

Thomas D Schneider

List of Publications by Year in descending order

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58
papers

9,268
citations

117453

34
h-index

149479

56
g-index

97
all docs

97
docs citations

97
times ranked

9218
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequence logos: a new way to display consensus sequences. <i>Nucleic Acids Research</i> , 1990, 18, 6097-6100.	6.5	2,940
2	Information content of binding sites on nucleotide sequences. <i>Journal of Molecular Biology</i> , 1986, 188, 415-431.	2.0	872
3	Characterization of translational initiation sites in <i>E. coli</i> . <i>Nucleic Acids Research</i> , 1982, 10, 2971-2996.	6.5	729
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.	6.5	649
5	Redox-dependent shift of OxyR-DNA contacts along an extended DNA-binding site: A mechanism for differential promoter selection. <i>Cell</i> , 1994, 78, 897-909.	13.5	375
6	OxyR and SoxRS Regulation of <i>fur</i> . <i>Journal of Bacteriology</i> , 1999, 181, 4639-4643.	1.0	358
7	Information Content of Individual Genetic Sequences. <i>Journal of Theoretical Biology</i> , 1997, 189, 427-441.	0.8	283
8	Features of spliceosome evolution and function inferred from an analysis of the information at human splice sites. <i>Journal of Molecular Biology</i> , 1992, 228, 1124-1136.	2.0	254
9	Anatomy of <i>Escherichia coli</i> 70 promoters. <i>Nucleic Acids Research</i> , 2007, 35, 771-788.	6.5	209
10	Small membrane proteins found by comparative genomics and ribosome binding site models. <i>Molecular Microbiology</i> , 2008, 70, 1487-1501.	1.2	194
11	Information analysis of human splice site mutations. <i>Human Mutation</i> , 1998, 12, 153-171.	1.1	187
12	Quantitative analysis of the relationship between nucleotide sequence and functional activity. <i>Nucleic Acids Research</i> , 1986, 14, 6661-6679.	6.5	156
13	Quantitative analysis of ribosome binding sites in <i>E. coli</i> . <i>Nucleic Acids Research</i> , 1994, 22, 1287-1295.	6.5	147
14	The human XPC DNA repair gene: arrangement, splice site information content and influence of a single nucleotide polymorphism in a splice acceptor site on alternative splicing and function. <i>Nucleic Acids Research</i> , 2002, 30, 3624-3631.	6.5	146
15	Anatomy of <i>Escherichia coli</i> ribosome binding sites 1 Edited by D. Draper. <i>Journal of Molecular Biology</i> , 2001, 313, 215-228.	2.0	132
16	Computation-Directed Identification of OxyR DNA Binding Sites in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2001, 183, 4571-4579.	1.0	126
17	Theory of molecular machines. I. Channel capacity of molecular machines. <i>Journal of Theoretical Biology</i> , 1991, 148, 83-123.	0.8	105
18	Theory of molecular machines. II. Energy dissipation from molecular machines. <i>Journal of Theoretical Biology</i> , 1991, 148, 125-137.	0.8	100

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19	Discovery of Fur binding site clusters in Escherichia coli by information theory models. <i>Nucleic Acids Research</i> , 2007, 35, 6762-6777.	6.5	79
20	Xeroderma Pigmentosum-Variant Patients from America, Europe, and Asia. <i>Journal of Investigative Dermatology</i> , 2008, 128, 2055-2068.	0.3	76
21	Information Analysis of Sequences that Bind the Replication Initiator RepA. <i>Journal of Molecular Biology</i> , 1993, 233, 219-230.	2.0	71
22	A brief review of molecular information theory. <i>Nano Communication Networks</i> , 2010, 1, 173-180.	1.6	70
23	Excess information at bacteriophage T7 genomic promoters detected by a random cloning technique. <i>Nucleic Acids Research</i> , 1989, 17, 659-674.	6.5	69
24	Reading of DNA sequence logos: Prediction of major groove binding by information theory. <i>Methods in Enzymology</i> , 1996, 274, 445-455.	0.4	66
25	Xeroderma Pigmentosum Group C Splice Mutation Associated with Autism and Hypoglycinemia11An abstract of this manuscript was presented at the annual meeting of the Society for Investigative Dermatology in Washington, DC. <i>Journal of Investigative Dermatology</i> , 1998, 111, 791-796.	0.3	66
26	Two essential splice lariat branchpoint sequences in one intron in a xeroderma pigmentosum DNA repair gene: mutations result in reduced XPC mRNA levels that correlate with cancer risk. <i>Human Molecular Genetics</i> , 2003, 13, 343-352.	1.4	63
27	A design for computer nucleic-acid-sequence storage, retrieval, and manipulation. <i>Nucleic Acids Research</i> , 1982, 10, 3013-3024.	6.5	60
28	Interdependence of the position and orientation of SoxS binding sites in the transcriptional activation of the class I subset of Escherichia coli superoxide-inducible promoters. <i>Molecular Microbiology</i> , 1999, 34, 414-430.	1.2	56
29	Using information content and base frequencies to distinguish mutations from genetic polymorphisms in splice junction recognition sites. <i>Human Mutation</i> , 1995, 6, 74-76.	1.1	55
30	Consensus sequence Zen. <i>Applied Bioinformatics</i> , 2002, 1, 111-9.	1.7	49
31	Delila system tools. <i>Nucleic Acids Research</i> , 1984, 12, 129-140.	6.5	45
32	Information theory based T7-like promoter models: classification of bacteriophages and differential evolution of promoters and their polymerases. <i>Nucleic Acids Research</i> , 2005, 33, 6172-6187.	6.5	45
33	Using sequence logos and information analysis of Lrp DNA binding sites to investigate discrepancies between natural selection and SELEX. <i>Nucleic Acids Research</i> , 1999, 27, 882-887.	6.5	43
34	Fast multiple alignment of ungapped DNA sequences using information theory and a relaxation method. <i>Discrete Applied Mathematics</i> , 1996, 71, 259-268.	0.5	39
35	Replication Control of Plasmid P1 and Its Host Chromosome: The Common Ground. <i>Progress in Molecular Biology and Translational Science</i> , 1997, 57, 145-186.	1.9	38
36	Measuring Molecular Information. <i>Journal of Theoretical Biology</i> , 1999, 201, 87-92.	0.8	37

