Resource Summary Report

Generated by <u>dkNET</u> on May 17, 2025

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

Funding:

Resource Name: BiSeq

Resource ID: SCR_012993

Alternate IDs: OMICS_00620

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250420T014628+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 28 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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.

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.

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.

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 Filip1I 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.

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

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.

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.

Sakurai K, et al. (2019) DNA methylome of human neonatal umbilical cord: Enrichment of differentially methylated regions compared to umbilical cord blood DNA at transcription factor genes involved in body patterning and effects of maternal folate deficiency or children's sex. PloS one, 14(5), e0214307.

Gomez-Cabrero D, et al. (2019) STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. Scientific data, 6(1), 256.