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: software resource, web application

Defining Citation: PMID:20459626

Keywords: bisulfite sequencing, dna methylation, quality control

Funding:

Availability: Freely available for academic use, Commercial use with purchase of a commercial license

Resource Name: BISMA

Resource ID: SCR_000688

Alternate IDs: OMICS_00592

Record Creation Time: 20220129T080203+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 12 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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) CRIg, 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.