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List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

14,082
citations

159585

30
h-index

214800

47
g-index

82
all docs

82
docs citations

82
times ranked

14532
citing authors

#	ARTICLE	IF	CITATIONS
1	Polypolish: Short-read polishing of long-read bacterial genome assemblies. <i>PLoS Computational Biology</i> , 2022, 18, e1009802.	3.2	210
2	Kaptive 2.0: updated capsule and lipopolysaccharide locus typing for the <i>Klebsiella pneumoniae</i> species complex. <i>Microbial Genomics</i> , 2022, 8, .	2.0	52
3	Linear plasmids in <i>Klebsiella</i> and other Enterobacteriaceae. <i>Microbial Genomics</i> , 2022, 8, .	2.0	3
4	Genomic dissection of <i>Klebsiella pneumoniae</i> infections in hospital patients reveals insights into an opportunistic pathogen. <i>Nature Communications</i> , 2022, 13, .	12.8	51
5	Genomic adaptations to an endolithic lifestyle in the coral-associated alga <i>Ostreobium</i> . <i>Current Biology</i> , 2021, 31, 1393-1402.e5.	3.9	40
6	Rapid Whole Genome Sequencing of Serotype K1 Hypervirulent <i>Klebsiella pneumoniae</i> from an Undocumented Chinese Migrant. <i>Case Reports in Infectious Diseases</i> , 2021, 2021, 1-5.	0.5	2
7	Silent spread of mobile colistin resistance gene <i>mcr-9.1</i> on IncHI2 $\hat{=}$ superplasmids $\hat{=}$ ™ in clinical carbapenem-resistant Enterobacterales. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1856.e7-1856.e13.	6.0	37
8	Genomic surveillance of antimicrobial resistant bacterial colonisation and infection in intensive care patients. <i>BMC Infectious Diseases</i> , 2021, 21, 683.	2.9	18
9	A genomic surveillance framework and genotyping tool for <i>Klebsiella pneumoniae</i> and its related species complex. <i>Nature Communications</i> , 2021, 12, 4188.	12.8	394
10	Recovery of small plasmid sequences via Oxford Nanopore sequencing. <i>Microbial Genomics</i> , 2021, 7, .	2.0	44
11	Tricycler: consensus long-read assemblies for bacterial genomes. <i>Genome Biology</i> , 2021, 22, 266.	8.8	175
12	GeneMates: an R package for detecting horizontal gene co-transfer between bacteria using gene-gene associations controlled for population structure. <i>BMC Genomics</i> , 2020, 21, 658.	2.8	9
13	Genome-Resolved Metagenomics and Detailed Geochemical Speciation Analyses Yield New Insights into Microbial Mercury Cycling in Geothermal Springs. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	19
14	Diversity and evolution of surface polysaccharide synthesis loci in Enterobacterales. <i>ISME Journal</i> , 2020, 14, 1713-1730.	9.8	40
15	The inflated mitochondrial genomes of siphonous green algae reflect processes driving expansion of noncoding DNA and proliferation of introns. <i>PeerJ</i> , 2020, 8, e8273.	2.0	21
16	Dissecting the molecular evolution of fluoroquinolone-resistant <i>Shigella sonnei</i> . <i>Nature Communications</i> , 2019, 10, 4828.	12.8	41
17	Performance of neural network basecalling tools for Oxford Nanopore sequencing. <i>Genome Biology</i> , 2019, 20, 129.	8.8	1,971
18	Distinct evolutionary dynamics of horizontal gene transfer in drug resistant and virulent clones of <i>Klebsiella pneumoniae</i> . <i>PLoS Genetics</i> , 2019, 15, e1008114.	3.5	228

