

Resource Summary Report

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RSEG

RRID:SCR_007695

Type: Tool

Proper Citation

RSEG (RRID:SCR_007695)

Resource Information

URL: <http://smithlab.usc.edu/histone/rseg/>

Proper Citation: RSEG (RRID:SCR_007695)

Description: Software package aimed to analyze ChIP-Seq data, especially for identifying genomic regions and their boundaries marked by diffusive histone modification markers, such as H3K36me3 and H3K27me3.

Abbreviations: RSEG

Resource Type: software resource

Defining Citation: [PMID:21325299](#)

Availability: Free

Resource Name: RSEG

Resource ID: SCR_007695

Alternate IDs: OMICS_00459

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260725T190644+0000

Ratings and Alerts

No rating or validation information has been found for RSEG.

No alerts have been found for RSEG.

Data and Source Information

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Costello KR, et al. (2021) Sequence features of retrotransposons allow for epigenetic variability. *eLife*, 10.

Cheng EC, et al. (2021) The Essential Function of SETDB1 in Homologous Chromosome Pairing and Synapsis during Meiosis. *Cell reports*, 34(1), 108575.

Ji L, et al. (2020) TOPORS, a tumor suppressor protein, contributes to the maintenance of higher-order chromatin architecture. *Biochimica et biophysica acta. Gene regulatory mechanisms*, 1863(5), 194518.

Chiang M, et al. (2019) Polymer Modeling Predicts Chromosome Reorganization in Senescence. *Cell reports*, 28(12), 3212.

Plissonneau C, et al. (2018) Pangenome analyses of the wheat pathogen *Zymoseptoria tritici* reveal the structural basis of a highly plastic eukaryotic genome. *BMC biology*, 16(1), 5.

Kim KY, et al. (2018) Uhrf1 regulates active transcriptional marks at bivalent domains in pluripotent stem cells through Setd1a. *Nature communications*, 9(1), 2583.

Fu S, et al. (2018) Differential analysis of chromatin accessibility and histone modifications for predicting mouse developmental enhancers. *Nucleic acids research*, 46(21), 11184.

Brescia P, et al. (2018) MEF2B Instructs Germinal Center Development and Acts as an Oncogene in B Cell Lymphomagenesis. *Cancer cell*, 34(3), 453.

Salzberg AC, et al. (2017) Genome-wide mapping of histone H3K9me2 in acute myeloid leukemia reveals large chromosomal domains associated with massive gene silencing and sites of genome instability. *PloS one*, 12(3), e0173723.

Centeno TP, et al. (2016) Genome-wide chromatin and gene expression profiling during memory formation and maintenance in adult mice. *Scientific data*, 3, 160090.

Gallego Romero I, et al. (2015) A panel of induced pluripotent stem cells from chimpanzees: a resource for comparative functional genomics. *eLife*, 4, e07103.

Schotanus K, et al. (2015) Histone modifications rather than the novel regional centromeres of *Zymoseptoria tritici* distinguish core and accessory chromosomes. *Epigenetics & chromatin*, 8, 41.

Zhou X, et al. (2014) Epigenetic modifications are associated with inter-species gene expression variation in primates. *Genome biology*, 15(12), 547.

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