

Martha L Bulyk

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

7,690
citations

159585

30
h-index

168389

53
g-index

83
all docs

83
docs citations

83
times ranked

9729
citing authors

#	ARTICLE	IF	CITATIONS
1	Diversity and Complexity in DNA Recognition by Transcription Factors. <i>Science</i> , 2009, 324, 1720-1723.	12.6	874
2	Compact, universal DNA microarrays to comprehensively determine transcription-factor binding site specificities. <i>Nature Biotechnology</i> , 2006, 24, 1429-1435.	17.5	612
3	Variation in Homeodomain DNA Binding Revealed by High-Resolution Analysis of Sequence Preferences. <i>Cell</i> , 2008, 133, 1266-1276.	28.9	552
4	Genome-wide analysis of ETS-family DNA-binding in vitro and in vivo. <i>EMBO Journal</i> , 2010, 29, 2147-2160.	7.8	497
5	High-resolution DNA-binding specificity analysis of yeast transcription factors. <i>Genome Research</i> , 2009, 19, 556-566.	5.5	365
6	Evaluation of methods for modeling transcription factor sequence specificity. <i>Nature Biotechnology</i> , 2013, 31, 126-134.	17.5	341
7	Direct Promoter Repression by BCL11A Controls the Fetal to Adult Hemoglobin Switch. <i>Cell</i> , 2018, 173, 430-442.e17.	28.9	328
8	Universal protein-binding microarrays for the comprehensive characterization of the DNA-binding specificities of transcription factors. <i>Nature Protocols</i> , 2009, 4, 393-411.	12.0	322
9	Additivity in protein-DNA interactions: how good an approximation is it?. <i>Nucleic Acids Research</i> , 2002, 30, 4442-4451.	14.5	284
10	Nucleotides of transcription factor binding sites exert interdependent effects on the binding affinities of transcription factors. <i>Nucleic Acids Research</i> , 2002, 30, 1255-1261.	14.5	282
11	Genomic Regions Flanking E-Box Binding Sites Influence DNA Binding Specificity of bHLH Transcription Factors through DNA Shape. <i>Cell Reports</i> , 2013, 3, 1093-1104.	6.4	280
12	UniPROBE, update 2015: new tools and content for the online database of protein-binding microarray data on protein-DNA interactions. <i>Nucleic Acids Research</i> , 2015, 43, D117-D122.	14.5	252
13	Transcription factor-DNA binding: beyond binding site motifs. <i>Current Opinion in Genetics and Development</i> , 2017, 43, 110-119.	3.3	245
14	A Multiparameter Network Reveals Extensive Divergence between <i>C. elegans</i> bHLH Transcription Factors. <i>Cell</i> , 2009, 138, 314-327.	28.9	242
15	Principles of dimer-specific gene regulation revealed by a comprehensive characterization of NF- κ B family DNA binding. <i>Nature Immunology</i> , 2012, 13, 95-102.	14.5	188
16	Neural-specific Sox2 input and differential Gli-binding affinity provide context and positional information in Shh-directed neural patterning. <i>Genes and Development</i> , 2012, 26, 2802-2816.	5.9	158
17	DNA-binding specificity changes in the evolution of forkhead transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12349-12354.	7.1	150
18	The NF- κ B Genomic Landscape in Lymphoblastoid B Cells. <i>Cell Reports</i> , 2014, 8, 1595-1606.	6.4	147

