

Resource Summary Report

Generated by [dkNET](#) on Jul 30, 2026

RopeBWT2

RRID:SCR_002673

Type: Tool

Proper Citation

RopeBWT2 (RRID:SCR_002673)

Resource Information

URL: <https://github.com/lh3/ropebwt2>

Proper Citation: RopeBWT2 (RRID:SCR_002673)

Description: A software tool for constructing the FM-index for a collection of DNA sequences. It works by incrementally inserting one or multiple sequences into an existing pseudo-BWT position by position, starting from the end of the sequences. This algorithm can be largely considered a mixture of BCR and dynamic FM-index. Nonetheless, ropeBWT2 is unique in that it may implicitly sort the input into reverse lexicographical order (RLO) or reverse-complement lexicographical order (RCLO) while building the index.

Resource Type: software resource

Defining Citation: [PMID:25107872](#)

Keywords: standalone software, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: RopeBWT2

Resource ID: SCR_002673

Alternate IDs: biotools:ropebwt2, OMICS_05300

Alternate URLs: <https://bio.tools/ropebwt2>

License: MIT License

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260725T190527+0000

Ratings and Alerts

No rating or validation information has been found for RopeBWT2.

No alerts have been found for RopeBWT2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

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

Aoyagi LN, et al. (2025) Diversity and characterization of the ammonia-oxidizing bacteria responsible for nitrification in tea field soils. *Scientific reports*, 15(1), 33221.

Salcher MM, et al. (2025) Bringing the uncultivated microbial majority of freshwater ecosystems into culture. *Nature communications*, 16(1), 7971.

Wong HL, et al. (2024) Ubiquitous genome streamlined Acidobacteriota in freshwater environments. *ISME communications*, 4(1), ycae124.

Zong L, et al. (2024) An optimized workflow of full-length transcriptome sequencing for accurate fusion transcript identification. *RNA biology*, 21(1), 122.

Li H, et al. (2024) BWT construction and search at the terabase scale. *Bioinformatics (Oxford, England)*, 40(12).

Mak QXC, et al. (2023) Polishing De Novo Nanopore Assemblies of Bacteria and Eukaryotes With FMLRC2. *Molecular biology and evolution*, 40(3).

Szandar K, et al. (2022) Breaking the limits - multichromosomal structure of an early eudicot *Pulsatilla patens* mitogenome reveals extensive RNA-editing, longest repeats and chloroplast derived regions among sequenced land plant mitogenomes. *BMC plant biology*, 22(1), 109.

Eisfeldt J, et al. (2020) Discovery of Novel Sequences in 1,000 Swedish Genomes. *Molecular biology and evolution*, 37(1), 18.

Sawicki J, et al. (2020) The Increase of Simple Sequence Repeats during Diversification of Marchantiidae, An Early Land Plant Lineage, Leads to the First Known Expansion of Inverted Repeats in the Evolutionarily-Stable Structure of Liverwort Plastomes. *Genes*, 11(3).

Morgan AP, et al. (2016) Whole Genome Sequence of Two Wild-Derived *Mus musculus domesticus* Inbred Strains, LEWES/EiJ and ZALENDE/EiJ, with Different Diploid Numbers. *G3 (Bethesda, Md.)*, 6(12), 4211.