

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>

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

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: 20260804T043636+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 131 mentions in open access literature.

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

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).

Falentin C, et al. (2025) Chromosome level assembly of five Brassica rapa and oleracea accessions expand the resistance genes reservoir. *Scientific data*, 12(1), 2016.

Yue H, et al. (2025) Enzyme Repertoires and Genomic Insights into Lycium barbarum Pectin Polysaccharide Biosynthesis. *Genomics, proteomics & bioinformatics*, 22(6).

LaMere S, et al. (2025) Epigenetic motifs distinguishing endogenous from exogenous retroviral integrants. *Journal of virology*, 99(10), e0077525.

Dean AAC, et al. (2025) An algorithm for annotation and classification of T. cruzi MASP sequences: towards a better understanding of the parasite genetic variability. *BMC genomics*, 26(1), 194.

Massonnet M, et al. (2025) Evolutionary conservation of the grape sex-determining region in angiosperms and emergence of dioecy in Vitaceae. *Nature communications*, 16(1), 6047.

Teixeira M, et al. (2025) Genome reannotation and gland-specific transcriptome analysis identify new effector candidates in Meloidogyne chitwoodi. *PLoS pathogens*, 21(11), e1013075.

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

Teterina AA, et al. (2025) Pervasive Conservation of Intron Number and Other Genetic Elements Revealed by a Chromosome-level Genome Assembly of the Hyper-polymorphic Nematode Caenorhabditis brenneri. *Genome biology and evolution*, 17(3).

Cunha VAS, et al. (2025) Genome of the Myiasis-Causing Fly Chrysomya bezziana, the Old-World Screwworm. *Genome biology and evolution*, 17(8).

Zhang S, et al. (2025) Haplotype-resolved t2t genome of *paliurus hemsleyanus* provides insights into rhamnaceae evolution and genome biology. *Communications biology*, 8(1), 1744.

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

Robbins MD, et al. (2025) Haplotype-resolved genome assembly of 'Manhattan' perennial ryegrass (*Lolium perenne* L.) and characterization of drought responsive late embryogenesis abundant genes. *BMC genomics*, 26(1), 1125.

Pianezza R, et al. (2025) The ongoing invasion of the endogenous retrovirus Kuruka in natural *Drosophila melanogaster* populations. *bioRxiv : the preprint server for biology*.

Gaccione L, et al. (2025) Graph-based pangenomes and pan-phenome provide a cornerstone for eggplant biology and breeding. *Nature communications*, 16(1), 9919.

Safronov O, et al. (2025) Independent evolution of betulin biosynthesis in *Inonotus obliquus*. *Scientific reports*, 15(1), 21319.

Lu J, et al. (2025) Haplotype-resolved chromosome-level genome assembly of *Fragaria × ananassa* Duch. cv. 'Yuexin'. *Scientific data*, 12(1), 974.

Bulzu PA, et al. (2025) Lineage-specific expansions of polinton-like viruses in photosynthetic cryptophytes. *Microbiome*, 13(1), 154.

Balouz V, et al. (2025) A divide-and-conquer approach to uncover the genomic structure of the highly virulent RA strain of *Trypanosoma cruzi*. *Scientific reports*, 15(1), 40000.

Moya ND, et al. (2025) *Caenorhabditis briggsae* ancestral genomic hyper-diversity contrasts with globally distributed genome-wide haplotypes. *bioRxiv : the preprint server for biology*.