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19	Distinguishing direct versus indirect transcription factor-DNA interactions. <i>Genome Research</i> , 2009, 19, 2090-2100.	5.5	128
20	Survey of variation in human transcription factors reveals prevalent DNA binding changes. <i>Science</i> , 2016, 351, 1450-1454.	12.6	114
21	Curated collection of yeast transcription factor DNA binding specificity data reveals novel structural and gene regulatory insights. <i>Genome Biology</i> , 2011, 12, R125.	9.6	103
22	Precise temporal control of the eye regulatory gene <i>Pax6</i> via enhancer-binding site affinity. <i>Genes and Development</i> , 2010, 24, 980-985.	5.9	97
23	Non-DNA-binding cofactors enhance DNA-binding specificity of a transcriptional regulatory complex. <i>Molecular Systems Biology</i> , 2011, 7, 555.	7.2	95
24	Systematic identification of mammalian regulatory motifs' target genes and functions. <i>Nature Methods</i> , 2008, 5, 347-353.	19.0	86
25	Transcriptional Silencers in <i>Drosophila</i> Serve a Dual Role as Transcriptional Enhancers in Alternate Cellular Contexts. <i>Molecular Cell</i> , 2020, 77, 324-337.e8.	9.7	85
26	Protein Binding Microarrays (PBMs) for Rapid, High-Throughput Characterization of the Sequence Specificities of DNA Binding Proteins. , 2006, 338, 245-260.		71
27	A Comprehensive <i>Drosophila melanogaster</i> Transcription Factor Interactome. <i>Cell Reports</i> , 2019, 27, 955-970.e7.	6.4	66
28	EP300 Selectively Controls the Enhancer Landscape of <i>MYCN</i> -Amplified Neuroblastoma. <i>Cancer Discovery</i> , 2022, 12, 730-751.	9.4	64
29	Diversification of Transcription Factor Paralogs via Noncanonical Modularity in C2H2 Zinc Finger DNA Binding. <i>Molecular Cell</i> , 2014, 55, 640-648.	9.7	56
30	A Motif Co-Occurrence Approach for Genome-Wide Prediction of Transcription-Factor-Binding Sites in <i>Escherichia coli</i> . <i>Genome Research</i> , 2004, 14, 201-208.	5.5	55
31	Highly parallel assays of tissue-specific enhancers in whole <i>Drosophila</i> embryos. <i>Nature Methods</i> , 2013, 10, 774-780.	19.0	55
32	Transcriptional Silencers: Driving Gene Expression with the Brakes On. <i>Trends in Genetics</i> , 2021, 37, 514-527.	6.7	45
33	Differential Occupancy of Two GA-Binding Proteins Promotes Targeting of the <i>Drosophila</i> Dosage Compensation Complex to the Male X Chromosome. <i>Cell Reports</i> , 2018, 22, 3227-3239.	6.4	39
34	Identification of Human Lineage-Specific Transcriptional Coregulators Enabled by a Glossary of Binding Modules and Tunable Genomic Backgrounds. <i>Cell Systems</i> , 2017, 5, 187-201.e7.	6.2	34
35	[13] Analysis of Sequence Specificities of DNA-Binding Proteins with Protein Binding Microarrays. <i>Methods in Enzymology</i> , 2006, 410, 279-299.	1.0	32
36	Differential regulation of mesodermal gene expression by <i>Drosophila</i> cell type-specific Forkhead transcription factors. <i>Development (Cambridge)</i> , 2012, 139, 1457-1466.	2.5	32

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37	Bispecific Forkhead Transcription Factor FoxN3 Recognizes Two Distinct Motifs with Different DNA Shapes. <i>Molecular Cell</i> , 2019, 74, 245-253.e6.	9.7	31
38	LIN28B regulates transcription and potentiates MYCN-induced neuroblastoma through binding to ZNF143 at target gene promoters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16516-16526.	7.1	31
39	Context influences on TALEâ€™DNA binding revealed by quantitative profiling. <i>Nature Communications</i> , 2015, 6, 7440.	12.8	30
40	Phosphorylation of the chromatin remodeling factor DPF3a induces cardiac hypertrophy through releasing HEY repressors from DNA. <i>Nucleic Acids Research</i> , 2016, 44, 2538-2553.	14.5	30
41	Ancient mechanisms for the evolution of the bicoid homeodomain's function in fly development. <i>ELife</i> , 2018, 7, .	6.0	28
42	Jury remains out on simple models of transcription factor specificity. <i>Nature Biotechnology</i> , 2011, 29, 483-484.	17.5	27
43	A feed-forward relay integrates the regulatory activities of Bicoid and Orthodenticle via sequential binding to suboptimal sites. <i>Genes and Development</i> , 2018, 32, 723-736.	5.9	24
44	Common variants in signaling transcription-factor-binding sites drive phenotypic variability in red blood cell traits. <i>Nature Genetics</i> , 2020, 52, 1333-1345.	21.4	24
45	Diversification of transcription factorâ€™DNA interactions and the evolution of gene regulatory networks. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2018, 10, e1423.	6.6	22
46	Interspecies analysis of MYC targets identifies tRNA synthetases as mediators of growth and survival in MYC-overexpressing cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14614-14619.	7.1	14
47	Biological code breaking in the 21st century. <i>Molecular Systems Biology</i> , 2006, 2, 2006.0018.	7.2	10
48	A ChIP-exo screen of 887 Protein Capture Reagents Program transcription factor antibodies in human cells. <i>Genome Research</i> , 2021, 31, 1663-1679.	5.5	9
49	Lineage-specific control of convergent differentiation by a Forkhead repressor. <i>Development (Cambridge)</i> , 2021, 148, .	2.5	9
50	MEDEA: analysis of transcription factor binding motifs in accessible chromatin. <i>Genome Research</i> , 2020, 30, 736-748.	5.5	8
51	Context and number of noncanonical repeat variable diresidues impede the design of TALE proteins with improved DNA targeting. <i>Protein Science</i> , 2020, 29, 606-616.	7.6	3
52	Quantitative-enhancer-FACS-seq (QeFS) reveals epistatic interactions among motifs within transcriptional enhancers in developing <i>Drosophila</i> tissue. <i>Genome Biology</i> , 2021, 22, 348.	8.8	3
53	IDENTIFICATION OF CELL CYCLE-REGULATED, PUTATIVE HYPHAL GENES IN CANDIDA ALBICANS. , 2011, , .		2
54	FUNCTIONAL TRENDS IN STRUCTURAL CLASSES OF THE DNA BINDING DOMAINS OF REGULATORY TRANSCRIPTION FACTORS. , 2007, , .		1