

Gary D Stormo

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/907392/publications.pdf>

Version: 2024-02-01

173
papers

17,449
citations

16451

64
h-index

15266

126
g-index

178
all docs

178
docs citations

178
times ranked

16050
citing authors

#	ARTICLE	IF	CITATIONS
1	Information content of binding sites on nucleotide sequences. <i>Journal of Molecular Biology</i> , 1986, 188, 415-431.	4.2	872
2	Characterization of translational initiation sites in <i>E. coli</i> . <i>Nucleic Acids Research</i> , 1982, 10, 2971-2996.	14.5	729
3	Comparative Genomics Identifies a Flagellar and Basal Body Proteome that Includes the BBS5 Human Disease Gene. <i>Cell</i> , 2004, 117, 541-552.	28.9	721
4	Use of the "Perceptron" algorithm to distinguish translational initiation sites in <i>E. coli</i> . <i>Nucleic Acids Research</i> , 1982, 10, 2997-3011.	14.5	649
5	An improved map of conserved regulatory sites for <i>Saccharomyces cerevisiae</i> . <i>BMC Bioinformatics</i> , 2006, 7, 113.	2.6	617
6	The AP-1 transcription factor Batf controls TH17 differentiation. <i>Nature</i> , 2009, 460, 405-409.	27.8	524
7	Sequence requirements of the hammerhead RNA self-cleavage reaction. <i>Biochemistry</i> , 1990, 29, 10695-10702.	2.5	489
8	Splicing signals in <i>Drosophila</i> : intron size, information content, and consensus sequences. <i>Nucleic Acids Research</i> , 1992, 20, 4255-4262.	14.5	419
9	Analysis of Homeodomain Specificities Allows the Family-wide Prediction of Preferred Recognition Sites. <i>Cell</i> , 2008, 133, 1277-1289.	28.9	401
10	Identifying protein-binding sites from unaligned DNA fragments.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1989, 86, 1183-1187.	7.1	400
11	Translation initiation in <i>Escherichia coli</i> : sequences within the ribosome-binding site. <i>Molecular Microbiology</i> , 1992, 6, 1219-1229.	2.5	329
12	Specificity, free energy and information content in protein-DNA interactions. <i>Trends in Biochemical Sciences</i> , 1998, 23, 109-113.	7.5	312
13	The Neuropeptide Pigment-Dispersing Factor Coordinates Pacemaker Interactions in the <i>Drosophila</i> Circadian System. <i>Journal of Neuroscience</i> , 2004, 24, 7951-7957.	3.6	296
14	Identifying constraints on the higher-order structure of RNA: continued development and application of comparative sequence analysis methods. <i>Nucleic Acids Research</i> , 1992, 20, 5785-5795.	14.5	285
15	Additivity in protein-DNA interactions: how good an approximation is it?. <i>Nucleic Acids Research</i> , 2002, 30, 4442-4451.	14.5	284
16	Innate Host Defense Requires TFE8-Mediated Transcription of Cytoprotective and Antimicrobial Genes. <i>Immunity</i> , 2014, 40, 896-909.	14.3	284
17	[7] High-level translation initiation. <i>Methods in Enzymology</i> , 1990, 185, 89-93.	1.0	270
18	Determining the specificity of protein-DNA interactions. <i>Nature Reviews Genetics</i> , 2010, 11, 751-760.	16.3	264

