

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: software application, data processing software, data analysis software, service resource, software 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: 20260804T043659+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 [ASWG](#) .

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.

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

Yin M, et al. (2025) The haplotype-resolved genome assembly of an ancient citrus variety provides insights into the domestication history and fruit trait formation of loose-skin mandarins. *Genome biology*, 26(1), 61.

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

Zhu Z, et al. (2025) Chromosome-Level Genome Assembly and Annotation of the Amur Rat Snake *Elaphe schrenckii*. *Genome biology and evolution*, 17(5).

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

Kadiwala J, et al. (2025) The First Genome Assembly Of The Dogwhelk *Nucella lapillus*, a Bioindicator Species For The Marine Environment. *Scientific data*, 12(1), 704.

Ben Romdhane W, et al. (2025) De novo, high-quality assembly and annotation of the halophyte grass *Aeluropus litoralis* draft genome and identification of A20/AN1 zinc finger protein family. *BMC plant biology*, 25(1), 556.

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

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

Yen EC, et al. (2025) Chromosome-level genome assembly and methylome profile yield insights for the conservation of endangered loggerhead sea turtles. *GigaScience*, 14.

Yang W, et al. (2025) A haplotype-resolved chromosomal-level genome assembly of *Oxalis articulata*. *Scientific data*, 12(1), 856.

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.

Dong WY, et al. (2025) Chromosome-level genome assembly of the parasitoid wasp *Aenasius arizonensis*. *Scientific data*, 12(1), 809.

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.

Lind AL, et al. (2025) Contiguous and complete assemblies of *Blastocystis* gut microbiome-associated protists reveal evolutionary diversification to host ecology. *Genome research*, 35(6), 1377.

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