

Resource Summary Report

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BISMA

RRID:SCR_000688

Type: Tool

Proper Citation

BISMA (RRID:SCR_000688)

Resource Information

URL: <http://services.ibc.uni-stuttgart.de/BDPC/BISMA/>

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Description: An online tool for the analysis of bisulfite sequencing DNA methylation data. The software has specificity and quality control functions that allow the user to compile a set of sequences.

Synonyms: Bisulfite Sequencing DNA Methylation Analysis, BISMA: Analysis of primary bisulfite sequencing data manual

Resource Type: web application, software resource

Defining Citation: [PMID:20459626](#)

Keywords: bisulfite sequencing, dna methylation, quality control

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: BISMA

Resource ID: SCR_000688

Alternate IDs: OMICS_00592

Record Creation Time: 20220129T080203+0000

Record Last Update: 20260728T043101+0000

Ratings and Alerts

No rating or validation information has been found for BISMA.

No alerts have been found for BISMA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Tatarakis A, et al. (2025) Requirements for establishment and epigenetic stability of mammalian heterochromatin. *Molecular cell*, 85(18), 3388.

Guo D, et al. (2022) iMyoblasts for ex vivo and in vivo investigations of human myogenesis and disease modeling. *eLife*, 11.

Mazurek S, et al. (2021) Disruption of RING and PHD Domains of TRIM28 Evokes Differentiation in Human iPSCs. *Cells*, 10(8).

Yang BH, et al. (2019) TCF1 and LEF1 Control Treg Competitive Survival and Tfr Development to Prevent Autoimmune Diseases. *Cell reports*, 27(12), 3629.

Periyasamy P, et al. (2018) Epigenetic Promoter DNA Methylation of miR-124 Promotes HIV-1 Tat-Mediated Microglial Activation via MECP2-STAT3 Axis. *The Journal of neuroscience : the official journal of the Society for Neuroscience*, 38(23), 5367.

Alvizi L, et al. (2017) Differential methylation is associated with non-syndromic cleft lip and palate and contributes to penetrance effects. *Scientific reports*, 7(1), 2441.

Yuan X, et al. (2017) CRlg, a tissue-resident macrophage specific immune checkpoint molecule, promotes immunological tolerance in NOD mice, via a dual role in effector and regulatory T cells. *eLife*, 6.

Rani L, et al. (2017) Genome-wide DNA methylation profiling integrated with gene expression profiling identifies PAX9 as a novel prognostic marker in chronic lymphocytic leukemia. *Clinical epigenetics*, 9, 57.

Veith N, et al. (2016) Mechanisms underlying epigenetic and transcriptional heterogeneity in Chinese hamster ovary (CHO) cell lines. *BMC biotechnology*, 16, 6.

Das S, et al. (2016) Influence of Repressive Histone and DNA Methylation upon D4Z4 Transcription in Non-Myogenic Cells. *PloS one*, 11(7), e0160022.

Li Z, et al. (2015) Gadd45a promotes DNA demethylation through TDG. *Nucleic acids research*, 43(8), 3986.

Megiorni F, et al. (2014) Deep Sequencing the microRNA profile in rhabdomyosarcoma reveals down-regulation of miR-378 family members. *BMC cancer*, 14, 880.

Guo F, et al. (2014) Active and passive demethylation of male and female pronuclear DNA in the mammalian zygote. *Cell stem cell*, 15(4), 447.