

Resource Summary Report

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Cornell University Biotechnology Resource Center Transcriptional Regulation and Expression Core Facility

RRID:SCR_022532

Type: Tool

Proper Citation

Cornell University Biotechnology Resource Center Transcriptional Regulation and Expression Core Facility (RRID:SCR_022532)

Resource Information

URL: <https://www.biotech.cornell.edu/core-facilities-brc/facilities/transcriptional-regulation-expression-facility-trex>

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Description: Facility offers genomics profiling services including RNAseq, small RNA sequencing, and ATACseq.

Abbreviations: TREx

Synonyms: Transcriptional Regulation and Expression Facility, BRC Transcriptional Regulation and Expression Facility

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

Keywords: USEEdit, ABRF, genomics profiling services, RNAseq, small RNA sequencing, ATACseq

Resource Name: Cornell University Biotechnology Resource Center Transcriptional Regulation and Expression Core Facility

Resource ID: SCR_022532

Alternate IDs: ABRF_1471

Alternate URLs: <https://coremarketplace.org/?FacilityID=1471&citation=1>

Record Creation Time: 20220702T050148+0000

Ratings and Alerts

No rating or validation information has been found for Cornell University Biotechnology Resource Center Transcriptional Regulation and Expression Core Facility.

No alerts have been found for Cornell University Biotechnology Resource Center Transcriptional Regulation and Expression Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Ramsaran LN, et al. (2026) Investigation of gene stability in equine luteal tissue during mid-diestrus phase and early pregnancy - Research Article. BMC veterinary research.

Yu YT, et al. (2025) Genome sequence of Equine Erythrovirus 1, identified in the United States. Microbiology resource announcements, 14(3), e0089724.

Patel Y, et al. (2025) A mutation in RNA polymerase imparts resistance to β -lactams by preventing dysregulation of amino acid and nucleotide metabolism. Cell reports, 44(2), 115268.

Murrell CM, et al. (2025) TITAN-RNA: A hybrid-capture sequencing panel detects known and unknown Flaviviridae for diagnostics and vector surveillance. bioRxiv : the preprint server for biology.

Reboul G, et al. (2025) Analysis of the microbiota of raw commercial feline diets to prioritize food safety investigations. Communications biology, 8(1), 1349.

Zhu H, et al. (2025) An efficient framework to decipher microRNA regulatory programs applied to T cells. Genes and immunity.

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

Ganapathi Sankaran D, et al. (2025) Gene-regulatory programs that specify age-related differences during thymocyte development. Cell reports, 44(7), 115903.

Iu DS, et al. (2024) Transcriptional reprogramming primes CD8⁺ T cells toward exhaustion in Myalgic encephalomyelitis/chronic fatigue syndrome. Proceedings of the National Academy of Sciences of the United States of America, 121(50), e2415119121.

Watson NB, et al. (2024) The gene regulatory basis of bystander activation in CD8+ T cells. *Science immunology*, 9(92), eadf8776.

Olarte-Castillo XA, et al. (2023) Detection and characterization of novel luchacoviruses, genus Alphacoronavirus, shed in saliva and feces of meso-carnivores in the northeastern United States. *bioRxiv : the preprint server for biology*.

Olarte-Castillo XA, et al. (2023) Detection and characterization of novel luchacoviruses, genus Alphacoronavirus, in saliva and feces of meso-carnivores in the northeastern United States. *Journal of virology*, 97(11), e0082923.

Sosnicki DM, et al. (2023) Segmental differentiation of the murine epididymis: identification of segment-specific, GM1-enriched vesicles and regulation by luminal fluid factors†. *Biology of reproduction*, 109(6), 864.