# **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.

Abbreviations: RnBeads

Resource Type: software resource

Funding:

Resource Name: RnBeads

Resource ID: SCR\_010958

Alternate IDs: OMICS\_00800

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250420T014516+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

Source: SciCrunch Registry

### **Usage and Citation Metrics**

We found 276 mentions in open access literature.

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

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.

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

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.

English A, et al. (2024) Genomic, Proteomic, and Phenotypic Biomarkers of COVID-19 Severity: Protocol for a Retrospective Observational Study. JMIR research protocols, 13, e50733.

Win PW, et al. (2024) Simultaneous assessment of mitochondrial DNA copy number and nuclear epigenetic age towards predictive models of development and aging. BMC research notes, 17(1), 21.

Nair VD, et al. (2024) Protocol for high-throughput DNA methylation profiling in rat tissues using automated reduced representation bisulfite sequencing. STAR protocols, 5(2), 103007.

Nair VD, et al. (2024) Molecular adaptations in response to exercise training are associated with tissue-specific transcriptomic and epigenomic signatures. Cell genomics, 4(6), 100421.

Thomas D, et al. (2024) Nitric oxide inhibits ten-eleven translocation DNA demethylases to regulate 5mC and 5hmC across the genome. Research square.

Sultanov R, et al. (2024) TP63-TRIM29 axis regulates enhancer methylation and chromosomal instability in prostate cancer. Epigenetics & chromatin, 17(1), 6.

Danielewicz H, et al. (2024) Cord blood methylation at TNFRSF17 is associated with early allergic phenotypes. Immunologic research, 72(6), 1259.

Das S, et al. (2024) Universal penalized regression (Elastic-net) model with differentially methylated promoters for oral cancer prediction. European journal of medical research, 29(1), 458.

Dalton GD, et al. (2024) Transcriptome analysis identifies an ASD-Like phenotype in

oligodendrocytes and microglia from C58/J amygdala that is dependent on sex and sociability. Behavioral and brain functions : BBF, 20(1), 14.

Yu Z, et al. (2024) DNA methylation profiling identifies TBKBP1 as potent amplifier of cytotoxic activity in CMV-specific human CD8+ T cells. PLoS pathogens, 20(9), e1012581.

Ressler JM, et al. (2024) DNA Methylation Signatures Correlate with Response to Immune Checkpoint Inhibitors in Metastatic Melanoma. Targeted oncology, 19(2), 263.

Kristjansson D, et al. (2024) Sex differences in DNA methylation variations according to ART conception-evidence from the Norwegian mother, father, and child cohort study. Scientific reports, 14(1), 22904.

Nishizawa Y, et al. (2024) Epigenetic signals associated with delirium replicated across four independent cohorts. Translational psychiatry, 14(1), 275.

Pinton A, et al. (2024) PHF6-altered T-ALL Harbor Epigenetic Repressive Switch at Bivalent Promoters and Respond to 5-Azacitidine and Venetoclax. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(1), 94.

Zhang W, et al. (2024) Critical evaluation of the reliability of DNA methylation probes on the Illumina MethylationEPIC v1.0 BeadChip microarrays. Epigenetics, 19(1), 2333660.

Crombach A, et al. (2024) Differential methylation of linoleic acid pathway genes is associated with PTSD symptoms - a longitudinal study with Burundian soldiers returning from a war zone. Translational psychiatry, 14(1), 32.

Daenekas B, et al. (2024) Conumee 2.0: enhanced copy-number variation analysis from DNA methylation arrays for humans and mice. Bioinformatics (Oxford, England), 40(2).