## **Resource Summary Report**

Generated by dkNET on Apr 28, 2025

# **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

Funding:

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:** 20250420T014332+0000

## **Ratings and Alerts**

No rating or validation information has been found for MethylSeekR.

#### Data and Source Information

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 51 mentions in open access literature.

**Listed below are recent publications.** The full list is available at dkNET.

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.

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

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

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.

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.

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.

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. 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 cancerspecific 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.

Hu X, et al. (2021) Evolution of DNA methylome from precancerous lesions to invasive lung adenocarcinomas. Nature communications, 12(1), 687.

Wang T, et al. (2021) Integrative Epigenome Map of the Normal Human Prostate Provides Insights Into Prostate Cancer Predisposition. Frontiers in cell and developmental biology, 9, 723676.

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

Stoyanova E, et al. (2021) 5-Hydroxymethylcytosine-mediated active demethylation is required for mammalian neuronal differentiation and function. eLife, 10.