

Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

MethylSeekR

RRID:SCR_006513

Type: Tool

Proper Citation

MethylSeekR (RRID:SCR_006513)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/MethylSeekR.html>

Proper Citation: MethylSeekR (RRID:SCR_006513)

Description: A software package for the discovery of regulatory regions from Bis-seq data.

Abbreviations: MethylSeekR

Synonyms: MethylSeekR - Segmentation of Bis-seq data

Resource Type: software resource

Availability: GNU General Public License, v2 or greater

Resource Name: MethylSeekR

Resource ID: SCR_006513

Alternate IDs: OMICS_00607

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260725T190625+0000

Ratings and Alerts

No rating or validation information has been found for MethylSeekR.

No alerts have been found for MethylSeekR.

Data and Source Information

Usage and Citation Metrics

We found 54 mentions in open access literature.

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

Liu Y, et al. (2025) The genomic and epigenomic landscape of iridocorneal endothelial syndrome. *Genes & diseases*, 12(3), 101448.

Messingschlager M, et al. (2025) DNA methylation changes during acute COVID-19 are associated with long-term transcriptional dysregulation in patients' airway epithelial cells. *EMBO molecular medicine*, 17(5), 923.

Spector BL, et al. (2025) Methylation patterns of the nasal epigenome of hospitalized SARS-CoV-2 positive patients reveal insights into molecular mechanisms of COVID-19. *BMC medical genomics*, 18(1), 62.

Lehle JD, et al. (2024) An in vitro approach reveals molecular mechanisms underlying endocrine disruptor-induced epimutagenesis. *eLife*, 13.

Lorzadeh A, et al. (2024) DNA methylation-dependent and -independent binding of CDX2 directs activation of distinct developmental and homeostatic genes. *bioRxiv : the preprint server for biology*.

Balaramane D, et al. (2024) MethyLasso: a segmentation approach to analyze DNA methylation patterns and identify differentially methylated regions from whole-genome datasets. *Nucleic acids research*, 52(21), e98.

Angeloni A, et al. (2024) Extensive DNA methylome rearrangement during early lamprey embryogenesis. *Nature communications*, 15(1), 1977.

Tiedemann RL, et al. (2024) UHRF1 ubiquitin ligase activity supports the maintenance of low-density CpG methylation. *Nucleic acids research*, 52(22), 13733.

Fukagawa A, et al. (2023) Genomic and epigenomic integrative subtypes of renal cell carcinoma in a Japanese cohort. *Nature communications*, 14(1), 8383.

Bienkowska A, et al. (2023) Development of an epigenetic clock to predict visual age progression of human skin. *Frontiers in aging*, 4, 1258183.

Ballard JWO, et al. (2023) The Australasian dingo archetype: de novo chromosome-length genome assembly, DNA methylome, and cranial morphology. *GigaScience*, 12.

Feng Y, et al. (2023) A DNA methylation haplotype block landscape in human tissues and preimplantation embryos reveals regulatory elements defined by comethylation patterns. *Genome research*, 33(12), 2041.

Ballard JWO, et al. (2023) The Australasian dingo archetype: De novo chromosome-length genome assembly, DNA methylome, and cranial morphology. *bioRxiv : the preprint*

server for biology.

Zheng Y, et al. (2023) Comprehensive analyses of partially methylated domains and differentially methylated regions in esophageal cancer reveal both cell-type- and cancer-specific epigenetic regulation. *Genome biology*, 24(1), 193.

Field MA, et al. (2022) The Australian dingo is an early offshoot of modern breed dogs. *Science advances*, 8(16), eabm5944.

Ka-Yue Chow L, et al. (2022) Epigenomic landscape study reveals molecular subtypes and EBV-associated regulatory epigenome reprogramming in nasopharyngeal carcinoma. *EBioMedicine*, 86, 104357.

Li J, et al. (2022) Dnmt3a knockout in excitatory neurons impairs postnatal synapse maturation and increases the repressive histone modification H3K27me3. *eLife*, 11.

Zhou Q, et al. (2022) ASMdb: a comprehensive database for allele-specific DNA methylation in diverse organisms. *Nucleic acids research*, 50(D1), D60.

Edwards RJ, et al. (2021) Chromosome-length genome assembly and structural variations of the primal Basenji dog (*Canis lupus familiaris*) genome. *BMC genomics*, 22(1), 188.

Derrien J, et al. (2021) The DNA methylation landscape of multiple myeloma shows extensive inter- and inpatient heterogeneity that fuels transcriptomic variability. *Genome medicine*, 13(1), 127.