Caroline Colijn

List of Publications by Year
in descending order

77 papers	4,048 citations	182225 30 h-index	182931 54 g-index
107 all docs	107 docs citations	107 times ranked	6630 citing authors

#	Article	IF	Citations
1	Long-Term Persistence of Spike Protein Antibody and Predictive Modeling of Antibody Dynamics After Infection With Severe Acute Respiratory Syndrome Coronavirus 2. Clinical Infectious Diseases, 2022, 74, 1220-1229.	2.9	45
2	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
3	The role of prisons in disseminating tuberculosis in Brazil: A genomic epidemiology study. The Lancet Regional Health Americas, 2022, 9, 100186.	1.5	10
4	Analyzing Phylogenetic Trees with a Tree Lattice Coordinate System and a Graph Polynomial. Systematic Biology, 2022, 71, 1378-1390.	2.7	7
5	Phylogeography and transmission of M. tuberculosis in Moldova: A prospective genomic analysis. PLoS Medicine, 2022, 19, e1003933.	3.9	16
6	Mathematical modeling of COVID-19 in British Columbia: An age-structured model with time-dependent contact rates. Epidemics, 2022, 39, 100559.	1.5	12
7	The need for linked genomic surveillance of SARS-CoV-2. Canada Communicable Disease Report, 2022, 48, 131-139.	0.6	13
8	Negative frequency-dependent selection and asymmetrical transformation stabilise multi-strain bacterial population structures. ISME Journal, 2021, 15, 1523-1538.	4.4	17
9	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
10	Importance of COVID-19 vaccine efficacy in older age groups. Vaccine, 2021, 39, 2020-2023.	1.7	50
11	How much leeway is there to relax COVID-19 control measures?. Epidemics, 2021, 35, 100453.	1.5	15
12	Estimating Genetic Similarity Matrices Using Phylogenies. Journal of Computational Biology, 2021, 28, 587-600.	0.8	6
13	COVID-19 in schools: Mitigating classroom clusters in the context of variable transmission. PLoS Computational Biology, 2021, 17, e1009120.	1.5	34
14	The origins and potential future of SARS-CoV-2 variants of concern in the evolving COVID-19 pandemic. Current Biology, 2021, 31, R918-R929.	1.8	246
15	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
16	Evolution and emergence of multidrug-resistant Mycobacterium tuberculosis in Chisinau, Moldova. Microbial Genomics, 2021, 7, .	1.0	5
17	Vaccine rollout strategies: The case for vaccinating essential workers early. PLOS Global Public Health, 2021, 1, e0000020.	0.5	25
18	Long time frames to detect the impact of changing COVID-19 measures, Canada, March to July 2020. Eurosurveillance, 2021, 26, .	3.9	0

