

Resource Summary Report

Generated by [dkNET](#) on Apr 27, 2025

SAAP-RRBS

RRID:SCR_006516

Type: Tool

Proper Citation

SAAP-RRBS (RRID:SCR_006516)

Resource Information

URL: <https://code.google.com/p/saap-rrbs/>

Proper Citation: SAAP-RRBS (RRID:SCR_006516)

Description: Streamlined Analysis and Annotation Pipeline for reduced representation bisulfite sequencing.

Abbreviations: SAAP-RRBS

Synonyms: Streamlined Analysis and Annotation Pipeline for reduced representation bisulfite sequencing

Resource Type: software resource

Keywords: genomics, next generation sequencing

Funding:

Availability: GNU General Public License, v3, Acknowledgement requested

Resource Name: SAAP-RRBS

Resource ID: SCR_006516

Alternate IDs: OMICS_00612

Record Creation Time: 20220129T080236+0000

Record Last Update: 20250420T014332+0000

Ratings and Alerts

No rating or validation information has been found for SAAP-RRBS.

No alerts have been found for SAAP-RRBS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

El Khoury LY, et al. (2021) Identification of DNA methylation signatures associated with poor outcome in lower-risk Stage, Size, Grade and Necrosis (SSIGN) score clear cell renal cell cancer. *Clinical epigenetics*, 13(1), 12.

Mathison AJ, et al. (2021) KrasG12D induces changes in chromatin territories that differentially impact early nuclear reprogramming in pancreatic cells. *Genome biology*, 22(1), 289.

Ballester V, et al. (2020) Novel methylated DNA markers accurately discriminate Lynch syndrome associated colorectal neoplasia. *Epigenomics*, 12(24), 2173.

Zhou D, et al. (2018) Distinctive epigenomes characterize glioma stem cells and their response to differentiation cues. *Genome biology*, 19(1), 43.

Day SE, et al. (2017) Alterations of sorbin and SH3 domain containing 3 (SORBS3) in human skeletal muscle following Roux-en-Y gastric bypass surgery. *Clinical epigenetics*, 9, 96.

Day SE, et al. (2016) Next-generation sequencing methylation profiling of subjects with obesity identifies novel gene changes. *Clinical epigenetics*, 8, 77.

Gervin K, et al. (2016) Intra-individual changes in DNA methylation not mediated by cell-type composition are correlated with aging during childhood. *Clinical epigenetics*, 8, 110.

Sun Z, et al. (2015) Base resolution methylome profiling: considerations in platform selection, data preprocessing and analysis. *Epigenomics*, 7(5), 813.