#	ARTICLE	IF	CITATIONS
19	Identification of a Novel cis-Regulatory Element Involved in the Heat Shock Response in <i>Caenorhabditis elegans</i> Using Microarray Gene Expression and Computational Methods. <i>Genome Research</i> , 2002, 12, 701-712.	5.5	262
20	Application of genome-wide expression analysis to human health and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4801-4806.	7.1	238
21	Combining phylogenetic data with co-regulated genes to identify regulatory motifs. <i>Bioinformatics</i> , 2003, 19, 2369-2380.	4.1	227
22	Identification of consensus patterns in unaligned DNA sequences known to be functionally related. <i>Bioinformatics</i> , 1990, 6, 81-92.	4.1	222
23	Selection of optimal DNA oligos for gene expression arrays. <i>Bioinformatics</i> , 2001, 17, 1067-1076.	4.1	213
24	An Iterated loop matching approach to the prediction of RNA secondary structures with pseudoknots. <i>Bioinformatics</i> , 2004, 20, 58-66.	4.1	213
25	enoLOGOS: a versatile web tool for energy normalized sequence logos. <i>Nucleic Acids Research</i> , 2005, 33, W389-W392.	14.5	199
26	Target Selectivity of Vertebrate Notch Proteins. <i>Journal of Biological Chemistry</i> , 2006, 281, 5106-5119.	3.4	197
27	Identification of Protein Coding Regions In Genomic DNA. <i>Journal of Molecular Biology</i> , 1995, 248, 1-18.	4.2	195
28	Finding the most significant common sequence and structure motifs in a set of RNA sequences. <i>Nucleic Acids Research</i> , 1997, 25, 3724-3732.	14.5	188
29	Inferring Binding Energies from Selected Binding Sites. <i>PLoS Computational Biology</i> , 2009, 5, e1000590.	3.2	188
30	Identification of coding regions in genomic DNA sequences: an application of dynamic programming and neural networks. <i>Nucleic Acids Research</i> , 1993, 21, 607-613.	14.5	180
31	Modeling the specificity of protein-DNA interactions. <i>Quantitative Biology</i> , 2013, 1, 115-130.	0.5	173
32	Non-independence of Mnt repressor-operator interaction determined by a new quantitative multiple fluorescence relative affinity (QuMFRA) assay. <i>Nucleic Acids Research</i> , 2001, 29, 2471-2478.	14.5	169
33	Influence of the period-dependent circadian clock on diurnal, circadian, and aperiodic gene expression in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9562-9567.	7.1	167
34	[13] Consensus patterns in DNA. <i>Methods in Enzymology</i> , 1990, 183, 211-221.	1.0	165
35	Quantitative analysis demonstrates most transcription factors require only simple models of specificity. <i>Nature Biotechnology</i> , 2011, 29, 480-483.	17.5	161
36	Quantitative analysis of the relationship between nucleotide sequence and functional activity. <i>Nucleic Acids Research</i> , 1986, 14, 6661-6679.	14.5	156

#	ARTICLE	IF	CITATIONS
37	Direct, Androgen Receptor-Mediated Regulation of the FKBP5 Gene via a Distal Enhancer Element. <i>Endocrinology</i> , 2006, 147, 590-598.	2.8	151
38	Quantitative analysis of ribosome binding sites in E.coli. <i>Nucleic Acids Research</i> , 1994, 22, 1287-1295.	14.5	147
39	Autogenous regulatory site on the bacteriophage T4 gene 32 messenger RNA. <i>Journal of Molecular Biology</i> , 1988, 201, 517-535.	4.2	146
40	Translational regulation of expression of the bacteriophage T4 lysozyme gene. <i>Nucleic Acids Research</i> , 1986, 14, 5813-5826.	14.5	139
41	Pairwise local structural alignment of RNA sequences with sequence similarity less than 40%. <i>Bioinformatics</i> , 2005, 21, 1815-1824.	4.1	138
42	Expectation maximization algorithm for identifying protein-binding sites with variable lengths from unaligned DNA fragments. <i>Journal of Molecular Biology</i> , 1992, 223, 159-170.	4.2	132
43	A consensus sequence for binding of Lrp to DNA. <i>Journal of Bacteriology</i> , 1995, 177, 4872-4880.	2.2	130
44	Improved Models for Transcription Factor Binding Site Identification Using Nonindependent Interactions. <i>Genetics</i> , 2012, 191, 781-790.	2.9	123
45	Discovering common stem-loop motifs in unaligned RNA sequences. <i>Nucleic Acids Research</i> , 2001, 29, 2135-2144.	14.5	122
46	lacZ translation initiation mutations. <i>Journal of Molecular Biology</i> , 1984, 177, 663-683.	4.2	115
47	An optimized two-finger archive for ZFN-mediated gene targeting. <i>Nature Methods</i> , 2012, 9, 588-590.	19.0	114
48	A Comparative Genomics Approach to Prediction of New Members of Regulons. <i>Genome Research</i> , 2001, 11, 566-584.	5.5	113
49	Autoregulation of gene expression. <i>Journal of Molecular Biology</i> , 1982, 162, 795-818.	4.2	111
50	Probabilistic Code for DNA Recognition by Proteins of the EGR Family. <i>Journal of Molecular Biology</i> , 2002, 323, 701-727.	4.2	109
51	Expression profiling using random genomic DNA microarrays identifies differentially expressed genes associated with three major developmental stages of the protozoan parasite <i>Leishmania major</i> . <i>Molecular and Biochemical Parasitology</i> , 2004, 136, 71-86.	1.1	109
52	Redefining fundamental concepts of transcription initiation in bacteria. <i>Nature Reviews Genetics</i> , 2020, 21, 699-714.	16.3	100
53	Translation Initiation. , 1986, , 195-224.		96
54	Computer Methods for Analyzing Sequence Recognition of Nucleic Acids. <i>Annual Review of Biophysics and Biophysical Chemistry</i> , 1988, 17, 241-263.	12.2	95

