Resource Summary Report

Generated by dkNET on Apr 29, 2025

CompleteMOTIFs

RRID:SCR_010878
Type: Tool

Proper Citation

CompleteMOTIFs (RRID:SCR_010878)

Resource Information

URL: http://cmotifs.tchlab.org/

Proper Citation: CompleteMOTIFs (RRID:SCR_010878)

Description: Data analysis service providing a motif discovery platform developed to help biologists to find novel as well as known motifs in their peak datasets from transcription factor (TF) binding experiments such as ChIP-seq and ChIP-chip.

Abbreviations: cMOTIFs

Resource Type: production service resource, data analysis service, analysis service resource, service resource

Defining Citation: PMID:21183585

Funding:

Availability: Account required, For academic use

Resource Name: CompleteMOTIFs

Resource ID: SCR_010878

Alternate IDs: OMICS_00478

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250429T055446+0000

Ratings and Alerts

No rating or validation information has been found for CompleteMOTIFs.

No alerts have been found for CompleteMOTIFs.

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 dkNET.

Calderari S, et al. (2018) Molecular genetics of the transcription factor GLIS3 identifies its dual function in beta cells and neurons. Genomics, 110(2), 98.

Tam KJ, et al. (2017) Androgen receptor transcriptionally regulates semaphorin 3C in a GATA2-dependent manner. Oncotarget, 8(6), 9617.

Dressaire C, et al. (2015) BolA is a transcriptional switch that turns off motility and turns on biofilm development. mBio, 6(1), e02352.

Meyer KD, et al. (2012) Comprehensive analysis of mRNA methylation reveals enrichment in 3' UTRs and near stop codons. Cell, 149(7), 1635.