

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

RnBeads

RRID:SCR_010958

Type: Tool

Proper Citation

RnBeads (RRID:SCR_010958)

Resource Information

URL: <http://rnbeads.bioinf.mpi-inf.mpg.de/>

Proper Citation: RnBeads (RRID:SCR_010958)

Description: An R package for comprehensive analysis of DNA methylation data obtained with any experimental protocol that provides single-CpG resolution, including Infinium 450K microarray and bisulfite sequencing protocols, but also MeDIP-seq and MBD-seq., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: RnBeads

Resource Type: software resource

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: RnBeads

Resource ID: SCR_010958

Alternate IDs: OMICS_00800

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260912T195726+0000

Ratings and Alerts

No rating or validation information has been found for RnBeads.

No alerts have been found for RnBeads.

Data and Source Information

Usage and Citation Metrics

We found 299 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Parker H, et al. (2026) High-risk molecular features may eclipse genomic complexity in predicting chronic lymphocytic leukemia outcomes; UK clinical trial insights. *Leukemia*, 40(4), 816.

Tout I, et al. (2025) The integrative genomic and functional immunological analyses of colorectal cancer initiating cells to modulate stemness properties and the susceptibility to immune responses. *Journal of translational medicine*, 23(1), 193.

Chicón-Bosch M, et al. (2025) Multi-omics profiling reveals key factors involved in Ewing sarcoma metastasis. *Molecular oncology*, 19(4), 1002.

Werr L, et al. (2025) TERT Expression and Clinical Outcome in Pulmonary Carcinoids. *Journal of clinical oncology : official journal of the American Society of Clinical Oncology*, 43(2), 214.

Zhang T, et al. (2025) Deciphering lung adenocarcinoma evolution and the role of LINE-1 retrotransposition. *bioRxiv : the preprint server for biology*.

Ochoa E, et al. (2025) Germline variants in UHRF1 are associated with multilocus imprinting disturbance in humans and mice. *Proceedings of the National Academy of Sciences of the United States of America*, 122(34), e2505884122.

Razzaq A, et al. (2025) Exploring Differentially Methylated Genes among Preterm Birth and Full-Term Birth. *Lifestyle genomics*, 18(1), 76.

Mertens J, et al. (2025) An accelerated human in-vitro aging model mimics in-vivo aging and facilitates dynamic testing of anti-aging compounds. *Research square*.

Bejaoui Y, et al. (2025) The role of protective genetic variants in modulating epigenetic aging. *GeroScience*, 47(4), 5995.

Palczewski MB, et al. (2025) Nitric oxide inhibits ten-eleven translocation DNA demethylases to regulate 5mC and 5hmC across the genome. *Nature communications*, 16(1), 1732.

Rodriguez-Sosa A, et al. (2025) Multiomic Sequencing Reveals Distinctive Gene Expression and Epigenetic Alterations Associated With Primary Sclerosing Cholangitis Development in Treatment-Naïve Pediatric Ulcerative Colitis. *Gastro hep advances*, 4(3), 100586.

Umrath F, et al. (2025) Revitalizing the Epigenome of Adult Jaw Periosteal Cells: Enhancing Diversity in iPSC-Derived Mesenchymal Stem Cells (iMSCs). *Cells*, 14(9).

Melhorn P, et al. (2025) Methylation Profiles Differ According to Clinical Characteristics in Well-Differentiated Neuroendocrine Tumors of the Lung. *Endocrine pathology*, 36(1), 6.

Loi E, et al. (2025) DNA Methylation in macrophages infected with *Leishmania* spp. in different culture conditions. *Emerging microbes & infections*, 14(1), 2508766.

Scherer M, et al. (2025) Clonal tracing with somatic epimutations reveals dynamics of blood ageing. *Nature*, 643(8071), 478.

Pirini F, et al. (2025) Comprehensive genetic and epigenetic characterization of Lynch-like syndrome patients. *International journal of cancer*, 157(4), 788.

Stasi A, et al. (2025) mTOR Inhibition limits LPS induced acute kidney injury and ameliorates hallmarks of cellular senescence. *Scientific reports*, 15(1), 9635.

Berg F, et al. (2025) Development and validation of a novel cell type estimation method for targeted bisulfite sequencing data. *Epigenomics*, 17(6), 389.

Welsh H, et al. (2025) Age-related changes in DNA methylation in a sample of elderly Brazilians. *Clinical epigenetics*, 17(1), 17.

Eulalio T, et al. (2025) regionalpcs improve discovery of DNA methylation associations with complex traits. *Nature communications*, 16(1), 368.