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19	Genome-resolved metagenomics of an autotrophic thiocyanate-remediating microbial bioreactor consortium. <i>Water Research</i> , 2019, 158, 106-117.	11.3	11
20	Convergence of virulence and MDR in a single plasmid vector in MDR <i>Klebsiella pneumoniae</i> ST15. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1218-1222.	3.0	93
21	Complete Genome Sequence of A388, an Antibiotic-Resistant <i>Acinetobacter baumannii</i> Global Clone 1 Isolate from Greece. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	16
22	Emergence and rapid global dissemination of CTX-M-15-associated <i>Klebsiella pneumoniae</i> strain ST307. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 577-581.	3.0	137
23	Small IncQ1 and Col-Like Plasmids Harboring <i>bla</i> _{KPC-2} and Non-Tn <i>4401</i> Elements (NTE <i>bla</i> _{KPC} -IId) in High-Risk Lineages of <i>Klebsiella pneumoniae</i> CG258. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	27
24	Benchmarking of long-read assemblers for prokaryote whole genome sequencing. <i>F1000Research</i> , 2019, 8, 2138.	1.6	128
25	Evolution of a clade of <i>Acinetobacter baumannii</i> global clone 1, lineage 1 via acquisition of carbapenem- and aminoglycoside-resistance genes and dispersion of ISAba1. <i>Microbial Genomics</i> , 2019, 5, .	2.0	49
26	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. <i>Microbial Genomics</i> , 2019, 5, .	2.0	171
27	Insights from the revised complete genome sequences of <i>Acinetobacter baumannii</i> strains AB307-0294 and ACICU belonging to global clones 1 and 2. <i>Microbial Genomics</i> , 2019, 5, .	2.0	12
28	Benchmarking of long-read assemblers for prokaryote whole genome sequencing. <i>F1000Research</i> , 2019, 8, 2138.	1.6	115
29	Badread: simulation of error-prone long reads. <i>Journal of Open Source Software</i> , 2019, 4, 1316.	4.6	73
30	Kaptive Web: User-Friendly Capsule and Lipopolysaccharide Serotype Prediction for <i>Klebsiella</i> Genomes. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	239
31	Antimicrobial-Resistant <i>Klebsiella pneumoniae</i> Carriage and Infection in Specialized Geriatric Care Wards Linked to Acquisition in the Referring Hospital. <i>Clinical Infectious Diseases</i> , 2018, 67, 161-170.	5.8	108
32	Genetic diversity, mobilisation and spread of the yersiniabactin-encoding mobile element ICEKp in <i>Klebsiella pneumoniae</i> populations. <i>Microbial Genomics</i> , 2018, 4, .	2.0	197
33	Deepbiner: Demultiplexing barcoded Oxford Nanopore reads with deep convolutional neural networks. <i>PLoS Computational Biology</i> , 2018, 14, e1006583.	3.2	171
34	Complete Genome Sequence of WM99c, an Antibiotic-Resistant <i>Acinetobacter baumannii</i> Global Clone 2 (GC2) Strain Representing an Australian GC2 Lineage. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	5
35	Tracking key virulence loci encoding aerobactin and salmochelin siderophore synthesis in <i>Klebsiella pneumoniae</i> . <i>Genome Medicine</i> , 2018, 10, 77.	8.2	153
36	Morphological, genomic and transcriptomic responses of <i>Klebsiella pneumoniae</i> to the last-line antibiotic colistin. <i>Scientific Reports</i> , 2018, 8, 9868.	3.3	20

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37	Population genomics of hypervirulent <i>Klebsiella pneumoniae</i> clonal-group 23 reveals early emergence and rapid global dissemination. <i>Nature Communications</i> , 2018, 9, 2703.	12.8	205
38	Evolution of carbapenem resistance in <i>Acinetobacter baumannii</i> during a prolonged infection. <i>Microbial Genomics</i> , 2018, 4, .	2.0	49
39	Gastrointestinal Carriage Is a Major Reservoir of <i>Klebsiella pneumoniae</i> Infection in Intensive Care Patients. <i>Clinical Infectious Diseases</i> , 2017, 65, 208-215.	5.8	381
40	Completing bacterial genome assemblies with multiplex MinION sequencing. <i>Microbial Genomics</i> , 2017, 3, e000132.	2.0	559
41	Unicycler: Resolving bacterial genome assemblies from short and long sequencing reads. <i>PLoS Computational Biology</i> , 2017, 13, e1005595.	3.2	5,135
42	Identification of <i>Klebsiella</i> capsule synthesis loci from whole genome data. <i>Microbial Genomics</i> , 2016, 2, e000102.	2.0	372
43	Microbial mercury methylation in Antarctic sea ice. <i>Nature Microbiology</i> , 2016, 1, 16127.	13.3	158
44	Inducible colistin resistance via a disrupted plasmid-borne <i>mcr-1</i> gene in a 2008 Vietnamese <i>Shigella sonnei</i> isolate. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2314-2317.	3.0	82
45	Repeated local emergence of carbapenem-resistant <i>Acinetobacter baumannii</i> in a single hospital ward. <i>Microbial Genomics</i> , 2016, 2, e000050.	2.0	65
46	ISMMapper: identifying transposase insertion sites in bacterial genomes from short read sequence data. <i>BMC Genomics</i> , 2015, 16, 667.	2.8	119
47	Bandage: interactive visualization of <i>de novo</i> genome assemblies. <i>Bioinformatics</i> , 2015, 31, 3350-3352.	4.1	1,671
48	Benchmarking of long-read assemblers for prokaryote whole genome sequencing. <i>F1000Research</i> , 0, 8, 2138.	1.6	5
49	Benchmarking of long-read assemblers for prokaryote whole genome sequencing. <i>F1000Research</i> , 0, 8, 2138.	1.6	17