

Resource Summary Report

Generated by [dkNET](#) on Sep 11, 2026

[ramr](#)

RRID:SCR_024408

Type: Tool

Proper Citation

ramr (RRID:SCR_024408)

Resource Information

URL: <https://bioconductor.org/packages/ramr/>

Proper Citation: ramr (RRID:SCR_024408)

Description: Software R package for detection of low frequency aberrant methylation events in large data sets obtained by methylation profiling using array or high-throughput bisulfite sequencing. Provides functions to visualize found aberrantly methylated regions, to generate sets of all possible regions to be used as reference sets for enrichment analysis, and to generate biologically relevant test data sets for performance evaluation of AMR/DMR search algorithms.

Synonyms: rare aberrantly methylated regions

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:34383893](#)

Keywords: rare aberrantly methylated regions, low frequency aberrant methylation events detection, visualize found aberrantly methylated regions,

Funding: K.G. Jebsen foundation ;
Norwegian Cancer Society ;
Norwegian Health Region West ;
Norwegian Research Council

Availability: Free, Available for download, Freely available

Resource Name: ramr

Resource ID: SCR_024408

Alternate URLs: <https://github.com/BBCG/ramr>

License: Artistic-2.0

Record Creation Time: 20230912T050221+0000

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Ratings and Alerts

No rating or validation information has been found for ramr.

No alerts have been found for ramr.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.