

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

117625
34
h-index

149698
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. Nucleic Acids Research, 1990, 18, 6097-6100.	14.5	2,940
2	Information content of binding sites on nucleotide sequences. Journal of Molecular Biology, 1986, 188, 415-431.	4.2	872
3	Characterization of translational initiation sites in <i>E. coli</i> . Nucleic Acids Research, 1982, 10, 2971-2996.	14.5	729
4	Use of the "Perceptron" algorithm to distinguish translational initiation sites in <i>E. coli</i> . Nucleic Acids Research, 1982, 10, 2997-3011.	14.5	649
5	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
6	OxyR and SoxRS Regulation of <i>fur</i> . Journal of Bacteriology, 1999, 181, 4639-4643.	2.2	358
7	Information Content of Individual Genetic Sequences. Journal of Theoretical Biology, 1997, 189, 427-441.	1.7	283
8	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
9	Anatomy of <i>Escherichia coli</i> 70 promoters. Nucleic Acids Research, 2007, 35, 771-788.	14.5	209
10	Small membrane proteins found by comparative genomics and ribosome binding site models. Molecular Microbiology, 2008, 70, 1487-1501.	2.5	194
11	Information analysis of human splice site mutations. Human Mutation, 1998, 12, 153-171.	2.5	187
12	Quantitative analysis of the relationship between nucleotide sequence and functional activity. Nucleic Acids Research, 1986, 14, 6661-6679.	14.5	156
13	Quantitative analysis of ribosome binding sites in <i>E. coli</i> . Nucleic Acids Research, 1994, 22, 1287-1295.	14.5	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. Nucleic Acids Research, 2002, 30, 3624-3631.	14.5	146
15	Anatomy of <i>Escherichia coli</i> ribosome binding sites 1 Edited by D. Draper. Journal of Molecular Biology, 2001, 313, 215-228.	4.2	132
16	Computation-Directed Identification of OxyR DNA Binding Sites in <i>Escherichia coli</i> . Journal of Bacteriology, 2001, 183, 4571-4579.	2.2	126
17	Theory of molecular machines. I. Channel capacity of molecular machines. Journal of Theoretical Biology, 1991, 148, 83-123.	1.7	105
18	Theory of molecular machines. II. Energy dissipation from molecular machines. Journal of Theoretical Biology, 1991, 148, 125-137.	1.7	100

#	ARTICLE	IF	CITATIONS
19	Discovery of Fur binding site clusters in Escherichia coli by information theory models. Nucleic Acids Research, 2007, 35, 6762-6777.	14.5	79
20	Xeroderma Pigmentosum-Variant Patients from America, Europe, and Asia. Journal of Investigative Dermatology, 2008, 128, 2055-2068.	0.7	76
21	Information Analysis of Sequences that Bind the Replication Initiator RepA. Journal of Molecular Biology, 1993, 233, 219-230.	4.2	71
22	A brief review of molecular information theory. Nano Communication Networks, 2010, 1, 173-180.	2.9	70
23	Excess information at bacteriophage T7 genomic promoters detected by a random cloning technique. Nucleic Acids Research, 1989, 17, 659-674.	14.5	69
24	Reading of DNA sequence logos: Prediction of major groove binding by information theory. Methods in Enzymology, 1996, 274, 445-455.	1.0	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. Journal of Investigative Dermatology, 1998, 111, 791-796.	0.7	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. Human Molecular Genetics, 2003, 13, 343-352.	2.9	63
27	A design for computer nucleic-acid-sequence storage, retrieval, and manipulation. Nucleic Acids Research, 1982, 10, 3013-3024.	14.5	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. Molecular Microbiology, 1999, 34, 414-430.	2.5	56
29	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
30	Consensus sequence Zen. Applied Bioinformatics, 2002, 1, 111-9.	1.6	49
31	Delila system tools. Nucleic Acids Research, 1984, 12, 129-140.	14.5	45
32	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
33	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
34	Fast multiple alignment of ungapped DNA sequences using information theory and a relaxation method. Discrete Applied Mathematics, 1996, 71, 259-268.	0.9	39
35	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
36	Measuring Molecular Information. Journal of Theoretical Biology, 1999, 201, 87-92.	1.7	37

#	ARTICLE	IF	CITATIONS
37	CorreLogo: an online server for 3D sequence logos of RNA and DNA alignments. <i>Nucleic Acids Research</i> , 2006, 34, W405-W411.	14.5	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.	14.5	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.	14.5	30
40	Discovery of novel tumor suppressor p53 response elements using information theory. <i>Nucleic Acids Research</i> , 2008, 36, 3828-3833.	14.5	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.	3.8	25
42	Molecular flip-flops formed by overlapping Fis sites. <i>Nucleic Acids Research</i> , 2003, 31, 6663-6673.	14.5	16
43	Claude Shannon: Biologist [information theory used in biology]. <i>IEEE Engineering in Medicine and Biology Magazine</i> , 2006, 25, 30-33.	0.8	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.	3.5	12
45	Twenty-five Years of Delila and Molecular Information Theory. <i>Biological Theory</i> , 2006, 1, 250-260.	1.5	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.	2.2	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.	14.5	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.	2.5	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.	2.5	8
50	Elements in the λ immunity region regulate phage development: beyond the "Genetic Switch". <i>Molecular Microbiology</i> , 2019, 112, 1798-1813.	2.5	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 σ^{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.	14.5	7
53	Identification of a Cryptic Bacterial Promoter in Mouse (<i>mdr1a</i>) P-Glycoprotein cDNA. <i>PLoS ONE</i> , 2015, 10, e0136396.	2.5	5
54	Restriction enzymes use a 24 dimensional coding space to recognize 6 base long DNA sequences. <i>PLoS ONE</i> , 2019, 14, e0222419.	2.5	4

#	ARTICLE	IF	CITATIONS
55	Some Lessons for Molecular Biology from Information Theory. Studies in Fuzziness and Soft Computing, 2003, , 229-237.	0.8	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, .	2.2	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