

# Resource Summary Report

Generated by [Kravitz](#) on Sep 17, 2026

## Wgsim

RRID:SCR\_013269

Type: Tool

### Proper Citation

Wgsim (RRID:SCR\_013269)

### Resource Information

**URL:** <https://github.com/lh3/wgsim>

**Proper Citation:** Wgsim (RRID:SCR\_013269)

**Description:** A small tool for simulating sequence reads from a reference genome.

**Abbreviations:** Wgsim

**Resource Type:** software resource

**Resource Name:** Wgsim

**Resource ID:** SCR\_013269

**Alternate IDs:** OMICS\_00260

**Record Creation Time:** 20220129T080315+0000

**Record Last Update:** 20260912T195801+0000

### Ratings and Alerts

No rating or validation information has been found for Wgsim.

No alerts have been found for Wgsim.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

### Usage and Citation Metrics

We found 171 mentions in open access literature.

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

Shi M, et al. (2026) Optimising Genome-Wide Detection of Runs of Homozygosity: Impacts of Reference Genome Quality and Sequencing Parameters on Inbreeding Assessment. *Molecular ecology resources*, 26(1), e70084.

Torres-Gonzalez E, et al. (2026) Mammalian mitochondrial DNA accumulates insertions and deletions with age in energetically demanding tissues. *Molecular biology and evolution*, 43(3).

W Runge AK, et al. (2026) Probing the zooarchaeological record across time and space for ancient pathogen DNA. *Nature communications*, 17(1).

Aoki K, et al. (2025) Tracking Antimicrobial Resistant Organisms Timely: a workflow validation study for successive core-genome SNP-based nosocomial transmission analysis. *JAC-antimicrobial resistance*, 7(3), dlaf069.

Huang S, et al. (2025) Performance testing for the sensitivity and resolution of low-pass WGS for small CNV detection. *BMC medical genomics*, 18(1), 203.

Guo MH, et al. (2025) Polygenic burden of short tandem repeat expansions promotes risk for Alzheimer's disease. *Nature communications*, 16(1), 1126.

Feng JW, et al. (2025) A haplotype-resolved pangenome of the barley wild relative *Hordeum bulbosum*. *Nature*, 645(8080), 429.

Verbiest MA, et al. (2025) Genotyping short tandem repeats across copy number alterations, aneuploidies, and polyploid organisms. *Communications biology*, 8(1), 1437.

Lo BW, et al. (2025) Genome-Wide Demographic Analyses of Balaenid Whales Revealed Complex History of Gene Flow Associated with Past Climate Oscillation. *Genome biology and evolution*, 17(5).

Sun S, et al. (2025) Analysis wheat wild relatives *Thinopyrum intermedium* and *Roegneria kamoji* genomes reveal different polyploid evolution paths. *Nature communications*, 16(1), 7693.

Bolognini D, et al. (2024) Global diversity, recurrent evolution, and recent selection on amylase structural haplotypes in humans. *bioRxiv : the preprint server for biology*.

Satake A, et al. (2024) Somatic mutation rates scale with time not growth rate in long-lived tropical trees. *eLife*, 12.

Yang X, et al. (2024) Pindel-TD: A Tandem Duplication Detector Based on A Pattern Growth Approach. *Genomics, proteomics & bioinformatics*, 22(1).

Coombes B, et al. (2024) Introgressions lead to reference bias in wheat RNA-seq analysis. *BMC biology*, 22(1), 56.

Hassan JA, et al. (2024) *Solanum pimpinellifolium* exhibits complex genetic resistance to *Pseudomonas syringae* pv. tomato. *Frontiers in plant science*, 15, 1416078.

Qiao L, et al. (2024) ViroISDC: a method for calling integration sites of hepatitis B virus based on feature encoding. *BMC bioinformatics*, 25(1), 177.

Azizpour A, et al. (2024) Graph-based self-supervised learning for repeat detection in metagenomic assembly. *Genome research*, 34(9), 1468.

R??dai Z, et al. (2024) An overlooked phenomenon: complex interactions of potential error sources on the quality of bacterial de novo genome assemblies. *BMC genomics*, 25(1), 45.

Yu W, et al. (2024) Comprehensive assessment of 11 de novo HiFi assemblers on complex eukaryotic genomes and metagenomes. *Genome research*, 34(2), 326.

Bolognini D, et al. (2024) Recurrent evolution and selection shape structural diversity at the amylase locus. *Nature*, 634(8034), 617.