Resource Summary Report

Generated by SPARC SAWG 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 SPARC SAWG .

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.