Christina Boucher

List of Publications by Year
in descending order

44 papers	1,674 citations	430874 18 h-index	345221 36 g-index
47 all docs	47 docs citations	47 times ranked	2355 citing authors

#	Article	IF	Citations
1	Finding Maximal Exact Matches Using the r-Index. Journal of Computational Biology, 2022, 29, 188-194.	1.6	4
2	MONI: A Pangenomic Index for Finding Maximal Exact Matches. Journal of Computational Biology, 2022, 29, 169-187.	1.6	23
3	Towards routine employment of computational tools for antimicrobial resistance determination via high-throughput sequencing. Briefings in Bioinformatics, 2022, 23, .	6.5	3
4	Computational graph pangenomics: a tutorial on data structures and their applications. Natural Computing, 2022, 21, 81-108.	3.0	22
5	Syotti: scalable bait design for DNA enrichment. Bioinformatics, 2022, 38, i177-i184.	4.1	3
6	AMR-meta: a k-mer and metafeature approach to classify antimicrobial resistance from high-throughput short-read metagenomics data. GigaScience, 2022, 11, .	6.4	8
7	Succinct dynamic de Bruijn graphs. Bioinformatics, 2021, 37, 1946-1952.	4.1	8
8	Data structures based on k-mers for querying large collections of sequencing data sets. Genome Research, 2021, 31, 1-12.	5.5	67
9	PFP Compressed Suffix Trees. , 2021, 2021, 60-72.		7
10	Buffering updates enables efficient dynamic de Bruijn graphs. Computational and Structural Biotechnology Journal, 2021, 19, 4067-4078.	4.1	6
11	Fast and efficient Rmap assembly using the Bi-labelled de Bruijn graph. Algorithms for Molecular Biology, 2021, 16, 6.	1.2	2
12	Pan-genomic matching statistics for targeted nanopore sequencing. IScience, 2021, 24, 102696.	4.1	15
13	Propensity score synthetic augmentation matching using generative adversarial networks (PSSAM-GAN). Computer Methods and Programs in Biomedicine Update, 2021, 1, 100020.	3.7	8
14	Fast and exact quantification of motif occurrences in biological sequences. BMC Bioinformatics, 2021, 22, 445.	2.6	2
15	Exploring Prediction of Antimicrobial Resistance Based on Protein Solvent Accessibility Variation. Frontiers in Genetics, 2021, 12, 564186.	2.3	3
16	Metagenome SNP calling via read-colored de Bruijn graphs. Bioinformatics, 2021, 36, 5275-5281.	4.1	8
17	Fast and accurate correction of optical mapping data via spaced seeds. Bioinformatics, 2020, 36, 682-689.	4.1	5
18	MEGARes 2.0: a database for classification of antimicrobial drug, biocide and metal resistance determinants in metagenomic sequence data. Nucleic Acids Research, 2020, 48, D561-D569.	14.5	227

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19	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12522-12523.	7.1	68
20	Efficient Construction of a Complete Index for Pan-Genomics Read Alignment. Journal of Computational Biology, 2020, 27, 500-513.	1.6	35
21	Matching Reads to Many Genomes with the r-Index. Journal of Computational Biology, 2020, 27, 514-518.	1.6	6
22	Mobilization of Antibiotic Resistance: Are Current Approaches for Colocalizing Resistomes and Mobilomes Useful?. Frontiers in Microbiology, 2020, 11, 1376.	3.5	33
23	Hierarchical Hidden Markov models enable accurate and diverse detection of antimicrobial resistance sequences. Communications Biology, 2019, 2, 294.	4.4	31
24	Sequencing Technologies and Analyses: Where Have We Been and Where Are We Going?. IScience, 2019, 18, 37-41.	4.1	31
25	Characterization of the Microbial Resistome in Conventional and â€œRaised Without Antibioticsâ€•Beef and Dairy Production Systems. Frontiers in Microbiology, 2019, 10, 1980.	3.5	58
26	Building large updatable colored de Bruijn graphs via merging. Bioinformatics, 2019, 35, i51-i60.	4.1	42
27	Aligning optical maps to de Bruijn graphs. Bioinformatics, 2019, 35, 3250-3256.	4.1	4
28	Genomic Comparison Reveals Natural Occurrence of Clinically Relevant Multidrug-Resistant Extended-Spectrum-Î²-Lactamase-Producing Escherichia coli Strains. Applied and Environmental Microbiology, 2019, 85, .	3.1	29
29	Kohdista: an efficient method to index and query possible Rmap alignments. Algorithms for Molecular Biology, 2019, 14, 25.	1.2	6
30	A Cautionary Report for Pathogen Identification Using Shotgun Metagenomics; A Comparison to Aerobic Culture and Polymerase Chain Reaction for Salmonella enterica Identification. Frontiers in Microbiology, 2019, 10, 2499.	3.5	27
31	Counting motifs in dynamic networks. BMC Systems Biology, 2018, 12, 6.	3.0	11
32	Investigating Effects of Tulathromycin Metaphylaxis on the Fecal Resistome and Microbiome of Commercial Feedlot Cattle Early in the Feeding Period. Frontiers in Microbiology, 2018, 9, 1715.	3.5	78
33	Error correcting optical mapping data. GigaScience, 2018, 7, .	6.4	14
34	Practical dynamic de Bruijn graphs. Bioinformatics, 2018, 34, 4189-4195.	4.1	18
35	MEGARes: an antimicrobial resistance database for high throughput sequencing. Nucleic Acids Research, 2017, 45, D574-D580.	14.5	328
36	Succinct colored de Bruijn graphs. Bioinformatics, 2017, 33, 3181-3187.	4.1	99

#	ARTICLE	IF	CITATIONS
37	Targeted Enrichment for Pathogen Detection and Characterization in Three Felid Species. Journal of Clinical Microbiology, 2017, 55, 1658-1670.	3.9	25
38	aPPRove: An HMM-Based Method for Accurate Prediction of RNA-Pentatricopeptide Repeat Protein Binding Events. PLoS ONE, 2016, 11, e0160645.	2.5	14
39	Use of Metagenomic Shotgun Sequencing Technology To Detect Foodborne Pathogens within the Microbiome of the Beef Production Chain. Applied and Environmental Microbiology, 2016, 82, 2433-2443.	3.1	132
40	The SLOW GROWTH3 Pentatricopeptide Repeat Protein Is Required for the Splicing of Mitochondrial <i>NADH Dehydrogenase Subunit7</i> Intron 2 in Arabidopsis. Plant Physiology, 2015, 168, 490-501.	4.8	73
41	Variable-Order de Bruijn Graphs. , 2015, , .		39
42	Misassembly detection using paired-end sequence reads and optical mapping data. Bioinformatics, 2015, 31, i80-i88.	4.1	41
43	Genome Sequences of Strain ATCC 29281 and Pin and Northern Red Oak Isolates of Lonsdalea quercina subsp. <i>quercina</i>. Genome Announcements, 2014, 2, .	0.8	4
44	On the Hardness of Counting and Sampling Center Strings. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1843-1846.	3.0	0