DNAshape: a method for the high-throughput predictio genomic scale

Citation Report

#	ARTICLE	IF	CITATIONS
1	Search by proteins for their DNA target site: 1. The effect of DNA conformation on protein sliding. Nucleic Acids Research, 2014, 42, 12404-12414.	6.5	47
2	Protein–DNA binding: complexities and multi-protein codes. Nucleic Acids Research, 2014, 42, 2099-2111.	6.5	186
3	Experimental mapping of DNA duplex shape enabled by global lineshape analyses of a nucleotide-independent nitroxide probe. Nucleic Acids Research, 2014, 42, e140-e140.	6.5	14
4	cgDNA: a software package for the prediction of sequence-dependent coarse-grain free energies of B-form DNA. Nucleic Acids Research, 2014, 42, e153-e153.	6.5	34
5	Protein˜DNA binding in the absence of specific base-pair recognition. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17140-17145.	3.3	96
6	Prediction of nucleosome rotational positioning in yeast and human genomes based on sequence-dependent DNA anisotropy. BMC Bioinformatics, 2014, 15, 313.	1.2	17
7	TFBSshape: a motif database for DNA shape features of transcription factor binding sites. Nucleic Acids Research, 2014, 42, D148-D155.	6.5	111
8	Covariation between homeodomain transcription factors and the shape of their DNA binding sites. Nucleic Acids Research, 2014, 42, 430-441.	6.5	54
9	OnTheFly: a database of *Drosophila melanogaster* transcription factors and their binding sites. Nucleic Acids Research, 2014, 42, D167-D171.	6.5	43
10	Conformations of p53 response elements in solution deduced using site-directed spin labeling and Monte Carlo sampling. Nucleic Acids Research, 2014, 42, 2789-2797.	6.5	23
11	Determining causality and consequence of expression quantitative trait loci. Human Genetics, 2014, 133, 727-735.	1.8	58
12	Coregulation of Transcription Factor Binding and Nucleosome Occupancy through DNA Features of Mammalian Enhancers. Molecular Cell, 2014, 54, 844-857.	4.5	195
13	Mechanical Model of DNA Allostery. Journal of Physical Chemistry Letters, 2014, 5, 3831-3835.	2.1	24
14	Absence of a simple code: how transcription factors read the genome. Trends in Biochemical Sciences, 2014, 39, 381-399.	3.7	447
15	Exploring comprehensive within-motif dependence of transcription factor binding in Escherichia coli. Scientific Reports, 2015, 5, 17021.	1.6	3
16	A Novel AT-Rich DNA Recognition Mechanism for Bacterial Xenogeneic Silencer MvaT. PLoS Pathogens, 2015, 11, e1004967.	2.1	53
17	Genome-wide features of neuroendocrine regulation in Drosophila by the basic helix-loop-helix transcription factor DIMMED. Nucleic Acids Research, 2015, 43, 2199-2215.	6.5	23
18	An ancient protein-DNA interaction underlying metazoan sex determination. Nature Structural and Molecular Biology, 2015, 22, 442-451.	3.6	93

#	Article	IF	Citations
19	Anthracyclines induce double-strand DNA breaks at active gene promoters. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2015, 773, 9-15.	0.4	80
20	ChIP-nexus enables improved detection of in vivo transcription factor binding footprints. Nature Biotechnology, 2015, 33, 395-401.	9.4	220
21	A DNA shape-based regulatory score improves position-weight matrix-based recognition of transcription factor binding sites. Bioinformatics, 2015, 31, 3445-3450.	1.8	18
22	Multiscale modelling of DNA mechanics. Journal of Physics Condensed Matter, 2015, 27, 323102.	0.7	13
23	Quantitative modeling of transcription factor binding specificities using DNA shape. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4654-4659.	3.3	218
24	Unraveling determinants of transcription factor binding outside the core binding site. Genome Research, 2015, 25, 1018-1029.	2.4	146
25	Shapely DNA attracts the right partner. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4516-4517.	3.3	3
26	GBshape: a genome browser database for DNA shape annotations. Nucleic Acids Research, 2015, 43, D103-D109.	6.5	58
