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 (RRID:SCR_010994)

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, writting 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

Funding:

Availability: Restricted

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 64 mentions in open access literature.

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

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.

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), bpae074.

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.

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.

Roncalli V, et al. (2022) Physiological acclimatization in high-latitude zooplankton. Molecular ecology, 31(6), 1753.

Barnhart MH, et al. (2022) Phenotypic and transcriptomic responses of cultivated sunflower seedlings (Helianthus annuus L.) to four abiotic stresses. PloS one, 17(9), e0275462.

Seidel DS, et al. (2022) Impact of concentrations of camphor on the in vitro mixed ruminal microorganism fermentation from goats selected for consumption of low and high levels of Juniperus spp.-2. Translational animal science, 6(3), txac098.

Welch CB, et al. (2021) Evaluation of the Fecal Bacterial Communities of Angus Steers With Divergent Feed Efficiencies Across the Lifespan From Weaning to Slaughter. Frontiers in veterinary science, 8, 597405.

Naimi S, et al. (2021) Direct impact of commonly used dietary emulsifiers on human gut microbiota. Microbiome, 9(1), 66.

Roncalli V, et al. (2021) Post-diapause transcriptomic restarts: insight from a high-latitude copepod. BMC genomics, 22(1), 409.

Chalopin D, et al. (2021) Integrated Genomic Analyses From Low-Depth Sequencing Help Resolve Phylogenetic Incongruence in the Bamboos (Poaceae: Bambusoideae). Frontiers in plant science, 12, 725728.