

Resource Summary Report

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Rockefeller University Genomics Resource Center Core Facility

RRID:SCR_020986

Type: Tool

Proper Citation

Rockefeller University Genomics Resource Center Core Facility (RRID:SCR_020986)

Resource Information

URL: <http://www.rockefeller.edu/genomics/>

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Description: Core offers services and instruments to support genomics research. Houses Illumina NovaSeq, NextSeq, MiSeq sequencers, 10X Genomics Chromium Single Cell System, and Life Technologies QuantStudio 12K flex realtime PCR system. Provides several accessory instruments for sample quantity and quality validation: Agilent Bioanalyzer, Agilent TapeStation, NanoDrop spectrophotometer, and Qubit spectrophotometer. Offers full services for genomic DNA-Seq and RNA-Seq, specializing in preparation of libraries from very small amount of starting total RNA. Users can also prepare their own libraries and use the center's sequencing-only services. Offers free consultations on experimental designs, library preparation options, sequencer choice, sequencing depth and coverage, and biological replicates. Performs initial sequencing data analysis for all users, and can assist with downstream analysis.

Synonyms: Genomics Resource Center

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

Keywords: USEdit, ABRF

Resource Name: Rockefeller University Genomics Resource Center Core Facility

Resource ID: SCR_020986

Alternate IDs: ABRF_430

Alternate URLs: <https://coremarketplace.org/?FacilityID=430>

Record Creation Time: 20220129T080353+0000

Ratings and Alerts

No rating or validation information has been found for Rockefeller University Genomics Resource Center Core Facility.

No alerts have been found for Rockefeller University Genomics Resource Center Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Yatim A, et al. (2026) Human LFA-1 governs T cell immune surveillance of the skin. *Science immunology*, 11(116), eadz8360.

Obado SO, et al. (2026) Division of labor in trypanosome RNA processing and export through expanded Mex67 paralogs. *Nucleic acids research*, 54(1).

Patriotis AL, et al. (2026) The conserved N-terminal SANT1-binding domain (SBD) of EZH2 regulates PRC2 activity. *Genes & development*, 40(9-10), 650.

Liu S, et al. (2026) Radial-glia-to-astrocyte trans-differentiation and astrocyte transcriptional convergence are coordinated by CEH-43/DLX in *C. elegans*. *bioRxiv : the preprint server for biology*.

Yeung JL, et al. (2026) CDK4/6 inhibition induces a senescence-associated secretory phenotype via delayed NF- κ B activation. *Life science alliance*, 9(9).

Lee U, et al. (2025) Comparative single-cell analysis of transcriptional bursting reveals the role of genome organization in de novo transcript origination. *Proceedings of the National Academy of Sciences of the United States of America*, 122(18), e2425618122.

Chapa CM, et al. (2025) RNA-Seq dataset of wild type and PRC2 mutant mouse embryonic stem cells undergoing ground state conversion. *Data in brief*, 62, 111957.

Lee U, et al. (2024) Comparative single cell analysis of transcriptional bursting reveals the role of genome organization on de novo transcript origination. *bioRxiv : the preprint server for biology*.

Cross FR, et al. (2023) Expanding and improving nanobody repertoires using a yeast display method: Targeting SARS-CoV-2. *The Journal of biological chemistry*, 299(3), 102954.

Biegler MT, et al. (2022) Induction of an immortalized songbird cell line allows for gene characterization and knockout by CRISPR-Cas9. *Scientific reports*, 12(1), 4369.