

Colin J Worby

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

1,297
citations

516710

16
h-index

526287

27
g-index

32
all docs

32
docs citations

32
times ranked

2154
citing authors

#	ARTICLE	IF	CITATIONS
1	Establishing the role of the gut microbiota in susceptibility to recurrent urinary tract infections. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	17
2	StrainGE: a toolkit to track and characterize low-abundance strains in complex microbial communities. <i>Genome Biology</i> , 2022, 23, 74.	8.8	35
3	Inter-species geographic signatures for tracing horizontal gene transfer and long-term persistence of carbapenem resistance. <i>Genome Medicine</i> , 2022, 14, 37.	8.2	15
4	Drinking water chlorination has minor effects on the intestinal flora and resistomes of Bangladeshi children. <i>Nature Microbiology</i> , 2022, 7, 620-629.	13.3	9
5	Longitudinal multi-omics analyses link gut microbiome dysbiosis with recurrent urinary tract infections in women. <i>Nature Microbiology</i> , 2022, 7, 630-639.	13.3	54
6	Face mask use in the general population and optimal resource allocation during the COVID-19 pandemic. <i>Nature Communications</i> , 2020, 11, 4049.	12.8	250
7	Acquisition of Antibiotic-Resistant Bacteria by U.S. International Travelers. <i>New England Journal of Medicine</i> , 2020, 382, 1372-1374.	27.0	20
8	Acquisition and Long-term Carriage of Multidrug-Resistant Organisms in US International Travelers. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa543.	0.9	21
9	Phylogeography of rubella virus in Asia: Vaccination and demography shape synchronous outbreaks. <i>Epidemics</i> , 2019, 28, 100346.	3.0	7
10	Model diagnostics and refinement for phylodynamic models. <i>PLoS Computational Biology</i> , 2019, 15, e1006955.	3.2	3
11	On the Relative Role of Different Age Groups During Epidemics Associated With Respiratory Syncytial Virus. <i>Journal of Infectious Diseases</i> , 2018, 217, 238-244.	4.0	34
12	On the Role of Different Age Groups and Pertussis Vaccines During the 2012 Outbreak in Wisconsin. <i>Open Forum Infectious Diseases</i> , 2018, 5, ofy082.	0.9	6
13	Bayesian reconstruction of transmission within outbreaks using genomic variants. <i>PLoS Computational Biology</i> , 2018, 14, e1006117.	3.2	69
14	Population effect of influenza vaccination under co-circulation of non-vaccine variants and the case for a bivalent A/H3N2 vaccine component. <i>Epidemics</i> , 2017, 19, 74-82.	3.0	4
15	Shared Genomic Variants: Identification of Transmission Routes Using Pathogen Deep-Sequence Data. <i>American Journal of Epidemiology</i> , 2017, 186, 1209-1216.	3.4	84
16	THE REAL McCOIL: A method for the concurrent estimation of the complexity of infection and SNP allele frequency for malaria parasites. <i>PLoS Computational Biology</i> , 2017, 13, e1005348.	3.2	93
17	Penicillin Resistance of Nonvaccine Type Pneumococcus before and after PCV13 Introduction, United States. <i>Emerging Infectious Diseases</i> , 2017, 23, 1012-1015.	4.3	13
18	Reconstructing transmission trees for communicable diseases using densely sampled genetic data. <i>Annals of Applied Statistics</i> , 2016, 10, 395-417.	1.1	52

#	ARTICLE	IF	CITATIONS
19	Microbial Genomics of Ancient Plagues and Outbreaks. Trends in Microbiology, 2016, 24, 978-990.	7.7	50
20	Identifying the effect of patient sharing on between-hospital genetic differentiation of methicillin-resistant Staphylococcus aureus. Genome Medicine, 2016, 8, 18.	8.2	20
21	More Research Is Needed to Quantify Risks, Benefits, and Cost-Effectiveness of Universal Mupirocin Usage. Clinical Infectious Diseases, 2016, 62, 1193.2-1194.	5.8	0
22	Examining the role of different age groups and of vaccination during the 2012 Minnesota pertussis outbreak. Scientific Reports, 2015, 5, 13182.	3.3	20
23	'SEEDY' (Simulation of Evolutionary and Epidemiological Dynamics): An R Package to Follow Accumulation of Within-Host Mutation in Pathogens. PLoS ONE, 2015, 10, e0129745.	2.5	24
24	Impact of mupirocin resistance on the transmission and control of healthcare-associated MRSA. Journal of Antimicrobial Chemotherapy, 2015, 70, dkv249.	3.0	21
25	On the relative role of different age groups in influenza epidemics. Epidemics, 2015, 13, 10-16.	3.0	128
26	Within-Host Bacterial Diversity Hinders Accurate Reconstruction of Transmission Networks from Genomic Distance Data. PLoS Computational Biology, 2014, 10, e1003549.	3.2	148
27	The Distribution of Pairwise Genetic Distances: A Tool for Investigating Disease Transmission. Genetics, 2014, 198, 1395-1404.	2.9	43
28	Estimating the Effectiveness of Isolation and Decolonization Measures in Reducing Transmission of Methicillin-resistant Staphylococcus aureus in Hospital General Wards. American Journal of Epidemiology, 2013, 177, 1306-1313.	3.4	43