

Resource Summary Report

Generated by [dkNET](#) on Aug 17, 2026

[cgmapotools](#)

RRID:SCR_020950

Type: Tool

Proper Citation

cgmapotools (RRID:SCR_020950)

Resource Information

URL: <https://cgmaptools.github.io>

Proper Citation: cgmapotools (RRID:SCR_020950)

Description: Software package for DNA methylation analysis. Used for context-wise, gene-wise, bin-wise, region-wise and sample-wise analysis and visualizations. Used to improve precision of heterozygous SNV calls and supports allele-specific methylation detection and visualization in bisulfite-sequencing data.

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

Defining Citation: [PMID:28968643](#)

Keywords: DNA methylomes analysis, DNA methylomes, context-wise analysis, gene-wise analysis, bin-wise analysis, region-wise analysis, sample-wise analysis, bisulfite sequencing data, allele specific methylation detection

Funding: National Key Research and Development Program of China ;
National Natural Science Foundation of China

Availability: Free, Available for download, Freely available

Resource Name: cgmapotools

Resource ID: SCR_020950

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260817T040637+0000

Ratings and Alerts

No rating or validation information has been found for cgmapotools.

No alerts have been found for cgmapotools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Zhang W, et al. (2022) TARSII and CARSII: Two approaches for SNP-independent identification of germline differentially methylated regions in mammals. STAR protocols, 3(2), 101240.

Chu C, et al. (2021) Analysis of developmental imprinting dynamics in primates using SNP-free methods to identify imprinting defects in cloned placenta. Developmental cell, 56(20), 2826.

Catania S, et al. (2020) Evolutionary Persistence of DNA Methylation for Millions of Years after Ancient Loss of a De Novo Methyltransferase. Cell, 180(2), 263.