

Christina Boucher

List of Publications by Year in descending order

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Version: 2024-02-01

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 | MEGARes: an antimicrobial resistance database for high throughput sequencing. <i>Nucleic Acids Research</i> , 2017, 45, D574-D580. | 14.5 | 328 |
| 2 | MEGARes 2.0: a database for classification of antimicrobial drug, biocide and metal resistance determinants in metagenomic sequence data. <i>Nucleic Acids Research</i> , 2020, 48, D561-D569. | 14.5 | 227 |
| 3 | Use of Metagenomic Shotgun Sequencing Technology To Detect Foodborne Pathogens within the Microbiome of the Beef Production Chain. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2433-2443. | 3.1 | 132 |
| 4 | Succinct colored de Bruijn graphs. <i>Bioinformatics</i> , 2017, 33, 3181-3187. | 4.1 | 99 |
| 5 | Investigating Effects of Tulathromycin Metaphylaxis on the Fecal Resistome and Microbiome of Commercial Feedlot Cattle Early in the Feeding Period. <i>Frontiers in Microbiology</i> , 2018, 9, 1715. | 3.5 | 78 |
| 6 | The SLOW GROWTH3 Pentatricopeptide Repeat Protein Is Required for the Splicing of Mitochondrial <i>ndh7</i> Intron 2 in Arabidopsis. <i>Plant Physiology</i> , 2015, 168, 490-501. | 4.8 | 73 |
| 7 | Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523. | 7.1 | 68 |
| 8 | Data structures based on <i>k</i> -mers for querying large collections of sequencing data sets. <i>Genome Research</i> , 2021, 31, 1-12. | 5.5 | 67 |
| 9 | Characterization of the Microbial Resistome in Conventional and "Raised Without Antibiotics" Beef and Dairy Production Systems. <i>Frontiers in Microbiology</i> , 2019, 10, 1980. | 3.5 | 58 |
| 10 | Building large updatable colored de Bruijn graphs via merging. <i>Bioinformatics</i> , 2019, 35, i51-i60. | 4.1 | 42 |
| 11 | Misassembly detection using paired-end sequence reads and optical mapping data. <i>Bioinformatics</i> , 2015, 31, i80-i88. | 4.1 | 41 |
| 12 | Variable-Order de Bruijn Graphs. , 2015, , . | | 39 |
| 13 | Efficient Construction of a Complete Index for Pan-Genomics Read Alignment. <i>Journal of Computational Biology</i> , 2020, 27, 500-513. | 1.6 | 35 |
| 14 | Mobilization of Antibiotic Resistance: Are Current Approaches for Colocalizing Resistomes and Mobilomes Useful?. <i>Frontiers in Microbiology</i> , 2020, 11, 1376. | 3.5 | 33 |
| 15 | Hierarchical Hidden Markov models enable accurate and diverse detection of antimicrobial resistance sequences. <i>Communications Biology</i> , 2019, 2, 294. | 4.4 | 31 |
| 16 | Sequencing Technologies and Analyses: Where Have We Been and Where Are We Going?. <i>IScience</i> , 2019, 18, 37-41. | 4.1 | 31 |
| 17 | Genomic Comparison Reveals Natural Occurrence of Clinically Relevant Multidrug-Resistant Extended-Spectrum- β -Lactamase-Producing <i>Escherichia coli</i> Strains. <i>Applied and Environmental Microbiology</i> , 2019, 85, . | 3.1 | 29 |
| 18 | A Cautionary Report for Pathogen Identification Using Shotgun Metagenomics; A Comparison to Aerobic Culture and Polymerase Chain Reaction for <i>Salmonella enterica</i> Identification. <i>Frontiers in Microbiology</i> , 2019, 10, 2499. | 3.5 | 27 |

