

Resource Summary Report

Generated by T1D on Jul 31, 2026

bsseq

RRID:SCR_001072

Type: Tool

Proper Citation

bsseq (RRID:SCR_001072)

Resource Information

URL: <http://www.bioconductor.org/packages/2.13/bioc/html/bsseq.html>

Proper Citation: bsseq (RRID:SCR_001072)

Description: R package with tools for analyzing and visualizing bisulfite sequencing data.

Synonyms: bsseq - Analyze manage and store bisulfite sequencing data

Resource Type: data processing software, sequence analysis software, data analysis software, software resource, software application

Keywords: bisulfite sequencing, analyze, r, sequence analysis software, data analysis software, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: bsseq

Resource ID: SCR_001072

Alternate IDs: OMICS_01847, biotools:bsseq

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

License: Artistic-2.0

Record Creation Time: 20220129T080205+0000

Record Last Update: 20260731T042605+0000

Ratings and Alerts

No rating or validation information has been found for bsseq.

No alerts have been found for bsseq.

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 [T1D](#).

Lo EKW, et al. (2023) Comprehensive DNA Methylation Analysis Indicates That Pancreatic Intraepithelial Neoplasia Lesions Are Acinar-Derived and Epigenetically Primed for Carcinogenesis. *Cancer research*, 83(11), 1905.

Gallon J, et al. (2023) DNA Methylation Landscapes of Prostate Cancer Brain Metastasis Are Shaped by Early Driver Genetic Alterations. *Cancer research*, 83(8), 1203.

Mordaunt CE, et al. (2020) Cord blood DNA methylome in newborns later diagnosed with autism spectrum disorder reflects early dysregulation of neurodevelopmental and X-linked genes. *Genome medicine*, 12(1), 88.

Chun HE, et al. (2019) Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. *Cell reports*, 29(8), 2338.

Lu X, et al. (2017) Single-base resolution methylomes of upland cotton (*Gossypium hirsutum* L.) reveal epigenome modifications in response to drought stress. *BMC genomics*, 18(1), 297.

Li Y, et al. (2017) Genome-wide comparative analysis of DNA methylation between soybean cytoplasmic male-sterile line NJCMS5A and its maintainer NJCMS5B. *BMC genomics*, 18(1), 596.

Hao Y, et al. (2016) Genome-wide DNA methylation profiles changes associated with constant heat stress in pigs as measured by bisulfite sequencing. *Scientific reports*, 6, 27507.

Yang C, et al. (2016) DNA Methylation Patterns in the Hypothalamus of Female Pubertal Goats. *PloS one*, 11(10), e0165327.