

Resource Summary Report

Generated by SPARC SAWG on Sep 15, 2026

Marmal-aid

RRID:SCR_010956

Type: Tool

Proper Citation

Marmal-aid (RRID:SCR_010956)

Resource Information

URL: <http://marmal-aid.org/>

Proper Citation: Marmal-aid (RRID:SCR_010956)

Description: A combined database and R package that allows you to investigate the methylation state of regions of interest across the genome.

Abbreviations: Marmal-aid

Resource Type: data or information resource, database, software resource

Defining Citation: [PMID:24330312](#)

Availability: Acknowledgement requested

Resource Name: Marmal-aid

Resource ID: SCR_010956

Alternate IDs: OMICS_00796

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260912T195726+0000

Ratings and Alerts

No rating or validation information has been found for Marmal-aid.

No alerts have been found for Marmal-aid.

Data and Source Information

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Kondrup K, et al. (2026) Genome-wide methylome profiling of cell-free DNA enables prognostication of patients with castration-resistant prostate cancer. *British journal of cancer*, 135(1), 127.

Macartney-Coxson D, et al. (2020) DNA methylation in blood-Potential to provide new insights into cell biology. *PloS one*, 15(11), e0241367.

Bjerre MT, et al. (2020) Epigenetic Analysis of Circulating Tumor DNA in Localized and Metastatic Prostate Cancer: Evaluation of Clinical Biomarker Potential. *Cells*, 9(6).

Bjerre MT, et al. (2019) Aberrant DOCK2, GRASP, HIF3A and PKFP Hypermethylation has Potential as a Prognostic Biomarker for Prostate Cancer. *International journal of molecular sciences*, 20(5).

Saffari A, et al. (2018) Estimation of a significance threshold for epigenome-wide association studies. *Genetic epidemiology*, 42(1), 20.

Feber A, et al. (2017) UroMark-a urinary biomarker assay for the detection of bladder cancer. *Clinical epigenetics*, 9, 8.

Mundbjerg K, et al. (2017) Identifying aggressive prostate cancer foci using a DNA methylation classifier. *Genome biology*, 18(1), 3.

Benton MC, et al. (2017) Methylome-wide association study of whole blood DNA in the Norfolk Island isolate identifies robust loci associated with age. *Aging*, 9(3), 753.

Macartney-Coxson D, et al. (2017) Genome-wide DNA methylation analysis reveals loci that distinguish different types of adipose tissue in obese individuals. *Clinical epigenetics*, 9, 48.

Jeyapalan JN, et al. (2016) DNA methylation analysis of paediatric low-grade astrocytomas identifies a tumour-specific hypomethylation signature in pilocytic astrocytomas. *Acta neuropathologica communications*, 4(1), 54.

Blackburn J, et al. (2016) Damage-inducible intragenic demethylation of the human TP53 tumor suppressor gene is associated with transcription from an alternative intronic promoter. *Molecular carcinogenesis*, 55(12), 1940.

Noor DAM, et al. (2016) Genome-wide methylation analysis identifies genes silenced in non-seminoma cell lines. *NPJ genomic medicine*, 1, 15009.

Field MG, et al. (2016) Epigenetic reprogramming and aberrant expression of PRAME are associated with increased metastatic risk in Class 1 and Class 2 uveal melanomas.

Oncotarget, 7(37), 59209.

Lim AM, et al. (2016) Genome-scale methylation assessment did not identify prognostic biomarkers in oral tongue carcinomas. *Clinical epigenetics*, 8, 74.

Dai W, et al. (2015) Comparative methylome analysis in solid tumors reveals aberrant methylation at chromosome 6p in nasopharyngeal carcinoma. *Cancer medicine*, 4(7), 1079.

Benton MC, et al. (2015) An analysis of DNA methylation in human adipose tissue reveals differential modification of obesity genes before and after gastric bypass and weight loss. *Genome biology*, 16(1), 8.

Hillman SL, et al. (2015) Novel DNA methylation profiles associated with key gene regulation and transcription pathways in blood and placenta of growth-restricted neonates. *Epigenetics*, 10(1), 50.

Charlton J, et al. (2014) Methylome analysis identifies a Wilms tumor epigenetic biomarker detectable in blood. *Genome biology*, 15(8), 434.

Lowe R, et al. (2013) Marmal-aid--a database for Infinium HumanMethylation450. *BMC bioinformatics*, 14, 359.

Lowe R, et al. (2013) Report on the 2nd Annual Infinium Humanmethylation450 Array Workshop: 15 April 2013 QMUL, London, UK. *Epigenetics*, 8(10), 1123.