

# Resource Summary Report

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

## 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:** data analysis service, service resource, production service resource, analysis 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:** 20260801T191017+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](#)

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## Usage and Citation Metrics

We found 4 mentions in open access literature.

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

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.