

Resource Summary Report

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BiSeq

RRID:SCR_012993

Type: Tool

Proper Citation

BiSeq (RRID:SCR_012993)

Resource Information

URL: <http://www.bioconductor.org/packages/2.12/bioc/html/BiSeq.html>

Proper Citation: BiSeq (RRID:SCR_012993)

Description: Software package that provides useful classes and functions to handle and analyze targeted bisulfite sequencing (BS) data such as reduced-representation bisulfite sequencing (RRBS) data.

Abbreviations: BiSeq

Resource Type: software resource

Resource Name: BiSeq

Resource ID: SCR_012993

Alternate IDs: OMICS_00620

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260808T190006+0000

Ratings and Alerts

No rating or validation information has been found for BiSeq.

No alerts have been found for BiSeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 30 mentions in open access literature.

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

Lecuyer G, et al. (2025) Recurrent spontaneous miscarriages from sperm after ABVD chemotherapy in a patient with Hodgkin's lymphoma: sperm DNA and methylation profiling. *Asian journal of andrology*, 27(5), 598.

Pereyra S, et al. (2025) Cost-effective promoter methylation analysis via target long-read bisulfite sequencing: a case study in severe preterm birth. *BMC medical genomics*, 18(1), 122.

King SE, et al. (2025) Prenatal maternal stress in rats alters the epigenetic and transcriptomic landscape of the maternal-fetal interface across four generations. *Communications biology*, 8(1), 38.

Oganezovi N, et al. (2024) Long-term effects of myo-inositol on traumatic brain injury: Epigenomic and transcriptomic studies. *IBRO neuroscience reports*, 16, 291.

Boman J, et al. (2024) Regulatory and evolutionary impact of DNA methylation in two songbird species and their naturally occurring F1 hybrids. *BMC biology*, 22(1), 124.

Donato L, et al. (2024) The genomic mosaic of mitochondrial dysfunction: Decoding nuclear and mitochondrial epigenetic contributions to maternally inherited diabetes and deafness pathogenesis. *Heliyon*, 10(14), e34756.

Andrade-Brito DE, et al. (2024) Neuronal-specific methylome and hydroxymethylome analysis reveal significant loci associated with alcohol use disorder. *Frontiers in genetics*, 15, 1345410.

Andrade-Brito DE, et al. (2023) Neuronal-specific methylome and hydroxymethylome analysis reveal replicated and novel loci associated with alcohol use disorder. *medRxiv* : the preprint server for health sciences.

Schaffner SL, et al. (2022) Alpha-synuclein overexpression induces epigenomic dysregulation of glutamate signaling and locomotor pathways. *Human molecular genetics*, 31(21), 3694.

Diddens J, et al. (2021) DNA Methylation Regulates Transcription Factor-Specific Neurodevelopmental but Not Sexually Dimorphic Gene Expression Dynamics in Zebra Finch Telencephalon. *Frontiers in cell and developmental biology*, 9, 583555.

Quilter CR, et al. (2021) Identification of methylation changes associated with positive and negative growth deviance in Gambian infants using a targeted methyl sequencing approach of genomic DNA. *FASEB bioAdvances*, 3(4), 205.

Taman H, et al. (2021) DNA hypo-methylation facilitates anti-inflammatory responses in severe ulcerative colitis. *PloS one*, 16(4), e0248905.

Roth K, et al. (2021) Clinically relevant aberrant Filip1l DNA methylation detected in a murine model of cutaneous squamous cell carcinoma. *EBioMedicine*, 67, 103383.

Orjuela S, et al. (2020) The DNA hypermethylation phenotype of colorectal cancer liver metastases resembles that of the primary colorectal cancers. *BMC cancer*, 20(1), 290.

Wang X, et al. (2020) Exploring DNA Methylation Profiles Altered in Cryptogenic Hepatocellular Carcinomas by High-Throughput Targeted DNA Methylation Sequencing: A Preliminary Study for Cryptogenic Hepatocellular Carcinoma. *OncoTargets and therapy*, 13, 9901.

Mulder CL, et al. (2020) Comparison of DNA methylation patterns of parentally imprinted genes in placenta derived from IVF conceptions in two different culture media. *Human reproduction (Oxford, England)*, 35(3), 516.

Szymczak S, et al. (2020) DNA methylation QTL analysis identifies new regulators of human longevity. *Human molecular genetics*, 29(7), 1154.

Ejarque M, et al. (2019) Adipose tissue mitochondrial dysfunction in human obesity is linked to a specific DNA methylation signature in adipose-derived stem cells. *International journal of obesity (2005)*, 43(6), 1256.

Huh I, et al. (2019) Detecting differential DNA methylation from sequencing of bisulfite converted DNA of diverse species. *Briefings in bioinformatics*, 20(1), 33.

Adam AC, et al. (2019) Profiling DNA methylation patterns of zebrafish liver associated with parental high dietary arachidonic acid. *PloS one*, 14(8), e0220934.