

Caroline Colijn

List of Publications by Year in descending order

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Version: 2024-02-01

77
papers

4,048
citations

159525

30
h-index

161767

54
g-index

107
all docs

107
docs citations

107
times ranked

6088
citing authors

#	ARTICLE	IF	CITATIONS
1	Evidence for transmission of COVID-19 prior to symptom onset. <i>ELife</i> , 2020, 9, .	2.8	259
2	The origins and potential future of SARS-CoV-2 variants of concern in the evolving COVID-19 pandemic. <i>Current Biology</i> , 2021, 31, R918-R929.	1.8	246
3	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, .	1.8	192
4	Bayesian Inference of Infectious Disease Transmission from Whole-Genome Sequence Data. <i>Molecular Biology and Evolution</i> , 2014, 31, 1869-1879.	3.5	191
5	Genomic infectious disease epidemiology in partially sampled and ongoing outbreaks. <i>Molecular Biology and Evolution</i> , 2017, 34, msw075.	3.5	181
6	Mixed-Strain <i>Mycobacterium tuberculosis</i> Infections and the Implications for Tuberculosis Treatment and Control. <i>Clinical Microbiology Reviews</i> , 2012, 25, 708-719.	5.7	172
7	<scp>treespace</scp>: Statistical exploration of landscapes of phylogenetic trees. <i>Molecular Ecology Resources</i> , 2017, 17, 1385-1392.	2.2	158
8	No coexistence for free: Neutral null models for multistrain pathogens. <i>Epidemics</i> , 2009, 1, 2-13.	1.5	130
9	Antimicrobials: a global alliance for optimizing their rational use in intra-abdominal infections (AGORA). <i>World Journal of Emergency Surgery</i> , 2016, 11, 33.	2.1	130
10	Mapping Phylogenetic Trees to Reveal Distinct Patterns of Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 2735-2743.	3.5	121
11	Beyond the SNP Threshold: Identifying Outbreak Clusters Using Inferred Transmissions. <i>Molecular Biology and Evolution</i> , 2019, 36, 587-603.	3.5	121
12	Interpreting whole genome sequencing for investigating tuberculosis transmission: a systematic review. <i>BMC Medicine</i> , 2016, 14, 21.	2.3	117
13	Simultaneous inference of phylogenetic and transmission trees in infectious disease outbreaks. <i>PLoS Computational Biology</i> , 2017, 13, e1005495.	1.5	93
14	Internal migration and transmission dynamics of tuberculosis in Shanghai, China: an epidemiological, spatial, genomic analysis. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 788-795.	4.6	85
15	What is the mechanism for persistent coexistence of drug-susceptible and drug-resistant strains of <i>Streptococcus pneumoniae</i> ?. <i>Journal of the Royal Society Interface</i> , 2010, 7, 905-919.	1.5	83
16	Phylogenetic tree shapes resolve disease transmission patterns. <i>Evolution, Medicine and Public Health</i> , 2014, 2014, 96-108.	1.1	72
17	Spontaneous Emergence of Multiple Drug Resistance in Tuberculosis before and during Therapy. <i>PLoS ONE</i> , 2011, 6, e18327.	1.1	71
18	Quantifying the impact of COVID-19 control measures using a Bayesian model of physical distancing. <i>PLoS Computational Biology</i> , 2020, 16, e1008274.	1.5	67

