

# 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:** 20260808T185925+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 [SPARC SAWG](#) .

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.