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List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

8,379
citations

109321

35
h-index

155660

55
g-index

83
all docs

83
docs citations

83
times ranked

13417
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	28.9	843
2	Occurrence of carbapenemase-producing <i>Klebsiella pneumoniae</i> and <i>Escherichia coli</i> in the European survey of carbapenemase-producing Enterobacteriaceae (EuSCAPE): a prospective, multinational study. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 153-163.	9.1	522
3	Epidemic of carbapenem-resistant <i>Klebsiella pneumoniae</i> in Europe is driven by nosocomial spread. <i>Nature Microbiology</i> , 2019, 4, 1919-1929.	13.3	476
4	Microreact: visualizing and sharing data for genomic epidemiology and phylogeography. <i>Microbial Genomics</i> , 2016, 2, e000093.	2.0	470
5	Phandango: an interactive viewer for bacterial population genomics. <i>Bioinformatics</i> , 2018, 34, 292-293.	4.1	468
6	A genomic portrait of the emergence, evolution, and global spread of a methicillin-resistant <i>Staphylococcus aureus</i> pandemic. <i>Genome Research</i> , 2013, 23, 653-664.	5.5	412
7	Recent Asian origin of chytrid fungi causing global amphibian declines. <i>Science</i> , 2018, 360, 621-627.	12.6	389
8	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. <i>Cell Reports</i> , 2021, 35, 109292.	6.4	375
9	Dense genomic sampling identifies highways of pneumococcal recombination. <i>Nature Genetics</i> , 2014, 46, 305-309.	21.4	371
10	Rapid Sequence-Based Identification of Gonococcal Transmission Clusters in a Large Metropolitan Area. <i>Journal of Infectious Diseases</i> , 2004, 189, 1497-1505.	4.0	340
11	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	12.6	335
12	EpiCollect: Linking Smartphones to Web Applications for Epidemiology, Ecology and Community Data Collection. <i>PLoS ONE</i> , 2009, 4, e6968.	2.5	306
13	The multilocus sequence typing network: mlst.net. <i>Nucleic Acids Research</i> , 2005, 33, W728-W733.	14.5	235
14	Genomic Evidence for the Evolution of <i>Streptococcus equi</i> : Host Restriction, Increased Virulence, and Genetic Exchange with Human Pathogens. <i>PLoS Pathogens</i> , 2009, 5, e1000346.	4.7	197
15	Whole-Genome Sequencing for Routine Pathogen Surveillance in Public Health: a Population Snapshot of Invasive <i>Staphylococcus aureus</i> in Europe. <i>MBio</i> , 2016, 7, .	4.1	192
16	Molecular tracing of the emergence, adaptation, and transmission of hospital-associated methicillin-resistant <i>Staphylococcus aureus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9107-9112.	7.1	174
17	Genomic epidemiology of the UK outbreak of the emerging human fungal pathogen <i>Candida auris</i> . <i>Emerging Microbes and Infections</i> , 2018, 7, 1-12.	6.5	169
18	Pneumococcal lineages associated with serotype replacement and antibiotic resistance in childhood invasive pneumococcal disease in the post-PCV13 era: an international whole-genome sequencing study. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 759-769.	9.1	165

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19	Public health surveillance of multidrug-resistant clones of <i>Neisseria gonorrhoeae</i> in Europe: a genomic survey. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 758-768.	9.1	164
20	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895.	12.6	142
21	Predicted Functions and Linkage Specificities of the Products of the <i>Streptococcus pneumoniae</i> Capsular Biosynthetic Loci. <i>Journal of Bacteriology</i> , 2007, 189, 7856-7876.	2.2	114
22	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. <i>Nature Communications</i> , 2018, 9, 5094.	12.8	98
23	Host migration impacts on the phylogeography of Lyme Borreliosis spirochaete species in Europe. <i>Environmental Microbiology</i> , 2011, 13, 184-192.	3.8	97
24	Integrated chromosomal and plasmid sequence analyses reveal diverse modes of carbapenemase gene spread among <i>Klebsiella pneumoniae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25043-25054.	7.1	97
25	The Promise of Whole Genome Pathogen Sequencing for the Molecular Epidemiology of Emerging Aquaculture Pathogens. <i>Frontiers in Microbiology</i> , 2017, 8, 121.	3.5	80
26	Whole genome resequencing of the human parasite <i>Schistosoma mansoni</i> reveals population history and effects of selection. <i>Scientific Reports</i> , 2016, 6, 20954.	3.3	72
27	Phylogenetic and phylodynamic approaches to understanding and combating the early SARS-CoV-2 pandemic. <i>Nature Reviews Genetics</i> , 2022, 23, 547-562.	16.3	70
28	Pneumococcal Capsule Synthesis Locus <i>cps</i> as Evolutionary Hotspot with Potential to Generate Novel Serotypes by Recombination. <i>Molecular Biology and Evolution</i> , 2017, 34, 2537-2554.	8.9	65
29	Building a genomic framework for prospective MRSA surveillance in the United Kingdom and the Republic of Ireland. <i>Genome Research</i> , 2016, 26, 263-270.	5.5	63
30	A community-driven resource for genomic epidemiology and antimicrobial resistance prediction of <i>Neisseria gonorrhoeae</i> at Pathogenwatch. <i>Genome Medicine</i> , 2021, 13, 61.	8.2	63
31	Integrating whole-genome sequencing within the National Antimicrobial Resistance Surveillance Program in the Philippines. <i>Nature Communications</i> , 2020, 11, 2719.	12.8	62
32	A global resource for genomic predictions of antimicrobial resistance and surveillance of <i>Salmonella</i> Typhi at pathogenwatch. <i>Nature Communications</i> , 2021, 12, 2879.	12.8	56
33	Emergence and clonal spread of colistin resistance due to multiple mutational mechanisms in carbapenemase-producing <i>Klebsiella pneumoniae</i> in London. <i>Scientific Reports</i> , 2017, 7, 12711.	3.3	55
34	CLIMB-COVID: continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance. <i>Genome Biology</i> , 2021, 22, 196.	8.8	53
35	Genomic Analysis and Comparison of Two Gonorrhea Outbreaks. <i>MBio</i> , 2016, 7, .	4.1	51
36	Rapid Genomic Characterization and Global Surveillance of <i>Klebsiella</i> Using Pathogenwatch. <i>Clinical Infectious Diseases</i> , 2021, 73, S325-S335.	5.8	47