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37	CorreLogo: an online server for 3D sequence logos of RNA and DNA alignments. <i>Nucleic Acids Research</i> , 2006, 34, W405-W411.	6.5	32
38	70% efficiency of bistate molecular machines explained by information theory, high dimensional geometry and evolutionary convergence. <i>Nucleic Acids Research</i> , 2010, 38, 5995-6006.	6.5	31
39	Correlation between binding rate constants and individual information of <i>E. coli</i> Fis binding sites. <i>Nucleic Acids Research</i> , 2007, 35, 5275-5283.	6.5	30
40	Discovery of novel tumor suppressor p53 response elements using information theory. <i>Nucleic Acids Research</i> , 2008, 36, 3828-3833.	6.5	30
41	Promoter variants in the MSMB gene associated with prostate cancer regulate MSMB/NCOA4 fusion transcripts. <i>Human Genetics</i> , 2012, 131, 1453-1466.	1.8	25
42	Molecular flip-flops formed by overlapping Fis sites. <i>Nucleic Acids Research</i> , 2003, 31, 6663-6673.	6.5	16
43	Claude Shannon: Biologist [information theory used in biology]. <i>IEEE Engineering in Medicine and Biology Magazine</i> , 2006, 25, 30-33.	1.1	14
44	Genome-Wide Transcriptional Regulation and Chromosome Structural Arrangement by GalR in <i>E. coli</i> . <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 74.	1.6	12
45	Twenty-five Years of Delila and Molecular Information Theory. <i>Biological Theory</i> , 2006, 1, 250-260.	0.8	11
46	Identification of an Intragenic Ribosome Binding Site That Affects Expression of the <i>uncB</i> Gene of the <i>Escherichia coli</i> Proton-Translocating ATPase (<i>unc</i>) Operon. <i>Journal of Bacteriology</i> , 1998, 180, 3940-3945.	1.0	11
47	Comparative analysis of tandem T7-like promoter containing regions in enterobacterial genomes reveals a novel group of genetic islands. <i>Nucleic Acids Research</i> , 2006, 34, 1133-1147.	6.5	10
48	Redundant designations of BRCA1 intron 11 splicing mutation; c. 4216-2A>G; IVS11-2A>G; L78833, 37698, A>G. <i>Human Mutation</i> , 2000, 16, 264-264.	1.1	8
49	An unusual feature associated with <i>LEE1</i> P1 promoters in enteropathogenic <i>Escherichia coli</i> (EPEC). <i>Molecular Microbiology</i> , 2012, 83, 612-622.	1.2	8
50	Elements in the $\hat{\nu}$ immunity region regulate phage development: beyond the "Genetic Switch"™. <i>Molecular Microbiology</i> , 2019, 112, 1798-1813.	1.2	8
51	Logos for amino-acid preferences in different backbone packing density regions of protein structural classes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1156-1165.	2.5	7
52	Density of $\hat{\nu}$ 70 promoter-like sites in the intergenic regions dictates the redistribution of RNA polymerase during osmotic stress in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2019, 47, 3970-3985.	6.5	7
53	Identification of a Cryptic Bacterial Promoter in Mouse (<i>mdr1a</i>) P-Glycoprotein cDNA. <i>PLoS ONE</i> , 2015, 10, e0136396.	1.1	5
54	Restriction enzymes use a 24 dimensional coding space to recognize 6 base long DNA sequences. <i>PLoS ONE</i> , 2019, 14, e0222419.	1.1	4

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55	Some Lessons for Molecular Biology from Information Theory. Studies in Fuzziness and Soft Computing, 2003, , 229-237.	0.6	4
56	An Evolutionary/Biochemical Connection between Promoter- and Primer-Dependent Polymerases Revealed by Systematic Evolution of Ligands by Exponential Enrichment. Journal of Bacteriology, 2018, 200, .	1.0	2
57	New Approaches in Mathematical Biology: Information Theory and Molecular Machines. , 1996, , 313-321.		2
58	Visual Display of Sequence Conservation as an Aid to Taxonomic Classification Using PCR Amplification. , 1995, , 21-32.		1