

# Resource Summary Report

Generated by [dkNET](#) on Apr 30, 2025

## GenomeTools

RRID:SCR\_016120

Type: Tool

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### Proper Citation

GenomeTools (RRID:SCR\_016120)

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### 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, sequence analysis software, software resource, data processing software, software toolkit, software application

**Defining Citation:** [PMID:24091398](#)

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

**Funding:**

**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:** 20250430T060051+0000

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## Ratings and Alerts

No rating or validation information has been found for GenomeTools.

No alerts have been found for GenomeTools.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 113 mentions in open access literature.

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

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

Lee S, et al. (2025) Chromosome-scale genome assembly of Korean goosegrass (*Eleusine indica*). *Scientific data*, 12(1), 156.

Penumarthy LR, et al. (2024) A new chromosome-level genome assembly and annotation of *Cryptosporidium meleagridis*. *bioRxiv : the preprint server for biology*.

Bai Y, et al. (2024) Genome-wide characterization and comparison of endogenous retroviruses among 3 duck reference genomes. *Poultry science*, 103(5), 103543.

Carpinteyro-Ponce J, et al. (2024) The Complex Landscape of Structural Divergence Between the *Drosophila pseudoobscura* and *D. persimilis* Genomes. *Genome biology and evolution*, 16(3).

Talbot SC, et al. (2024) A first look at the genome structure of hexaploid "Mitcham" peppermint (*Mentha × piperita* L.). *G3 (Bethesda, Md.)*, 14(12).

Glick L, et al. (2024) Phylogenetic Analysis of 590 Species Reveals Distinct Evolutionary Patterns of Intron-Exon Gene Structures Across Eukaryotic Lineages. *Molecular biology and evolution*, 41(12).

Männer L, et al. (2024) Chromosome-level genome assembly of the sacoglossan sea slug *Elysia timida* (Risso, 1818). *BMC genomics*, 25(1), 941.

Yang T, et al. (2024) A telomere-to-telomere gap-free reference genome assembly of avocado provides useful resources for identifying genes related to fatty acid biosynthesis and disease resistance. *Horticulture research*, 11(7), uhae119.

Talbot SC, et al. (2024) A haplotype-resolved chromosome-level assembly and annotation of European hazelnut (*C. avellana* cv. Jefferson) provides insight into mechanisms of eastern filbert blight resistance. *G3 (Bethesda, Md.)*, 14(6).

Cuello C, et al. (2024) The Madagascar palm genome provides new insights on the evolution of Apocynaceae specialized metabolism. *Heliyon*, 10(6), e28078.

Liang X, et al. (2024) Genome comparisons reveal accessory genes crucial for the evolution of apple Glomerella leaf spot pathogenicity in *Colletotrichum* fungi. *Molecular plant pathology*, 25(4), e13454.

Al-Yazeedi T, et al. (2024) The contribution of an X chromosome QTL to non-Mendelian inheritance and unequal chromosomal segregation in *Auanema freiburgense*. *Genetics*, 227(1).

Chen G, et al. (2024) Adaptive expansion of ERVK solo-LTRs is associated with Passeriformes speciation events. *Nature communications*, 15(1), 3151.

Moawad AS, et al. (2024) Evolution of Endogenous Retroviruses in the Subfamily of Caprinae. *Viruses*, 16(3).

Teterina AA, et al. (2024) Pervasive conservation of intron number and other genetic elements revealed by a chromosome-level genomic assembly of the hyper-polymorphic nematode *Caenorhabditis brenneri*. *bioRxiv : the preprint server for biology*.

Huerlimann R, et al. (2024) The transcriptional landscape underlying larval development and metamorphosis in the Malabar grouper (*Epinephelus malabaricus*). *eLife*, 13.

Kim BY, et al. (2024) Single-fly genome assemblies fill major phylogenomic gaps across the Drosophilidae Tree of Life. *PLoS biology*, 22(7), e3002697.

Zhang Z, et al. (2024) Complete telomere-to-telomere genomes uncover virulence evolution conferred by chromosome fusion in oomycete plant pathogens. *Nature communications*, 15(1), 4624.

Olumakaiye R, et al. (2024) Identification of a terpene synthase arsenal using long-read sequencing and genome assembly of *Aspergillus wentii*. *BMC genomics*, 25(1), 1141.