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37	Europe-wide expansion and eradication of multidrug-resistant <i>Neisseria gonorrhoeae</i> lineages: a genomic surveillance study. <i>Lancet Microbe</i> , The, 2022, 3, e452-e463.	7.3	44
38	The changing epidemiology of carbapenemase-producing <i>Klebsiella pneumoniae</i> in Italy: toward polyclonal evolution with emergence of high-risk lineages. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 355-361.	3.0	43
39	OutbreakTools: A new platform for disease outbreak analysis using the R software. <i>Epidemics</i> , 2014, 7, 28-34.	3.0	37
40	High susceptibility to zoliflodacin and conserved target (GyrB) for zoliflodacin among 1209 consecutive clinical <i>Neisseria gonorrhoeae</i> isolates from 25 European countries, 2018. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1221-1228.	3.0	31
41	EpiCollect+: linking smartphones to web applications for complex data collection projects. <i>F1000Research</i> , 2014, 3, 199.	1.6	31
42	High-Resolution Genomic Profiling of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Isolates: A Multicentric Retrospective Indian Study. <i>Clinical Infectious Diseases</i> , 2021, 73, S300-S307.	5.8	30
43	Clones and Clusters of Antimicrobial-Resistant <i>Klebsiella</i> From Southwestern Nigeria. <i>Clinical Infectious Diseases</i> , 2021, 73, S308-S315.	5.8	26
44	Development and worldwide use of non-lethal, and minimal population-level impact, protocols for the isolation of amphibian chytrid fungi. <i>Scientific Reports</i> , 2018, 8, 7772.	3.3	24
45	Complexity of Genomic Epidemiology of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Isolates in Colombia Urges the Reinforcement of Whole Genome Sequencing-Based Surveillance Programs. <i>Clinical Infectious Diseases</i> , 2021, 73, S290-S299.	5.8	22
46	Population genetic structuring of methicillin-resistant <i>Staphylococcus aureus</i> clone EMRSA-15 within UK reflects patient referral patterns. <i>Microbial Genomics</i> , 2017, 3, e000113.	2.0	19
47	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. <i>GigaScience</i> , 2022, 11, .	6.4	18
48	Genome Sequencing Identifies Previously Unrecognized <i>Klebsiella pneumoniae</i> Outbreaks in Neonatal Intensive Care Units in the Philippines. <i>Clinical Infectious Diseases</i> , 2021, 73, S316-S324.	5.8	12
49	Genomic Epidemiology of CC30 Methicillin-Resistant <i>Staphylococcus aureus</i> Strains from Argentina Reveals Four Major Clades with Distinctive Genetic Features. <i>MSphere</i> , 2021, 6, .	2.9	11
50	Globetrotting strangles: the unbridled national and international transmission of <i>Streptococcus equi</i> between horses. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
51	Genomic surveillance of <i>Neisseria gonorrhoeae</i> in the Philippines, 2013–2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021, 12, 17-25.	0.6	3
52	Genomic surveillance of <i>Pseudomonas aeruginosa</i> in the Philippines, 2013–2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021, 12, 4-18.	0.6	3
53	Conservation of vaccine antigen sequences encoded by sequenced strains of <i>Streptococcus equi</i> subsp. <i>equi</i> . <i>Equine Veterinary Journal</i> , 2023, 55, 92-101.	1.7	3
54	Genomic surveillance of <i>Acinetobacter baumannii</i> in the Philippines, 2013–2014. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021, 12, 46-60.	0.6	1