

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 29, 2026

[findMotif.pl](#)

RRID:SCR_016417

Type: Tool

Proper Citation

findMotif.pl (RRID:SCR_016417)

Resource Information

URL: <http://homer.ucsd.edu/homer/microarray/index.html>

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Description: Software tool to analyze the promoters of genes and look for motifs that are enriched in the target gene promoters relative to other promoters. Used for gene based analysis to provide a list of genes that should contain the same elements, such as genes that are co-regulated. It includes gene ontology analysis and can be used to look for RNA motifs in mRNAs.

Resource Type: software application, data analysis software, sequence analysis software, software resource, data processing software, software toolkit

Keywords: analyze, promoter, gene, motif, target, relative, same, element, ontology, RNA, mRNA

Availability: Free, Available for download, Freely available

Resource Name: findMotif.pl

Resource ID: SCR_016417

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260729T044417+0000

Ratings and Alerts

No rating or validation information has been found for findMotif.pl.

No alerts have been found for findMotif.pl.

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 [SPARC SAWG](#) .

Ramdas Nair A, et al. (2022) A permissive epigenetic landscape facilitates distinct transcriptional signatures of activating transcription factor 6 in the liver. *Genomics*, 114(1), 107.

Gans I, et al. (2020) Klf9 is a key feedforward regulator of the transcriptomic response to glucocorticoid receptor activity. *Scientific reports*, 10(1), 11415.

Antonova A, et al. (2019) Heat-Shock Protein 90 Controls the Expression of Cell-Cycle Genes by Stabilizing Metazoan-Specific Host-Cell Factor HCFC1. *Cell reports*, 29(6), 1645.

Tiwari N, et al. (2018) Stage-Specific Transcription Factors Drive Astroglialogenesis by Remodeling Gene Regulatory Landscapes. *Cell stem cell*, 23(4), 557.