

Resource Summary Report

Generated by [NIF](#) on Aug 30, 2026

DWGSIM

RRID:SCR_002342

Type: Tool

Proper Citation

DWGSIM (RRID:SCR_002342)

Resource Information

URL: <https://github.com/nh13/DWGSIM>

Proper Citation: DWGSIM (RRID:SCR_002342)

Description: Whole Genome Simulator for Next-Generation Sequencing.

Abbreviations: DWGSIM

Resource Type: software resource

Keywords: next-generation sequencing, whole genome simulation

Availability: GNU General Public License, v2

Resource Name: DWGSIM

Resource ID: SCR_002342

Alternate IDs: OMICS_00249

Alternate URLs: <https://sources.debian.org/src/dwgsim/>

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260829T182118+0000

Ratings and Alerts

No rating or validation information has been found for DWGSIM.

No alerts have been found for DWGSIM.

Data and Source Information

Usage and Citation Metrics

We found 53 mentions in open access literature.

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

Kang M, et al. (2026) AmpliFuse: an amplicon simulation tool with enhanced chimera generation for Illumina platforms. Microbiology resource announcements, 15(2), e0143925.

Battistella E, et al. (2025) Graph-based deep reinforcement learning for haplotype assembly with Ralphi. Genome research, 35(12), 2617.

Bahk K, et al. (2024) SigAlign: an alignment algorithm guided by explicit similarity criteria. Nucleic acids research, 52(15), 8717.

Hu T, et al. (2024) Comparison of the DNBSEQ platform and Illumina HiSeq 2000 for bacterial genome assembly. Scientific reports, 14(1), 1292.

Chen J, et al. (2024) CropGS-Hub: a comprehensive database of genotype and phenotype resources for genomic prediction in major crops. Nucleic acids research, 52(D1), D1519.

Diener C, et al. (2024) Metagenomic estimation of dietary intake from human stool. bioRxiv : the preprint server for biology.

Yang H, et al. (2024) Kssdtree: an interactive Python package for phylogenetic analysis based on sketching technique. Bioinformatics (Oxford, England), 40(10).

Wang S, et al. (2023) SpecHLA enables full-resolution HLA typing from sequencing data. Cell reports methods, 3(9), 100589.

Villalba de la Peña M, et al. (2023) Chromatin structure influences rate and spectrum of spontaneous mutations in Neurospora crassa. Genome research, 33(4), 599.

Weiner S, et al. (2023) CNAsim: improved simulation of single-cell copy number profiles and DNA-seq data from tumors. Bioinformatics (Oxford, England), 39(7).

Ajaykumar A, et al. (2022) Integrative Comparison of Burrows-Wheeler Transform-Based Mapping Algorithm with de Bruijn Graph for Identification of Lung/Liver Cancer-Specific Gene. Journal of microbiology and biotechnology, 32(2), 149.

Hayden HS, et al. (2022) Genome Capture Sequencing Selectively Enriches Bacterial DNA and Enables Genome-Wide Measurement of Intrastrain Genetic Diversity in Human Infections. mBio, 13(5), e0142422.

Wang Y, et al. (2021) 2-kupl: mapping-free variant detection from DNA-seq data of matched samples. BMC bioinformatics, 22(1), 304.

Kolodziej MC, et al. (2021) A membrane-bound ankyrin repeat protein confers race-specific leaf rust disease resistance in wheat. *Nature communications*, 12(1), 956.

Hawari MA, et al. (2021) SomatoSim: precision simulation of somatic single nucleotide variants. *BMC bioinformatics*, 22(1), 109.

B?inda K, et al. (2021) Simplitigs as an efficient and scalable representation of de Bruijn graphs. *Genome biology*, 22(1), 96.

Xu P, et al. (2021) ClipSV: improving structural variation detection by read extension, spliced alignment and tree-based decision rules. *NAR genomics and bioinformatics*, 3(1), lqab003.

Liang KC, et al. (2021) MetaVelvet-DL: a MetaVelvet deep learning extension for de novo metagenome assembly. *BMC bioinformatics*, 22(Suppl 6), 427.

Bush SJ, et al. (2020) Evaluation of methods for detecting human reads in microbial sequencing datasets. *Microbial genomics*, 6(7).

He C, et al. (2020) Factorial estimating assembly base errors using k-mer abundance difference (KAD) between short reads and genome assembled sequences. *NAR genomics and bioinformatics*, 2(3), lqaa075.