

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 18, 2026

BSmooth-align

RRID:SCR_000013

Type: Tool

Proper Citation

BSmooth-align (RRID:SCR_000013)

Resource Information

URL: <https://github.com/BenLangmead/bsmooth-align>

Proper Citation: BSmooth-align (RRID:SCR_000013)

Description: Software statistics and alignment pipeline that performs the alignment of bisulfite sequence reads and tabulates read-level methylation measurements.

Resource Type: alignment software, data analysis software, data processing software, image analysis software, software application, software resource

Keywords: bisulfite sequence, read-level methylation, bisulfite sequence reads alignment,

Availability: Free, Available for download, Freely available

Resource Name: BSmooth-align

Resource ID: SCR_000013

Alternate IDs: OMICS_01846

License: GPL v3, Apache License

License URLs: <https://help.github.com/articles/github-terms-of-service/>

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260912T195501+0000

Ratings and Alerts

No rating or validation information has been found for BSmooth-align.

No alerts have been found for BSmooth-align.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.