Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 8, 2025

SISSRs

RRID:SCR_010866
Type: Tool

Proper Citation

SISSRs (RRID:SCR_010866)

Resource Information

URL: http://sissrs.rajajothi.com/

Proper Citation: SISSRs (RRID:SCR_010866)

Description: Anl algorithm for precise identification of binding sites from short reads generated from ChIP-Seq experiments.

Abbreviations: SISSRs

Synonyms: Site Identification from Short Sequence Reads

Resource Type: software resource

Defining Citation: PMID:18684996, PMID:22130889

Keywords: perl, bio.tools

Funding:

Resource Name: SISSRs

Resource ID: SCR_010866

Alternate IDs: biotools:sissrs, OMICS_00463

Alternate URLs: https://bio.tools/sissrs

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250214T183139+0000

Ratings and Alerts

No rating or validation information has been found for SISSRs.

No alerts have been found for SISSRs.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Kim HJ, et al. (2020) Transcriptional network dynamics during the progression of pluripotency revealed by integrative statistical learning. Nucleic acids research, 48(4), 1828.

Jeon H, et al. (2020) Comparative analysis of commonly used peak calling programs for ChIP-Seq analysis. Genomics & informatics, 18(4), e42.

Kolmykov SK, et al. (2019) Population size estimation for quality control of ChIP-Seq datasets. PloS one, 14(8), e0221760.

Hagey DW, et al. (2018) SOX2 regulates common and specific stem cell features in the CNS and endoderm derived organs. PLoS genetics, 14(2), e1007224.

Hagey DW, et al. (2016) Distinct transcription factor complexes act on a permissive chromatin landscape to establish regionalized gene expression in CNS stem cells. Genome research, 26(7), 908.

Kondrakhin Y, et al. (2016) Prediction of protein-DNA interactions of transcription factors linking proteomics and transcriptomics data. EuPA open proteomics, 13, 14.

Han Y, et al. (2016) Integrating Epigenomics into the Understanding of Biomedical Insight. Bioinformatics and biology insights, 10, 267.

Kulakovskiy IV, et al. (2016) HOCOMOCO: expansion and enhancement of the collection of transcription factor binding sites models. Nucleic acids research, 44(D1), D116.

Donczew M, et al. (2016) ParA and ParB coordinate chromosome segregation with cell elongation and division during Streptomyces sporulation. Open biology, 6(4), 150263.

de Taffin M, et al. (2015) Genome-Wide Mapping of Collier In Vivo Binding Sites Highlights Its Hierarchical Position in Different Transcription Regulatory Networks. PloS one, 10(7), e0133387.

Wang J, et al. (2015) Comprehensive genome-wide transcription factor analysis reveals that a combination of high affinity and low affinity DNA binding is needed for human gene regulation. BMC genomics, 16 Suppl 7(Suppl 7), S12.

Sahlén P, et al. (2015) Genome-wide mapping of promoter-anchored interactions with close to single-enhancer resolution. Genome biology, 16(1), 156.

Wang A, et al. (2015) Systematically dissecting the global mechanism of miRNA functions in mouse pluripotent stem cells. BMC genomics, 16(1), 490.

Tran NT, et al. (2014) A survey of motif finding Web tools for detecting binding site motifs in ChIP-Seq data. Biology direct, 9, 4.

Carvalho BS, et al. (2013) The challenges of delivering bioinformatics training in the analysis of high-throughput data. Briefings in bioinformatics, 14(5), 538.

Xiao X, et al. (2013) Genome-wide identification of Polycomb target genes in human embryonic stem cells. Gene, 518(2), 425.