

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 12, 2026

GENOME

RRID:SCR_008949

Type: Tool

Proper Citation

GENOME (RRID:SCR_008949)

Resource Information

URL: <http://www.sph.umich.edu/csg/liang/genome/>

Proper Citation: GENOME (RRID:SCR_008949)

Description: Software application to simulate sequences drawn from a population under the Wright-Fisher neutral model. The purpose of this program is to simulate sequences on the whole genome scale within practical time. (entry from Genetic Analysis Software)

Abbreviations: GENOME

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, c++, unix, solaris, linux, ms-windows

Resource Name: GENOME

Resource ID: SCR_008949

Alternate IDs: nlx_154347

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260912T200238+0000

Ratings and Alerts

No rating or validation information has been found for GENOME.

No alerts have been found for GENOME.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 63 mentions in open access literature.

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

Hang H, et al. (2025) SP1-Mediated Glycolytic Reprogramming Promotes Tumorigenesis and Progression in Pancreatic Cancer. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), e10071.

Ahrend F, et al. (2025) Protocol for assembling, prioritizing, and characterizing piRNA clusters using the piRNA Cluster Builder. *STAR protocols*, 6(2), 103759.

McNair K, et al. (2024) PRFect: a tool to predict programmed ribosomal frameshifts in prokaryotic and viral genomes. *BMC bioinformatics*, 25(1), 82.

Takasaki A, et al. (2024) Gesture imitation performance in community-dwelling older people: assessment of a gesture imitation task in the screening and diagnosis of mild cognitive impairment and dementia. *Psychogeriatrics : the official journal of the Japanese Psychogeriatric Society*, 24(2), 404.

Mulet I, et al. (2024) TET3 regulates terminal cell differentiation at the metabolic level. *Nature communications*, 15(1), 9749.

Hamazaki K, et al. (2024) AI-assisted selection of mating pairs through simulation-based optimized progeny allocation strategies in plant breeding. *Frontiers in plant science*, 15, 1361894.

Fujino T, et al. (2024) A chromosome-level genome assembly of a model conifer plant, the Japanese cedar, *Cryptomeria japonica* D. Don. *BMC genomics*, 25(1), 1039.

Hu M, et al. (2024) Identification of genomic diversity and selection signatures in Luxi cattle using whole-genome sequencing data. *Animal bioscience*, 37(3), 461.

Zhang Y, et al. (2024) Sbn1 mediates cell-cell communication between neural stem cells and microglia through small extracellular vesicles. *Cell & bioscience*, 14(1), 125.

Jiang L, et al. (2023) Genome insights into the plant growth-promoting bacterium *Saccharibacillus brassicae* ATSA2T. *AMB Express*, 13(1), 9.

Zhong Y, et al. (2023) RBFOX1 and Working Memory: From Genome to Transcriptome Revealed Posttranscriptional Mechanism Separate From Attention-Deficit/Hyperactivity Disorder. *Biological psychiatry global open science*, 3(4), 1042.

Zhao K, et al. (2022) Hemgn Protects Hematopoietic Stem and Progenitor Cells Against Transplantation Stress Through Negatively Regulating IFN- γ Signaling. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 9(5), e2103838.

Goyal A, et al. (2022) Horizontal gene transfer drives the evolution of dependencies in bacteria. *iScience*, 25(5), 104312.

Yang Z, et al. (2022) Degree of Freedom of Gene Expression in *Saccharomyces cerevisiae*. *Microbiology spectrum*, 10(2), e0083821.

Burke CG, et al. (2021) DNA Methylation Patterns in CD4⁺ T Cells of Naïve and Influenza A Virus-Infected Mice Developmentally Exposed to an Aryl Hydrocarbon Receptor Ligand. *Environmental health perspectives*, 129(1), 17007.

Kozmin SG, et al. (2021) Dissecting Highly Mutagenic Processing of Complex Clustered DNA Damage in Yeast *Saccharomyces cerevisiae*. *Cells*, 10(9).

Pereira LM, et al. (2020) In-depth transcriptome reveals the potential biotechnological application of *Bothrops jararaca* venom gland. *The journal of venomous animals and toxins including tropical diseases*, 26, e20190058.

Bhati M, et al. (2020) Assessing genomic diversity and signatures of selection in Original Braunvieh cattle using whole-genome sequencing data. *BMC genomics*, 21(1), 27.

Nishimura T, et al. (2020) A proteogenomic profile of early lung adenocarcinomas by protein co-expression network and genomic alteration analysis. *Scientific reports*, 10(1), 13604.

Fan X, et al. (2020) Single-base methylome profiling of the giant kelp *Saccharina japonica* reveals significant differences in DNA methylation to microalgae and plants. *The New phytologist*, 225(1), 234.