

Resource Summary Report

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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: 20260725T190747+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 161 mentions in open access literature.

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

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.

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.

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.

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.

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

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.

Becher H, et al. (2023) Assembly-free quantification of vagrant DNA inserts. *Molecular ecology resources*, 23(5), 1002.

Guo MH, et al. (2023) Polygenic burden of short tandem repeat expansions promote risk for Alzheimer's disease. *medRxiv : the preprint server for health sciences*.

Guo A, et al. (2023) JASPER: A fast genome polishing tool that improves accuracy of genome assemblies. *PLoS computational biology*, 19(3), e1011032.