Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 13, 2025

SIPeS

RRID:SCR_010865
Type: Tool

Proper Citation

SIPeS (RRID:SCR_010865)

Resource Information

URL: http://gmdd.shgmo.org/Computational-Biology/ChIP-Seq/download/SIPeS

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Description: An algorithm that allows researchers to identify transcript factor binding sites from paired-end sequencing reads. SIPeS uses a dynamic baseline directly through the piling up of fragments to effectively find peaks, overcoming the disadvantage of estimating the average length of DNA fragments from singled-end sequencing achieving more powerful prediction binding sites with high sensitivity and specificity.

Abbreviations: SIPeS

Synonyms: SIPeS - Site Identification from Paired-end Sequencing, Site Identification from Paired-end Sequencing

Resource Type: software resource

Defining Citation: PMID:20144209

Funding:

Availability: Free to academic users, Non-commercial, Commercial requires permission

Resource Name: SIPeS

Resource ID: SCR_010865

Alternate IDs: OMICS_00462

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250410T070026+0000

Ratings and Alerts

No rating or validation information has been found for SIPeS.

No alerts have been found for SIPeS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Finlayson J, et al. (2025) Adults With Intellectual Disabilities and Incontinence: Assessment and Toileting Issues. Journal of intellectual disability research : JIDR, 69(2), 165.

Arcangeli L, et al. (2020) Attitudes of Mainstream and Special-Education Teachers toward Intellectual Disability in Italy: The Relevance of Being Teachers. International journal of environmental research and public health, 17(19).

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.

Wang C, et al. (2010) An effective approach for identification of in vivo protein-DNA binding sites from paired-end ChIP-Seq data. BMC bioinformatics, 11, 81.