

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 28, 2026

Repitools

RRID:SCR_013242

Type: Tool

Proper Citation

Repitools (RRID:SCR_013242)

Resource Information

URL: <http://www.bioconductor.org/packages/2.9/bioc/html/Repitools.html>

Proper Citation: Repitools (RRID:SCR_013242)

Description: Software tools for the analysis of enrichment-based epigenomic data.

Abbreviations: Repitools

Resource Type: software resource

Resource Name: Repitools

Resource ID: SCR_013242

Alternate IDs: OMICS_00619

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260725T190750+0000

Ratings and Alerts

No rating or validation information has been found for Repitools.

No alerts have been found for Repitools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Wang YF, et al. (2025) Echs1-mediated histone crotonylation facilitates zygotic genome activation and expression of repetitive elements in early mammalian embryos. *Nature communications*, 16(1), 5630.

Balachandran S, et al. (2024) STIGMA: Single-cell tissue-specific gene prioritization using machine learning. *American journal of human genetics*, 111(2), 338.

Petrova V, et al. (2022) Increased chromatin accessibility facilitates intron retention in specific cell differentiation states. *Nucleic acids research*, 50(20), 11563.

Lensch S, et al. (2022) Dynamic spreading of chromatin-mediated gene silencing and reactivation between neighboring genes in single cells. *eLife*, 11.

Natoli M, et al. (2021) Transcriptional analysis of multiple ovarian cancer cohorts reveals prognostic and immunomodulatory consequences of ERV expression. *Journal for immunotherapy of cancer*, 9(1).

Moreland BS, et al. (2019) A model of pulldown alignments from SssI-treated DNA improves DNA methylation prediction. *BMC bioinformatics*, 20(1), 431.

Du Q, et al. (2019) Replication timing and epigenome remodelling are associated with the nature of chromosomal rearrangements in cancer. *Nature communications*, 10(1), 416.

Toubiana S, et al. (2019) Persistent epigenetic memory impedes rescue of the telomeric phenotype in human ICF iPSCs following DNMT3B correction. *eLife*, 8.

Samudyata , et al. (2019) Interaction of Sox2 with RNA binding proteins in mouse embryonic stem cells. *Experimental cell research*, 381(1), 129.

Lipponen A, et al. (2018) Transcription factors Tp73, Cebp α , Pax6, and Spi1 rather than DNA methylation regulate chronic transcriptomics changes after experimental traumatic brain injury. *Acta neuropathologica communications*, 6(1), 17.

Kamdar SN, et al. (2016) Dynamic interplay between locus-specific DNA methylation and hydroxymethylation regulates distinct biological pathways in prostate carcinogenesis. *Clinical epigenetics*, 8, 32.

Singhal H, et al. (2016) Genomic agonism and phenotypic antagonism between estrogen and progesterone receptors in breast cancer. *Science advances*, 2(6), e1501924.

Devailly G, et al. (2015) Dynamics of MBD2 deposition across methylated DNA regions during malignant transformation of human mammary epithelial cells. *Nucleic acids research*, 43(12), 5838.

Valensisi C, et al. (2015) cChIP-seq: a robust small-scale method for investigation of histone modifications. *BMC genomics*, 16, 1083.

Devailly G, et al. (2015) Variable reproducibility in genome-scale public data: A case study using ENCODE ChIP sequencing resource. *FEBS letters*, 589(24 Pt B), 3866.

Locke WJ, et al. (2015) Coordinated epigenetic remodelling of transcriptional networks occurs during early breast carcinogenesis. *Clinical epigenetics*, 7(1), 52.

Kanu N, et al. (2015) SETD2 loss-of-function promotes renal cancer branched evolution through replication stress and impaired DNA repair. *Oncogene*, 34(46), 5699.

Dubin MJ, et al. (2015) DNA methylation in *Arabidopsis* has a genetic basis and shows evidence of local adaptation. *eLife*, 4, e05255.

Gloss BS, et al. (2012) Integrative genome-wide expression and promoter DNA methylation profiling identifies a potential novel panel of ovarian cancer epigenetic biomarkers. *Cancer letters*, 318(1), 76.

Statham AL, et al. (2012) Bisulfite sequencing of chromatin immunoprecipitated DNA (BisChIP-seq) directly informs methylation status of histone-modified DNA. *Genome research*, 22(6), 1120.