

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: 20260903T234456+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 [kravitz2](#) .

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.

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

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).

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).

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

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).

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.

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

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).

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).

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

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.

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

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

Li S, et al. (2026) Genome-wide identification of the DFR gene family in *Dracaena cambodiana* and its expression analysis under wound stress. *BMC plant biology*, 26(1).

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).

Xue Y, et al. (2026) Characterization of the OsEXO70 gene family and their response to salt stress in rice. *BMC genomics*, 27(1).

Zhang D, et al. (2026) Genome-Wide Identification of the CCCH Gene Family and Functional Exploration of MdC3H49 Under Drought Stress Response in Apple (*Malus domestica*). *Plants (Basel, Switzerland)*, 15(8).

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