

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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

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: 20260905T132555+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 10 mentions in open access literature.

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

Oatman SR, et al. (2026) Integrative epigenomic landscape of Alzheimer's Disease brains reveals oligodendrocyte molecular perturbations associated with tau. Nature communications, 17(1).

Matchett CL, et al. (2026) Discovery and Validation of Molecular Biomarkers for Differentiation of Nondysplastic Barrett's Esophagus from High-grade Dysplasia and Esophageal Adenocarcinoma. Cancer prevention research (Philadelphia, Pa.), 19(1), 49.

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.

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.

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.