

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

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: 20260905T132439+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 2472 mentions in open access literature.

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

Liu S, et al. (2026) Adaptive evolution of Agaricomycetes laccases follows wood lignin diversification in plants. *Applied and environmental microbiology*, 92(2), e0197125.

Zhou Y, et al. (2026) Genome-wide identification and gene expression analysis of AhNHXs in peanut. *BMC plant biology*, 26(1).

Sun M, et al. (2026) Identification of the ZmDUF966 Gene Family in Maize, Analysis of Its Expression Under Cold Stress, and Preliminary Investigation of the ZmDUF966-10 Regulatory Network. *Biology*, 15(6).

Miu Y, et al. (2026) Genome-Wide Identification of the SWEET Gene Family and Functional Analysis of LpSWEET13 in Perennial Ryegrass Under Drought Stress. *Plants (Basel, Switzerland)*, 15(4).

Wu P, et al. (2026) A novel TetR-type repressor directly modulates precursor supply and utilization for erythromycin biosynthesis. *Synthetic and systems biotechnology*, 13, 132.

Zhu M, et al. (2026) Genome-Wide Evolution and Stress-Responsive Regulation of 2-Oxoglutarate-Dependent Dioxygenases in *Gossypium*. *Genes*, 17(2).

Wang FH, et al. (2026) Genome-wide identification and functional analysis of the WRKY transcription factor family in *Reynoutria japonica* reveals its role in balancing growth and

abiotic stress tolerance. BMC plant biology, 26(1).

Mascoli A, et al. (2026) Sex- and stage-dependent expression of gonadal soma-derived factor paralogues reveals functional and evolutionary divergence in European sea bass (*Dicentrarchus labrax*). Frontiers in endocrinology, 17, 1779674.

Cortolezzis Y, et al. (2026) RPA hyperphosphorylation hinders the resolution of R-loops and G-quadruplex-associated R-loops during RAS-driven senescence. Nucleic acids research, 54(7).

Zhao Y, et al. (2026) Identification of StbZIP in Potato (*Solanum tuberosum* L.) and StbZIP104 Enhances Cold Resistance. Plants (Basel, Switzerland), 15(10).

Li D, et al. (2026) Integrated ATAC-seq and mRNA-seq analyses on granulosa cells identify key regulators of follicle selection in chickens. Journal of animal science and biotechnology, 17(1).

Wang X, et al. (2026) Comprehensive analysis of the GeBP gene family in cucumber highlights functional divergence in fruit development and stress tolerance. BMC plant biology, 26(1).

Ji P, et al. (2026) The CiWOX13-CiWOX14 Complex Regulates CiBGLU21 to Promote Graft Union Formation by Modulating Cell Wall Synthesis in *Carya illinoensis*. Plants (Basel, Switzerland), 15(2).

Weng L, et al. (2026) Compound Inflorescence (S) represses fruit growth and seed development in tomato. Molecular horticulture, 6(1), 5.

Zhao L, et al. (2026) Characterization of the BPC genes in alfalfa and functional verification of MsBPC10 in salt tolerance. BMC plant biology, 26(1).

Liu C, et al. (2026) Characterization of a novel aminoglycoside resistance gene, aadA34, identified from *Serratia ureilytica* S24. Frontiers in microbiology, 17, 1765554.

Centonze A, et al. (2026) A Plastic EMP1⁺ to LGR5⁺ Cell State Conversion as a Bypass to KRASG12D Pharmacologic Inhibition in Metastatic Colorectal Cancer. Cancer discovery, 16(2), 320.

Yu K, et al. (2026) An α -Hydrolase GmABHD6 Controls Seed Oil Content and Yield in Soybean. Plant biotechnology journal, 24(4), 2040.

Chen D, et al. (2026) Genome-wide identification, evolutionary diversification and developmental expression of the Sox gene family in three brachyuran crabs. BMC genomics, 27(1).

Xu Y, et al. (2026) Histone 3 lysine 36 trimethylation by SETD2 shapes an epigenetic landscape in intestinal stem cells to orchestrate lipid metabolism and attenuate cell senescence. Cell death & disease, 17(1).