27	Deconvolving the Recognition of DNA Shape from Sequence. Cell, 2015, 161, 307-318.	13.5	174
28	Operator recognition by the ROK transcription factor family members, NagC and Mlc. Nucleic Acids Research, 2015, 43, 361-372.	6.5	11
29	Survey of protein–DNA interactions in Aspergillus oryzae on a genomic scale. Nucleic Acids Research, 2015, 43, 4429-4446.	6.5	9
30	Molecular mechanisms of ribosomal protein gene coregulation. Genes and Development, 2015, 29, 1942-1954.	2.7	116
32	ChEC-seq kinetics discriminates transcription factor binding sites by DNA sequence and shape in vivo. Nature Communications, 2015, 6, 8733.	5.8	153
33	Searching target sites on DNA by proteins: Role of DNA dynamics under confinement. Nucleic Acids Research, 2015, 43, 9176-9186.	6.5	37
34	A widespread role of the motif environment in transcription factor binding across diverse protein families. Genome Research, 2015, 25, 1268-1280.	2.4	134
35	High-Resolution Profiling of Drosophila Replication Start Sites Reveals a DNA Shape and Chromatin Signature of Metazoan Origins. Cell Reports, 2015, 11, 821-834.	2.9	72
36	Evolving insights on how cytosine methylation affects protein-DNA binding. Briefings in Functional Genomics, 2015, 14, 61-73.	1.3	122
37	Quantitative modeling of gene expression using DNA shape features of binding sites. Nucleic Acids Research, 2016, 44, e120-e120.	6.5	16

#	Article	IF	Citations
38	Interactions of two large antiviral polyamides with the long control region of HPV16. Biochimie, 2016, 127, 103-114.	1.3	11
39	Computational challenges in modeling gene regulatory events. Transcription, 2016, 7, 188-195.	1.7	7
40	Xenogeneic Silencing and Its Impact on Bacterial Genomes. Annual Review of Microbiology, 2016, 70, 199-213.	2.9	79
41	Coarse‐grained models for studying protein diffusion along <scp>DNA</scp>. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2016, 6, 515-531.	6.2	25
42	Fine‐tuning of choline metabolism is important for pneumococcal colonization. Molecular Microbiology, 2016, 100, 972-988.	1.2	44
43	DNA supercoiling is a fundamental regulatory principle in the control of bacterial gene expression. Biophysical Reviews, 2016, 8, 89-100.	1.5	89
44	An exploration of the space Of DNA structural properties using an evolutionary algorithm. , 2016, , .		0
45	DNA Structure Helps Predict Protein Binding. Cell Systems, 2016, 3, 216-218.	2.9	4
46	The Impact of Gene Silencing on Horizontal Gene Transfer and Bacterial Evolution. Advances in Microbial Physiology, 2016, 69, 157-186.	1.0	41
47	How motif environment influences transcription factor search dynamics: Finding a needle in a haystack. BioEssays, 2016, 38, 605-612.	1.2	48
48	PionX sites mark the X chromosome for dosage compensation. Nature, 2016, 537, 244-248.	13.7	65
49	DNA Shape Features Improve Transcription Factor Binding Site Predictions InÂVivo. Cell Systems, 2016, 3, 278-286.e4.	2.9	119
50	DNA supercoiling is a fundamental regulatory principle in the control of bacterial gene expression. Biophysical Reviews, 2016, 8, 209-220.	1.5	73
51	Evaluating the impact of single nucleotide variants on transcription factor binding. Nucleic Acids Research, 2016, 44, gkw691.	6.5	35
52	Bacterial pathogen gene regulation: a DNA-structure-centred view of a protein-dominated domain. Clinical Science, 2016, 130, 1165-1177.	1.8	11
53	Sequences flanking the core-binding site modulate glucocorticoid receptor structure and activity. Nature Communications, 2016, 7, 12621.	5.8	48
54	Genomic Nucleosome Organization Reconstituted with Pure Proteins. Cell, 2016, 167, 709-721.e12.	13.5	227
55	Affinity and competition for TBP are molecular determinants of gene expression noise. Nature Communications, 2016, 7, 10417.	5.8	55

#	ARTICLE	IF	CITATIONS
56	Onco-Regulon: an integrated database and software suite for site specific targeting of transcription factors of cancer genes. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw116.	1.4	2
