

Resource Summary Report

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Georgia Genomics and Bioinformatics Core at the University of Georgia

RRID:SCR_010994

Type: Tool

Proper Citation

Georgia Genomics and Bioinformatics Core at the University of Georgia
(RRID:SCR_010994)

Resource Information

URL: <https://dna.uga.edu/>

Proper Citation: Georgia Genomics and Bioinformatics Core at the University of Georgia
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Description: Core laboratory for nucleic acid sequencing and bioinformatics. Used for research support, education, and training. Services include genomic techniques and applications, sequencing technologies, and bioinformatics analyses, writing letters of support for grant applications submitted to funding agencies. GGBC operates multiple platforms for short-, long-, and single-molecule sequencing reads (i.e., Illumina MiSeq and NextSeq, PacBio Sequel, and Oxford Nanopore MinIon).

Abbreviations: GGBC

Synonyms: Georgia Genomics & Bioinformatics Core, Georgia Genomics and Bioinformatics Core at UGA, University of Georgia Genomics Facility, Georgia Genomics and Bioinformatics Core

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

Keywords: nucleic, acid, sequencing, labs, analysis, equipment, genomic, technique, analysis, grant, application

Resource Name: Georgia Genomics and Bioinformatics Core at the University of Georgia

Resource ID: SCR_010994

Alternate IDs: SciEx_9234

Old URLs: <http://www.scienceexchange.com/facilities/georgia-genomics-facility-uga>,
<http://www.scienceexchange.com/facilities/georgia-genomics-facility-uga>

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Ratings and Alerts

No rating or validation information has been found for Georgia Genomics and Bioinformatics Core at the University of Georgia.

No alerts have been found for Georgia Genomics and Bioinformatics Core at the University of Georgia.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 71 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Kim JY, et al. (2025) Stress-induced changes in endogenous TP53 mRNA 5' regulatory region. The Journal of biological chemistry, 301(4), 108418.

Tuma TT, et al. (2025) Tonoplast sucrose transporter SUT4-dependent sugar partitioning modulates phenological transitions and reproductive success in poplar. The Plant journal : for cell and molecular biology, 124(4), e70554.

Deguchi M, et al. (2025) A compendium of nonredundant short polymerase III promoters for CRISPR applications. Plant physiology, 198(3).

Chen J, et al. (2025) Horizontal Transfer and Recombination Fuel Ty4 Retrotransposon Evolution in Saccharomyces. Genome biology and evolution, 17(1).

Li C, et al. (2025) Cell-type-aware regulatory landscapes governing monoterpene indole alkaloid biosynthesis in the medicinal plant Catharanthus roseus. The New phytologist, 245(1), 347.

Mars Brisbin M, et al. (2025) Exploring the Phaeosphere: Characterizing the microbiomes of Phaeocystis antarctica colonies from the coastal Southern Ocean and laboratory culture. Journal of phycology.

De Santiago A, et al. (2025) Pseudoalteromonas is a novel symbiont of marine invertebrates that exhibits broad patterns of phyllosymbiosis. bioRxiv : the preprint server for biology.

Wuthrich KL, et al. (2025) Beating the heat: a lowland tropical lizard expresses heat shock protein networks in response to acute thermal stress. Integrative and comparative biology.

Hannon-Hatfield JA, et al. (2024) Evolution of a Restriction Factor by Domestication of a Yeast Retrotransposon. Molecular biology and evolution, 41(3).

Ridley RS, et al. (2024) Potential routes of plastics biotransformation involving novel plastizymes revealed by global multi-omic analysis of plastic associated microbes. Scientific reports, 14(1), 8798.

Gupta A, et al. (2024) OpenCell: A low-cost, open-source, 3-in-1 device for DNA extraction. PloS one, 19(5), e0298857.

Ousset MJ, et al. (2024) Improved SARS-CoV-2 RNA recovery in wastewater matrices using a CTAB-based extraction method. Journal of virological methods, 327, 114918.

Muyanl? EB, et al. (2024) RT-qPCR based quantitative analysis of ARO and ADH genes in *Saccharomyces cerevisiae* and *Metschnikowia pulcherrima* strains growth white grape juice. Molecular biology reports, 51(1), 547.

Nevone A, et al. (2024) SmaRT M-Seq: an optimized step-by-step protocol for M protein sequencing in monoclonal gammopathies. Biology methods & protocols, 9(1), bpa074.

Chen J, et al. (2023) Horizontal transfer and recombination fuel Ty4 retrotransposon evolution in *Saccharomyces*. bioRxiv : the preprint server for biology.

Hartline DK, et al. (2023) De novo transcriptomes of six calanoid copepods (Crustacea): a resource for the discovery of novel genes. Scientific data, 10(1), 242.

Cohen O, et al. (2023) Effect of sulfadoxine-pyrimethamine chemoprophylaxis in pregnant women on selection of the new *P. falciparum* dhps quintuple mutant carrying the I431V mutation. The Journal of antimicrobial chemotherapy, 78(3), 665.

Gurung RL, et al. (2023) A Guide to Genome-Wide Association Study Design for Diabetic Retinopathy. Methods in molecular biology (Clifton, N.J.), 2678, 49.

Ruybal-Pesántez S, et al. (2023) Molecular epidemiology of continued *Plasmodium falciparum* disease transmission after an outbreak in Ecuador. Frontiers in tropical diseases, 4.

Barnhart MH, et al. (2022) Transcriptomics of developing wild sunflower seeds from the extreme ends of a latitudinal gradient differing in seed oil composition. Plant direct, 6(7), e423.