

Resource Summary Report

Generated by [Kravitz](#) on Sep 17, 2026

[motifRG](#)

RRID:SCR_012602

Type: Tool

Proper Citation

motifRG (RRID:SCR_012602)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/motifRG.html>

Proper Citation: motifRG (RRID:SCR_012602)

Description: Software tools for discriminative motif discovery using regression methods.

Abbreviations: motifRG

Synonyms: motifRG - A package for discriminative motif discovery designed for high throughput sequencing dataset

Resource Type: software resource

Defining Citation: [PMID:24162561](#)

Availability: Free

Resource Name: motifRG

Resource ID: SCR_012602

Alternate IDs: OMICS_00487

Record Creation Time: 20220129T080311+0000

Record Last Update: 20260912T195751+0000

Ratings and Alerts

No rating or validation information has been found for motifRG.

No alerts have been found for motifRG.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Vaklavas C, et al. (2020) Hallmarks and Determinants of Oncogenic Translation Revealed by Ribosome Profiling in Models of Breast Cancer. *Translational oncology*, 13(2), 452.

Wreczycka K, et al. (2019) HOT or not: examining the basis of high-occupancy target regions. *Nucleic acids research*, 47(11), 5735.

Zhang S, et al. (2019) FisherMP: fully parallel algorithm for detecting combinatorial motifs from large ChIP-seq datasets. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 26(3), 231.

Zhang H, et al. (2017) WSMD: weakly-supervised motif discovery in transcription factor ChIP-seq data. *Scientific reports*, 7(1), 3217.

Uyar B, et al. (2017) RCAS: an RNA centric annotation system for transcriptome-wide regions of interest. *Nucleic acids research*, 45(10), e91.