57	A predicted T4 secretion system and conserved DNA-repeats identified in a subset of related Arthrobacter plasmids. Microbiological Research, 2016, 191, 32-37.	2.5	18
58	The role of structural parameters in DNA cyclization. BMC Bioinformatics, 2016, 17, 68.	1.2	7
59	Roles of cofactors and chromatin accessibility in Hox protein target specificity. Epigenetics and Chromatin, 2016, 9, 1.	1.8	68
60	Multiscale simulation of DNA. Current Opinion in Structural Biology, 2016, 37, 29-45.	2.6	124
61	DNAshapeR: an R/Bioconductor package for DNA shape prediction and feature encoding. Bioinformatics, 2016, 32, 1211-1213.	1.8	142
62	Integrated microfluidic approach for quantitative high-throughput measurements of transcription factor binding affinities. Nucleic Acids Research, 2016, 44, e51-e51.	6.5	18
63	Binding of transcription factor GabR to DNA requires recognition of DNA shape at a location distinct from its cognate binding site. Nucleic Acids Research, 2016, 44, 1411-1420.	6.5	35
64	Predicting gene expression in massively parallel reporter assays: A comparative study. Human Mutation, 2017, 38, 1240-1250.	1.1	39
65	Transcription factor family–specific <scp>DNA</scp> shape readout revealed by quantitative specificity models. Molecular Systems Biology, 2017, 13, 910.	3.2	105
66	Genome-wide uniformity of human 'open' pre-initiation complexes. Genome Research, 2017, 27, 15-26.	2.4	22
67	A high-order representation and classification method for transcription factor binding sites recognition in Escherichia coli. Artificial Intelligence in Medicine, 2017, 75, 16-23.	3.8	3
68	Systems Genetics as a Tool to Identify Master Genetic Regulators in Complex Disease. Methods in Molecular Biology, 2017, 1488, 337-362.	0.4	11
69	Genome-wide prediction of minor-groove electrostatic potential enables biophysical modeling of protein–DNA binding. Nucleic Acids Research, 2017, 45, 12565-12576.	6.5	63
70	Correspondence: Reply to 'DNA shape is insufficient to explain binding'. Nature Communications, 2017, 8, 15644.	5.8	1
71	Differences in DNA Binding Specificity of Floral Homeotic Protein Complexes Predict Organ-Specific Target Genes. Plant Cell, 2017, 29, 1822-1835.	3.1	50
72	Correspondence: DNA shape is insufficient to explain binding. Nature Communications, 2017, 8, 15643.	5.8	9
73	Predicting conformational ensembles and genome-wide transcription factor binding sites from DNA sequences. Scientific Reports, 2017, 7, 4071.	1.6	11

#	Article	IF	Citations
74	Features of genomic organization in a nucleotide-resolution molecular model of the Escherichia coli chromosome. Nucleic Acids Research, 2017, 45, 7541-7554.	6.5	48
75	DNA sequence+shape kernel enables alignment-free modeling of transcription factor binding. Bioinformatics, 2017, 33, 3003-3010.	1.8	25
76	Importance of the Sequence-Directed DNA Shape for Specific Binding Site Recognition by the Estrogen-Related Receptor. Frontiers in Endocrinology, 2017, 8, 140.	1.5	12
77	Binding of high mobility group A proteins to the mammalian genome occurs as a function of AT-content. PLoS Genetics, 2017, 13, e1007102.	1.5	16
78	An efficient algorithm for improving structure-based prediction of transcription factor binding sites. BMC Bioinformatics, 2017, 18, 342.	1.2	12
79	DNA microstructure influences selective binding of small molecules designed to target mixed-site DNA sequences. Nucleic Acids Research, 2017, 45, 1297-1306.	6.5	9
80	Predicting Variation of DNA Shape Preferences in Protein-DNA Interaction in Cancer Cells with a New Biophysical Model. Genes, 2017, 8, 233.	1.0	6
81	CERENKOV. , 2017, , .		3
82	Expanding the repertoire of DNA shape features for genome-scale studies of transcription factor binding. Nucleic Acids Research, 2017, 45, 12877-12887.	6.5	81