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|----|---|-----|-----------|
| 19 | Targeted Enrichment for Pathogen Detection and Characterization in Three Felid Species. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1658-1670. | 3.9 | 25 |
| 20 | MONI: A Pangenomic Index for Finding Maximal Exact Matches. <i>Journal of Computational Biology</i> , 2022, 29, 169-187. | 1.6 | 23 |
| 21 | Computational graph pangenomics: a tutorial on data structures and their applications. <i>Natural Computing</i> , 2022, 21, 81-108. | 3.0 | 22 |
| 22 | Practical dynamic de Bruijn graphs. <i>Bioinformatics</i> , 2018, 34, 4189-4195. | 4.1 | 18 |
| 23 | Pan-genomic matching statistics for targeted nanopore sequencing. <i>IScience</i> , 2021, 24, 102696. | 4.1 | 15 |
| 24 | aPPRove: An HMM-Based Method for Accurate Prediction of RNA-Pentatricopeptide Repeat Protein Binding Events. <i>PLoS ONE</i> , 2016, 11, e0160645. | 2.5 | 14 |
| 25 | Error correcting optical mapping data. <i>GigaScience</i> , 2018, 7, . | 6.4 | 14 |
| 26 | Counting motifs in dynamic networks. <i>BMC Systems Biology</i> , 2018, 12, 6. | 3.0 | 11 |
| 27 | Succinct dynamic de Bruijn graphs. <i>Bioinformatics</i> , 2021, 37, 1946-1952. | 4.1 | 8 |
| 28 | Propensity score synthetic augmentation matching using generative adversarial networks (PSSAM-GAN). <i>Computer Methods and Programs in Biomedicine Update</i> , 2021, 1, 100020. | 3.7 | 8 |
| 29 | Metagenome SNP calling via read-colored de Bruijn graphs. <i>Bioinformatics</i> , 2021, 36, 5275-5281. | 4.1 | 8 |
| 30 | AMR-meta: a <i>k</i> -mer and metafeature approach to classify antimicrobial resistance from high-throughput short-read metagenomics data. <i>GigaScience</i> , 2022, 11, . | 6.4 | 8 |
| 31 | PFP Compressed Suffix Trees. , 2021, 2021, 60-72. | | 7 |
| 32 | Kohdista: an efficient method to index and query possible Rmap alignments. <i>Algorithms for Molecular Biology</i> , 2019, 14, 25. | 1.2 | 6 |
| 33 | Matching Reads to Many Genomes with the r-Index. <i>Journal of Computational Biology</i> , 2020, 27, 514-518. | 1.6 | 6 |
| 34 | Buffering updates enables efficient dynamic de Bruijn graphs. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4067-4078. | 4.1 | 6 |
| 35 | Fast and accurate correction of optical mapping data via spaced seeds. <i>Bioinformatics</i> , 2020, 36, 682-689. | 4.1 | 5 |
| 36 | Genome Sequences of Strain ATCC 29281 and Pin and Northern Red Oak Isolates of <i>Lonsdalea quercina</i> subsp. <i>quercina</i> . <i>Genome Announcements</i> , 2014, 2, . | 0.8 | 4 |

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|----|---|-----|-----------|
| 37 | Aligning optical maps to de Bruijn graphs. <i>Bioinformatics</i> , 2019, 35, 3250-3256. | 4.1 | 4 |
| 38 | Finding Maximal Exact Matches Using the r-Index. <i>Journal of Computational Biology</i> , 2022, 29, 188-194. | 1.6 | 4 |
| 39 | Exploring Prediction of Antimicrobial Resistance Based on Protein Solvent Accessibility Variation. <i>Frontiers in Genetics</i> , 2021, 12, 564186. | 2.3 | 3 |
| 40 | Towards routine employment of computational tools for antimicrobial resistance determination via high-throughput sequencing. <i>Briefings in Bioinformatics</i> , 2022, 23, . | 6.5 | 3 |
| 41 | Syotti: scalable bait design for DNA enrichment. <i>Bioinformatics</i> , 2022, 38, i177-i184. | 4.1 | 3 |
| 42 | Fast and efficient Rmap assembly using the Bi-labelled de Bruijn graph. <i>Algorithms for Molecular Biology</i> , 2021, 16, 6. | 1.2 | 2 |
| 43 | Fast and exact quantification of motif occurrences in biological sequences. <i>BMC Bioinformatics</i> , 2021, 22, 445. | 2.6 | 2 |
| 44 | On the Hardness of Counting and Sampling Center Strings. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1843-1846. | 3.0 | 0 |