

Resource Summary Report

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University of Minnesota Genomics Center Core Facility

RRID:SCR_012413

Type: Tool

Proper Citation

University of Minnesota Genomics Center Core Facility (RRID:SCR_012413)

Resource Information

URL: <https://genomics.umn.edu/>

Proper Citation: University of Minnesota Genomics Center Core Facility (RRID:SCR_012413)

Description: Provides genomic technologies and services to researchers and clinicians. Services include Next Generation Sequencing, Epigenomics, SARS-CoV-2 services, GBS, Third Generation Sequencing, NGS Library Creation, Sanger Sequencing, DNA and RNA Extraction, Gene Expression.

Abbreviations: UMGC

Synonyms: University of Minnesota Genomics Center, U of M Genomics Center, University of Minnesota Biomedical Genomics Center

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

Keywords: genomic technologies, Next Generation Sequencing, Epigenomics, SARS-CoV-2 services, GBS, Third Generation Sequencing, NGS Library Creation, Sanger Sequencing, DNA and RNA Extraction, Gene Expression

Availability: Open

Resource Name: University of Minnesota Genomics Center Core Facility

Resource ID: SCR_012413

Alternate IDs: SciEx_13150

Old URLs: <http://www.scienceexchange.com/facilities/biomedical-genomics-center>

Record Creation Time: 20220129T080310+0000

Ratings and Alerts

No rating or validation information has been found for University of Minnesota Genomics Center Core Facility.

No alerts have been found for University of Minnesota Genomics Center Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 80 mentions in open access literature.

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

Block AM, et al. (2026) The Mycobacterium tuberculosis ESX-5 secretion system enables carbon source utilization and growth in mice. *mBio*, 17(3), e0350025.

Kuhs MA, et al. (2026) Subinhibitory concentrations of antibiotics mediate primary metabolism and shape diverse species interactions among coevolved soil *Streptomyces*. *The ISME journal*, 20(1).

Urban-Olivares J, et al. (2026) The Copepoda mitogenome as a dynamic evolutionary landscape. *PloS one*, 21(6), e0350115.

Anderson SD, et al. (2026) Epigenetic biomarkers of mortality risk in mice under chronic social stress. *GeroScience*, 48(1), 1127.

Ontoy J, et al. (2026) Characterization of resistance to bacterial panicle blight in rice revealed by transcriptome and QTL mapping analyses. *Frontiers in plant science*, 17, 1857873.

Spike CA, et al. (2026) The SPN-4 Rbfox RNA-binding protein selects maternal mRNAs for CCR4-NOT-dependent clearance in early *Caenorhabditis elegans* embryos. *Development (Cambridge, England)*, 153(11).

Lou E, et al. (2025) SARS-CoV-2 infection drives local inflammation of the intestinal epithelium in immunocompromised patients with cancer. *iScience*, 28(9), 113438.

Etterson JR, et al. (2025) Domestication During Restoration: Unintentional Selection During Eight Generations of Wild Seed Propagation Reduces Herkogamy, Dichogamy and Heterozygosity in *Clarkia pulchella*. *Molecular ecology*, 34(24), e17655.

Ferretti P, et al. (2025) Assembly of the infant gut microbiome and resistome are linked to bacterial strains in mother's milk. *Nature communications*, 16(1), 11536.

Arias RS, et al. (2025) Characterizing phenotype variants of *Cercosporidium personatum*, causal agent of peanut late leaf spot disease, their morphology, genetics and metabolites. *Scientific reports*, 15(1), 1405.

Barb JJ, et al. (2025) Associations between sleep and the gut microbiome in adults with colorectal cancer and their caregivers. *Scientific reports*, 15(1), 32624.

Spike CA, et al. (2025) The SPN-4 Rbfox RNA-binding protein selects maternal mRNAs for CCR4-NOT-dependent clearance in early *Caenorhabditis elegans* embryos. *bioRxiv* : the preprint server for biology.

Islam R, et al. (2025) Macrophage Lyn Kinase Is a Sex-Specific Regulator of Post-Subarachnoid Hemorrhage Neuroinflammation. *Journal of the American Heart Association*, 14(9), e039409.

Blanco Mendana J, et al. (2025) Deterministic genetic barcoding for multiplexed behavioral and single-cell transcriptomic studies. *eLife*, 12.

Lembke HK, et al. (2025) Evaluating the Link between Efflux Pump Expression and Motility Phenotypes in *Pseudomonas aeruginosa* Treated with Virulence Inhibitors. *ACS infectious diseases*, 11(8), 2080.

Joyce LR, et al. (2025) Global genome analysis identifies glycolipids and lipoteichoic acid alanylation as contributors to group B streptococcal diabetic wound infection. *Cell reports*, 44(11), 116510.

Johnson KE, et al. (2024) Human cytomegalovirus in breast milk is associated with milk composition and the infant gut microbiome and growth. *Nature communications*, 15(1), 6216.

Gasca-Pineda J, et al. (2024) Conservation genomics of the wild pumpkin *Cucurbita radicans* in Central Mexico: The influence of a changing environment on the genetic diversity and differentiation of a rare species. *Journal of plant research*, 137(5), 799.

Paulson AL, et al. (2024) Discovery, Validation and Mechanistic Study of XPO1 Inhibition in the Treatment of Triple-Negative Breast Cancer. *Cancers*, 16(23).

Haeberle A, et al. (2024) Genotypic and phenotypic characterization of *Enterococcus faecalis* isolates from periprosthetic joint infections. *bioRxiv* : the preprint server for biology.