83	Quantum annealing versus classical machine learning applied to a simplified computational biology problem. Npj Quantum Information, 2018, 4, .	2.8	126
84	Genome-wide determinants of sequence-specific DNA binding of general regulatory factors. Genome Research, 2018, 28, 497-508.	2.4	44
85	Experimental maps of DNA structure at nucleotide resolution distinguish intrinsic from protein-induced DNA deformations. Nucleic Acids Research, 2018, 46, 2636-2647.	6.5	25
86	Relationship between histone modifications and transcription factor binding is protein family specific. Genome Research, 2018, 28, 321-333.	2.4	51
87	Comparison of discriminative motif optimization using matrix and DNA shape-based models. BMC Bioinformatics, 2018, 19, 86.	1.2	10
88	Divergence in DNA Specificity among Paralogous Transcription Factors Contributes to Their Differential InÂVivo Binding. Cell Systems, 2018, 6, 470-483.e8.	2.9	38
89	Comprehensive, high-resolution binding energy landscapes reveal context dependencies of transcription factor binding. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3702-E3711.	3.3	69
90	SelexGLM differentiates androgen and glucocorticoid receptor DNA-binding preference over an extended binding site. Genome Research, 2018, 28, 111-121.	2.4	32
91	Thermodynamic and first-principles biomolecular simulations applied to synthetic biology: promoter and aptamer designs. Molecular Systems Design and Engineering, 2018, 3, 19-37.	1.7	10

#	Article	IF	Citations
92	Eukaryotic and prokaryotic promoter databases as valuable tools in exploring the regulation of gene transcription: a comprehensive overview. Gene, 2018, 644, 38-48.	1.0	12
93	Flexibility and structure of flanking DNA impact transcription factor affinity for its core motif. Nucleic Acids Research, 2018, 46, 11883-11897.	6.5	62
94	Shared nucleotide flanks confer transcriptional competency to bZip core motifs. Nucleic Acids Research, 2018, 46, 8371-8384.	6.5	14
95	DNA Motif Recognition Modeling from Protein Sequences. IScience, 2018, 7, 198-211.	1.9	7
96	Predicting variant deleteriousness in non-human species: applying the CADD approach in mouse. BMC Bioinformatics, 2018, 19, 373.	1.2	10
97	Compound Shape Effects in Minor Groove Binding Affinity and Specificity for Mixed Sequence DNA. Journal of the American Chemical Society, 2018, 140, 14761-14769.	6.6	29
98	Intrinsic DNA Shape Accounts for Affinity Differences between Hox-Cofactor Binding Sites. Cell Reports, 2018, 24, 2221-2230.	2.9	31
99	MTF2 recruits Polycomb Repressive Complex 2 by helical-shape-selective DNA binding. Nature Genetics, 2018, 50, 1002-1010.	9.4	147
100	Analysis of Genetic Variation Indicates DNA Shape Involvement in Purifying Selection. Molecular Biology and Evolution, 2018, 35, 1958-1967.	3.5	14
101	<scp>DNA</scp> sequence and shape are predictive for meiotic crossovers throughout the plant kingdom. Plant Journal, 2018, 95, 686-699.	2.8	24
102	cgDNAweb: a web interface to the cgDNA sequence-dependent coarse-grain model of double-stranded DNA. Nucleic Acids Research, 2018, 46, W5-W10.	6.5	17
103	Human Enhancers Harboring Specific Sequence Composition, Activity, and Genome Organization Are Linked to the Immune Response. Genetics, 2018, 209, 1055-1071.	1.2	16
104	A unified approach for quantifying and interpreting <scp>DNA</scp> shape readout by transcription factors. Molecular Systems Biology, 2018, 14, e7902.	3.2	35
105	Systematic prediction of DNA shape changes due to CpG methylation explains epigenetic effects on proteinâ€"DNA binding. Epigenetics and Chromatin, 2018, 11, 6.	1.8	65
106	Structural Insights into the CRTC2â€"CREB Complex Assembly on CRE. Journal of Molecular Biology, 2018, 430, 1926-1939.	2.0	16
107	The floral homeotic protein <scp>SEPALLATA</scp>3 recognizes target <scp>DNA</scp> sequences by shape readout involving a conserved arginine residue in the <scp>MADS</scp>â€domain. Plant Journal, 2018, 95, 341-357.	2.8	17
