

Resource Summary Report

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MOSAiCS

RRID:SCR_010861

Type: Tool

Proper Citation

MOSAiCS (RRID:SCR_010861)

Resource Information

URL: <http://www.stat.wisc.edu/~keles/Software/mosaics/>

Proper Citation: MOSAiCS (RRID:SCR_010861)

Description: Software developed as a flexible mixture modeling approach for detecting peaks of one-sample (ChIP sample) or two-sample (ChIP sample and matched control sample) ChIP-seq data.

Abbreviations: MOSAiCS

Synonyms: MOdel-based one and two Sample Analysis and inference for ChIP-Seq Data

Resource Type: software resource

Resource Name: MOSAiCS

Resource ID: SCR_010861

Alternate IDs: OMICS_00448

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260725T190708+0000

Ratings and Alerts

No rating or validation information has been found for MOSAiCS.

No alerts have been found for MOSAiCS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 28 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Mannino G, et al. (2025) Somatic mutations in TBX3 promote hepatic clonal expansion by accelerating VLDL secretion. *The Journal of clinical investigation*, 135(18).

Delcourt CJF, et al. (2025) Carbon Emissions From Fires in Eastern Siberian Larch Forests. *Global change biology*, 31(5), e70247.

Martinez Pastor M, et al. (2024) TroR is the primary regulator of the iron homeostasis transcription network in the halophilic archaeon *Haloferax volcanii*. *Nucleic acids research*, 52(1), 125.

Hackley RK, et al. (2024) A conserved transcription factor controls gluconeogenesis via distinct targets in hypersaline-adapted archaea with diverse metabolic capabilities. *PLoS genetics*, 20(1), e1011115.

Sakrikar S, et al. (2023) The Hypersaline Archaeal Histones HpyA and HstA Are DNA Binding Proteins That Defy Categorization According to Commonly Used Functional Criteria. *mBio*, 14(2), e0344922.

Lakey BD, et al. (2022) The essential *Rhodobacter sphaeroides* CenKR two-component system regulates cell division and envelope biosynthesis. *PLoS genetics*, 18(6), e1010270.

Dong C, et al. (2021) INFIMA leverages multi-omics model organism data to identify effector genes of human GWAS variants. *Genome biology*, 22(1), 241.

Balderas D, et al. (2021) Genome Scale Analysis Reveals IscR Directly and Indirectly Regulates Virulence Factor Genes in Pathogenic *Yersinia*. *mBio*, 12(3), e0063321.

Darnell CL, et al. (2020) The Ribbon-Helix-Helix Domain Protein CdrS Regulates the Tubulin Homolog ftsZ2 To Control Cell Division in Archaea. *mBio*, 11(4).

Lemmer KC, et al. (2020) The NtrYX Two-Component System Regulates the Bacterial Cell Envelope. *mBio*, 11(3).

Banerjee R, et al. (2020) Tailoring a Global Iron Regulon to a Uropathogen. *mBio*, 11(2).

Demharter S, et al. (2019) HLA-DM Stabilizes the Empty MHCII Binding Groove: A Model Using Customized Natural Move Monte Carlo. *Journal of chemical information and modeling*, 59(6), 2894.

Fu S, et al. (2018) Differential analysis of chromatin accessibility and histone modifications for predicting mouse developmental enhancers. *Nucleic acids research*, 46(21), 11184.

Welch R, et al. (2017) Data exploration, quality control and statistical analysis of ChIP-exo/nexus experiments. *Nucleic acids research*, 45(15), e145.

Papale LA, et al. (2017) Early-life stress links 5-hydroxymethylcytosine to anxiety-related behaviors. *Epigenetics*, 12(4), 264.

Li R, et al. (2016) Misregulation of Alternative Splicing in a Mouse Model of Rett Syndrome. *PLoS genetics*, 12(6), e1006129.

Knapp B, et al. (2016) Exploring peptide/MHC detachment processes using hierarchical natural move Monte Carlo. *Bioinformatics (Oxford, England)*, 32(2), 181.

Demharter S, et al. (2016) Modeling Functional Motions of Biological Systems by Customized Natural Moves. *Biophysical journal*, 111(4), 710.

Stacy A, et al. (2016) Microbial Community Composition Impacts Pathogen Iron Availability during Polymicrobial Infection. *PLoS pathogens*, 12(12), e1006084.

Myers KS, et al. (2015) Defining bacterial regulons using ChIP-seq. *Methods (San Diego, Calif.)*, 86, 80.