

Resource Summary Report

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GenomeTools

RRID:SCR_016120

Type: Tool

Proper Citation

GenomeTools (RRID:SCR_016120)

Resource Information

URL: <http://genometools.org>

Proper Citation: GenomeTools (RRID:SCR_016120)

Description: Software toolkit for biological sequence analysis and -presentation combined into a single binary. It is used for genome analysis, efficient processing of structured genome annotations and contains binaries for sequence and annotation handling, sequence compression, index structure generation and access, annotation visualization.

Synonyms: GenomeTool, Genome Tools, Genome Tool

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource, software toolkit

Defining Citation: [PMID:24091398](#)

Keywords: analysis, genome, annotate, sequence, compress, visualization, single, binary, combine, structure, efficient

Availability: Free, Available for download

Resource Name: GenomeTools

Resource ID: SCR_016120

Alternate IDs: OMICS_16119

Alternate URLs: <https://sources.debian.org/src/genometools/>

License: ISC license

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260829T182531+0000

Ratings and Alerts

No rating or validation information has been found for GenomeTools.

No alerts have been found for GenomeTools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 150 mentions in open access literature.

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

Li K, et al. (2026) Telomere-to-Telomere Genomes Reveal that Multiscale Evolution Shapes the Largest Metabolic Arsenal of Diaporthe Fungi. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(27), e13287.

Fiesinger A, et al. (2026) The genome of the reef-building coral *Porites harrisoni* from the southern Persian/Arabian Gulf. *GigaByte* (Hong Kong, China), 2026, gigabyte174.

Rozenberg A, et al. (2026) Ontogenetic Sequence of Differential Gene Expression in Predator-Induced *Daphnia pulex*. *Molecular ecology*, 35(13), e70446.

Shipova AA, et al. (2026) From Adam's rib: the Siberian moth's female W chromosome is derived from its Z counterpart. *Molecular biology and evolution*, 43(3).

Wang B, et al. (2026) Global genomic diversity of the selfing nematode *Caenorhabditis tropicalis* correlates with geography. *bioRxiv : the preprint server for biology*.

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

Bates S, et al. (2026) OMAnnotator: a novel approach to building an annotated consensus genome sequence. *Bioinformatics advances*, 6(1), vbag015.

Li M, et al. (2026) De Novo Chromosome-Level Genome Assembly of 'Qing Zhou Mi' Landrace Peach and Analysis of Late Maturity and Fruit Weight Traits in Peach. *Plants* (Basel, Switzerland), 15(7).

Wei Y, et al. (2026) Unveiling the cryptic diversity and distribution of elements related to virophage mavirus through deep mining of pPolB proteins. *Virologica Sinica*, 41(2), 371.

Wang YY, et al. (2026) A Near Telomere-to-Telomere Genome of *Belamcanda chinensis* Provides Insights Into Genome Evolution and the Biosynthesis of Characteristic Isoflavones. *Plant biotechnology journal*, 24(6), 4285.

Ringeval A, et al. (2026) Multi-omics characterization of toxin expression and producing organs in the predatory gastropods *Monoplex corrugatus* and *Stramonita haemastoma*.

BMC genomics, 27(1).

Cheng X, et al. (2026) MUTE drives asymmetric divisions to form stomatal subsidiary cells in Crassulaceae succulents. *Science advances*, 12(13), eaeb8145.

Kriti D, et al. (2026) Chromosome-scale genome assembly and characterization of *Saccharomycopsis schoenii*, a necrotrophic predatory yeast. *G3 (Bethesda, Md.)*, 16(5).

Zhang J, et al. (2026) Polymorphism and evolutionary origins of accessory chromosomes in the basidiomycete *Tremella fuciformis*. *Nature communications*, 17(1).

Pinosio S, et al. (2026) The FORGENIUS Genomic Resources: New Genotyping Tools and Genomic Data for 23 Forest Tree Species and Their Genetic Conservation Units. *Molecular ecology resources*, 26(3), e70115.

Davis JM, et al. (2026) Benchmarking methods for genome annotation using nanopore direct RNA in a non-model crop plant. *Bioinformatics advances*, 6(1), vbag030.

Gottschalk C, et al. (2026) Improved genome assembly of double haploid *Prunus persica* siblings 'Lovell 2D' and 'Lovell 5D' and the peach NLRome. *Scientific reports*, 16(1).

van Rengs WMJ, et al. (2026) Wild tomato genome assemblies reveal structural variants and repeat content act as recombination barriers. *Nature communications*, 17(1).

Yang T, et al. (2025) Chromosome-level genome assembly provides insights into flavonoid biosynthesis in stems and leaves and fatty acid biosynthesis in kernels of *Erythralum scandens*. *BMC plant biology*, 25(1), 1000.

Zhao Z, et al. (2025) Evolutionary Consequences of Unusually Large Pericentric TE-rich Regions in the Genome of a Neotropical Fig Wasp. *Genome biology and evolution*, 17(9).