#	ARTICLE	IF	CITATIONS
55	Gene-Finding Approaches for Eukaryotes. <i>Genome Research</i> , 2000, 10, 394-397.	5.5	95
56	Is there a code for protein-DNA recognition? Probab(ilstical)ly?. <i>BioEssays</i> , 2002, 24, 466-475.	2.5	94
57	A graph theoretical approach for predicting common RNA secondary structure motifs including pseudoknots in unaligned sequences. <i>Bioinformatics</i> , 2004, 20, 1591-1602.	4.1	92
58	Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015, 6, 6363.	12.8	91
59	Do mRNAs act as direct sensors of small molecules to control their expression?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 9465-9467.	7.1	85
60	Quantitative specificity of the Mnt repressor. <i>Journal of Molecular Biology</i> , 1997, 271, 178-194.	4.2	81
61	Combining SELEX with quantitative assays to rapidly obtain accurate models of protein-DNA interactions. <i>Nucleic Acids Research</i> , 2005, 33, e141-e141.	14.5	75
62	Detection of deletions in the mitochondrial genome of <i>Caenorhabditis elegans</i> . <i>Nucleic Acids Research</i> , 1994, 22, 1075-1078.	14.5	73
63	Computational technique for improvement of the position-weight matrices for the DNA/protein binding sites. <i>Nucleic Acids Research</i> , 2005, 33, 2290-2301.	14.5	73
64	ScerTF: a comprehensive database of benchmarked position weight matrices for <i>Saccharomyces</i> species. <i>Nucleic Acids Research</i> , 2012, 40, D162-D168.	14.5	73
65	Global analysis of <i>Drosophila</i> Cys2-His2 zinc finger proteins reveals a multitude of novel recognition motifs and binding determinants. <i>Genome Research</i> , 2013, 23, 928-940.	5.5	70
66	Excess information at bacteriophage T7 genomic promoters detected by a random cloning technique. <i>Nucleic Acids Research</i> , 1989, 17, 659-674.	14.5	69
67	[2] <i>Escherichia coli</i> promoter sequences: Analysis and prediction. <i>Methods in Enzymology</i> , 1996, 273, 30-42.	1.0	69
68	Review of the algal biology program within the National Alliance for Advanced Biofuels and Bioproducts. <i>Algal Research</i> , 2017, 22, 187-215.	4.6	69
69	Identifying the conserved network of cis-regulatory sites of a eukaryotic genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 17400-17405.	7.1	68
70	An improved predictive recognition model for Cys2-His2 zinc finger proteins. <i>Nucleic Acids Research</i> , 2014, 42, 4800-4812.	14.5	66
71	A systematic model to predict transcriptional regulatory mechanisms based on overrepresentation of transcription factor binding profiles. <i>Genome Research</i> , 2006, 16, 405-413.	5.5	65
72	Identification of Cilia Genes That Affect Cell-Cycle Progression Using Whole-Genome Transcriptome Analysis in <i>Chlamydomonas reinhardtii</i> . <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 979-991.	1.8	64

