Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 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: 20260905T132722+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 PRECISE-TBI .

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.