

Resource Summary Report

Generated by [NIF](#) on Apr 20, 2025

GimmeMotifs

RRID:SCR_001146

Type: Tool

Proper Citation

GimmeMotifs (RRID:SCR_001146)

Resource Information

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

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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.

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

Funding:

Availability: MIT License, Acknowledgement requested

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: 20250420T014022+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 3 mentions in open access literature.

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

Manjón 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.