

# Resource Summary Report

Generated by [dkNET](#) on Sep 8, 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:** 20260905T132651+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 [dkNET](#) .

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.

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.

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

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) Marmalaid--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.