## Thomas D Schneider

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7104878/publications.pdf

Version: 2024-02-01

58 papers 9,268 citations

34 h-index 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.	2.5	4
2	Elements in the l̂» immunity region regulate phage development: beyond the â€~Genetic Switch'. Molecular Microbiology, 2019, 112, 1798-1813.	2.5	8
3	Density of Ïf70 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.	14.5	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, .	2.2	2
5	Genome-Wide Transcriptional Regulation and Chromosome Structural Arrangement by GalR in E. coli. Frontiers in Molecular Biosciences, 2016, 3, 74.	3.5	12
6	Identification of a Cryptic Bacterial Promoter in Mouse (mdr1a) P-Glycoprotein cDNA. PLoS ONE, 2015, 10, e0136396.	2.5	5
7	Promoter variants in the MSMB gene associated with prostate cancer regulate MSMB/NCOA4 fusion transcripts. Human Genetics, 2012, 131, 1453-1466.	3.8	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.	2.5	8
9	A brief review of molecular information theory. Nano Communication Networks, 2010, 1, 173-180.	2.9	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.	14.5	31
11	Xeroderma Pigmentosum-Variant Patients from America, Europe, and Asia. Journal of Investigative Dermatology, 2008, 128, 2055-2068.	0.7	76
12	Small membrane proteins found by comparative genomics and ribosome binding site models. Molecular Microbiology, 2008, 70, 1487-1501.	2.5	194
13	Discovery of novel tumor suppressor p53 response elements using information theory. Nucleic Acids Research, 2008, 36, 3828-3833.	14.5	30
14	Correlation between binding rate constants and individual information of E. coli Fis binding sites. Nucleic Acids Research, 2007, 35, 5275-5283.	14.5	30
15	Anatomy of Escherichia coli $\parallel f$ 70 promoters. Nucleic Acids Research, 2007, 35, 771-788.	14.5	209
16	Discovery of Fur binding site clusters in Escherichia coli by information theory models. Nucleic Acids Research, 2007, 35, 6762-6777.	14.5	79
17	Claude Shannon: Biologist [information theory used in biology]. IEEE Engineering in Medicine and Biology Magazine, 2006, 25, 30-33.	0.8	14
18	CorreLogo: an online server for 3D sequence logos of RNA and DNA alignments. Nucleic Acids Research, 2006, 34, W405-W411.	14.5	32

#	Article	IF	CITATIONS
19	Twenty-five Years of Delila and Molecular Information Theory. Biological Theory, 2006, 1, 250-260.	1.5	11
20	Comparative analysis of tandem T7-like promoter containing regions in enterobacterial genomes reveals a novel group of genetic islands. Nucleic Acids Research, 2006, 34, 1133-1147.	14.5	10
21	Information theory based T7-like promoter models: classification of bacteriophages and differential evolution of promoters and their polymerases. Nucleic Acids Research, 2005, 33, 6172-6187.	14.5	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. Human Molecular Genetics, 2003, 13, 343-352.	2.9	63
23	Molecular flip-flops formed by overlapping Fis sites. Nucleic Acids Research, 2003, 31, 6663-6673.	14.5	16
24	Some Lessons for Molecular Biology from Information Theory. Studies in Fuzziness and Soft Computing, 2003, , 229-237.	0.8	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. Nucleic Acids Research, 2002, 30, 3624-3631.	14.5	146
26	Consensus sequence Zen. Applied Bioinformatics, 2002, 1, 111-9.	1.6	49
27	Anatomy of Escherichia coli ribosome binding sites 1 1Edited by D. Draper. Journal of Molecular Biology, 2001, 313, 215-228.	4.2	132
28	Computation-Directed Identification of OxyR DNA Binding Sites in Escherichia coli. Journal of Bacteriology, 2001, 183, 4571-4579.	2.2	126
29	Redundant designations of BRCA1 intron 11 splicing mutation; c. 4216-2A>G; IVS11-2A>G; L78833, 37698, A>G. Human Mutation, 2000, 16, 264-264.	2.5	8
30	Logos for amino-acid preferences in different backbone packing density regions of protein structural classes. Acta Crystallographica Section D: Biological Crystallography, 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. Nucleic Acids Research, 1999, 27, 882-887.	14.5	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. Molecular Microbiology, 1999, 34, 414-430.	2.5	56
33	Measuring Molecular Information. Journal of Theoretical Biology, 1999, 201, 87-92.	1.7	37
34	OxyR and SoxRS Regulation of <i>fur</i> . Journal of Bacteriology, 1999, 181, 4639-4643.	2.2	358
35	Information analysis of human splice site mutations. Human Mutation, 1998, 12, 153-171.	2.5	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. Journal of Investigative Dermatology, 1998, 111, 791-796.	0.7	66

#	Article	IF	CITATIONS
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. Journal of Bacteriology, 1998, 180, 3940-3945.	2.2	11
38	Replication Control of Plasmid P1 and Its Host Chromosome: The Common Ground. Progress in Molecular Biology and Translational Science, 1997, 57, 145-186.	1.9	38
39	Information Content of Individual Genetic Sequences. Journal of Theoretical Biology, 1997, 189, 427-441.	1.7	283
40	Fast multiple alignment of ungapped DNA sequences using information theory and a relaxation method. Discrete Applied Mathematics, 1996, 71, 259-268.	0.9	39
41	Reading of DNA sequence logos: Prediction of major groove binding by information theory. Methods in Enzymology, 1996, 274, 445-455.	1.0	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. Human Mutation, 1995, 6, 74-76.	2.5	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. Cell, 1994, 78, 897-909.	28.9	375
46	Quantitative analysis of ribosome binding sites in E.coli. Nucleic Acids Research, 1994, 22, 1287-1295.	14.5	147
47	Information Analysis of Sequences that Bind the Replication Initiator RepA. Journal of Molecular Biology, 1993, 233, 219-230.	4.2	71
48	Features of spliceosome evolution and function inferred from an analysis of the information at human splice sites. Journal of Molecular Biology, 1992, 228, 1124-1136.	4.2	254
49	Theory of molecular machines. I. Channel capacity of molecular machines. Journal of Theoretical Biology, 1991, 148, 83-123.	1.7	105
50	Theory of molecular machines. II. Energy dissipation from molecular machines. Journal of Theoretical Biology, 1991, 148, 125-137.	1.7	100
51	Sequence logos: a new way to display consensus sequences. Nucleic Acids Research, 1990, 18, 6097-6100.	14.5	2,940
52	Excess information at bacteriophage T7 genomic promoters detected by a random cloning technique. Nucleic Acids Research, 1989, 17, 659-674.	14.5	69
53	Information content of binding sites on nucleotide sequences. Journal of Molecular Biology, 1986, 188, 415-431.	4.2	872
54	Quantitative analysis of the relationship between nucleotide sequence and functional activity. Nucleic Acids Research, 1986, 14, 6661-6679.	14.5	156

#	Article	IF	CITATION
55	Delila system tools. Nucleic Acids Research, 1984, 12, 129-140.	14.5	45
56	A design for computer nucleic-acid-sequence storage, retrieval, and manipulation. Nucleic Acids Research, 1982, 10, 3013-3024.	14.5	60
57	Characterization of translational initiation sites inE. coli. Nucleic Acids Research, 1982, 10, 2971-2996.	14.5	729
58	Use of the â€~Perceptron' algorithm to distinguish translational initiation sites inE. coli. Nucleic Acids Research, 1982, 10, 2997-3011.	14.5	649