108	Prediction of regulatory motifs from human Chip-sequencing data using a deep learning framework. Nucleic Acids Research, 2019, 47, 7809-7824.	6.5	47
109	An integrative approach identifies direct targets of the late viral transcription complex and an expanded promoter recognition motif in Kaposiâ€™s sarcoma-associated herpesvirus. PLoS Pathogens, 2019, 15, e1007774.	2.1	16

#	Article	IF	Citations
110	Satb1 integrates DNA binding site geometry and torsional stress to differentially target nucleosome-dense regions. Nature Communications, 2019, 10, 3221.	5.8	33
111	Co-SELECT reveals sequence non-specific contribution of DNA shape to transcription factor binding in vitro. Nucleic Acids Research, 2019, 47, 6632-6641.	6.5	15
112	Mutations of R882 change flanking sequence preferences of the DNA methyltransferase DNMT3A and cellular methylation patterns. Nucleic Acids Research, 2019, 47, 11355-11367.	6.5	49
113	TFBSshape: an expanded motif database for DNA shape features of transcription factor binding sites. Nucleic Acids Research, 2020, 48, D246-D255.	6.5	27
114	Singing the Crusades: French and Occitan Lyric Responses to the Crusading Movements, 1137–1336, by Linda Paterson, in collaboration with Luca Barbieri, Ruth Harvey and Anna Radaelli, and with an appendix by Marjolaine Raguin-Barthelmebs. English Historical Review, 2019, , .	0.0	0
115	Thermodynamics and site stoichiometry of DNA binding by a large antiviral hairpin polyamide. Biochimie, 2019, 157, 149-157.	1.3	7
116	Structural basis for DNA recognition by FOXC2. Nucleic Acids Research, 2019, 47, 3752-3764.	6.5	36
117	Meta‐analysis of massively parallel reporter assays enables prediction of regulatory function across cell types. Human Mutation, 2019, 40, 1299-1313.	1.1	15
118	YeasTSS: an integrative web database of yeast transcription start sites. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	34
119	MTTFsite: cross-cell type TF binding site prediction by using multi-task learning. Bioinformatics, 2019, 35, 5067-5077.	1.8	24
120	Massively Parallel Assays and Quantitative Sequence–Function Relationships. Annual Review of Genomics and Human Genetics, 2019, 20, 99-127.	2.5	101
121	Redox Sensing by PecS from the Plant Pathogen Pectobacterium atrosepticum and Its Effect on Gene Expression and the Conformation of PecS-Bound Promoter DNA. Biochemistry, 2019, 58, 2564-2575.	1.2	5
122	A New Generation of Minor-Groove-Binding–Heterocyclic Diamidines That Recognize G·C Base Pairs in an AT Sequence Context. Molecules, 2019, 24, 946.	1.7	23
123	Bispecific Forkhead Transcription Factor FoxN3 Recognizes Two Distinct Motifs with Different DNA Shapes. Molecular Cell, 2019, 74, 245-253.e6.	4.5	31
124	Deciphering the Gene Regulatory Landscape Encoded in DNA Biophysical Features. IScience, 2019, 21, 638-649.	1.9	7
125	Trinucleotide Base Pair Stacking Free Energy for Understanding TF-DNA Recognition and the Functions of SNPs. Frontiers in Chemistry, 2018, 6, 666.	1.8	5
126	Small Sequence‐Sensitive Compounds for Specific Recognition of the G‹…C Base Pair in DNA Minor Groove. Chemistry - A European Journal, 2020, 26, 4539-4551.	1.7	5
127	A novel method *SEProm* for prokaryotic promoter prediction based on DNA structure and energetics. Bioinformatics, 2020, 36, 2375-2384.	1.8	12

#	Article	IF	Citations
128	Landscape of DNA binding signatures of myocyte enhancer factor-2B reveals a unique interplay of base and shape readout. Nucleic Acids Research, 2020, 48, 8529-8544.	6.5	17
129	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. PLoS Genetics, 2020, 16, e1009027.	1.5	7
130	Alternative Activation of Macrophages Is Accompanied by Chromatin Remodeling Associated with Lineage-Dependent DNA Shape Features Flanking PU.1 Motifs. Journal of Immunology, 2020, 205, 1070-1083.	0.4	7
