Resource Summary Report

Generated by NIF on Apr 29, 2025

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

Funding:

Resource Name: Repitools

Resource ID: SCR_013242

Alternate IDs: OMICS_00619

Record Creation Time: 20220129T080315+0000

Record Last Update: 20250420T014637+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 20 mentions in open access literature.

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

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

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.

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.

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

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.

Robinson MD, et al. (2012) Copy-number-aware differential analysis of quantitative DNA sequencing data. Genome research, 22(12), 2489.