

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;
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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 [SPARC SAWG](#) .

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

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.

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

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.

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

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

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

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

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

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

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).

Shohat H, et al. (2026) A neofunctionalized flowering antagonist created an evolutionary contingency that channeled Solanaceae adaptation. *bioRxiv : the preprint server for biology*.

Shan X, et al. (2026) Chromosome-level genome assembly of Siberian kale (*Brassica napus* subsp. *pabularia*). *Scientific data*, 13(1).

Vu DQ, et al. (2026) A chromosome-scale genome assembly of *Tigridiopalma magnifica*. *Scientific data*, 13(1).

Cr??peault O, et al. (2026) Genomic and transcriptomic basis of morphological and life cycle diversity in the prasinophyte alga *Pseudoscourfieldia marina*. *Communications biology*, 9(1).

Jiang K, et al. (2026) Telomere-to-telomere-level genome assembly and annotation of the Zi goose *Anser cygnoides*. *Scientific data*, 13(1).

Sobreiro MB, et al. (2026) De Novo Chromosome-Level Assembly of the Endangered *Pilocarpus Microphyllus* Highlights Genomic Resources for Conservation and Sustainable Pilocarpine Extraction. *Genome biology and evolution*, 18(3).

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.

Zeng Z, et al. (2026) Highly heterozygous *Citrus changshan-huyou* Y. B. Chang originated from ancient hybridization between mandarin and pummelo and displayed distinct tissue-specific allelic imbalance. *The plant genome*, 19(2), e70232.