Resource Summary Report

Generated by NIF on Apr 18, 2025

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, service resource, core facility

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

Funding:

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

Record Last Update: 20250418T055314+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 61 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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.

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

Snell A, et al. (2024) Arginine impacts aggregation, biofilm formation, and antibiotic susceptibility in Enterococcus faecalis. bioRxiv : the preprint server for biology.

Haeberle AL, et al. (2024) Genotypic and phenotypic characterization of Enterococcus faecalis isolates from periprosthetic joint infections. Microbiology spectrum, 12(8), e0056524.

Snell AP, et al. (2024) Arginine impacts aggregation, biofilm formation, and antibiotic susceptibility in Enterococcus faecalis. FEMS microbes, 5, xtae030.

Allert M, et al. (2024) Assembly, stability, and dynamics of the infant gut microbiome are linked to bacterial strains and functions in mother's milk. bioRxiv : the preprint server for biology.

Alegria AD, et al. (2024) High-throughput genetic manipulation of multicellular organisms using a machine-vision guided embryonic microinjection robot. Genetics, 226(4).

Jones I, et al. (2024) Isolation, characterization, and genetic manipulation of cold-tolerant, manganese-oxidizing Pseudomonas sp. strains. Applied and environmental microbiology, 90(9), e0051024.

Johnson KE, et al. (2024) Human milk variation is shaped by maternal genetics and impacts the infant gut microbiome. Cell genomics, 4(10), 100638.

Kim SJ, et al. (2024) Spatially resolved gene expression profiles of fibrosing interstitial lung diseases. Scientific reports, 14(1), 26470.

Lee A, et al. (2024) Serotonin Transporter (SLC6A4) and FK506-Binding Protein 5 (FKBP5) Genotype and Methylation Relationships with Response to Meditation in Veterans with PTSD. Molecular neurobiology, 61(11), 9608.

Block AM, et al. (2024) Transposon sequencing reveals metabolic pathways essential for Mycobacterium tuberculosis infection. PLoS pathogens, 20(3), e1011663.

Gómez Quijano MJ, et al. (2024) Genetic differentiation across a steep and narrow environmental gradient: Quantitative genetic and genomic insights into Lake Superior populations of Quercus rubra. Molecular ecology, 33(17), e17483.

Kaur N, et al. (2024) Insights into the genetic architecture of Phytophthora capsici root rot resistance in chile pepper (Capsicum spp.) from multi-locus genome-wide association study. BMC plant biology, 24(1), 416.

Castell-Miller CV, et al. (2024) Interactive transcriptome analyses of Northern Wild Rice (Zizania palustris L.) and Bipolaris oryzae show convoluted communications during the early stages of fungal brown spot development. Frontiers in plant science, 15, 1350281.

Johnson KE, et al. (2023) Human Cytomegalovirus in breast milk is associated with milk composition, the infant gut microbiome, and infant growth. bioRxiv : the preprint server for biology.

Razzoli M, et al. (2023) Contextual modifiers of healthspan, lifespan, and epigenome in mice under chronic social stress. Proceedings of the National Academy of Sciences of the United

States of America, 120(16), e2211755120.

Smoniewski CM, et al. (2023) Circular mitochondrial-encoded mRNAs are a distinct subpopulation of mitochondrial mRNA in Trypanosoma brucei. Scientific reports, 13(1), 7825.