

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 18, 2026

QDMR

RRID:SCR_007162

Type: Tool

Proper Citation

QDMR (RRID:SCR_007162)

Resource Information

URL: <http://202.97.205.78/epidiff/QDMRTutorial.jsp>

Proper Citation: QDMR (RRID:SCR_007162)

Description: Software that provides a quantitative approach to quantify methylation difference and identify DMRs from genome-wide methylation profiles by adapting Shannon entropy.

Abbreviations: QDMR

Resource Type: software resource

Resource Name: QDMR

Resource ID: SCR_007162

Alternate IDs: OMICS_00623

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260912T195650+0000

Ratings and Alerts

No rating or validation information has been found for QDMR.

No alerts have been found for QDMR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Xu B, et al. (2024) Identification of colon cancer subtypes based on multi-omics data-construction of methylation markers for immunotherapy. *Frontiers in oncology*, 14, 1335670.

Kosten C, et al. (2024) Evaluating the effectiveness of prompt engineering for knowledge graph question answering. *Frontiers in artificial intelligence*, 7, 1454258.

Liu Y, et al. (2022) Excavation of Molecular Subtypes of Endometrial Cancer Based on DNA Methylation. *Genes*, 13(11).

Lian Q, et al. (2020) DNA methylation data-based molecular subtype classification and prediction in patients with gastric cancer. *Cancer cell international*, 20, 349.

Chen W, et al. (2019) DNA methylation-based classification and identification of renal cell carcinoma prognosis-subgroups. *Cancer cell international*, 19, 185.

Su J, et al. (2018) Homeobox oncogene activation by pan-cancer DNA hypermethylation. *Genome biology*, 19(1), 108.

Tian S, et al. (2016) DNA Methylation Heterogeneity Patterns in Breast Cancer Cell Lines. *Cancer informatics*, 15(Supple 4), 1.

Liu H, et al. (2013) Quantitative epigenetic co-variation in CpG islands and co-regulation of developmental genes. *Scientific reports*, 3, 2576.