Resource Summary Report

Generated by <u>dkNET</u> on Apr 30, 2025

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

Funding:

Availability: Artistic License, GNU General Public License

Resource Name: BSeQC

Resource ID: SCR_005428

Alternate IDs: OMICS_00572

Record Creation Time: 20220129T080230+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 <u>dkNET</u>.

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.

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.

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

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.