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

Proper Citation: WTDBG (RRID:SCR_017225)

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: image analysis software, data processing software, sequence analysis software, software application, software resource, alignment software, data 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: 20250411T055934+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 51 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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.

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.

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

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).

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.

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.

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.

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.

Zhu C, et al. (2022) Insights into chromosomal evolution and sex determination of Pseudobagrus ussuriensis (Bagridae, Siluriformes) based on a chromosome-level genome. DNA research : an international journal for rapid publication of reports on genes and genomes, 29(4).

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

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

Winter S, et al. (2022) A Chromosome-Scale Genome Assembly of the Okapi (Okapia johnstoni). The Journal of heredity, 113(5), 568.

Cosma BM, et al. (2022) Evaluating long-read de novo assembly tools for eukaryotic genomes: insights and considerations. GigaScience, 12.

Wang H, et al. (2022) A Chromosome-level assembly of the Japanese eel genome, insights into gene duplication and chromosomal reorganization. GigaScience, 11.

Barros CP, et al. (2022) A new haplotype-resolved turkey genome to enable turkey genetics and genomics research. GigaScience, 12.

Mu X, et al. (2022) Identification of candidate sex-specific genomic regions in male and female Asian arowana genomes. GigaScience, 11.