

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 2026

## BSSim

RRID:SCR\_001212

Type: Tool

### Proper Citation

BSSim (RRID:SCR\_001212)

### Resource Information

**URL:** <http://122.228.158.106/BSSim/>

**Proper Citation:** BSSim (RRID:SCR\_001212)

**Description:** Software to mimic various methylation level and bisulfite conversion rate in CpG, CHG and CHH context, respectively. It can also simulate genetic variations that are divergent from the reference sequence along with the sequencing error and quality distributions. In the output, both directional/non-directional, various read length, single/paired-end reads and alignment data in the SAM format can be generated. BSSim is a cross-platform BS-seq simulator offers output read datasets not only suitable for Illumina's Solexa, but also for Roche's 454 and Applied Biosystems' SOLiD.

**Abbreviations:** BSSim

**Synonyms:** BSSim: Bisulfite sequencing simulator for next-generation sequencing

**Resource Type:** software resource

**Keywords:** bisulfite sequencing, simulator, next-generation sequencing, python, dna methylation, snp, read quality

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** BSSim

**Resource ID:** SCR\_001212

**Alternate IDs:** OMICS\_02130

**Record Creation Time:** 20220129T080206+0000

**Record Last Update:** 20260919T194936+0000

### Ratings and Alerts

No rating or validation information has been found for BSSim.

No alerts have been found for BSSim.

---

## 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](#) .

Xie Q, et al. (2014) A Bayesian framework to identify methylcytosines from high-throughput bisulfite sequencing data. PLoS computational biology, 10(9), e1003853.