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19	Fundamental limitations of contact tracing for COVID-19. Facets, 2021, 6, 1993-2001.	1.1	5
20	Network science inspires novel tree shape statistics. PLoS ONE, 2021, 16, e0259877.	1.1	7
21	Systematic comparison of coexistence in models of drug-sensitive and drug-resistant pathogen strains. Theoretical Population Biology, 2020, 133, 150-158.	0.5	11
22	Event-specific interventions to minimize COVID-19 transmission. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32038-32045.	3.3	51
23	Predicting the short-term success of human influenza virus variants with machine learning. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20200319.	1.2	13
24	A Maximum Entropy Method for the Prediction of Size Distributions. Entropy, 2020, 22, 312.	1.1	4
25	Designing ecologically optimized pneumococcal vaccines using population genomics. Nature Microbiology, 2020, 5, 473-485.	5.9	39
26	Genomic variant-identification methods may alter Mycobacterium tuberculosis transmission inferences. Microbial Genomics, 2020, 6, .	1.0	24
27	Transmission analysis of a large tuberculosis outbreak in London: a mathematical modelling study using genomic data. Microbial Genomics, 2020, 6, .	1.0	8
28	Quantifying the impact of COVID-19 control measures using a Bayesian model of physical distancing. PLoS Computational Biology, 2020, 16, e1008274.	1.5	67
29	Evidence for transmission of COVID-19 prior to symptom onset. ELife, 2020, 9, .	2.8	259
30	High-resolution mapping of tuberculosis transmission: Whole genome sequencing and phylogenetic modelling of a cohort from Valencia Region, Spain. PLoS Medicine, 2019, 16, e1002961.	3.9	62
31	Beyond the SNP Threshold: Identifying Outbreak Clusters Using Inferred Transmissions. Molecular Biology and Evolution, 2019, 36, 587-603.	3.5	121
32	Evaluating strategies for control of tuberculosis in prisons and prevention of spillover into communities: An observational and modeling study from Brazil. PLoS Medicine, 2019, 16, e1002737.	3.9	55
33	Transmission Trees on a Known Pathogen Phylogeny: Enumeration and Sampling. Molecular Biology and Evolution, 2019, 36, 1333-1343.	3.5	18
34	Phylogenies from dynamic networks. PLoS Computational Biology, 2019, 15, e1006761.	1.5	14
35	Mathematical modelling for antibiotic resistance control policy: do we know enough?. BMC Infectious Diseases, 2019, 19, 1011.	1.3	37
36	Internal migration and transmission dynamics of tuberculosis in Shanghai, China: an epidemiological, spatial, genomic analysis. Lancet Infectious Diseases, The, 2018, 18, 788-795.	4.6	85

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37	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. Wellcome Open Research, 2018, 3, 33.	0.9	42
38	Genome-based transmission modelling separates imported tuberculosis from recent transmission within an immigrant population. Microbial Genomics, 2018, 4, .	1.0	10
39	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
40	Genomic infectious disease epidemiology in partially sampled and ongoing outbreaks. Molecular Biology and Evolution, 2017, 34, msw075.	3.5	181
41	HIV-1 Full-Genome Phylogenetics of Generalized Epidemics in Sub-Saharan Africa: Impact of Missing Nucleotide Characters in Next-Generation Sequences. AIDS Research and Human Retroviruses, 2017, 33, 1083-1098.	0.5	18
42	<scp>treespace</scp>: Statistical exploration of landscapes of phylogenetic trees. Molecular Ecology Resources, 2017, 17, 1385-1392.	2.2	158
43	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. Molecular Biology and Evolution, 2017, 34, 185-203.	3.5	53
44	Host population structure and treatment frequency maintain balancing selection on drug resistance. Journal of the Royal Society Interface, 2017, 14, 20170295.	1.5	32
45	Toward Precision Healthcare: Context and Mathematical Challenges. Frontiers in Physiology, 2017, 8, 136.	1.3	28
46	Simultaneous inference of phylogenetic and transmission trees in infectious disease outbreaks. PLoS Computational Biology, 2017, 13, e1005495.	1.5	93
47	A curated genome-scale metabolic model of Bordetella pertussis metabolism. PLoS Computational Biology, 2017, 13, e1005639.	1.5	8
48	Convergent evolution and topologically disruptive polymorphisms among multidrug-resistant tuberculosis in Peru. PLoS ONE, 2017, 12, e0189838.	1.1	19
49	ClassTR: Classifying Within-Host Heterogeneity Based on Tandem Repeats with Application to Mycobacterium tuberculosis Infections. PLoS Computational Biology, 2016, 12, e1004475.	1.5	14
50	Asymptotic frequency of shapes in supercritical branching trees. Journal of Applied Probability, 2016, 53, 1143-1155.	0.4	11
51	Whole-Genome Sequencing for Routine Pathogen Surveillance in Public Health: a Population Snapshot of Invasive Staphylococcus aureus in Europe. MBio, 2016, 7, .	1.8	192
52	Antimicrobials: a global alliance for optimizing their rational use in intra-abdominal infections (AGORA). World Journal of Emergency Surgery, 2016, 11, 33.	2.1	130
53	Effects of memory on the shapes of simple outbreak trees. Scientific Reports, 2016, 6, 21159.	1.6	3
54	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