#	ARTICLE	IF	CITATIONS
73	Measuring quantitative effects of methylation on transcription factorâ€™DNA binding affinity. <i>Science Advances</i> , 2017, 3, eaao1799.	10.3	62
74	RNA Sampler: a new sampling based algorithm for common RNA secondary structure prediction and structural alignment. <i>Bioinformatics</i> , 2007, 23, 1883-1891.	4.1	61
75	A design for computer nucleic-acid-sequence storage, retrieval, and manipulation. <i>Nucleic Acids Research</i> , 1982, 10, 3013-3024.	14.5	60
76	Training the Next Generation of Informaticians: The Impact of "BISTI" and Bioinformatics--A Report from the American College of Medical Informatics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2004, 11, 167-172.	4.4	52
77	Sepsis gene expression profiling: Murine splenic compared with hepatic responses determined by using complementary DNA microarrays. <i>Critical Care Medicine</i> , 2002, 30, 2711-2721.	0.9	51
78	Making connections between novel transcription factors and their DNA motifs. <i>Genome Research</i> , 2005, 15, 312-320.	5.5	49
79	Sequence landscapes. <i>Nucleic Acids Research</i> , 1986, 14, 141-158.	14.5	47
80	Context-dependent DNA recognition code for C2H2 zinc-finger transcription factors. <i>Bioinformatics</i> , 2008, 24, 1850-1857.	4.1	47
81	RNA interference of achaete-scute homolog 1 in mouse prostate neuroendocrine cells reveals its gene targets and DNA binding sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 5559-5564.	7.1	46
82	High-Resolution Specificity from DNA Sequencing Highlights Alternative Modes of Lac Repressor Binding. <i>Genetics</i> , 2014, 198, 1329-1343.	2.9	46
83	Delila system tools. <i>Nucleic Acids Research</i> , 1984, 12, 129-140.	14.5	45
84	INJURY IN THE ERA OF GENOMICS. <i>Shock</i> , 2001, 15, 165-170.	2.1	43
85	Information Content and Free Energy in DNAâ€™Protein Interactions. <i>Journal of Theoretical Biology</i> , 1998, 195, 135-137.	1.7	41
86	SMARCD1 Contributes to the Regulation of Naive Pluripotency by Interacting with Histone Citrullination. <i>Cell Reports</i> , 2017, 18, 3117-3128.	6.4	40
87	Molecular Diagnostics in Sepsis: From Bedside to Bench. <i>Journal of the American College of Surgeons</i> , 2006, 203, 585-598.e1.	0.5	38
88	Identification of muscle-specific regulatory modules in <i>Caenorhabditis elegans</i> . <i>Genome Research</i> , 2007, 17, 348-357.	5.5	38
89	Novel Modeling of Combinatorial miRNA Targeting Identifies SNP with Potential Role in Bone Density. <i>PLoS Computational Biology</i> , 2012, 8, e1002830.	3.2	38
90	PolyMAPr: Programs for polymorphism database mining, annotation, and functional analysis. <i>Human Mutation</i> , 2005, 25, 110-117.	2.5	37