131	The RNA Polymerase Î± Subunit Recognizes the DNA Shape of the Upstream Promoter Element. Biochemistry, 2020, 59, 4523-4532.	1.2	12
132	Transcription Factor Binding Affinities and DNA Shape Readout. IScience, 2020, 23, 101694.	1.9	12
133	DNA sequence-dependent activity and base flipping mechanisms of DNMT1 regulate genome-wide DNA methylation. Nature Communications, 2020, 11, 3723.	5.8	48
134	Complex DNA sequence readout mechanisms of the DNMT3B DNA methyltransferase. Nucleic Acids Research, 2020, 48, 11495-11509.	6.5	16
135	Regulatory encoding of quantitative variation in spatial activity of a <i>Drosophila</i> enhancer. Science Advances, 2020, 6, .	4.7	18
136	Structural basis for the complex DNA binding behavior of the plant stem cell regulator WUSCHEL. Nature Communications, 2020, 11, 2223.	5.8	22
137	Epigenetic competition reveals density-dependent regulation and target site plasticity of phosphorothioate epigenetics in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 14322-14330.	3.3	25
138	pCADD: SNV prioritisation in Sus scrofa. Genetics Selection Evolution, 2020, 52, 4.	1.2	21
139	Context-Dependent Gene Regulation by Homeodomain Transcription Factor Complexes Revealed by Shape-Readout Deficient Proteins. Molecular Cell, 2020, 78, 152-167.e11.	4.5	26
140	Atomistic insight into sequence-directed DNA bending and minicircle formation propensity in the absence and presence of phased A-tracts. Journal of Computer-Aided Molecular Design, 2020, 34, 253-265.	1.3	6
141	Crystal structures of REF6 and its complex with DNA reveal diverse recognition mechanisms. Cell Discovery, 2020, 6, 17.	3.1	18
142	Extending the Ïƒ-Hole Motif for Sequence-Specific Recognition of the DNA Minor Groove. Biochemistry, 2020, 59, 1756-1768.	1.2	8
143	Predicting <i>in-vitro</i> Transcription Factor Binding Sites Using DNA Sequence + Shape. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 667-676.	1.9	44
145	Short-range template switching in great ape genomes explored using pair hidden Markov models. PLoS Genetics, 2021, 17, e1009221.	1.5	11
146	Correcting signal biases and detecting regulatory elements in STARR-seq data. Genome Research, 2021, 31, 877-889.	2.4	11

#	Article	IF	Citations
147	Competition for DNA binding between paralogous transcription factors determines their genomic occupancy and regulatory functions. Genome Research, 2021, 31, 1216-1229.	2.4	14
149	Genome information processing by the INO80 chromatin remodeler positions nucleosomes. Nature Communications, 2021, 12, 3231.	5.8	27
150	Predicting transcription factor binding sites using DNA shape features based on shared hybrid deep learning architecture. Molecular Therapy - Nucleic Acids, 2021, 24, 154-163.	2.3	27
151	Epigenetic Marks and Variation of Sequence-Based Information Along Genomic Regions Are Predictive of Recombination Hot/Cold Spots in Saccharomyces cerevisiae. Frontiers in Genetics, 2021, 12, 705038.	1.1	0
153	Insight into the sequence-specific elements leading to increased DNA bending and ligase-mediated circularization propensity by antitumor trabectedin. Journal of Computer-Aided Molecular Design, 2021, 35, 707-719.	1.3	2
154	Structural basis for glucocorticoid receptor recognition of both unmodified and methylated binding sites, precursors of a modern recognition element. Nucleic Acids Research, 2021, 49, 8923-8933.	6.5	3
155	The Active Mechanism of Nucleosome Depletion by Poly(dA:dT) Tracts In Vivo. International Journal of Molecular Sciences, 2021, 22, 8233.	1.8	11
157	Analysis of nucleoidâ€associated proteinâ€binding regions reveals DNA structural features influencing genome organization in MycobacteriumÂtuberculosis. FEBS Letters, 2021, 595, 2504-2521.	1.3	2
158	The bacterial iron sensor IdeR recognizes its DNA targets by indirect readout. Nucleic Acids Research, 2021, 49, 10120-10135.	6.5	6
