Resource Summary Report

Generated by Kravitz on Sep 19, 2026

BSmooth

RRID:SCR_005693
Type: Tool

Proper Citation

BSmooth (RRID:SCR_005693)

Resource Information

URL: http://rafalab.jhsph.edu/bsmooth/

Proper Citation: BSmooth (RRID:SCR_005693)

Description: A pipeline for analyzing whole genome bisulfite sequencing (WGBS) data.

Abbreviations: BSmooth

Resource Type: software resource

Resource Name: BSmooth

Resource ID: SCR_005693

Alternate IDs: OMICS_00581

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260912T195630+0000

Ratings and Alerts

No rating or validation information has been found for BSmooth.

No alerts have been found for BSmooth.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 29 mentions in open access literature.

Listed below are recent publications. The full list is available at Kravitz .

Breen K, et al. (2026) Duration of contact sports play associated with aberrant DNA methylation in human frontal cortex. Research square.

DiFrank AJ, et al. (2026) Putative Imprinting Control Regions with Aberrant Blood-Based DNA Methylation are Associated with Hepatocellular Carcinoma Risk. Journal of hepatocellular carcinoma, 13, 605131.

Gansou Y, et al. (2026) A Functional Approach to Testing Overall Effect of Interaction Between DNA Methylation and SNPs. Statistics in medicine, 45(1-2), e70364.

Liu Y, et al. (2025) Long-read sequencing of single cell-derived melanoma subclones reveals divergent and parallel genomic and epigenomic evolutionary trajectories. bioRxiv : the preprint server for biology.

Lehle JD, et al. (2024) An in vitro approach reveals molecular mechanisms underlying endocrine disruptor-induced epimutagenesis. eLife, 13.

Benjamin KJM, et al. (2024) Analysis of gene expression in the postmortem brain of neurotypical Black Americans reveals contributions of genetic ancestry. Nature neuroscience, 27(6), 1064.

Baetens M, et al. (2024) Advancing diagnosis and early risk assessment of preeclampsia through noninvasive cell-free DNA methylation profiling. Clinical epigenetics, 16(1), 182.

Donato L, et al. (2024) The genomic mosaic of mitochondrial dysfunction: Decoding nuclear and mitochondrial epigenetic contributions to maternally inherited diabetes and deafness pathogenesis. Heliyon, 10(14), e34756.

Luo X, et al. (2023) Recall DNA methylation levels at low coverage sites using a CNN model in WGBS. PLoS computational biology, 19(6), e1011205.

Perzel Mandell KA, et al. (2022) Molecular phenotypes associated with antipsychotic drugs in the human caudate nucleus. Molecular psychiatry, 27(4), 2061.

Park B, et al. (2022) Particulate matter air pollution exposure disrupts the Nrf2 pathway in sinonasal epithelium via epigenetic alterations in a murine model. International forum of allergy & rhinology, 12(11), 1424.

Stenz L, et al. (2022) Altered DNA methylation in estrogen-responsive repetitive sequences of spermatozoa of infertile men with shortened anogenital distance. Clinical epigenetics, 14(1), 185.

Singh D, et al. (2021) Koala methylomes reveal divergent and conserved DNA methylation signatures of X chromosome regulation. Proceedings. Biological sciences, 288(1945), 20202244.

Kapourani CA, et al. (2021) scMET: Bayesian modeling of DNA methylation heterogeneity at single-cell resolution. Genome biology, 22(1), 114.

Lutz PE, et al. (2021) Non-CG methylation and multiple histone profiles associate child abuse with immune and small GTPase dysregulation. Nature communications, 12(1), 1132.

Liu P, et al. (2021) Altered DNA methylation pattern reveals epigenetic regulation of Hox genes in thoracic aortic dissection and serves as a biomarker in disease diagnosis. Clinical epigenetics, 13(1), 124.

Perzel Mandell KA, et al. (2021) Genome-wide sequencing-based identification of methylation quantitative trait loci and their role in schizophrenia risk. Nature communications, 12(1), 5251.

Deng M, et al. (2020) DNA methylation dynamics during zygotic genome activation in goat. Theriogenology, 156, 144.

Lutsik P, et al. (2020) Globally altered epigenetic landscape and delayed osteogenic differentiation in H3.3-G34W-mutant giant cell tumor of bone. Nature communications, 11(1), 5414.

Ma Y, et al. (2020) Methylation silencing of TGF-?? receptor type II is involved in malignant transformation of esophageal squamous cell carcinoma. Clinical epigenetics, 12(1), 25.