

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 2, 2026

SIOMICS

RRID:SCR_011990

Type: Tool

Proper Citation

SIOMICS (RRID:SCR_011990)

Resource Information

URL: <http://www.eecs.ucf.edu/~xiaoman/SIOMICS/SIOMICS.html>

Proper Citation: SIOMICS (RRID:SCR_011990)

Description: A software to de novo identify motifs in large sequence datasets such as those from ChIP-seq experiments.

Abbreviations: SIOMICS

Synonyms: SIOMICS--Systematic Identification Of Motifs In ChIP-Seq data, SIOMICS - Systematic Identification Of Motifs In ChIP-Seq data .

Resource Type: software resource

Defining Citation: [PMID:24322294](#)

Availability: Free

Resource Name: SIOMICS

Resource ID: SCR_011990

Alternate IDs: OMICS_01805

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260801T190434+0000

Ratings and Alerts

No rating or validation information has been found for SIOMICS.

No alerts have been found for SIOMICS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Wang S, et al. (2022) A systematic study of motif pairs that may facilitate enhancer-promoter interactions. *Journal of integrative bioinformatics*, 19(1).

Zhang Y, et al. (2022) A systematic study of HIF1A cofactors in hypoxic cancer cells. *Scientific reports*, 12(1), 18962.

Wang S, et al. (2020) Shared distal regulatory regions may contribute to the coordinated expression of human ribosomal protein genes. *Genomics*, 112(4), 2886.

Wang Y, et al. (2017) Prognostic cancer gene signatures share common regulatory motifs. *Scientific reports*, 7(1), 4750.

Perez-Zamorano B, et al. (2017) Identification of cis-regulatory sequences reveals potential participation of Iola and Deaf1 transcription factors in *Anopheles gambiae* innate immune response. *PloS one*, 12(10), e0186435.

Zheng Y, et al. (2015) Comprehensive discovery of DNA motifs in 349 human cells and tissues reveals new features of motifs. *Nucleic acids research*, 43(1), 74.

Duffy DJ, et al. (2015) Integrative omics reveals MYCN as a global suppressor of cellular signalling and enables network-based therapeutic target discovery in neuroblastoma. *Oncotarget*, 6(41), 43182.

Ding J, et al. (2014) SIOMICS: a novel approach for systematic identification of motifs in ChIP-seq data. *Nucleic acids research*, 42(5), e35.