

# Discovering Novel Sequence Motifs with MEME

Current Protocols in Bioinformatics

00, Unit 2.4

DOI: [10.1002/0471250953.bi0204s00](https://doi.org/10.1002/0471250953.bi0204s00)

Citation Report

#	ARTICLE	IF	CITATIONS
1	PathoGeneâ„¢: a pathogen coding sequence discovery and analysis resource. <i>BioTechniques</i> , 2004, 37, 218-222.	0.8	3
2	Genome-wide analysis of SREBP-1 binding in mouse liver chromatin reveals a preference for promoter proximal binding to a new motif. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 13765-13769.	3.3	85
3	Motif discovery and motif finding from genome-mapped DNase footprint data. <i>Bioinformatics</i> , 2009, 25, 2318-2325.	1.8	35
4	Cancer-associated regulation of alternative splicing. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 670-676.	3.6	327
5	The evolutionary diversification of LSF and Grainyhead transcription factors preceded the radiation of basal animal lineages. <i>BMC Evolutionary Biology</i> , 2010, 10, 101.	3.2	37
6	A feed-forward loop amplifies nutritional regulation of PNPLA3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7892-7897.	3.3	319
7	Three Paralogous LysR-Type Transcriptional Regulators Control Sulfur Amino Acid Supply in <i>Streptococcus mutans</i> . <i>Journal of Bacteriology</i> , 2010, 192, 3464-3473.	1.0	24
8	Genome-wide interrogation of hepatic FXR reveals an asymmetric IR-1 motif and synergy with LRH-1. <i>Nucleic Acids Research</i> , 2010, 38, 6007-6017.	6.5	79
9	A global role for KLF1 in erythropoiesis revealed by ChIP-seq in primary erythroid cells. <i>Genome Research</i> , 2010, 20, 1052-1063.	2.4	180
10	Genome-wide Localization of SREBP-2 in Hepatic Chromatin Predicts a Role in Autophagy. <i>Cell Metabolism</i> , 2011, 13, 367-375.	7.2	147
11	Visualization and Exploration of Conserved Regulatory Modules Using ReXSpecies 2. <i>BMC Evolutionary Biology</i> , 2011, 11, 267.	3.2	3
12	Computational study of associations between histone modification and protein-DNA binding in yeast genome by integrating diverse information. <i>BMC Genomics</i> , 2011, 12, 172.	1.2	5
13	Reshaping of global gene expression networks and sex-biased gene expression by integration of a young gene. <i>EMBO Journal</i> , 2012, 31, 2798-2809.	3.5	44
14	TFBS detection algorithm using distance metrics based on center of mass and polyphase mapping. , 2012, , .		1
15	Profile-based short linear protein motif discovery. <i>BMC Bioinformatics</i> , 2012, 13, 104.	1.2	14
16	Genome-wide analysis of hepatic LRH-1 reveals a promoter binding preference and suggests a role in regulating genes of lipid metabolism in concert with FXR. <i>BMC Genomics</i> , 2012, 13, 51.	1.2	40
17	MicroRNA Cancer Regulation. <i>Advances in Experimental Medicine and Biology</i> , 2013, , .	0.8	17
18	Cytosine methylation changes in enhancer regions of core pro-fibrotic genes characterize kidney fibrosis development. <i>Genome Biology</i> , 2013, 14, R108.	13.9	187

