

# Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](https://www.fdi-lab.org) on Apr 15, 2025

## motifRG

RRID:SCR\_012602

Type: Tool

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### Proper Citation

motifRG (RRID:SCR\_012602)

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### 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](https://pubmed.ncbi.nlm.nih.gov/24162561/)

**Funding:**

**Availability:** Free

**Resource Name:** motifRG

**Resource ID:** SCR\_012602

**Alternate IDs:** OMICS\_00487

**Record Creation Time:** 20220129T080311+0000

**Record Last Update:** 20250410T070253+0000

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### Ratings and Alerts

No rating or validation information has been found for motifRG.

No alerts have been found for motifRG.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 5 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

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.