

Resource Summary Report

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Wisconsin University Great Lakes Genomics Center Core Facility

RRID:SCR_017838

Type: Tool

Proper Citation

Wisconsin University Great Lakes Genomics Center Core Facility (RRID:SCR_017838)

Resource Information

URL: <http://www.greatlakesgenomics.uwm.edu>

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Description: Core provides services which include massively parallel sequencing on Illumina MiSeq, traditional Sanger sequencing, fragment analysis, quantitative PCR, nucleic acid extractions and QC, and digital PCR. Offers various level of service for Sanger sequencing and qPCR from full service to ready to load plates. Trains researchers in laboratory techniques and provide protocols. Each MiSeq sequencing project and qPCR project is unique and specifically designed so experimental design should be discussed before collecting samples.

Synonyms: Great Lakes Genomics Center

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

Keywords: Sequencing, Illumina, Sanger, fragment, analysis, quantitative, nucleic, acid, extraction, PCR, qPCR, MiSeq, service, core, ABRF

Availability: Open

Resource Name: Wisconsin University Great Lakes Genomics Center Core Facility

Resource ID: SCR_017838

Alternate IDs: ABRF_623

Record Creation Time: 20220129T080337+0000

Record Last Update: 20260804T043646+0000

Ratings and Alerts

No rating or validation information has been found for Wisconsin University Great Lakes Genomics Center Core Facility.

No alerts have been found for Wisconsin University Great Lakes Genomics Center Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Schussman MK, et al. (2026) Environmental reservoirs account for high levels of carbapenem resistance genes in wastewater. *Microbiology spectrum*, e0173725.

Dey R, et al. (2025) Quorum sensing regulators and non-ribosomal peptide synthetases govern antibacterial secretions in *Xenorhabdus szentirmaii*. *Frontiers in microbiology*, 16, 1560663.

Burmeister AR, et al. (2024) A tradeoff between bacteriophage resistance and bacterial motility is mediated by the Rcs phosphorelay in *Escherichia coli*. *Microbiology (Reading, England)*, 170(8).

Schumann PG, et al. (2022) RNA-seq reveals potential gene biomarkers in fathead minnows (*Pimephales promelas*) for exposure to treated wastewater effluent. *Environmental science. Processes & impacts*, 24(10), 1708.

LaMartina EL, et al. (2022) Full-Length 16S rRNA Gene Sequences from Raw Sewage Samples Spanning Geographic and Seasonal Gradients in Conveyance Systems across the United States. *Microbiology resource announcements*, 11(7), e0031922.

Euclide PT, et al. (2022) A new GTSeq resource to facilitate multijurisdictional research and management of walleye *Sander vitreus*. *Ecology and evolution*, 12(12), e9591.

Fasola TR, et al. (2016) Antidiabetic and antioxidant effects of *Croton lobatus* L. in alloxan-induced diabetic rats. *Journal of intercultural ethnopharmacology*, 5(4), 364.