Resource Summary Report

Generated by dkNET on Apr 21, 2025

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

Funding:

Resource Name: MOSAiCS

Resource ID: SCR_010861

Alternate IDs: OMICS_00448

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250420T014512+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 26 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

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.

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.

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

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

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).

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.

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

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

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

Lopez-Anido C, et al. (2015) Differential Sox10 genomic occupancy in myelinating glia. Glia, 63(11), 1897.

Imam S, et al. (2015) CceR and AkgR regulate central carbon and energy metabolism in alphaproteobacteria. mBio, 6(1).