

# Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

## SAAP-RRBS

RRID:SCR\_006516

Type: Tool

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### Proper Citation

SAAP-RRBS (RRID:SCR\_006516)

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### 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:** 20260912T195641+0000

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### 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 [kravitz2](#) .

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.