159	Deciphering the mechanical properties of <scp>Bâ€DNA</scp> duplex. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, e1575.	6.2	18
160	Symphony of the DNA flexibility and sequence environment orchestrates p53 binding to its responsive elements. Gene, 2021, 803, 145892.	1.0	2
161	Humanizing the yeast origin recognition complex. Nature Communications, 2021, 12, 33.	5.8	24
162	Genome-wide prediction of topoisomerase IIÎ² binding by architectural factors and chromatin accessibility. PLoS Computational Biology, 2021, 17, e1007814.	1.5	8
163	Dissecting and predicting different types of binding sites in nucleic acids based on structural information. Briefings in Bioinformatics, 2022, 23, .	3.2	4
172	A machine learning approach for predicting CRISPR-Cas9 cleavage efficiencies and patterns underlying its mechanism of action. PLoS Computational Biology, 2017, 13, e1005807.	1.5	147
173	Expansion of GA Dinucleotide Repeats Increases the Density of CLAMP Binding Sites on the X-Chromosome to Promote Drosophila Dosage Compensation. PLoS Genetics, 2016, 12, e1006120.	1.5	48
174	The folded k-spectrum kernel: A machine learning approach to detecting transcription factor binding sites with gapped nucleotide dependencies. PLoS ONE, 2017, 12, e0185570.	1.1	4
175	ShapeGTB: the role of local DNA shape in prioritization of functional variants in human promoters with machine learning. PeerJ, 2018, 6, e5742.	0.9	2

#	Article	IF	Citations
188	Crystal Structures of REF6 and Its Complex with DNA Reveal Diverse Recognition Mechanisms. SSRN Electronic Journal, 0, , .	0.4	0
192	Comprehensive understanding of Tn5 insertion preference improves transcription regulatory element identification. NAR Genomics and Bioinformatics, 2021, 3, lqab094.	1.5	8
193	RBPSpot: Learning on appropriate contextual information for RBP binding sites discovery. IScience, 2021, 24, 103381.	1.9	7
195	A New Method Combining DNA Shape Features to Improve the Prediction Accuracy of Transcription Factor Binding Sites. Lecture Notes in Computer Science, 2020, , 79-89.	1.0	2
198	Ultra-high-throughput analysis of functional biomolecules using in vitro selection and bioinformatics. Bioscience, Biotechnology and Biochemistry, 2020, 84, 1767-1774.	0.6	1
202	Loss of PRC2 subunits primes lineage choice during exit of pluripotency. Nature Communications, 2021, 12, 6985.	5.8	23
203	Predicting in-vitro DNA protein binding with a spatially aligned fusion of sequence and shape. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	1
204	A framework for mutational signature analysis based on DNA shape parameters. PLoS ONE, 2022, 17, e0262495.	1.1	4
205	SENIES: DNA Shape Enhanced Two-layer Deep Learning Predictor for the Identification of Enhancers and Their Strength. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, PP, 1-1.	1.9	3
206	Characterization and *in vitro* testing of newly isolated lytic bacteriophages for theÂbiocontrol of *Pseudomonas aeruginosa*. Future Microbiology, 2022, 17, 111-141.	1.0	7
207	Delineation of the DNA Structural Features of Eukaryotic Core Promoter Classes. ACS Omega, 2022, 7, 5657-5669.	1.6	11
208	Prediction of Transcription Factor Binding Sites Using Deep Learning Combined with DNA Sequences and Shape Feature Data. , 2021, , .		0
209	Prediction of Enhancers in DNA Sequence Data using a Hybrid CNN-DLSTM Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 1327-1336.	1.9	23
210	GC content strongly influences the role of poly(dA) in the intrinsic nucleosome positioning in *Saccharomyces cerevisiae*. Yeast, 2022, 39, 262-271.	0.8	2
213	Thermodynamic Factors That Drive Sequence-Specific DNA Binding of Designed, Synthetic Minor Groove Binding Agents. Life, 2022, 12, 681.	1.1	2
214	Genome-wide promoter assembly in *E. coli* measured at single-base resolution. Genome Research, 2022, , .	2.4	1
