

Resource Summary Report

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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: analysis service resource, service resource, data analysis service, production service resource

Defining Citation: [PMID:21183585](#)

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: 20260728T043344+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 [nidm-terms](#) .

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.