

Resource Summary Report

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BSeQC

RRID:SCR_005428

Type: Tool

Proper Citation

BSeQC (RRID:SCR_005428)

Resource Information

URL: <http://code.google.com/p/bseqc/>

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Description: A quality control software package specially for bisulfite sequencing experiments. It can comprehensively evaluate the quality of BS-seq experiments and automatically trim nucleotides with potential technical biases. In addition, BSeQC also support removing duplicate reads and keeping one copy of the overlapping segment in paired-end sequencing.

Abbreviations: BSeQC

Synonyms: BSeQC: Quality Control of bisulfite sequencing experiments

Resource Type: software resource

Keywords: bisulfite sequencing, bisulfite, sequencing

Availability: Artistic License, GNU General Public License

Resource Name: BSeQC

Resource ID: SCR_005428

Alternate IDs: OMICS_00572

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260725T190606+0000

Ratings and Alerts

No rating or validation information has been found for BSeQC.

No alerts have been found for BSeQC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Laajala E, et al. (2022) Permutation-based significance analysis reduces the type 1 error rate in bisulphite sequencing data analysis of human umbilical cord blood samples. *Epigenetics*, 17(12), 1608.

Gu T, et al. (2018) DNMT3A and TET1 cooperate to regulate promoter epigenetic landscapes in mouse embryonic stem cells. *Genome biology*, 19(1), 88.

Li J, et al. (2018) Decoding the dynamic DNA methylation and hydroxymethylation landscapes in endodermal lineage intermediates during pancreatic differentiation of hESC. *Nucleic acids research*, 46(6), 2883.

Lin X, et al. (2017) Sparse conserved under-methylated CpGs are associated with high-order chromatin structure. *Genome biology*, 18(1), 163.

Lio CW, et al. (2016) Tet2 and Tet3 cooperate with B-lineage transcription factors to regulate DNA modification and chromatin accessibility. *eLife*, 5.

Sun Z, et al. (2015) Base resolution methylome profiling: considerations in platform selection, data preprocessing and analysis. *Epigenomics*, 7(5), 813.