#	ARTICLE	IF	CITATIONS
91	Training of the next generation of biostatisticians: a call to action in the U.S.. <i>Statistics in Medicine</i> , 2006, 25, 3415-3429.	1.6	37
92	Recognition models to predict DNA-binding specificities of homeodomain proteins. <i>Bioinformatics</i> , 2012, 28, i84-i89.	4.1	36
93	Spec-seq: determining protein-DNA-binding specificity by sequencing. <i>Briefings in Functional Genomics</i> , 2015, 14, 30-38.	2.7	35
94	The bacteriophage T4regA gene: primary sequence of a translational repressor. <i>Nucleic Acids Research</i> , 1984, 12, 5979-5993.	14.5	34
95	Mining genome databases to identify and understand new gene regulatory systems. <i>Current Opinion in Microbiology</i> , 2002, 5, 149-153.	5.1	34
96	BEEM: estimation of binding energy models using HT-SELEX data. <i>Bioinformatics</i> , 2017, 33, 2288-2295.	4.1	34
97	PromoLign: A database for upstream region analysis and SNPs. <i>Human Mutation</i> , 2004, 23, 534-539.	2.5	33
98	ILM: a web server for predicting RNA secondary structures with pseudoknots. <i>Nucleic Acids Research</i> , 2004, 32, W146-W149.	14.5	32
99	Discovering structural <i>cis</i> regulatory elements by modeling the behaviors of mRNAs. <i>Molecular Systems Biology</i> , 2009, 5, 268.	7.2	32
100	Response Element Composition Governs Correlations between Binding Site Affinity and Transcription in Glucocorticoid Receptor Feed-forward Loops. <i>Journal of Biological Chemistry</i> , 2015, 290, 19756-19769.	3.4	32
101	Role of gene expression microarray analysis in finding complex disease genes. <i>Genetic Epidemiology</i> , 2002, 23, 37-56.	1.3	31
102	Specificity of the Mnt protein determined by binding to randomized operators.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 5699-5703.	7.1	30
103	Computational identification and functional validation of regulatory motifs in cartilage-expressed genes. <i>Genome Research</i> , 2007, 17, 1438-1447.	5.5	30
104	Maximally Efficient Modeling of DNA Sequence Motifs at All Levels of Complexity. <i>Genetics</i> , 2011, 187, 1219-1224.	2.9	30
105	Quantitative profiling of selective Sox/POU pairing on hundreds of sequences in parallel by Coop-seq. <i>Nucleic Acids Research</i> , 2017, 45, 832-845.	14.5	30
106	Putting the Leishmania genome to work: functional genomics by transposon trapping and expression profiling. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2002, 357, 47-53.	4.0	27
107	Computational identification of the Spo0A-phosphate regulon that is essential for the cellular differentiation and development in Gram-positive spore-forming bacteria. <i>Nucleic Acids Research</i> , 2003, 31, 6891-6903.	14.5	27
108	Novel transcription regulatory elements in <i>Caenorhabditis elegans</i> muscle genes. <i>Genome Research</i> , 2004, 14, 2457-2468.	5.5	27

#	ARTICLE	IF	CITATIONS
109	Using defined finger-finger interfaces as units of assembly for constructing zinc-finger nucleases. <i>Nucleic Acids Research</i> , 2013, 41, 2455-2465.	14.5	27
110	Computational identification of the normal and perturbed genetic networks involved in myeloid differentiation and acute promyelocytic leukemia. <i>Genome Biology</i> , 2008, 9, R38.	9.6	26
111	Exploring the DNA-recognition potential of homeodomains. <i>Genome Research</i> , 2012, 22, 1889-1898.	5.5	26
112	An Overview of RNA Sequence Analyses: Structure Prediction, ncRNA Gene Identification, and RNAi Design. <i>Current Protocols in Bioinformatics</i> , 2013, 43, 12.1.1-12.1.3.	25.8	26
113	A modified bacterial one-hybrid system yields improved quantitative models of transcription factor specificity. <i>Nucleic Acids Research</i> , 2011, 39, e83-e83.	14.5	25
114	Analysis of <i>Chlamydomonas reinhardtii</i> Genome Structure Using Large-Scale Sequencing of Regions on Linkage Groups I and III. <i>Journal of Eukaryotic Microbiology</i> , 2003, 50, 145-155.	1.7	24
115	Genome wide screens in yeast to identify potential binding sites and target genes of DNA-binding proteins. <i>Nucleic Acids Research</i> , 2008, 36, e8-e8.	14.5	24
116	PAP: a comprehensive workbench for mammalian transcriptional regulatory sequence analysis. <i>Nucleic Acids Research</i> , 2007, 35, W238-W244.	14.5	23
117	Quantitative analysis of EGR proteins binding to DNA: assessing additivity in both the binding site and the protein. <i>BMC Bioinformatics</i> , 2005, 6, 176.	2.6	22
118	A global approach to identify differentially expressed genes in cDNA (two-color) microarray experiments. <i>Bioinformatics</i> , 2007, 23, 2073-2079.	4.1	22
119	Multi-alphabet consensus algorithm for identification of low specificity protein-DNA interactions. <i>Nucleic Acids Research</i> , 1995, 23, 1434-1440.	14.5	21
120	An Introduction to Sequence Similarity (Homology) Searching. <i>Current Protocols in Bioinformatics</i> , 2009, 27, Unit 3.1 3.1.1-7.	25.8	21
121	Novel sequence-based method for identifying transcription factor binding sites in prokaryotic genomes. <i>Bioinformatics</i> , 2010, 26, 2672-2677.	4.1	21
122	A nutrient-sensitive interaction between Sirt1 and HNF1 α regulates <i>Crp</i> expression. <i>Aging Cell</i> , 2011, 10, 305-317.	6.7	21
123	Discovering cis-Regulatory RNAs in <i>Shewanella</i> Genomes by Support Vector Machines. <i>PLoS Computational Biology</i> , 2009, 5, e1000338.	3.2	20
124	Discriminative motif optimization based on perceptron training. <i>Bioinformatics</i> , 2014, 30, 941-948.	4.1	19
125	Inherent limitations of probabilistic models for protein-DNA binding specificity. <i>PLoS Computational Biology</i> , 2017, 13, e1005638.	3.2	19
126	TRANSCRIPTIONAL PROFILES OF HUMAN EPITHELIAL CELLS IN RESPONSE TO HEAT. <i>Shock</i> , 2008, 29, 623-630.	2.1	19

