

Resource Summary Report

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WTDBG

RRID:SCR_017225

Type: Tool

Proper Citation

WTDBG (RRID:SCR_017225)

Resource Information

URL: <https://github.com/ruanjue/wtdbg2.git>

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Description: Software tool as de novo sequence assembler for long noisy reads produced by PacBio or Oxford Nanopore Technologies. It assembles raw reads without error correction and then builds consensus from intermediate assembly output. Designed to assemble huge genomes in very limited time.

Synonyms: Wtdbg2, wtdgb, Wtdgb, wtdgb2

Resource Type: software application, data analysis software, sequence analysis software, software resource, data processing software, alignment software, image analysis software

Defining Citation: [PMID:31819265](#)

Keywords: sequence, assembler, de novo, long, noisy, read, likelihood, estimator, genome

Funding: NSFC ;
NHGRI R01 HG010040

Availability: Free, Available for download, Freely available

Resource Name: WTDBG

Resource ID: SCR_017225

Alternate IDs: OMICS_24025

Alternate URLs: <https://github.com/ruanjue/wtdbg>, <https://sources.debian.org/src/wtdbg2/>

License: GNU GPL v3.0

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260729T044432+0000

Ratings and Alerts

No rating or validation information has been found for WTDBG.

No alerts have been found for WTDBG.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 57 mentions in open access literature.

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

Qin H, et al. (2025) The complete genome assembly of *Astragalus membranaceus*: enabling more accurate genetic research. *GigaScience*, 14.

Xie S, et al. (2025) Extreme heterochiasmy and high rates of sex-reversed recombination result in large yet homomorphic sex chromosomes in the Emei moustache toad. *Genome research*, 35(6), 1325.

Márquez R, et al. (2025) A draft genome assembly for the dart-poison frog *Phylllobates terribilis*. *GigaByte (Hong Kong, China)*, 2025, gigabyte157.

Pan T, et al. (2025) Genomic insights and the conservation potential of captive breeding: The case of Chinese alligator. *Science advances*, 11(14), eadm7980.

Schall PZ, et al. (2025) Integrative Genotyping and Analysis of Canine Structural Variation Using Long-read and Short-read Data. *Genome biology and evolution*, 17(10).

Yu T, et al. (2025) Evolution of KoRV-A transcriptional silencing in wild koalas. *Cell*, 188(8), 2081.

Xu Y, et al. (2024) Chromosome-level genome of the poultry shaft louse *Menopon gallinae* provides insight into the host-switching and adaptive evolution of parasitic lice. *GigaScience*, 13(1).

Rüber L, et al. (2024) The genome sequence of the Dracula fish, *Danionella dracula* (Britz, Conway & Rüber, 2009). *Wellcome open research*, 9, 194.

Wang YS, et al. (2024) Chromosome-level genome assemblies of two littorinid marine snails indicate genetic basis of intertidal adaptation and ancient karyotype evolved from bilaterian ancestors. *GigaScience*, 13.

Souza-Borges CH, et al. (2024) De novo assembly and characterization of a highly degenerated ZW sex chromosome in the fish *Megaleporinus macrocephalus*. *GigaScience*, 13.

Jiang Z, et al. (2024) Gene flow and an anomaly zone complicate phylogenomic inference in a rapidly radiated avian family (*Prunellidae*). *BMC biology*, 22(1), 49.

Cheng Y, et al. (2024) A chromosome-level genome assembly of the *Echiura Urechis unicinctus*. *Scientific data*, 11(1), 90.

Gatins R, et al. (2024) Whole genome assembly and annotation of the King Angelfish (*Holacanthus passer*) gives insight into the evolution of marine fishes of the Tropical Eastern Pacific. *GigaByte (Hong Kong, China)*, 2024, gigabyte115.

Zhang Y, et al. (2024) A trade-off in evolution: the adaptive landscape of spiders without venom glands. *GigaScience*, 13.

Wolf M, et al. (2024) Near chromosome-level and highly repetitive genome assembly of the snake pipefish *Entelurus aequoreus* (*Syngnathiformes: Syngnathidae*). *GigaByte (Hong Kong, China)*, 2024, gigabyte105.

Yin X, et al. (2023) Comparative genomics of the medicinal plants *Lonicera macranthoides* and *L. japonica* provides insight into genus genome evolution and hederagenin-based saponin biosynthesis. *Plant biotechnology journal*, 21(11), 2209.

Zhang Z, et al. (2023) Chromosome-level genome assembly of *Dastarcus helophoroides* provides insights into CYP450 genes expression upon insecticide exposure. *Pest management science*, 79(4), 1467.

Kim HS, et al. (2022) KOREF_S1: phased, parental trio-binned Korean reference genome using long reads and Hi-C sequencing methods. *GigaScience*, 11.

Heckenhauer J, et al. (2022) Genome size evolution in the diverse insect order *Trichoptera*. *GigaScience*, 11.

Luo F, et al. (2022) A chromosome-level genome of the human blood fluke *Schistosoma japonicum* identifies the genomic basis of host-switching. *Cell reports*, 39(1), 110638.