

Resource Summary Report

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DREME

RRID:SCR_016860

Type: Tool

Proper Citation

DREME (RRID:SCR_016860)

Resource Information

URL: <http://meme-suite.org/tools/dreme>

Proper Citation: DREME (RRID:SCR_016860)

Description: Software tool to discover short, ungapped motifs (recurring, fixed-length patterns) that are relatively enriched in sequences compared with shuffled sequences or control sequences (sample output from sequences).

Synonyms: Discriminative Regular Expression Motif Elicitation, DREME

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Keywords: discover, short, ungapped, motif, sequence, compare, shuffled, control, sample, output, recurring, fixed, length, pattern, data

Availability: Free, Available for download, Freely available

Resource Name: DREME

Resource ID: SCR_016860

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260912T200217+0000

Ratings and Alerts

No rating or validation information has been found for DREME.

No alerts have been found for DREME.

Data and Source Information

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Zhao DY, et al. (2026) RNA-binding proteins TDP-43 and FUS promote R-loop resolution and regulate transcription termination. *The Journal of biological chemistry*, 302(5), 111348.

Xu T, et al. (2026) Genome-Wide Identification of Binding Motifs and Drought-Responsive Target Genes by the Transcription Factor ZmNAC20 in Maize. *Plants (Basel, Switzerland)*, 15(3).

Zhang S, et al. (2024) Knockdown of IGF2BP2 overcomes cisplatin-resistance in lung cancer through downregulating Spon2 gene. *Hereditas*, 161(1), 55.

Cerav EN, et al. (2024) Transcriptome-Wide N6-Methyladenosine (m6A) Methylation Analyses in a Compatible Wheat-Puccinia striiformis f. sp. tritici Interaction. *Plants (Basel, Switzerland)*, 13(7).

Zhao J, et al. (2023) Changes in m6A RNA methylation are associated with male sterility in wolfberry. *BMC plant biology*, 23(1), 456.

Ayyildiz D, et al. (2023) CAG repeat expansion in the Huntington's disease gene shapes linear and circular RNAs biogenesis. *PLoS genetics*, 19(10), e1010988.

Pan Y, et al. (2023) METTL3 drives NAFLD-related hepatocellular carcinoma and is a therapeutic target for boosting immunotherapy. *Cell reports. Medicine*, 4(8), 101144.

Wang S, et al. (2022) Comprehensive Analysis of Long Noncoding RNA Modified by m6A Methylation in Oxidative and Glycolytic Skeletal Muscles. *International journal of molecular sciences*, 23(9).

Broche J, et al. (2021) Genome-wide investigation of the dynamic changes of epigenome modifications after global DNA methylation editing. *Nucleic acids research*, 49(1), 158.

Alvelos MI, et al. (2021) The RNA-binding profile of the splicing factor SRSF6 in immortalized human pancreatic ??-cells. *Life science alliance*, 4(3).

Sanborn AL, et al. (2021) Simple biochemical features underlie transcriptional activation domain diversity and dynamic, fuzzy binding to Mediator. *eLife*, 10.

Zhang K, et al. (2021) The dynamics of N6-methyladenine RNA modification in interactions between rice and plant viruses. *Genome biology*, 22(1), 189.

Rozen-Gagnon K, et al. (2021) Argonaute-CLIP delineates versatile, functional RNAi networks in *Aedes aegypti*, a major vector of human viruses. *Cell host & microbe*, 29(5), 834.

Jiao J, et al. (2021) An age-downregulated ribosomal RpS28 protein variant regulates the muscle proteome. *G3* (Bethesda, Md.), 11(7).

Cheng B, et al. (2021) Profiling of RNA N⁶-Methyladenosine Methylation Reveals the Critical Role of m⁶A in Chicken Adipose Deposition. *Frontiers in cell and developmental biology*, 9, 590468.

Chetta M, et al. (2020) Rising Roles of Small Noncoding RNAs in Cotranscriptional Regulation: In Silico Study of miRNA and piRNA Regulatory Network in Humans. *Genes*, 11(5).

Rieger MA, et al. (2020) CLIP and Massively Parallel Functional Analysis of CELF6 Reveal a Role in Destabilizing Synaptic Gene mRNAs through Interaction with 3' UTR Elements. *Cell reports*, 33(12), 108531.

Reddington JP, et al. (2020) Lineage-Resolved Enhancer and Promoter Usage during a Time Course of Embryogenesis. *Developmental cell*, 55(5), 648.

Tu M, et al. (2020) Grapevine VlbZIP30 improves drought resistance by directly activating VvNAC17 and promoting lignin biosynthesis through the regulation of three peroxidase genes. *Horticulture research*, 7, 150.

Salvi E, et al. (2020) A Self-Organized PLT/Auxin/ARR-B Network Controls the Dynamics of Root Zonation Development in *Arabidopsis thaliana*. *Developmental cell*, 53(4), 431.