

Resource Summary Report

Generated by [dkNET](#) on Aug 16, 2026

Burrows-Wheeler transform

RRID:SCR_012304

Type: Tool

Proper Citation

Burrows-Wheeler transform (RRID:SCR_012304)

Resource Information

URL: <https://github.com/BEETL/BEETL>

Proper Citation: Burrows-Wheeler transform (RRID:SCR_012304)

Description: Software tool as data transformation algorithm that restructures data in such a way that the transformed message is more compressible. Used for large scale compression of genomic sequence databases.

Abbreviations: BWT

Synonyms: Burrows-Wheeler Transform

Resource Type: software resource

Defining Citation: [PMID:22556365](#)

Keywords: Large scale compression, data transformation, genomic sequence databases compression,

Availability: Free, Freely available

Resource Name: Burrows-Wheeler transform

Resource ID: SCR_012304

Alternate IDs: OMICS_00950

Record Creation Time: 20220129T080309+0000

Record Last Update: 20260815T182446+0000

Ratings and Alerts

No rating or validation information has been found for Burrows-Wheeler transform.

No alerts have been found for Burrows-Wheeler transform.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Treger TD, et al. (2025) Predisposition Footprints in the Somatic Genome of Wilms Tumors. *Cancer discovery*, 15(2), 286.

Ahmad SF, et al. (2023) Read-depth based approach on whole genome resequencing data reveals important insights into the copy number variation (CNV) map of major global buffalo breeds. *BMC genomics*, 24(1), 616.

Lesurf R, et al. (2022) Whole genome sequencing delineates regulatory, copy number, and cryptic splice variants in early onset cardiomyopathy. *NPJ genomic medicine*, 7(1), 18.

Socha M, et al. (2021) Position effects at the FGF8 locus are associated with femoral hypoplasia. *American journal of human genetics*, 108(9), 1725.

Zhong LH, et al. (2021) Molecular profiling of Chinese systemic anaplastic large cell lymphoma patients: novel evidence of genetic heterogeneity. *Annals of translational medicine*, 9(2), 128.

Migicovsky Z, et al. (2021) Genomic consequences of apple improvement. *Horticulture research*, 8(1), 9.

Choi YJ, et al. (2020) Family-based exome sequencing combined with linkage analyses identifies rare susceptibility variants of MUC4 for gastric cancer. *PloS one*, 15(7), e0236197.

Han S, et al. (2020) Role of NDP- and FZD4-Related Novel Mutations Identified in Patients with FEVR in Norrin/??-Catenin Signaling Pathway. *BioMed research international*, 2020, 7681926.