

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, service resource, data analysis software, source code, data analysis service, database, software resource, data or information resource, software application, production service resource, analysis service 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: Free, Freely available

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: 20260731T042623+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 2091 mentions in open access literature.

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

Vaishnav J, et al. (2026) Amiodarone disrupts thyroid hormone signaling networks governing early heart development in the chick embryo. General and comparative endocrinology, 376, 114871.

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.

Xing Q, et al. (2025) Genome-wide characterization of FAD gene family in Xanthoceras sorbifolium Bunge and germplasm assessment. PloS one, 20(3), e0318900.

Wang M, et al. (2025) Genome-wide characterization and expression profiling of the TGA gene family in sweet orange (Citrus sinensis) reveal CsTGA7 responses to multiple phytohormones and abiotic stresses. Frontiers in plant science, 16, 1530242.

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.

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).

Contreras E, et al. (2025) Regulation of HvASN1 expression by bZIP transcription factors during barley embryo development and germination. *Planta*, 262(1), 20.

Auzane A, et al. (2025) A Novel Pathosystem With the Model Plant *Arabidopsis thaliana* for Defining the Molecular Basis of *Taphrina* Infections. *Environmental microbiology reports*, 17(3), e70118.

Li L, et al. (2025) Genome-wide identification of CDPKs in jujube and expression profile analysis in response to multiple biological processes. *Frontiers in plant science*, 16, 1593446.

Wu A, et al. (2025) GhMYB102 affects cotton fibre elongation and secondary wall thickening by regulating GhIRX10 in cotton. *Plant biotechnology journal*, 23(4), 1329.

Han X, et al. (2025) Diversity and genomics of bacteriome-associated symbionts in treehopper *Darthula hardwickii* (Hemiptera: Aetalionidae) and implications of their nutritional functions. *Applied and environmental microbiology*, 91(4), e0173824.

Wang G, et al. (2025) Integrated metabolome analysis and transcript profiles revealed a potential role of SWEETs in sugar accumulation during Carrot taproot development. *BMC plant biology*, 25(1), 470.

Manna T, et al. (2025) Investigations on genomic, topological and structural properties of diguanylate cyclases involved in *Vibrio cholerae* biofilm signalling using in silico techniques: Promising drug targets in combating cholera. *Current research in structural biology*, 9, 100166.

Chouaibi Y, et al. (2025) Durum wheat nuclear factor Y (NF-Y) a subfamily: structure, phylogeny, and expression analysis in response to hormones and abiotic stresses. *Functional & integrative genomics*, 25(1), 102.

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.

Luo X, et al. (2025) Domain characteristics, classification and expression profiles in response to various abiotic stresses of four HD-Zip subfamilies in tea plant. *BMC plant biology*, 25(1), 751.

Liu Y, et al. (2025) Phosphoproteomics analysis of acid stress response of *Alicyclobacillus acidoterrestris* in response to acid stress. *Applied microbiology and biotechnology*, 109(1), 141.

Vega-Baray B, et al. (2025) Repression of *ctrA* and *chpT* by a transcriptional regulator of the Xre family that is expressed by RpoN3 and its cognate activator protein in *Cereibacter sphaeroides*. *PloS one*, 20(4), e0321186.