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19	High-resolution mapping of tuberculosis transmission: Whole genome sequencing and phylogenetic modelling of a cohort from Valencia Region, Spain. <i>PLoS Medicine</i> , 2019, 16, e1002961.	3.9	62
20	Evaluating strategies for control of tuberculosis in prisons and prevention of spillover into communities: An observational and modeling study from Brazil. <i>PLoS Medicine</i> , 2019, 16, e1002737.	3.9	55
21	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , 2017, 34, 185-203.	3.5	53
22	Event-specific interventions to minimize COVID-19 transmission. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 32038-32045.	3.3	51
23	Importance of COVID-19 vaccine efficacy in older age groups. <i>Vaccine</i> , 2021, 39, 2020-2023.	1.7	50
24	Long-Term Persistence of Spike Protein Antibody and Predictive Modeling of Antibody Dynamics After Infection With Severe Acute Respiratory Syndrome Coronavirus 2. <i>Clinical Infectious Diseases</i> , 2022, 74, 1220-1229.	2.9	45
25	How the Dynamics and Structure of Sexual Contact Networks Shape Pathogen Phylogenies. <i>PLoS Computational Biology</i> , 2013, 9, e1003105.	1.5	43
26	Community-Wide Isoniazid Preventive Therapy Drives Drug-Resistant Tuberculosis: A Model-Based Analysis. <i>Science Translational Medicine</i> , 2013, 5, 180ra49.	5.8	42
27	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. <i>Wellcome Open Research</i> , 2018, 3, 33.	0.9	42
28	The Distribution of Fitness Costs of Resistance-Confering Mutations Is a Key Determinant for the Future Burden of Drug-Resistant Tuberculosis: A Model-Based Analysis. <i>Clinical Infectious Diseases</i> , 2015, 61, S147-S154.	2.9	40
29	Designing ecologically optimized pneumococcal vaccines using population genomics. <i>Nature Microbiology</i> , 2020, 5, 473-485.	5.9	39
30	How competition governs whether moderate or aggressive treatment minimizes antibiotic resistance. <i>eLife</i> , 2015, 4, .	2.8	39
31	OutbreakTools: A new platform for disease outbreak analysis using the R software. <i>Epidemics</i> , 2014, 7, 28-34.	1.5	37
32	Mathematical modelling for antibiotic resistance control policy: do we know enough?. <i>BMC Infectious Diseases</i> , 2019, 19, 1011.	1.3	37
33	COVID-19 in schools: Mitigating classroom clusters in the context of variable transmission. <i>PLoS Computational Biology</i> , 2021, 17, e1009120.	1.5	34
34	Errors in reported degrees and respondent driven sampling: Implications for bias. <i>Drug and Alcohol Dependence</i> , 2014, 142, 120-126.	1.6	33
35	Host population structure and treatment frequency maintain balancing selection on drug resistance. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20170295.	1.5	32
36	Latent Coinfection and the Maintenance of Strain Diversity. <i>Bulletin of Mathematical Biology</i> , 2009, 71, 247-263.	0.9	30

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37	A phylogeny-based sampling strategy and power calculator informs genome-wide associations study design for microbial pathogens. <i>Genome Medicine</i> , 2014, 6, 101.	3.6	30
38	The dynamics of sexual contact networks: Effects on disease spread and control. <i>Theoretical Population Biology</i> , 2012, 81, 89-96.	0.5	29
39	Toward Precision Healthcare: Context and Mathematical Challenges. <i>Frontiers in Physiology</i> , 2017, 8, 136.	1.3	28
40	Declaring a tuberculosis outbreak over with genomic epidemiology. <i>Microbial Genomics</i> , 2016, 2, e000060.	1.0	27
41	Vaccine rollout strategies: The case for vaccinating essential workers early. <i>PLOS Global Public Health</i> , 2021, 1, e0000020.	0.5	25
42	Genomic variant-identification methods may alter Mycobacterium tuberculosis transmission inferences. <i>Microbial Genomics</i> , 2020, 6, .	1.0	24
43	How could preventive therapy affect the prevalence of drug resistance? Causes and consequences. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140306.	1.8	19
44	Convergent evolution and topologically disruptive polymorphisms among multidrug-resistant tuberculosis in Peru. <i>PLoS ONE</i> , 2017, 12, e0189838.	1.1	19
45	HIV-1 Full-Genome Phylogenetics of Generalized Epidemics in Sub-Saharan Africa: Impact of Missing Nucleotide Characters in Next-Generation Sequences. <i>AIDS Research and Human Retroviruses</i> , 2017, 33, 1083-1098.	0.5	18
46	Transmission Trees on a Known Pathogen Phylogeny: Enumeration and Sampling. <i>Molecular Biology and Evolution</i> , 2019, 36, 1333-1343.	3.5	18
47	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. <i>Wellcome Open Research</i> , 0, 3, 33.	0.9	18
48	Negative frequency-dependent selection and asymmetrical transformation stabilise multi-strain bacterial population structures. <i>ISME Journal</i> , 2021, 15, 1523-1538.	4.4	17
49	Phylogeography and transmission of M. tuberculosis in Moldova: A prospective genomic analysis. <i>PLoS Medicine</i> , 2022, 19, e1003933.	3.9	16
50	How much leeway is there to relax COVID-19 control measures?. <i>Epidemics</i> , 2021, 35, 100453.	1.5	15
51	ClassTR: Classifying Within-Host Heterogeneity Based on Tandem Repeats with Application to Mycobacterium tuberculosis Infections. <i>PLoS Computational Biology</i> , 2016, 12, e1004475.	1.5	14
52	Phylogenies from dynamic networks. <i>PLoS Computational Biology</i> , 2019, 15, e1006761.	1.5	14
53	Whole-genome sequencing of Mycobacterium tuberculosis for rapid diagnostics and beyond. <i>Lancet Respiratory Medicine</i> , 2016, 4, 6-8.	5.2	13
54	Predicting the short-term success of human influenza virus variants with machine learning. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200319.	1.2	13

