Resource Summary Report

Generated by NIF on Apr 22, 2025

Bs-Seeker2

RRID:SCR_020948
Type: Tool

Proper Citation

Bs-Seeker2 (RRID:SCR_020948)

Resource Information

URL: https://guoweilong.github.io/BS_Seeker2/index.html

Proper Citation: Bs-Seeker2 (RRID:SCR_020948)

Description: Software tool as versatile aligning pipeline for bisulfite sequencing data. Used for mapping bisulfite sequencing data and generating DNA methylomes. Improves mappability over existing aligners by using local alignment. Maps reads from RRBS library by building special indexes with improved efficiency and accuracy. Provides additional function for filtering out reads with incomplete bisulfite conversion, which is useful in minimizing overestimation of DNA methylation levels.

Synonyms: Bisulfite Sequencing Seeker2, BS Seeker2

Resource Type: software resource, sequence analysis software, data analysis software, data processing software, software application

Defining Citation: PMID:24206606

Keywords: Versatile aligning pipeline, bisulfite sequencing data, mapping bisulfite sequencing data, generating DNA methylomes, DNA methylation level, reads mapping, Reduced Represented Bisulfite Sequencing library, bio.tools

Funding: Institute of Genomics and Proteomics at UCLA ;
NBRPC 2012CB316503;
China Scholarship Council

Availability: Free, Available for download, Freely available

Resource Name: Bs-Seeker2

Resource ID: SCR_020948

Alternate IDs: biotools:bs-seeker2

Alternate URLs: http://pellegrini.mcdb.ucla.edu/BS_Seeker2/, https://bio.tools/bs-seeker2

Record Creation Time: 20220129T080353+0000

Record Last Update: 20250422T060144+0000

Ratings and Alerts

No rating or validation information has been found for Bs-Seeker2.

No alerts have been found for Bs-Seeker2.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Lizamore D, et al. (2021) Elevated transcription of transposable elements is accompanied by het-siRNA-driven de novo DNA methylation in grapevine embryogenic callus. BMC genomics, 22(1), 676.

Bourguet P, et al. (2020) DNA polymerase epsilon is required for heterochromatin maintenance in Arabidopsis. Genome biology, 21(1), 283.