#	ARTICLE	IF	CITATIONS
127	Improving Gene-finding in <i>Chlamydomonas reinhardtii</i> : GreenGenie2. <i>BMC Genomics</i> , 2009, 10, 210.	2.8	18
128	The <i>cis</i> -regulatory map of <i>Shewanella</i> genomes. <i>Nucleic Acids Research</i> , 2008, 36, 5376-5390.	14.5	17
129	Conserved Motifs and Prediction of Regulatory Modules in <i>Caenorhabditis elegans</i> . <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 469-481.	1.8	17
130	Analysis of five presumptive protein-coding sequences clustered between the primosome genes, 41 and 61, of bacteriophages T4, T2, and T6. <i>Journal of Virology</i> , 1993, 67, 2305-2316.	3.4	17
131	Specificity of the Mnt Protein. <i>Journal of Molecular Biology</i> , 1993, 229, 821-826.	4.2	16
132	Quantitative modeling of DNA-protein interactions: effects of amino acid substitutions on binding specificity of the Mnt repressor. <i>Nucleic Acids Research</i> , 2004, 32, 4026-4032.	14.5	16
133	DNA Motif Databases and Their Uses. <i>Current Protocols in Bioinformatics</i> , 2015, 51, 2.15.1-2.15.6.	25.8	16
134	Editing efficiency of a <i>Drosophila</i> gene correlates with a distant splice site selection. <i>Rna</i> , 2005, 11, 563-566.	3.5	15
135	Alternative Splicing During the <i>Chlamydomonas reinhardtii</i> Cell Cycle. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3797-3810.	1.8	15
136	Evidence for Active Maintenance of Inverted Repeat Structures Identified by a Comparative Genomic Approach. <i>PLoS ONE</i> , 2007, 2, e262.	2.5	14
137	EVOLUTION: Heirlooms in the Attic. <i>Science</i> , 2003, 302, 997-999.	12.6	13
138	A quantitative understanding of lac repressor's binding specificity and flexibility. <i>Quantitative Biology</i> , 2015, 3, 69-80.	0.5	13
139	PromFD 1.0: a computer program that predicts eukaryotic pol II promoters using strings and IMD matrices. <i>Bioinformatics</i> , 1997, 13, 29-35.	4.1	12
140	[22] Probing information content of DNA-binding sites. <i>Methods in Enzymology</i> , 1991, 208, 458-468.	1.0	11
141	Putting numbers on the network connections. <i>BioEssays</i> , 2007, 29, 717-721.	2.5	11
142	Quantitative specificity of STAT1 and several variants. <i>Nucleic Acids Research</i> , 2017, 45, 8199-8207.	14.5	11
143	Autoregulation of yeast ribosomal proteins discovered by efficient search for feedback regulation. <i>Communications Biology</i> , 2020, 3, 761.	4.4	11
144	Directed Evolution of an Enhanced POU Reprogramming Factor for Cell Fate Engineering. <i>Molecular Biology and Evolution</i> , 2021, 38, 2854-2868.	8.9	11

