Bronislava BrejovÃ¡

List of Publications by Year
in descending order

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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	The Schistosoma japonicum genome reveals features of hostâ€“parasite interplay. Nature, 2009, 460, 345-351.	27.8	635
2	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	27.8	541
3	The genome of the hydatid tapeworm Echinococcus granulosus. Nature Genetics, 2013, 45, 1168-1175.	21.4	260
4	The common marmoset genome provides insight into primate biology and evolution. Nature Genetics, 2014, 46, 850-857.	21.4	225
5	DeepNano: Deep recurrent neural networks for base calling in MinION nanopore reads. PLoS ONE, 2017, 12, e0178751.	2.5	186
6	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	5.5	125
7	Evolution of linear chromosomes and multipartite genomes in yeast mitochondria. Nucleic Acids Research, 2011, 39, 4202-4219.	14.5	69
8	Sequencing the genome of Marssonina brunnea reveals fungus-poplar co-evolution. BMC Genomics, 2012, 13, 382.	2.8	61
9	Massive programmed translational jumping in mitochondria. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5926-5931.	7.1	58
10	OPTIMAL SPACED SEEDS FOR HOMOLOGOUS CODING REGIONS. Journal of Bioinformatics and Computational Biology, 2004, 01, 595-610.	0.8	48
11	ExonHunter: a comprehensive approach to gene finding. Bioinformatics, 2005, 21, i57-i65.	4.1	45
12	Vector seeds: An extension to spaced seeds. Journal of Computer and System Sciences, 2005, 70, 364-380.	1.2	42
13	Targeted discovery of novel human exons by comparative genomics. Genome Research, 2007, 17, 1763-1773.	5.5	42
14	A draft genome sequence of the elusive giant squid, Architeuthis dux. GigaScience, 2020, 9, .	6.4	37
15	A SARS-CoV-2 mutant from B.1.258 lineage with âˆ†H69/âˆ†V70 deletion in the Spike protein circulating in Central Europe in the fall 2020. Virus Genes, 2021, 57, 556-560.	1.6	27
16	A Possible Role for Short Introns in the Acquisition of Stroma-Targeting Peptides in the Flagellate Euglena gracilis. DNA Research, 2010, 17, 223-231.	3.4	26
17	Surveillance of SARS-CoV-2 lineage B.1.1.7 in Slovakia using a novel, multiplexed RT-qPCR assay. Scientific Reports, 2021, 11, 20494.	3.3	24
18	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

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19	Analyzing variants of Shellsort. Information Processing Letters, 2001, 79, 223-227.	0.6	21
20	DeepNano-blitz: a fast base caller for MinION nanopore sequencers. Bioinformatics, 2020, 36, 4191-4192.	4.1	21
21	Nanopore base calling on the edge. Bioinformatics, 2021, 37, 4661-4667.	4.1	20
22	How Big is that Genome? Estimating Genome Size and Coverage from k-mer Abundance Spectra. Lecture Notes in Computer Science, 2015, , 199-209.	1.3	18
23	Mitochondrial genome of the basidiomycetous yeast Jaminaea angkorensis. Current Genetics, 2014, 60, 49-59.	1.7	17
24	Mosaicism in old trees and its patterns. Trees - Structure and Function, 2020, 34, 357-370.	1.9	17
25	Optimal Spaced Seeds for Hidden Markov Models, with Application to Homologous Coding Regions. Lecture Notes in Computer Science, 2003, , 42-54.	1.3	16
26	Nanopore sequencing of SARS-CoV-2: Comparison of short and long PCR-tiling amplicon protocols. PLoS ONE, 2021, 16, e0259277.	2.5	16
27	Dante: genotyping of known complex and expanded short tandem repeats. Bioinformatics, 2019, 35, 1310-1317.	4.1	15
28	Genome sequence of the opportunistic human pathogen Magnusiomyces capitatus. Current Genetics, 2019, 65, 539-560.	1.7	14
29	Monoclonal antibodies targeting two immunodominant epitopes on the Spike protein neutralize emerging SARS-CoV-2 variants of concern. EBioMedicine, 2022, 76, 103818.	6.1	14
30	Homology search for genes. Bioinformatics, 2007, 23, i97-i103.	4.1	13
31	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
32	Finding genes in Schistosoma japonicum: annotating novel genomes with help of extrinsic evidence. Nucleic Acids Research, 2009, 37, e52-e52.	14.5	13
33	Simplifying Flow Networks. Lecture Notes in Computer Science, 2000, , 192-201.	1.3	10
34	Finding hidden independent sets in interval graphs. Theoretical Computer Science, 2004, 310, 287-307.	0.9	8
35	Reconstructing Histories of Complex Gene Clusters on a Phylogeny. Journal of Computational Biology, 2010, 17, 1267-1279.	1.6	8
36	On-Line Viterbi Algorithm for Analysis of Long Biological Sequences. Lecture Notes in Computer Science, 2007, , 240-251.	1.3	8

