Colin J Worby

List of Publications by Year
in descending order

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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	Face mask use in the general population and optimal resource allocation during the COVID-19 pandemic. Nature Communications, 2020, 11, 4049.	12.8	250
2	Within-Host Bacterial Diversity Hinders Accurate Reconstruction of Transmission Networks from Genomic Distance Data. PLoS Computational Biology, 2014, 10, e1003549.	3.2	148
3	On the relative role of different age groups in influenza epidemics. Epidemics, 2015, 13, 10-16.	3.0	128
4	THE REAL McCOIL: A method for the concurrent estimation of the complexity of infection and SNP allele frequency for malaria parasites. PLoS Computational Biology, 2017, 13, e1005348.	3.2	93
5	Shared Genomic Variants: Identification of Transmission Routes Using Pathogen Deep-Sequence Data. American Journal of Epidemiology, 2017, 186, 1209-1216.	3.4	84
6	Bayesian reconstruction of transmission within outbreaks using genomic variants. PLoS Computational Biology, 2018, 14, e1006117.	3.2	69
7	Longitudinal multi-omics analyses link gut microbiome dysbiosis with recurrent urinary tract infections in women. Nature Microbiology, 2022, 7, 630-639.	13.3	54
8	Reconstructing transmission trees for communicable diseases using densely sampled genetic data. Annals of Applied Statistics, 2016, 10, 395-417.	1.1	52
9	Microbial Genomics of Ancient Plagues and Outbreaks. Trends in Microbiology, 2016, 24, 978-990.	7.7	50
10	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
11	The Distribution of Pairwise Genetic Distances: A Tool for Investigating Disease Transmission. Genetics, 2014, 198, 1395-1404.	2.9	43
12	StrainGE: a toolkit to track and characterize low-abundance strains in complex microbial communities. Genome Biology, 2022, 23, 74.	8.8	35
13	On the Relative Role of Different Age Groups During Epidemics Associated With Respiratory Syncytial Virus. Journal of Infectious Diseases, 2018, 217, 238-244.	4.0	34
14	'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
15	Impact of mupirocin resistance on the transmission and control of healthcare-associated MRSA. Journal of Antimicrobial Chemotherapy, 2015, 70, dkv249.	3.0	21
16	Acquisition and Long-term Carriage of Multidrug-Resistant Organisms in US International Travelers. Open Forum Infectious Diseases, 2020, 7, ofaa543.	0.9	21
17	Examining the role of different age groups and of vaccination during the 2012 Minnesota pertussis outbreak. Scientific Reports, 2015, 5, 13182.	3.3	20
18	Identifying the effect of patient sharing on between-hospital genetic differentiation of methicillin-resistant Staphylococcus aureus. Genome Medicine, 2016, 8, 18.	8.2	20

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19	Acquisition of Antibiotic-Resistant Bacteria by U.S. International Travelers. New England Journal of Medicine, 2020, 382, 1372-1374.	27.0	20
20	Establishing the role of the gut microbiota in susceptibility to recurrent urinary tract infections. Journal of Clinical Investigation, 2022, 132, .	8.2	17
21	Inter-species geographic signatures for tracing horizontal gene transfer and long-term persistence of carbapenem resistance. Genome Medicine, 2022, 14, 37.	8.2	15
22	Penicillin Resistance of Nonvaccine Type Pneumococcus before and after PCV13 Introduction, United States. Emerging Infectious Diseases, 2017, 23, 1012-1015.	4.3	13
23	Drinking water chlorination has minor effects on the intestinal flora and resistomes of Bangladeshi children. Nature Microbiology, 2022, 7, 620-629.	13.3	9
24	Phylogeography of rubella virus in Asia: Vaccination and demography shape synchronous outbreaks. Epidemics, 2019, 28, 100346.	3.0	7
25	On the Role of Different Age Groups and Pertussis Vaccines During the 2012 Outbreak in Wisconsin. Open Forum Infectious Diseases, 2018, 5, ofy082.	0.9	6
26	Population effect of influenza vaccination under co-circulation of non-vaccine variants and the case for a bivalent A/H3N2 vaccine component. Epidemics, 2017, 19, 74-82.	3.0	4
27	Model diagnostics and refinement for phylodynamic models. PLoS Computational Biology, 2019, 15, e1006955.	3.2	3
28	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