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55	The need for linked genomic surveillance of SARS-CoV-2. Canada Communicable Disease Report, 2022, 48, 131-139.	0.6	13
56	Competition, coinfection and strain replacement in models of Bordetella pertussis. Theoretical Population Biology, 2015, 103, 84-92.	0.5	12
57	Modelling the impact of household size distribution on the transmission dynamics of COVID-19. Journal of the Royal Society Interface, 2021, 18, 20210036.	1.5	12
58	The cost-effectiveness of alternative vaccination strategies for polyvalent meningococcal vaccines in Burkina Faso: A transmission dynamic modeling study. PLoS Medicine, 2018, 15, e1002495.	3.9	12
59	Mathematical modeling of COVID-19 in British Columbia: An age-structured model with time-dependent contact rates. Epidemics, 2022, 39, 100559.	1.5	12
60	Asymptotic frequency of shapes in supercritical branching trees. Journal of Applied Probability, 2016, 53, 1143-1155.	0.4	11
61	Systematic comparison of coexistence in models of drug-sensitive and drug-resistant pathogen strains. Theoretical Population Biology, 2020, 133, 150-158.	0.5	11
62	Genome-based transmission modelling separates imported tuberculosis from recent transmission within an immigrant population. Microbial Genomics, 2018, 4, .	1.0	10
63	The role of prisons in disseminating tuberculosis in Brazil: A genomic epidemiology study. The Lancet Regional Health Americas, 2022, 9, 100186.	1.5	10
64	Transmission analysis of a large tuberculosis outbreak in London: a mathematical modelling study using genomic data. Microbial Genomics, 2020, 6, .	1.0	8
65	A curated genome-scale metabolic model of Bordetella pertussis metabolism. PLoS Computational Biology, 2017, 13, e1005639.	1.5	8
66	Transmission dynamics are crucial to COVID-19 vaccination policy. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	7
67	Analyzing Phylogenetic Trees with a Tree Lattice Coordinate System and a Graph Polynomial. Systematic Biology, 2022, 71, 1378-1390.	2.7	7
68	Network science inspires novel tree shape statistics. PLoS ONE, 2021, 16, e0259877.	1.1	7
69	Estimating Genetic Similarity Matrices Using Phylogenies. Journal of Computational Biology, 2021, 28, 587-600.	0.8	6
70	Diverse drug-resistant subpopulations of <i>Mycobacterium tuberculosis</i> are sustained in continuous culture. Journal of the Royal Society Interface, 2016, 13, 20160745.	1.5	5
71	Evolution and emergence of multidrug-resistant <i>Mycobacterium tuberculosis</i> in Chisinau, Moldova. Microbial Genomics, 2021, 7, .	1.0	5
72	Fundamental limitations of contact tracing for COVID-19. Facets, 2021, 6, 1993-2001.	1.1	5

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73	A Maximum Entropy Method for the Prediction of Size Distributions. Entropy, 2020, 22, 312.	1.1	4
74	Effects of memory on the shapes of simple outbreak trees. Scientific Reports, 2016, 6, 21159.	1.6	3
75	Quantifying transmissibility of SARS-CoV-2 and impact of intervention within long-term healthcare facilities. Royal Society Open Science, 2022, 9, 211710.	1.1	2
76	Propagation through dynamic networks: Degree distribution and the spread of disease. , 2009, , .		0
77	Long time frames to detect the impact of changing COVID-19 measures, Canada, March to July 2020. Eurosurveillance, 2021, 26, .	3.9	0