

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, service resource, production service resource, analysis 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: 20260801T042805+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 20 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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.

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.

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

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

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

Cheng B, et al. (2021) Profiling of RNA N 6 -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 VlbZIP30 improves drought resistance by directly activating VvNAC17 and promoting lignin biosynthesis through the regulation of three peroxidase genes. *Horticulture research*, 7, 150.

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).

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.

Hasler D, et al. (2020) The Alazami 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.

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