# **Resource Summary Report**

Generated by dkNET on Apr 25, 2025

# **methyAnalysis**

RRID:SCR\_001290

Type: Tool

### **Proper Citation**

methyAnalysis (RRID:SCR\_001290)

#### **Resource Information**

URL: http://www.bioconductor.org/packages/release/bioc/html/methyAnalysis.html

Proper Citation: methyAnalysis (RRID:SCR\_001290)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. Software package for DNA methylation data analysis and visualization. A new class is defined to keep the chromosome location information together with the data. The current version of the package mainly focuses on analyzing the Illumina Infinium methylation array data, but most methods can be generalized to other methylation array or sequencing data.

**Abbreviations:** methyAnalysis

**Synonyms:** methyAnalysis - DNA methylation data analysis and visualization

**Resource Type:** software resource

**Defining Citation: PMID:21159174** 

**Keywords:** dna methylation, microarray, visualization

**Funding:** 

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: methyAnalysis

Resource ID: SCR 001290

Alternate IDs: OMICS\_02046

**Record Creation Time:** 20220129T080206+0000

**Record Last Update:** 20250420T014025+0000

## Ratings and Alerts

No rating or validation information has been found for methyAnalysis.

No alerts have been found for methyAnalysis.

#### Data and Source Information

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 9 mentions in open access literature.

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

McKinney BC, et al. (2019) DNA methylation in the human frontal cortex reveals a putative mechanism for age-by-disease interactions. Translational psychiatry, 9(1), 39.

Kan S, et al. (2019) DNA methylation profiling identifies potentially significant epigenetically-regulated genes in glioblastoma multiforme. Oncology letters, 18(2), 1679.

Janssens S, et al. (2018) Zika Virus Alters DNA Methylation of Neural Genes in an Organoid Model of the Developing Human Brain. mSystems, 3(1).

Daemen A, et al. (2018) HER2 is not a cancer subtype but rather a pan-cancer event and is highly enriched in AR-driven breast tumors. Breast cancer research: BCR, 20(1), 8.

Xu J, et al. (2017) An integrative analysis of DNA methylation in osteosarcoma. Journal of bone oncology, 9, 34.

Zhang K, et al. (2017) Screening of candidate key genes associated with human osteosarcoma using bioinformatics analysis. Oncology letters, 14(3), 2887.

Khuc E, et al. (2017) Comprehensive characterization of DNA methylation changes in Fuchs endothelial corneal dystrophy. PloS one, 12(4), e0175112.

Li D, et al. (2015) An evaluation of statistical methods for DNA methylation microarray data analysis. BMC bioinformatics, 16, 217.

Assenov Y, et al. (2014) Comprehensive analysis of DNA methylation data with RnBeads. Nature methods, 11(11), 1138.