

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	Restriction enzymes use a 24 dimensional coding space to recognize 6 base long DNA sequences. PLoS ONE, 2019, 14, e0222419.	1.1	4
2	Elements in the λ immunity region regulate phage development: beyond the "Genetic Switch"™. Molecular Microbiology, 2019, 112, 1798-1813.	1.2	8
3	Density of λ 70 promoter-like sites in the intergenic regions dictates the redistribution of RNA polymerase during osmotic stress in Escherichia coli. Nucleic Acids Research, 2019, 47, 3970-3985.	6.5	7
4	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
5	Genome-Wide Transcriptional Regulation and Chromosome Structural Arrangement by GalR in E. coli. Frontiers in Molecular Biosciences, 2016, 3, 74.	1.6	12
6	Identification of a Cryptic Bacterial Promoter in Mouse (mdr1a) P-Glycoprotein cDNA. PLoS ONE, 2015, 10, e0136396.	1.1	5
7	Promoter variants in the MSMB gene associated with prostate cancer regulate MSMB/NCOA4 fusion transcripts. Human Genetics, 2012, 131, 1453-1466.	1.8	25
8	An unusual feature associated with <i>LEE1</i> P1 promoters in enteropathogenic <i>Escherichia coli</i> (EPEC). Molecular Microbiology, 2012, 83, 612-622.	1.2	8
9	A brief review of molecular information theory. Nano Communication Networks, 2010, 1, 173-180.	1.6	70
10	70% efficiency of bistate molecular machines explained by information theory, high dimensional geometry and evolutionary convergence. Nucleic Acids Research, 2010, 38, 5995-6006.	6.5	31
11	Xeroderma Pigmentosum-Variant Patients from America, Europe, and Asia. Journal of Investigative Dermatology, 2008, 128, 2055-2068.	0.3	76
12	Small membrane proteins found by comparative genomics and ribosome binding site models. Molecular Microbiology, 2008, 70, 1487-1501.	1.2	194
13	Discovery of novel tumor suppressor p53 response elements using information theory. Nucleic Acids Research, 2008, 36, 3828-3833.	6.5	30
14	Correlation between binding rate constants and individual information of E. coli Fis binding sites. Nucleic Acids Research, 2007, 35, 5275-5283.	6.5	30
15	Anatomy of Escherichia coli λ 70 promoters. Nucleic Acids Research, 2007, 35, 771-788.	6.5	209
16	Discovery of Fur binding site clusters in Escherichia coli by information theory models. Nucleic Acids Research, 2007, 35, 6762-6777.	6.5	79
17	Claude Shannon: Biologist [information theory used in biology]. IEEE Engineering in Medicine and Biology Magazine, 2006, 25, 30-33.	1.1	14
18	CorreLogo: an online server for 3D sequence logos of RNA and DNA alignments. Nucleic Acids Research, 2006, 34, W405-W411.	6.5	32

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19	Twenty-five Years of Delila and Molecular Information Theory. <i>Biological Theory</i> , 2006, 1, 250-260.	0.8	11
20	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
21	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
22	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
23	Molecular flip-flops formed by overlapping Fis sites. <i>Nucleic Acids Research</i> , 2003, 31, 6663-6673.	6.5	16
24	Some Lessons for Molecular Biology from Information Theory. <i>Studies in Fuzziness and Soft Computing</i> , 2003, , 229-237.	0.6	4
25	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
26	Consensus sequence Zen. <i>Applied Bioinformatics</i> , 2002, 1, 111-9.	1.7	49
27	Anatomy of Escherichia coli ribosome binding sites 1 Edited by D. Draper. <i>Journal of Molecular Biology</i> , 2001, 313, 215-228.	2.0	132
28	Computation-Directed Identification of OxyR DNA Binding Sites in Escherichia coli. <i>Journal of Bacteriology</i> , 2001, 183, 4571-4579.	1.0	126
29	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
30	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
31	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
32	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
33	Measuring Molecular Information. <i>Journal of Theoretical Biology</i> , 1999, 201, 87-92.	0.8	37
34	OxyR and SoxRS Regulation of <i>fur</i> . <i>Journal of Bacteriology</i> , 1999, 181, 4639-4643.	1.0	358
35	Information analysis of human splice site mutations. <i>Human Mutation</i> , 1998, 12, 153-171.	1.1	187
36	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

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37	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
38	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
39	Information Content of Individual Genetic Sequences. <i>Journal of Theoretical Biology</i> , 1997, 189, 427-441.	0.8	283
40	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
41	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
42	New Approaches in Mathematical Biology: Information Theory and Molecular Machines. , 1996, , 313-321.		2
43	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
44	Visual Display of Sequence Conservation as an Aid to Taxonomic Classification Using PCR Amplification. , 1995, , 21-32.		1
45	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
46	Quantitative analysis of ribosome binding sites in E.coli. <i>Nucleic Acids Research</i> , 1994, 22, 1287-1295.	6.5	147
47	Information Analysis of Sequences that Bind the Replication Initiator RepA. <i>Journal of Molecular Biology</i> , 1993, 233, 219-230.	2.0	71
48	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
49	Theory of molecular machines. I. Channel capacity of molecular machines. <i>Journal of Theoretical Biology</i> , 1991, 148, 83-123.	0.8	105
50	Theory of molecular machines. II. Energy dissipation from molecular machines. <i>Journal of Theoretical Biology</i> , 1991, 148, 125-137.	0.8	100
51	Sequence logos: a new way to display consensus sequences. <i>Nucleic Acids Research</i> , 1990, 18, 6097-6100.	6.5	2,940
52	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
53	Information content of binding sites on nucleotide sequences. <i>Journal of Molecular Biology</i> , 1986, 188, 415-431.	2.0	872
54	Quantitative analysis of the relationship between nucleotide sequence and functional activity. <i>Nucleic Acids Research</i> , 1986, 14, 6661-6679.	6.5	156

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55	Delila system tools. Nucleic Acids Research, 1984, 12, 129-140.	6.5	45
56	A design for computer nucleic-acid-sequence storage, retrieval, and manipulation. Nucleic Acids Research, 1982, 10, 3013-3024.	6.5	60
57	Characterization of translational initiation sites inE. coli. Nucleic Acids Research, 1982, 10, 2971-2996.	6.5	729
58	Use of the "Perceptron" algorithm to distinguish translational initiation sites inE. coli. Nucleic Acids Research, 1982, 10, 2997-3011.	6.5	649