

Resource Summary Report

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GenomeScope

RRID:SCR_017014

Type: Tool

Proper Citation

GenomeScope (RRID:SCR_017014)

Resource Information

URL: <https://github.com/schatzlab/genomescope>

Proper Citation: GenomeScope (RRID:SCR_017014)

Description: Open source software package for fast genome analysis from unassembled short reads. Used to estimate genome heterozygosity, repeat content, and size from sequencing reads using a kmer-based statistical approach.

Abbreviations: Genomescope

Resource Type: data analysis software, software application, service resource, software resource, data processing software

Defining Citation: [PMID:28369201](#)

Keywords: genome, unassembled, sequenced, data, short, read, analysis, heterozygosity, repeat, content, size, kmer

Funding: NSF DBI 1350041;
NSF IOS 1237880;
NHGRI R01 HG006677

Availability: Free, Freely available,

Resource Name: GenomeScope

Resource ID: SCR_017014

Alternate URLs: <http://qb.cshl.edu/genomescope/>

License: Apache License 2.0

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250503T060654+0000

Ratings and Alerts

No rating or validation information has been found for GenomeScope.

No alerts have been found for GenomeScope.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 445 mentions in open access literature.

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

Liu J, et al. (2025) Chromosome-level genome assembly of the seasonally polyphenic scorpionfly (*Panorpa liui*). *Scientific data*, 12(1), 22.

Patankar HV, et al. (2025) A Chromosome level assembly of pomegranate (*Punica granatum* L.) variety grown in arid environment. *Scientific data*, 12(1), 73.

Yang Y, et al. (2025) A Chromosome-Scale Genome of *Trametes versicolor* and Transcriptome-Based Screening for Light-Induced Genes That Promote Triterpene Biosynthesis. *Journal of fungi (Basel, Switzerland)*, 11(1).

Choi S, et al. (2025) Chromosome-level genome assembly of *Salvia sclarea*. *Scientific data*, 12(1), 14.

Oriowo TO, et al. (2025) A chromosome-level, haplotype-resolved genome assembly and annotation for the Eurasian minnow (*Leuciscidae: Phoxinus phoxinus*) provide evidence of haplotype diversity. *GigaScience*, 14.

Guan DL, et al. (2025) A high-quality chromosome-level genome assembly of the mulberry looper, *Phthonandria atrilineata*. *Scientific data*, 12(1), 186.

Liu S, et al. (2025) Chromosome-level genome assembly and annotation of Japanese anchovy (*Engraulis japonicus*). *Scientific data*, 12(1), 134.

Lee S, et al. (2025) Chromosome-scale genome assembly of Korean goosegrass (*Eleusine*

indica). *Scientific data*, 12(1), 156.

Schöneberg Y, et al. (2025) Three Novel Spider Genomes Unveil Spidroin Diversification and Hox Cluster Architecture: *Ryuthela nishihirai* (Liphistiidae), *Uloborus plumipes* (Uloboridae) and *Cheiracanthium punctorium* (Cheiracanthiidae). *Molecular ecology resources*, 25(1), e14038.

Vea IM, et al. (2025) The B Chromosome of *Pseudococcus viburni*: A Selfish Chromosome that Exploits Whole-Genome Meiotic Drive. *Genome biology and evolution*, 17(1).

Cao LJ, et al. (2024) Nuclear and mitochondrial genomes of the plum fruit moth *Grapholita funebrana*. *Scientific data*, 11(1), 692.

Guenzi-Tiberi P, et al. (2024) LocoGSE, a sequence-based genome size estimator for plants. *Frontiers in plant science*, 15, 1328966.

Dong Z, et al. (2024) A high-quality chromosome-level genome assembly of the Chinese medaka *Oryzias sinensis*. *Scientific data*, 11(1), 322.

Markee A, et al. (2024) De Novo Long-Read Genome Assembly and Annotation of the Luna Moth (*Actias luna*) Fully Resolves Repeat-Rich Silk Genes. *Genome biology and evolution*, 16(7).

Songsungsan P, et al. (2024) A k-mer-based bulked segregant analysis approach to map seed traits in unphased heterozygous potato genomes. *G3 (Bethesda, Md.)*, 14(4).

Li X, et al. (2024) Large-scale gene expression alterations introduced by structural variation drive morphotype diversification in *Brassica oleracea*. *Nature genetics*, 56(3), 517.

Wang ZF, et al. (2024) Chromosome-level genome assembly and demographic history of *Euryodendron excelsum* in monotypic genus endemic to China. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 31(1).

Wang Y, et al. (2024) The evolution history of an allotetraploid mangrove tree analysed with a new tool Allo4D. *Plant biotechnology journal*, 22(6), 1491.

Sudalaimuthuasari N, et al. (2024) Near-chromosomal-level genome of the red palm weevil (*Rhynchophorus ferrugineus*), a potential resource for genome-based pest control. *Scientific data*, 11(1), 45.

Wang X, et al. (2024) De novo chromosome-level genome assembly of Chinese motherwort (*Leonurus japonicus*). *Scientific data*, 11(1), 55.