

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 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:** 20260725T190610+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 27 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

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

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.

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.

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.

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.

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.

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

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- $\beta$  receptor type II is involved in malignant transformation of esophageal squamous cell carcinoma. Clinical epigenetics, 12(1), 25.

Luz-Madrigal A, et al. (2020) DNA demethylation is a driver for chick retina regeneration. Epigenetics, 15(9), 998.

Wulfridge P, et al. (2019) Analyzing whole genome bisulfite sequencing data from highly divergent genotypes. Nucleic acids research, 47(19), e117.