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55	Interpreting whole genome sequencing for investigating tuberculosis transmission: a systematic review. BMC Medicine, 2016, 14, 21.	2.3	117
56	Mapping Phylogenetic Trees to Reveal Distinct Patterns of Evolution. Molecular Biology and Evolution, 2016, 33, 2735-2743.	3.5	121
57	Whole-genome sequencing of Mycobacterium tuberculosis for rapid diagnostics and beyond. Lancet Respiratory Medicine,the, 2016, 4, 6-8.	5.2	13
58	Declaring a tuberculosis outbreak over with genomic epidemiology. Microbial Genomics, 2016, 2, e000060.	1.0	27
59	How could preventive therapy affect the prevalence of drug resistance? Causes and consequences. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140306.	1.8	19
60	Competition, coinfection and strain replacement in models of Bordetella pertussis. Theoretical Population Biology, 2015, 103, 84-92.	0.5	12
61	The Distribution of Fitness Costs of Resistance-Conferring Mutations Is a Key Determinant for the Future Burden of Drug-Resistant Tuberculosis: A Model-Based Analysis. Clinical Infectious Diseases, 2015, 61, S147-S154.	2.9	40
62	How competition governs whether moderate or aggressive treatment minimizes antibiotic resistance. ELife, 2015, 4, .	2.8	39
63	A phylogeny-based sampling strategy and power calculator informs genome-wide associations study design for microbial pathogens. Genome Medicine, 2014, 6, 101.	3.6	30
64	Phylogenetic tree shapes resolve disease transmission patterns. Evolution, Medicine and Public Health, 2014, 2014, 96-108.	1.1	72
65	Bayesian Inference of Infectious Disease Transmission from Whole-Genome Sequence Data. Molecular Biology and Evolution, 2014, 31, 1869-1879.	3.5	191
66	OutbreakTools: A new platform for disease outbreak analysis using the R software. Epidemics, 2014, 7, 28-34.	1.5	37
67	Errors in reported degrees and respondent driven sampling: Implications for bias. Drug and Alcohol Dependence, 2014, 142, 120-126.	1.6	33
68	How the Dynamics and Structure of Sexual Contact Networks Shape Pathogen Phylogenies. PLoS Computational Biology, 2013, 9, e1003105.	1.5	43
69	Community-Wide Isoniazid Preventive Therapy Drives Drug-Resistant Tuberculosis: A Model-Based Analysis. Science Translational Medicine, 2013, 5, 180ra49.	5.8	42
70	Mixed-Strain Mycobacterium tuberculosis Infections and the Implications for Tuberculosis Treatment and Control. Clinical Microbiology Reviews, 2012, 25, 708-719.	5.7	172
71	The dynamics of sexual contact networks: Effects on disease spread and control. Theoretical Population Biology, 2012, 81, 89-96.	0.5	29
72	Spontaneous Emergence of Multiple Drug Resistance in Tuberculosis before and during Therapy. PLoS ONE, 2011, 6, e18327.	1.1	71

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73	What is the mechanism for persistent coexistence of drug-susceptible and drug-resistant strains of *Streptococcus pneumoniae* ?. Journal of the Royal Society Interface, 2010, 7, 905-919.	1.5	83
74	Latent Coinfection and the Maintenance of Strain Diversity. Bulletin of Mathematical Biology, 2009, 71, 247-263.	0.9	30
75	No coexistence for free: Neutral null models for multistrain pathogens. Epidemics, 2009, 1, 2-13.	1.5	130
76	Propagation through dynamic networks: Degree distribution and the spread of disease. , 2009, , .		0
77	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. Wellcome Open Research, 0, 3, 33.	0.9	18