

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

Defining Citation: [PMID:28369201](#)

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

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

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: 20260912T195847+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 800 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Li J, et al. (2026) A telomere-to-telomere genome assembly for *Cyperus difformis*. *Scientific data*, 13(1), 257.

Cortez J, et al. (2026) Reference genome of an irruptive migrant, the pine siskin (*Spinus pinus*). *The Journal of heredity*, 117(3), 469.

Rivera MG, et al. (2026) Genome assembly and annotation of a deep-diving pinniped, the northern elephant seal (*Mirounga angustirostris*). *The Journal of heredity*, 117(3), 512.

Hu Y, et al. (2026) The reference genome sequence of the scarlet follicle, *Sterculia lanceolata*, reveals a paleo-polyploidization and its impact on fruit quality and fruit dehiscence. *Functional & integrative genomics*, 26(1), 46.

Marques Silva B, et al. (2026) Pipeasm: a tool for automated large chromosome-scale genome assembly and evaluation. *Bioinformatics advances*, 6(1), vbaf326.

Pfeifer M, et al. (2026) High-quality haplotype-resolved genome assembly and annotation of *Malus baccata* 'Jackii'. *Scientific data*, 13(1), 14.

Petrohilos C, et al. (2026) When cells rebel: a comparative genomics investigation into marsupial cancer susceptibility. *Molecular biology and evolution*, 43(2).

de Souza Araujo N, et al. (2026) Retroelement expansions underlie genome evolution in stingless bees. *BMC genomics*, 27(1), 160.

Tengstedt ANB, et al. (2026) Evaluating inbreeding and assessing the risk of outbreeding depression in genetic rescue using whole-genome sequence data. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2526216122.

Hu QL, et al. (2026) Chromosome-level genome assembly of the predatory stink bug, *Eocanthecona furcellata* (Wolff). *Scientific data*, 13(1), 6.

Hallas JM, et al. (2026) A genome assembly for mule deer, *Odocoileus hemionus*, from Southern California. *The Journal of heredity*, 117(3), 502.

Han ZR, et al. (2026) Chromosome-level genome assembly of *Neoseiulus longispinosus* (Phytoseiidae). *Scientific data*, 13(1).

Cartealy IC, et al. (2026) Genome survey of nutmeg (*Myristica fragrans*) from Indonesia: genomic resource for Myristicaceae. *Frontiers in plant science*, 17, 1753954.

Wang M, et al. (2026) Chromosome-level genome assembly of the alpine extremophyte Tibetan snow lotus, *Saussurea hypsipeta* Diels. *Scientific data*, 13(1).

Zhang X, et al. (2026) A high-quality Chromosome-level genome assembly of *Gynostemma guangxiense* (Cucurbitaceae). *Scientific data*, 13(1).

Li X, et al. (2026) A chromosome-level genome assembly of two-spotted cricket, *Gryllus bimaculatus* (Orthoptera: Grylloidea). *Scientific data*, 13(1).

Yue Z, et al. (2026) Chromosome-level genome assembly and annotation of the termite *Reticulitermes chinensis* Snyder. *Scientific data*, 13(1).

Biello R, et al. (2026) Chromosome-level genome of the Adriatic sturgeon, *Acipenser naccarii*: A resource for polyploid fish genomics. *The Journal of heredity*, 117(4), 877.

Cheng Z, et al. (2026) A chromosome-level reference genome of an endangered plant *Craigia yunnanensis*. *Scientific data*, 13(1).

Schoonmaker AN, et al. (2026) A whole-genome assembly of St. Augustinegrass and visualizing diversity within the species. *The plant genome*, 19(1), e70144.