Resource Summary Report

Generated by dkNET on Aug 19, 2026

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. Desiged to assemble huge genomes in very limited time.

Synonyms: Wtdbg2, wtdgb, Wtdgb, wtdgb2

Resource Type: alignment software, sequence analysis software, software application, image analysis software, software resource, data analysis software, data processing 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: 20260819T044438+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 66 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET .

Lu Z, et al. (2026) The Rhus chinensis Genome Provides Insights Into Tannin, Flavonoid Biosynthesis, and Glandular Trichome Development. Plant biotechnology journal, 24(3), 988.

Doré G, et al. (2026) First draft genome of the decaploid species, Ludwigia grandiflora subsp. hexapetala, validated through gene expression. GigaByte (Hong Kong, China), 2026, gigabyte176.

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 Phyllobates terribilis. GigaByte (Hong Kong, China), 2025, gigabyte157.

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

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).

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.

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.

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

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.

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

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.

Herrera S, et al. (2023) Genome assembly of the deep-sea coral Lophelia pertusa. GigaByte (Hong Kong, China), 2023, gigabyte78.

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.

Yang Y, et al. (2023) Assembly of Genome and Resequencing Provide Insights into Genetic Differentiation between Parents of Hulong Hybrid Grouper (Epinephelus fuscoguttatus ? × E. lanceolatus ?). International journal of molecular sciences, 24(15).