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List of Publications by Year in descending order

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Version: 2024-02-01

70
papers

2,835
citations

430874

18
h-index

189892

50
g-index

80
all docs

80
docs citations

80
times ranked

5270
citing authors

#	ARTICLE	IF	CITATIONS
1	Monoclonal antibodies targeting two immunodominant epitopes on the Spike protein neutralize emerging SARS-CoV-2 variants of concern. <i>EBioMedicine</i> , 2022, 76, 103818.	6.1	14
2	Transcriptome and proteome profiling reveals complex adaptations of <i>Candida parapsilosis</i> cells assimilating hydroxyaromatic carbon sources. <i>PLoS Genetics</i> , 2022, 18, e1009815.	3.5	1
3	Markov chains improve the significance computation of overlapping genome annotations. <i>Bioinformatics</i> , 2022, 38, i203-i211.	4.1	0
4	Probabilistic Models of k-mer Frequencies (Extended Abstract). <i>Lecture Notes in Computer Science</i> , 2021, , 227-236.	1.3	0
5	Nanopore base calling on the edge. <i>Bioinformatics</i> , 2021, 37, 4661-4667.	4.1	20
6	A SARS-CoV-2 mutant from B.1.258 lineage with Δ H69/ Δ V70 deletion in the Spike protein circulating in Central Europe in the fall 2020. <i>Virus Genes</i> , 2021, 57, 556-560.	1.6	27
7	Surveillance of SARS-CoV-2 lineage B.1.1.7 in Slovakia using a novel, multiplexed RT-qPCR assay. <i>Scientific Reports</i> , 2021, 11, 20494.	3.3	24
8	Nanopore sequencing of SARS-CoV-2: Comparison of short and long PCR-tiling amplicon protocols. <i>PLoS ONE</i> , 2021, 16, e0259277.	2.5	16
9	Mosaicism in old trees and its patterns. <i>Trees - Structure and Function</i> , 2020, 34, 357-370.	1.9	17
10	A Linear-Time Algorithm for the Isometric Reconciliation of Unrooted Trees. <i>Algorithms</i> , 2020, 13, 225.	2.1	1
11	DeepNano-bltz: a fast base caller for MinION nanopore sequencers. <i>Bioinformatics</i> , 2020, 36, 4191-4192.	4.1	21
12	A draft genome sequence of the elusive giant squid, <i>Architeuthis dux</i> . <i>GigaScience</i> , 2020, 9, .	6.4	37
13	SWSPM: A Novel Alignment-Free DNA Comparison Method Based on Signal Processing Approaches. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431984907.	1.2	2
14	Genome Sequence of Flavor-Producing Yeast <i>Saprochaete suaveolens</i> NRRL Y-17571. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
15	Genome Sequence of an Arthroconidial Yeast, <i>Saprochaete fungicola</i> CBS 625.85. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
16	Genome Sequence of the Yeast <i>Saprochaete ingens</i> CBS 517.90. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
17	Dante: genotyping of known complex and expanded short tandem repeats. <i>Bioinformatics</i> , 2019, 35, 1310-1317.	4.1	15
18	Genome sequence of the opportunistic human pathogen <i>Magnusiomyces capitatus</i> . <i>Current Genetics</i> , 2019, 65, 539-560.	1.7	14

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19	Isometric gene tree reconciliation revisited. <i>Algorithms for Molecular Biology</i> , 2017, 12, 17.	1.2	1
20	Draft Genome Sequence of an Obligate Psychrophilic Yeast, <i>Candida psychrophila</i> NRRL Y-17665 T. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
21	DeepNano: Deep recurrent neural networks for base calling in MinION nanopore reads. <i>PLoS ONE</i> , 2017, 12, e0178751.	2.5	186
22	RNA motif search with data-driven element ordering. <i>BMC Bioinformatics</i> , 2016, 17, 216.	2.6	6
23	Isometric Gene Tree Reconciliation Revisited. <i>Lecture Notes in Computer Science</i> , 2016, , 40-51.	1.3	0
24	GAML: genome assembly by maximum likelihood. <i>Algorithms for Molecular Biology</i> , 2015, 10, 18.	1.2	6
25	Sequence annotation with HMMs: New problems and their complexity. <i>Information Processing Letters</i> , 2015, 115, 635-639.	0.6	0
26	Fishing in Read Collections: Memory Efficient Indexing for Sequence Assembly. <i>Lecture Notes in Computer Science</i> , 2015, , 188-198.	1.3	0
27	How Big is that Genome? Estimating Genome Size and Coverage from k-mer Abundance Spectra. <i>Lecture Notes in Computer Science</i> , 2015, , 199-209.	1.3	18
28	Massive programmed translational jumping in mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5926-5931.	7.1	58
29	Mitochondrial genome of the basidiomycetous yeast <i>Jaminalia angkorensis</i> . <i>Current Genetics</i> , 2014, 60, 49-59.	1.7	17
30	The common marmoset genome provides insight into primate biology and evolution. <i>Nature Genetics</i> , 2014, 46, 850-857.	21.4	225
31	Probabilistic approaches to alignment with tandem repeats. <i>Algorithms for Molecular Biology</i> , 2014, 9, 3.	1.2	4
32	Fast computation of a string duplication history under no-breakpoint-reuse. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2014, 372, 20130133.	3.4	2
33	The genome of the hydatid tapeworm <i>Echinococcus granulosus</i> . <i>Nature Genetics</i> , 2013, 45, 1168-1175.	21.4	260
34	Efficient routing in carrier-based mobile networks. <i>Theoretical Computer Science</i> , 2013, 509, 113-121.	0.9	3
35	Probabilistic Approaches to Alignment with Tandem Repeats. <i>Lecture Notes in Computer Science</i> , 2013, , 287-299.	1.3	0
36	Sequencing the genome of <i>Marssonina brunnea</i> reveals fungus-poplar co-evolution. <i>BMC Genomics</i> , 2012, 13, 382.	2.8	61