215	Bacterial H-NS contacts DNA at the same irregularly spaced sites in both bridged and hemi-sequestered linear filaments. IScience, 2022, 25, 104429.	1.9	7
216	DESSO-DB: A web database for sequence and shape motif analyses and identification. Computational and Structural Biotechnology Journal, 2022, 20, 3053-3058.	1.9	0

#	Article	IF	Citations
219	Chromatin accessibility shapes meiotic recombination in mouse primordial germ cells through assisting double-strand breaks and loop formation. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2022, , 194844.	0.9	0
220	Motif models proposing independent and interdependent impacts of nucleotides are related to high and low affinity transcription factor binding sites in Arabidopsis. Frontiers in Plant Science, 0, 13, .	1.7	4
221	<i>Pseudomonas</i>-tailed lytic phages: genome mechanical analysis and putative correlation with virion morphogenesis yield. Future Microbiology, 2022, 17, 1009-1026.	1.0	4
222	Deep learning for de-convolution of Smad2 versus Smad3 binding sites. BMC Genomics, 2022, 23, .	1.2	1
223	Structural mechanism of endonucleolytic processing of blocked DNA ends and hairpins by Mre11-Rad50. Molecular Cell, 2022, 82, 3513-3522.e6.	4.5	17
224	Towards a better understanding of TF-DNA binding prediction from genomic features. Computers in Biology and Medicine, 2022, 149, 105993.	3.9	10
225	CRISPR-OTE: Prediction of CRISPR On-Target Efficiency Based on Multi-Dimensional Feature Fusion. Irbm, 2023, 44, 100732.	3.7	1
226	The impact of G-quadruplex dynamics on inter-tetrad electronic couplings: a hybrid computational study. Physical Chemistry Chemical Physics, 2022, 24, 22513-22522.	1.3	0
227	Sequence-Specific Structural Features and Solvation Properties of Transcription Factor Binding DNA Motifs: Insights from Molecular Dynamics Simulation. Journal of Physical Chemistry B, 2022, 126, 9187-9206.	1.2	3
228	Using Fully Convolutional Network to Locate Transcription Factor Binding Sites Based on DNA Sequence and Conservation Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 2690-2699.	1.9	0
229	Structural basis for cell type specific DNA binding of C/EBPβ: The case of cell cycle inhibitor p15INK4b promoter. Journal of Structural Biology, 2022, 214, 107918.	1.3	1
230	Compound Shape and Substituent Effects in DNA Minor Groove Interactions. , 2022, , 1-39.		1
232	DeepPHiC: predicting promoter-centered chromatin interactions using a novel deep learning approach. Bioinformatics, 2023, 39, .	1.8	4
233	Machine learning in the estimation of CRISPR-Cas9 cleavage sites for plant system. Frontiers in Genetics, 0, 13, .	1.1	1
234	Structures of human TR4LBD–JAZF1 and TR4DBD–DNA complexes reveal the molecular basis of transcriptional regulation. Nucleic Acids Research, 2023, 51, 1443-1457.	6.5	1
235	cgNA+web : A Visual Interface to the cgNA+ Sequence-dependent Statistical Mechanics Model of Double-stranded Nucleic Acids. Journal of Molecular Biology, 2023, 435, 167978.	2.0	3
238	Bisulfite probing reveals DNA structural intricacies. Nucleic Acids Research, 0, , .	6.5	0
239	Sequence and chromatin features guide DNA double-strand break resection initiation. Molecular Cell, 2023, 83, 1237-1250.e15.	4.5	7

#	Article	IF	Citations
240	X-ray Structure Characterization of the Selective Recognition of AT Base Pair Sequences. ACS Bio & Med Chem Au, 2023, 3, 335-348.	1.7	3
242	Binding to the DNA Minor Groove by Heterocyclic Dications: from AT Specific to GC Recognition Compounds. Current Protocols, 2023, 3, .	1.3	0
244	DNA and RNA Structure. , 2022, , 20-95.		5
247	Convolutional Hybrid Kernel Network for in-vitro Transcription Factor Binding Sites. , 2023, , .		0
251	Compound Shape and Substituent Effects in DNA Minor Groove Interactions. , 2023, , 833-871.		0
257	Energy-driven genome regulation by ATP-dependent chromatin remodellers. Nature Reviews Molecular Cell Biology, 0, , .	16.1	2