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19	Control of Cellular Bcl-xL Levels by Deamidation-Regulated Degradation. <i>PLoS Biology</i> , 2013, 11, e1001588.	2.6	36
20	The Transcriptome of the Baculovirus <i>Autographa californica</i> Multiple Nucleopolyhedrovirus in <i>Trichoplusia ni</i> Cells. <i>Journal of Virology</i> , 2013, 87, 6391-6405.	1.5	152
21	Production of a reference transcriptome and transcriptomic database (EdwardsiellaBase) for the lined sea anemone, <i>Edwardsiella lineata</i> , a parasitic cnidarian. <i>BMC Genomics</i> , 2014, 15, 71.	1.2	58
22	<i>Serratia marcescens</i> Sh1A Pore-Forming Toxin Is Responsible for Early Induction of Autophagy in Host Cells and Is Transcriptionally Regulated by RcsB. <i>Infection and Immunity</i> , 2014, 82, 3542-3554.	1.0	64
23	Fusion transcript loci share many genomic features with non-fusion loci. <i>BMC Genomics</i> , 2015, 16, 1021.	1.2	16
24	DNA Motif Databases and Their Uses. <i>Current Protocols in Bioinformatics</i> , 2015, 51, 2.15.1-2.15.6.	25.8	16
25	Parallelisation of maximal patterns finding algorithm in biological sequences. , 2016, , .		0
26	PAR-CLIP: A Genomic Technique to Dissect RNA-Protein Interactions. , 2016, , 261-289.		0
27	Finding Similar Nucleotide Sequences Using Network BLAST Searches. <i>Current Protocols in Bioinformatics</i> , 2017, 58, 3.3.1-3.3.25.	25.8	12
28	Identification of 15 candidate structured noncoding RNA motifs in fungi by comparative genomics. <i>BMC Genomics</i> , 2017, 18, 785.	1.2	16
29	Epioncogene Networks: Identification of Epigenomic and Transcriptomic Cooperation by Multi-omics Integration of ChIP-Seq and RNA-Seq Data. <i>RNA Technologies</i> , 2018, , 129-151.	0.2	1
30	An Inter-Institutional and Inter-Disciplinary Collaborative Learning to in-silico Motif Discovery in Molecular Sequences. , 2019, , .		1
31	Expression profiling and in silico homology modeling of Inositol pentakisphosphate 2-kinase, a potential candidate gene for low phytate trait in soybean. <i>3 Biotech</i> , 2020, 10, 268.	1.1	4
32	Investigating the Role of FlhF Identifies Novel Interactions With Genes Involved in Flagellar Synthesis in <i>Campylobacter jejuni</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 460.	1.5	15
33	Expansion of the Transporter-Opsonin-G protein-coupled receptor superfamily with five new protein families. <i>PLoS ONE</i> , 2020, 15, e0231085.	1.1	11
36	Computational Study on Temperature Driven Structure-Function Relationship of Polysaccharide Producing Bacterial Glycosyl Transferase Enzyme. <i>Polymers</i> , 2021, 13, 1771.	2.0	10
37	MicroPIPE: validating an end-to-end workflow for high-quality complete bacterial genome construction. <i>BMC Genomics</i> , 2021, 22, 474.	1.2	25
38	RecA gene genetic diversity and its regulatory element analysis: The case of <i>Vibrio cholerae</i> . <i>Gene Reports</i> , 2021, 25, 101333.	0.4	0

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39	PAR-CLIP: A Method for Transcriptome-Wide Identification of RNA Binding Protein Interaction Sites. <i>Methods in Molecular Biology</i> , 2016, 1358, 153-173.	0.4	55
40	Integrated Expression Profiling and Genome-Wide Analysis of ChREBP Targets Reveals the Dual Role for ChREBP in Glucose-Regulated Gene Expression. <i>PLoS ONE</i> , 2011, 6, e22544.	1.1	130
41	Multiplex transcriptional characterizations across diverse bacterial species using cell-free systems. <i>Molecular Systems Biology</i> , 2019, 15, e8875.	3.2	54
42	Loss of p53-inducible long non-coding RNA LINC01021 increases chemosensitivity. <i>Oncotarget</i> , 2017, 8, 102783-102800.	0.8	13
46	A massively parallel reporter assay reveals focused and broadly encoded RNA localization signals in neurons. <i>Nucleic Acids Research</i> , 2022, 50, 10643-10664.	6.5	4
47	A Deep Learning-Based Approach for Pin-Pointing DNA-Binding in Protein Mutations. <i>Lecture Notes in Electrical Engineering</i> , 2022, , 467-479.	0.3	0
49	Site-directed mutagenesis improves the practical application of L-glutamic acid decarboxylase in <i>Escherichia coli</i> . <i>Engineering in Life Sciences</i> , 2023, 23, .	2.0	0