Resource Summary Report

Generated by dkNET on Apr 16, 2025

GENOME

RRID:SCR_008949
Type: Tool

Proper Citation

GENOME (RRID:SCR_008949)

Resource Information

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

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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 resource, software application

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

Funding:

Resource Name: GENOME

Resource ID: SCR_008949

Alternate IDs: nlx_154347

Record Creation Time: 20220129T080250+0000

Record Last Update: 20250416T063534+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 61 mentions in open access literature.

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

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) Sbno1 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-? 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.

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.

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.

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.

Nojiri Y, et al. (2020) Dissimilatory Nitrate Reduction to Ammonium and Responsible Microbes in Japanese Rice Paddy Soil. Microbes and environments, 35(4).

Lechuga-Vieco AV, et al. (2020) Cell identity and nucleo-mitochondrial genetic context modulate OXPHOS performance and determine somatic heteroplasmy dynamics. Science advances, 6(31), eaba5345.