

# 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:** access service resource, core facility, service resource

**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:** 20260904T000741+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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 8 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

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

Rg C, et al. (2026) A Practical Framework for GT-Seq Panel Optimization. *Molecular ecology resources*, 26(5), e70169.

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).

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.

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.

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.