

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: data analysis service, analysis service resource, production service resource, service resource

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

Funding:

Availability: Free, Available for download, Freely available

Resource Name: DREME

Resource ID: SCR_016860

Record Creation Time: 20220129T080332+0000

Record Last Update: 20250329T061205+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

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

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).

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.

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.

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

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).

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 β -cells. *Life science alliance*, 4(3).

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.

Tu M, et al. (2020) Grapevine VbZIP30 improves drought resistance by directly activating VvNAC17 and promoting lignin biosynthesis through the regulation of three peroxidase genes. *Horticulture research*, 7, 150.

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

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.

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).

Hasler D, et al. (2020) The Alzami Syndrome-Associated Protein LARP7 Guides U6 Small Nuclear RNA Modification and Contributes to Splicing Robustness. *Molecular cell*, 77(5), 1014.

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.

Liu Y, et al. (2019) Comparative analysis of miniature inverted-repeat transposable elements (MITEs) and long terminal repeat (LTR) retrotransposons in six Citrus species. *BMC plant biology*, 19(1), 140.

Maronedze C, et al. (2019) Drought Stress Causes Specific Changes to the Spliceosome and Stress Granule Components. *Frontiers in molecular biosciences*, 6, 163.