#	ARTICLE	IF	CITATIONS
145	Motif Discovery Using Expectation Maximization and Gibbs™ Sampling. <i>Methods in Molecular Biology</i> , 2010, 674, 85-95.	0.9	11
146	New Tricks for an Old Dogma. <i>Molecular Cell</i> , 2003, 11, 1419-1420.	9.7	10
147	Combinatorial <i>Cis</i> -regulation in <i>Saccharomyces</i> Species. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 653-667.	1.8	10
148	Comparison of discriminative motif optimization using matrix and DNA shape-based models. <i>BMC Bioinformatics</i> , 2018, 19, 86.	2.6	10
149	DNA sequence classification using DAWGs. <i>Lecture Notes in Computer Science</i> , 1997, , 339-352.	1.3	10
150	Translational Regulation in Bacteriophages. , 1987, , 27-49.		10
151	Modeling the Quantitative Specificity of DNA-Binding Proteins from Example Binding Sites. <i>PLoS ONE</i> , 2009, 4, e6736.	2.5	8
152	Quantitative profiling of BATF family proteins/JUNB/IRF hetero-trimers using Spec-seq. <i>BMC Molecular Biology</i> , 2018, 19, 5.	3.0	8
153	Quantitative DNA Sequencing to Determine the Relative Protein-DNA Binding Constants to Multiple DNA Sequences. <i>Analytical Biochemistry</i> , 1994, 219, 230-239.	2.4	7
154	Procom: a web-based tool to compare multiple eukaryotic proteomes. <i>Bioinformatics</i> , 2005, 21, 1693-1694.	4.1	7
155	An Overview of RNA Structure Prediction and Applications to RNA Gene Prediction and RNA i Design. <i>Current Protocols in Bioinformatics</i> , 2006, 13, Unit 12.1.	25.8	7
156	Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids. Richard Durbin , Sean R. Eddy , Anders Krogh , Graeme Mitchison. <i>Quarterly Review of Biology</i> , 2000, 75, 313-314.	0.1	6
157	Improved statistical methods reveal direct interactions between 16S and 23S rRNA. <i>Nucleic Acids Research</i> , 2000, 28, 4938-4943.	14.5	6
158	Specificity of Mnt 'master residue' obtained from in vivo and in vitro selections. <i>Nucleic Acids Research</i> , 2002, 30, 5539-5548.	14.5	6
159	<title>Probing protein: DNA interactions using a uniform monolayer of DNA and surface plasmon resonance</title>. , 2000, , .		5
160	Fast, Sensitive Discovery of Conserved Genome-Wide Motifs. <i>Journal of Computational Biology</i> , 2012, 19, 139-147.	1.6	5
161	DNA Structure Helps Predict Protein Binding. <i>Cell Systems</i> , 2016, 3, 216-218.	6.2	4
162	Coop-Seq Analysis Demonstrates that Sox2 Evokes Latent Specificities in the DNA Recognition by Pax6. <i>Journal of Molecular Biology</i> , 2017, 429, 3626-3634.	4.2	4

#	ARTICLE	IF	CITATIONS
163	An Introduction to Recognizing Functional Domains. Current Protocols in Bioinformatics, 2006, 15, Unit 2.1.	25.8	3
164	Using mRNAs lengths to accurately predict the alternatively spliced gene products in Caenorhabditis elegans. Bioinformatics, 2006, 22, 1239-1244.	4.1	3
165	An Introduction to Recognizing Functional Domains. Current Protocols in Bioinformatics, 2011, 34, Unit 2.1.	25.8	3
166	Assessing the Effects of Symmetry on Motif Discovery and Modeling. PLoS ONE, 2011, 6, e24908.	2.5	3
167	Detecting Coevolution of Functionally Related Proteins for Automated Protein Annotation. , 2010, , 99-105.		2
168	Determination of specificity influencing residues for key transcription factor families. Quantitative Biology, 2015, 3, 115-123.	0.5	2
169	An Introduction to Recognizing Functional Domains. Current Protocols in Bioinformatics, 2003, 00, 2.1.1.	25.8	1
170	An Overview of RNA Structure Prediction. Current Protocols in Bioinformatics, 2003, 4, 12.1.1.	25.8	0
171	Is Autogenous Posttranscriptional Gene Regulation Common?. RNA Technologies, 2018, , 217-227.	0.3	0
172	PLASTICITY OF THE HUMAN INNATE IMMUNE RESPONSE TO ACUTE INFECTION DURING CRITICAL ILLNESS: DEVELOPMENT OF THE RIBOLEUKOGRAM.. Critical Care Medicine, 2006, 34, A47.	0.9	0
173	Recognizing Functional Domains in Biological Sequences. , 1997, , 105-116.		0