

Resource Summary Report

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QUMA

RRID:SCR_010907

Type: Tool

Proper Citation

QUMA (RRID:SCR_010907)

Resource Information

URL: <http://quma.cdb.riken.jp/>

Proper Citation: QUMA (RRID:SCR_010907)

Description: You can easily align, visualize and quantify bisulfite sequence data for CpG methylation analysis.

Abbreviations: QUMA

Synonyms: QUantification tool for Methylation Analysis

Resource Type: software resource

Keywords: bio.tools

Resource Name: QUMA

Resource ID: SCR_010907

Alternate IDs: OMICS_00588, biotools:quma

Alternate URLs: <https://bio.tools/quma>

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260808T185925+0000

Ratings and Alerts

No rating or validation information has been found for QUMA.

No alerts have been found for QUMA.

Data and Source Information

Usage and Citation Metrics

We found 398 mentions in open access literature.

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

Santerre M, et al. (2026) HIV Vpr induces demethylation of the SNCA antisense promoter, leading to neurocognitive impairment. *Scientific reports*, 16(1), 6078.

Huang E, et al. (2026) OGDH mediates α -ketoglutarate-induced follicular development and antioxidative response by interacting with CAT/SOD2. *Biological research*, 59(1).

Xu J, et al. (2026) Ketogenic diet can inhibit epileptic seizures by inhibiting RGMA methylation to promote GluA1 palmitoylation in the epileptic rat model. *Nutrition & metabolism*, 23(1), 30.

Li T, et al. (2026) Innate immune sensing via the cGAS-STING pathway restricts extrachromosomal DNA-driven tumorigenesis. *bioRxiv : the preprint server for biology*.

Ju S, et al. (2026) A versatile VLP-mediated CRISPR-RNP platform for precise genome editing and durable epigenome silencing in cancer. *Molecular therapy. Nucleic acids*, 37(3), 102978.

Wu X, et al. (2026) Endogenous VEGF signaling acts as a guardian of human primed pluripotency. *Nature communications*, 17(1).

Yang F, et al. (2026) Inflammatory memory disables a DDR1 degradation checkpoint to enable pancreatic cancer growth. *bioRxiv : the preprint server for biology*.

Wan C, et al. (2026) Reconstitution of spermatogenesis and continuous generation of functional haploid germ cells in mouse testicular organoids. *Nature communications*, 17(1).

Zhang Q, et al. (2026) Construction of a DNA Methylation Map of Argali Hybrid Sheep During Mo Infection. *Microorganisms*, 14(3).

Yang Z, et al. (2026) Effects of Betaine on DNA Methylation Level, Expression Level, and Fat Synthesis of VNN1 in Goose Hepatocytes. *Animals : an open access journal from MDPI*, 16(4).

Wang Q, et al. (2026) DNA methylation regulation of CYP450-lipid metabolism by high-altitude hypoxia: linking neuroinflammation to cognitive impairment. *Journal of neuroinflammation*, 23(1).

Li J, et al. (2026) In vitro mimicking of humanized cardiogenesis under porcine condition. *Cell & bioscience*, 16(1), 22.

Hayashi Y, et al. (2025) Glial cells missing 1 triggers gliosis and angiogenesis after neonatal brain injury. *iScience*, 28(11), 113860.

Amistadi S, et al. (2025) Dissecting the epigenetic regulation of the fetal hemoglobin genes to unravel a novel therapeutic approach for β -hemoglobinopathies. *Nucleic acids research*, 53(13).

Zhou X, et al. (2025) Potentiating anti-tumor immunity by re-engaging immune synapse molecules. *Cell reports. Medicine*, 6(3), 101975.

Wang X, et al. (2025) DNA Methylation of Igf2r Promoter CpG Island 2 Governs Cis-Acting Inheritance and Gene Dosage in Equine Hybrids. *Biology*, 14(6).

Hashimoto K, et al. (2025) STAT1-mediated epigenetic regulation of LIN28A controls iPSC-derived platelet production through the let-7-RALB axis. *Blood advances*, 9(17), 4345.

Hali S, et al. (2025) Differentiation Defect Into GABAergic Neurons in Cerebral Organoids From Autism Patients. *CNS neuroscience & therapeutics*, 31(6), e70449.

Hara S, et al. (2025) Identification of maternal allele sequences of IG-DMR that are essential for neonatal viability. *PloS one*, 20(5), e0324882.

Qian W, et al. (2025) Selective identification of epigenetic regulators at methylated genomic sites by SelectID. *Nature communications*, 16(1), 3709.