

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

GimmeMotifs

RRID:SCR_001146

Type: Tool

Proper Citation

GimmeMotifs (RRID:SCR_001146)

Resource Information

URL: <http://131.174.198.125/bioinfo/gimmemotifs/>

Proper Citation: GimmeMotifs (RRID:SCR_001146)

Description: Software that provides a de novo motif prediction pipeline, especially suited for ChIP-seq datasets. It incorporates several existing motif prediction algorithms in an ensemble method to predict motifs and clusters these motifs using the WIC similarity scoring metric., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: GimmeMotifs

Synonyms: GimmeMotifs: a systematic de novo motif prediction pipeline

Resource Type: software resource

Defining Citation: [PMID:21081511](#)

Keywords: linux, chip-seq, motif, cluster, python, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GimmeMotifs

Resource ID: SCR_001146

Alternate IDs: biotools:gimmemotifs, OMICS_02150

Alternate URLs: <https://bio.tools/gimmemotifs>

Record Creation Time: 20220129T080205+0000

Record Last Update: 20260725T190456+0000

Ratings and Alerts

No rating or validation information has been found for GimmeMotifs.

No alerts have been found for GimmeMotifs.

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](#) .

Tingvall-Gustafsson J, et al. (2025) Chromatin interaction-based annotation of regulatory elements reveals dynamic promoter-enhancer interactions in lymphocyte development. iScience, 28(7), 112855.

Manj??n AG, et al. (2023) Perturbations in 3D genome organization can promote acquired drug resistance. Cell reports, 42(10), 113124.

Wei X, et al. (2022) HiCAR is a robust and sensitive method to analyze open-chromatin-associated genome organization. Molecular cell, 82(6), 1225.

Toenhake CG, et al. (2018) Chromatin Accessibility-Based Characterization of the Gene Regulatory Network Underlying Plasmodium falciparum Blood-Stage Development. Cell host & microbe, 23(4), 557.