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37	Discovery of RNA Motifs Using a Computational Pipeline that Allows Insertions in Paired Regions and Filtering of Candidate Sequences. <i>Methods in Molecular Biology</i> , 2012, 848, 145-158.	0.9	4
38	Fast Computation of a String Duplication History under No-Breakpoint-Reuse. <i>Lecture Notes in Computer Science</i> , 2011, , 144-155.	1.3	0
39	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	27.8	541
40	Evolution of linear chromosomes and multipartite genomes in yeast mitochondria. <i>Nucleic Acids Research</i> , 2011, 39, 4202-4219.	14.5	69
41	Routing in Carrier-Based Mobile Networks. <i>Lecture Notes in Computer Science</i> , 2011, , 222-233.	1.3	3
42	A Practical Algorithm for Ancestral Rearrangement Reconstruction. <i>Lecture Notes in Computer Science</i> , 2011, , 163-174.	1.3	7
43	Automated Segmentation of DNA Sequences with Complex Evolutionary Histories. <i>Lecture Notes in Computer Science</i> , 2011, , 1-13.	1.3	0
44	A Possible Role for Short Introns in the Acquisition of Stroma-Targeting Peptides in the Flagellate <i>Euglena gracilis</i> . <i>DNA Research</i> , 2010, 17, 223-231.	3.4	26
45	Reconstructing Histories of Complex Gene Clusters on a Phylogeny. <i>Journal of Computational Biology</i> , 2010, 17, 1267-1279.	1.6	8
46	The Highest Expected Reward Decoding for HMMs with Application to Recombination Detection. <i>Lecture Notes in Computer Science</i> , 2010, , 164-176.	1.3	1
47	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2009, 19, 2324-2333.	5.5	125
48	Finding genes in <i>Schistosoma japonicum</i> : annotating novel genomes with help of extrinsic evidence. <i>Nucleic Acids Research</i> , 2009, 37, e52-e52.	14.5	13
49	The <i>Schistosoma japonicum</i> genome reveals features of host-parasite interplay. <i>Nature</i> , 2009, 460, 345-351.	27.8	635
50	Predicting Gene Structures from Multiple RT-PCR Tests. <i>Lecture Notes in Computer Science</i> , 2009, , 181-193.	1.3	2
51	Reconstructing Histories of Complex Gene Clusters on a Phylogeny. <i>Lecture Notes in Computer Science</i> , 2009, , 150-163.	1.3	2
52	Targeted discovery of novel human exons by comparative genomics. <i>Genome Research</i> , 2007, 17, 1763-1773.	5.5	42
53	Homology search for genes. <i>Bioinformatics</i> , 2007, 23, i97-i103.	4.1	13
54	Advances in Hidden Markov Models for Sequence Annotation. , 2007, , 55-91.		6

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55	The most probable annotation problem in HMMs and its application to bioinformatics. Journal of Computer and System Sciences, 2007, 73, 1060-1077.	1.2	13
56	On-Line Viterbi Algorithm for Analysis of Long Biological Sequences. Lecture Notes in Computer Science, 2007, , 240-251.	1.3	8
57	Vector seeds: An extension to spaced seeds. Journal of Computer and System Sciences, 2005, 70, 364-380.	1.2	42
58	ExonHunter: a comprehensive approach to gene finding. Bioinformatics, 2005, 21, i57-i65.	4.1	45
59	Sharper Upper and Lower Bounds for an Approximation Scheme for Consensus-Pattern. Lecture Notes in Computer Science, 2005, , 1-10.	1.3	4
60	The Most Probable Labeling Problem in HMMs and Its Application to Bioinformatics. Lecture Notes in Computer Science, 2004, , 426-437.	1.3	0
61	OPTIMAL SPACED SEEDS FOR HOMOLOGOUS CODING REGIONS. Journal of Bioinformatics and Computational Biology, 2004, 01, 595-610.	0.8	48
62	Finding hidden independent sets in interval graphs. Theoretical Computer Science, 2004, 310, 287-307.	0.9	8
63	Vector Seeds: An Extension to Spaced Seeds Allows Substantial Improvements in Sensitivity and Specificity. Lecture Notes in Computer Science, 2003, , 39-54.	1.3	22
64	Optimal DNA Signal Recognition Models with a Fixed Amount of Intrasignal Dependency. Lecture Notes in Computer Science, 2003, , 78-94.	1.3	2
65	Optimal Spaced Seeds for Hidden Markov Models, with Application to Homologous Coding Regions. Lecture Notes in Computer Science, 2003, , 42-54.	1.3	16
66	Pattern Discovery. , 2003, , 491-521.		7
67	Finding Hidden Independent Sets in Interval Graphs. Lecture Notes in Computer Science, 2003, , 182-191.	1.3	0
68	A Better Method for Length Distribution Modeling in HMMs and Its Application to Gene Finding. Lecture Notes in Computer Science, 2002, , 190-202.	1.3	2
69	Analyzing variants of Shellsort. Information Processing Letters, 2001, 79, 223-227.	0.6	21
70	Simplifying Flow Networks. Lecture Notes in Computer Science, 2000, , 192-201.	1.3	10