

# Resource Summary Report

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## 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:** 20260725T190709+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 298 mentions in open access literature.

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

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.

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.

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

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.

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.

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.

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

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*.

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

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.

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).

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

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

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

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

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

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.

Leroy M, et al. (2025) Long-term outcome of oesophageal atresia in adolescence (TransEAsome): a national French cohort study protocol. *BMJ open*, 15(1), e086303.