

Resource Summary Report

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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: An 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

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: 20260725T190706+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 [nidm-terms](#) .

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.

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

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.

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

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

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

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.

Sahl??n 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.