.biotech.cornell.edu>

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 Genomics Core Facility.

No alerts have been found for Cornell University BRC Genomics Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 105 mentions in open access literature.

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

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

Garabello E, et al. (2026) Tunable low-rate genomic recombination with Cre-lox in *Escherichia coli*: a versatile tool for anoxic environmental biosensing and synthetic biology. *Applied and environmental microbiology*, 92(4), e0176825.

Wyer CAS, et al. (2026) Transcriptional response of spermathecal secretory cells to mating and receipt of seminal fluid proteins in *Aedes aegypti*. *iScience*, 29(6), 116301.

Powers ZM, et al. (2026) *Salmonella Typhi* asparaginase-dependent activation of GCN2 promotes bacterial killing in murine macrophages. *bioRxiv : the preprint server for biology*.

Odell J, et al. (2026) Antagonistic contributions of A-type and B-type lamins to LBR localization and dynamics. *Nucleus (Austin, Tex.)*, 17(1), 2673721.

Elpers MA, et al. (2026) Polarization increases nuclear stiffness in macrophages despite reduction in lamin A/C levels. *npj biological physics and mechanics*, 3(1), 8.

Odell J, et al. (2026) Antagonistic contributions of A-type and B-type lamins to LBR localization and dynamics. *bioRxiv : the preprint server for biology*.

Wang KT, et al. (2026) RoboA reinforces planarian stem cell fate through FoxA and Anosmin1a. *Nature communications*, 17(1).

El Kamali L, et al. (2026) Comprehensive investigation of SARS-CoV-2 intestinal pathogenesis in *Drosophila*. *iScience*, 29(5), 115621.

Bakhle K, et al. (2026) Epithelial-mesenchymal plasticity and immunosuppression in canine carcinomas reveals cross-species upregulation of CD109. *Communications biology*, 9(1).

Odell J, et al. (2026) A-type lamins anchor emerin at the inner nuclear membrane via two independent binding sites. *The Journal of biological chemistry*, 302(3), 111192.

Shohat H, et al. (2026) A neofunctionalized flowering antagonist created an evolutionary contingency that channeled Solanaceae adaptation. *bioRxiv : the preprint server for biology*.

Tabilas C, et al. (2026) Single-cell gene expression and TCR profiling reveal age-related differences in recent thymic emigrants. *iScience*, 29(5), 115582.

Pieples LA, et al. (2026) Identification of an F13A1 frameshift variant associated with factor XIII deficiency in a Coonhound dog with severe coagulopathy. *Journal of veterinary internal medicine*, 40(3).

Pendleton A, et al. (2026) Upwelling periodically disturbs the ecological assembly of microbial communities in Lake Ontario. *ISME communications*, 6(1), ycag023.

Carro MLM, et al. (2026) Argonaute proteins orchestrate Meiotic Sex Chromosome Inactivation and timing of the spermatogenic transcriptional program. *PLoS genetics*, 22(6), e1012217.

Powers ZM, et al. (2026) Salmonella Typhi asparaginase-dependent activation of GCN2 promotes bacterial killing in murine macrophages. *Infection and immunity*, 94(7), e0017826.

Walsky T, et al. (2026) Commercial washing and storage over shelf life impact bacterial communities more than the fungal communities on baby spinach. *Microbiology spectrum*, 14(7), e0400725.

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

Akopyan M, et al. (2026) Multiple chromosomal inversions modulate continuous local adaptation along a steep thermal cline. *Science (New York, N.Y.)*, 391(6789), 1015.