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37	Pattern Discovery. , 2003, , 491-521.		7
38	A Practical Algorithm for Ancestral Rearrangement Reconstruction. Lecture Notes in Computer Science, 2011, , 163-174.	1.3	7
39	Advances in Hidden Markov Models for Sequence Annotation. , 2007, , 55-91.		6
40	GAML: genome assembly by maximum likelihood. Algorithms for Molecular Biology, 2015, 10, 18.	1.2	6
41	RNA motif search with data-driven element ordering. BMC Bioinformatics, 2016, 17, 216.	2.6	6
42	Probabilistic approaches to alignment with tandem repeats. Algorithms for Molecular Biology, 2014, 9, 3.	1.2	4
43	Discovery of RNA Motifs Using a Computational Pipeline that Allows Insertions in Paired Regions and Filtering of Candidate Sequences. Methods in Molecular Biology, 2012, 848, 145-158.	0.9	4
44	Sharper Upper and Lower Bounds for an Approximation Scheme for Consensus-Pattern. Lecture Notes in Computer Science, 2005, , 1-10.	1.3	4
45	Efficient routing in carrier-based mobile networks. Theoretical Computer Science, 2013, 509, 113-121.	0.9	3
46	Routing in Carrier-Based Mobile Networks. Lecture Notes in Computer Science, 2011, , 222-233.	1.3	3
47	Optimal DNA Signal Recognition Models with a Fixed Amount of Intrasignal Dependency. Lecture Notes in Computer Science, 2003, , 78-94.	1.3	2
48	Fast computation of a string duplication history under no-breakpoint-reuse. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2014, 372, 20130133.	3.4	2
49	Draft Genome Sequence of an Obligate Psychrophilic Yeast, Candida psychrophila NRRL Y-17665 T. Genome Announcements, 2017, 5, .	0.8	2
50	SWSPM: A Novel Alignment-Free DNA Comparison Method Based on Signal Processing Approaches. Evolutionary Bioinformatics, 2019, 15, 117693431984907.	1.2	2
51	Predicting Gene Structures from Multiple RT-PCR Tests. Lecture Notes in Computer Science, 2009, , 181-193.	1.3	2
52	Reconstructing Histories of Complex Gene Clusters on a Phylogeny. Lecture Notes in Computer Science, 2009, , 150-163.	1.3	2
53	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
54	Isometric gene tree reconciliation revisited. Algorithms for Molecular Biology, 2017, 12, 17.	1.2	1

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55	Genome Sequence of Flavor-Producing Yeast Saprochaete suaveolens NRRL Y-17571. Microbiology Resource Announcements, 2019, 8, .	0.6	1
56	Genome Sequence of an Arthroconidial Yeast, Saprochaete fungicola CBS 625.85. Microbiology Resource Announcements, 2019, 8, .	0.6	1
57	Genome Sequence of the Yeast Saprochaete ingens CBS 517.90. Microbiology Resource Announcements, 2019, 8, .	0.6	1
58	A Linear-Time Algorithm for the Isometric Reconciliation of Unrooted Trees. Algorithms, 2020, 13, 225.	2.1	1
59	The Highest Expected Reward Decoding for HMMs with Application to Recombination Detection. Lecture Notes in Computer Science, 2010, , 164-176.	1.3	1
60	Transcriptome and proteome profiling reveals complex adaptations of Candida parapsilosis cells assimilating hydroxyaromatic carbon sources. PLoS Genetics, 2022, 18, e1009815.	3.5	1
61	The Most Probable Labeling Problem in HMMs and Its Application to Bioinformatics. Lecture Notes in Computer Science, 2004, , 426-437.	1.3	0
62	Fast Computation of a String Duplication History under No-Breakpoint-Reuse. Lecture Notes in Computer Science, 2011, , 144-155.	1.3	0
63	Sequence annotation with HMMs: New problems and their complexity. Information Processing Letters, 2015, 115, 635-639.	0.6	0
64	Fishing in Read Collections: Memory Efficient Indexing for Sequence Assembly. Lecture Notes in Computer Science, 2015, , 188-198.	1.3	0
65	Isometric Gene Tree Reconciliation Revisited. Lecture Notes in Computer Science, 2016, , 40-51.	1.3	0
66	Probabilistic Models of k-mer Frequencies (Extended Abstract). Lecture Notes in Computer Science, 2021, , 227-236.	1.3	0
67	Finding Hidden Independent Sets in Interval Graphs. Lecture Notes in Computer Science, 2003, , 182-191.	1.3	0
68	Automated Segmentation of DNA Sequences with Complex Evolutionary Histories. Lecture Notes in Computer Science, 2011, , 1-13.	1.3	0
69	Probabilistic Approaches to Alignment with Tandem Repeats. Lecture Notes in Computer Science, 2013, , 287-299.	1.3	0
70	Markov chains improve the significance computation of overlapping genome annotations. Bioinformatics, 2022, 38, i203-i211.	4.1	0