

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 processing software, data analysis software, software resource, software application, service resource

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: 20260805T044404+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 651 mentions in open access literature.

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

Wang YH, et al. (2026) Insights into dill (*Anethum graveolens*) flavor formation via integrative analysis of chromosomal-scale genome, metabolome and transcriptome. *Journal of advanced research*, 79, 847.

Bekavac M, et al. (2026) De novo genome assembly of Ansell's mole-rat (*Fukomys anselli*). *G3 (Bethesda, Md.)*, 16(1).

Cash EI, et al. (2025) Reference genome of the kidnapper ant, *Polyergus mexicanus*. *The Journal of heredity*, 116(3), 293.

Nagai S, et al. (2025) The draft genome sequences of the cosmopolitan centric diatom, the genus *Skeletonema*. *Scientific data*, 12(1), 1358.

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

Zhang L, et al. (2025) A high-quality chromosome-level genome assembly for the agricultural pest *Mythimna separata*. *Scientific data*, 12(1), 540.

Benoit M, et al. (2025) *Solanum* pan-genetics reveals paralogues as contingencies in crop engineering. *Nature*, 640(8057), 135.

Fu Z, et al. (2025) A chromosome-level genome assembly of Gray's grenadier anchovy, *Coilia grayii*. *Scientific data*, 12(1), 656.

Derilus D, et al. (2025) Chromosome-scale genome assembly and annotation of two geographically distinct strains of malaria vector *Anopheles albimanus*. *Scientific reports*, 15(1), 19448.

Lu K, et al. (2025) Chromosome-Level Genome and Variation Map of Eri Silkworm *Samia cynthia ricini*. *Biology*, 14(6).

Liu G, et al. (2025) From genome to gene expression: the genomic landscape of a hybrid species of *Eucalyptus urophylla* ?? *Eucalyptus grandis* and its divergence from parental species hybrid. *BMC plant biology*, 25(1), 1458.

- Kim S, et al. (2025) Comparative Genomics and Virulence Mechanisms to Identify Genes Related to Mucin O-Glycan Degradation and Pathogenicity in a Potentially Multidrug-Resistant *Clostridium tertium* Strain. *MicrobiologyOpen*, 14(6), e70169.
- Liu S, et al. (2025) Genome assembly and structural variations of Guyuan cattle. *Scientific data*, 12(1), 1863.
- Naktang C, et al. (2025) Chromosome-level assemblies of two hexaploid bamboos, *Thyrsostachys oliveri* and *Thyrsostachys siamensis*, provide a foundation for functional and comparative genomics studies. *GigaScience*, 14.
- Zhang X, et al. (2025) A telomere-to-telomere gap-free genome assembly of the striped catfish (*Pangasianodon hypophthalmus*). *Scientific data*, 12(1), 1890.
- Charvet S, et al. (2025) Nuclear genome assembly and annotation for the phagotrophic green alga *Nephroselmis pyriformis*. *Journal of phycology*, 61(6), 1566.
- Mora-Carrera E, et al. (2025) Genomic Patterns of Loss of Distyly and Polyploidization in Primroses. *Molecular biology and evolution*, 42(8).
- Ji X, et al. (2025) Mapping and identification of QTLs for low light tolerance traits in grapevine. *BMC plant biology*, 25(1), 927.
- Yen EC, et al. (2025) Chromosome-level genome assembly and methylome profile yield insights for the conservation of endangered loggerhead sea turtles. *GigaScience*, 14.
- Volpe E, et al. (2025) The reference genome of the human diploid cell line RPE-1. *Nature communications*, 16(1), 7751.