

Resource Summary Report

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MEME Suite - Motif-based sequence analysis tools

RRID:SCR_001783

Type: Tool

Proper Citation

MEME Suite - Motif-based sequence analysis tools (RRID:SCR_001783)

Resource Information

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

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Description: Suite of motif-based sequence analysis tools to discover motifs using MEME, DREME (DNA only) or GLAM2 on groups of related DNA or protein sequences; search sequence databases with motifs using MAST, FIMO, MCAST or GLAM2SCAN; compare a motif to all motifs in a database of motifs; associate motifs with Gene Ontology terms via their putative target genes, and analyze motif enrichment using SpaMo or CentriMo. Source code, binaries and a web server are freely available for noncommercial use.

Abbreviations: MEME Suite

Synonyms: The MEME Suite

Resource Type: data processing software, database, production service resource, data analysis software, software application, software resource, service resource, data analysis service, source code, analysis service resource, data or information resource

Defining Citation: [PMID:19458158](#), [DOI:10.1093/nar/gkl198](#)

Keywords: gene ontology, motif, comparative genomics, dna regulatory motif, dna sequence, dna, gene, transcription factor, genome, protein, analysis, function analysis, comparison, cluster, enrichment analysis, sequence analysis, bio.tools, FASEB list

Funding: NCRR R01 RR021692

Availability: Source code, Binaries and a web server: Free for academic use, Non-commercial, Acknowledgement requested, Copyrighted, See copyright notice

Resource Name: MEME Suite - Motif-based sequence analysis tools

Resource ID: SCR_001783

Alternate IDs: nif-0000-10298, biotools:meme_suite, OMICS_08103

Alternate URLs: https://bio.tools/meme_suite

Old URLs: http://meme.sdsc.edu/meme4_6_1/intro.html, <http://meme.nbcr.net/meme/>, <https://sources.debian.org/src/meme/>

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250326T060111+0000

Ratings and Alerts

No rating or validation information has been found for MEME Suite - Motif-based sequence analysis tools.

No alerts have been found for MEME Suite - Motif-based sequence analysis tools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1962 mentions in open access literature.

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

Li S, et al. (2025) Genome-Wide Identification and Expression Analysis Under Abiotic Stress of the Lipxygenase Gene Family in Maize (*Zea mays*). *Genes*, 16(1).

Zhao Y, et al. (2025) Genome-wide Characterization of the MBF1 Gene Family and Its Expression Pattern in Different Tissues and Under Stresses in *Medicago truncatula* and *Medicago sativa*. *International journal of molecular sciences*, 26(2).

Liang X, et al. (2025) Genome-Wide Identification of GmPIF Family and Regulatory Pathway Analysis of GmPIF3g in Different Temperature Environments. *International journal of molecular sciences*, 26(2).

Omari Alzahrani F, et al. (2025) Ammonium Transporter 1 (AMT1) Gene Family in Pomegranate: Genome-Wide Analysis and Expression Profiles in Response to Salt Stress. *Current issues in molecular biology*, 47(1).

Gabriel GC, et al. (2025) Mitotic block and epigenetic repression underlie neurodevelopmental defects and neurobehavioral deficits in congenital heart disease. *Nature communications*, 16(1), 469.

Aggarwal N, et al. (2025) Insights into expression and localization of HPV16 LCR-associated transcription factors and association with LCR activity in HNSCC. *Molecular therapy. Oncology*, 33(1), 200926.

Wang Y, et al. (2025) Chromatin accessibility profile and the role of PeAtf1 transcription factor in the postharvest pathogen *Penicillium expansum*. *Horticulture research*, 12(1), uhae264.

Zhang Z, et al. (2025) Ploidy levels influence cold tolerance of *Cyclocarya paliurus*: insight into the roles of WRKY genes. *BMC genomics*, 26(1), 31.

Adlakha A, et al. (2025) Interferon-gamma rescues dendritic cell calcineurin-dependent responses to *Aspergillus fumigatus* via Stat3 to Stat1 switching. *iScience*, 28(2), 111535.

Dong J, et al. (2025) ZNF143 binds DNA and stimulates transcription initiation to activate and repress direct target genes. *Nucleic acids research*, 53(2).

Shi H, et al. (2025) Coordinated regulation of two LacI family regulators, GvmR and GvmR2, on guvermectin production in *Streptomyces caniferus*. *Synthetic and systems biotechnology*, 10(1), 237.

Dong F, et al. (2025) TaSnRK3.23B, a CBL-interacting protein kinase of wheat, confers drought stress tolerance by promoting ROS scavenging in *Arabidopsis*. *BMC plant biology*, 25(1), 59.

Magnitov MD, et al. (2025) ZNF143 is a transcriptional regulator of nuclear-encoded mitochondrial genes that acts independently of looping and CTCF. *Molecular cell*, 85(1), 24.

Li Y, et al. (2025) Epitranscriptome profiles reveal participation of the RNA methyltransferase gene OsMTA1 in rice seed germination and salt stress response. *BMC plant biology*, 25(1), 115.

Park JY, et al. (2025) ChIP-mini: a low-input ChIP-exo protocol for elucidating DNA-binding protein dynamics in intracellular pathogens. *Nucleic acids research*, 53(3).

Feng X, et al. (2025) Genome-Wide Analysis of bZIP Transcription Factors and Expression Patterns in Response to Salt and Drought Stress in *Vaccinium corymbosum*. *International journal of molecular sciences*, 26(2).

Wang H, et al. (2025) BcWRKY25-BcWRKY33A-BcLRP1/BcCOW1 module promotes root

development for improved salt tolerance in Bok choy. Horticulture research, 12(1), uhae280.

Tong C, et al. (2025) Pangenome and pantranscriptome as the new reference for gene-family characterization: A case study of basic helix-loop-helix (bHLH) genes in barley. Plant communications, 6(1), 101190.

Wang X, et al. (2025) Genome-wide identification and functional roles relating to anthocyanin biosynthesis analysis in maize. BMC plant biology, 25(1), 57.

Chen X, et al. (2025) Integration of ATAC-Seq and RNA-Seq Reveals the Role of FaTIP1 in Red Light-Induced Fruit Ripening in Strawberry. International journal of molecular sciences, 26(2).