

Daniel J Wilson

List of Publications by Citations

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98
papers

9,375
citations

53
h-index

96
g-index

119
ext. papers

12,104
ext. citations

9.8
avg, IF

6.23
L-index

#	Paper	IF	Citations
98	Whole-genome sequencing to delineate Mycobacterium tuberculosis outbreaks: a retrospective observational study. <i>Lancet Infectious Diseases, The</i> , 2013 , 13, 137-46	25.5	615
97	Transforming clinical microbiology with bacterial genome sequencing. <i>Nature Reviews Genetics</i> , 2012 , 13, 601-612	30.1	508
96	Diverse sources of C. difficile infection identified on whole-genome sequencing. <i>New England Journal of Medicine</i> , 2013 , 369, 1195-205	59.2	471
95	ClonalFrameML: efficient inference of recombination in whole bacterial genomes. <i>PLoS Computational Biology</i> , 2015 , 11, e1004041	5	458
94	Whole-genome sequencing for prediction of Mycobacterium tuberculosis drug susceptibility and resistance: a retrospective cohort study. <i>Lancet Infectious Diseases, The</i> , 2015 , 15, 1193-1202	25.5	391
93	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. <i>Nature Communications</i> , 2015 , 6, 10063	17.4	348
92	Tracing the source of campylobacteriosis. <i>PLoS Genetics</i> , 2008 , 4, e1000203	6	309
91	Campylobacter genotyping to determine the source of human infection. <i>Clinical Infectious Diseases</i> , 2009 , 48, 1072-8	11.6	281
90	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018 , 379, 1403-1415	59.2	243
89	Within-host evolution of bacterial pathogens. <i>Nature Reviews Microbiology</i> , 2016 , 14, 150-62	22.2	239
88	Prediction of Staphylococcus aureus antimicrobial resistance by whole-genome sequencing. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 1182-91	9.7	218
87	Estimating diversifying selection and functional constraint in the presence of recombination. <i>Genetics</i> , 2006 , 172, 1411-25	4	210
86	Distribution of serogroups and genotypes among disease-associated and carried isolates of Neisseria meningitidis from the Czech Republic, Greece, and Norway. <i>Journal of Clinical Microbiology</i> , 2004 , 42, 5146-53	9.7	203
85	Effects of control interventions on Clostridium difficile infection in England: an observational study. <i>Lancet Infectious Diseases, The</i> , 2017 , 17, 411-421	25.5	202
84	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. <i>MBio</i> , 2016 , 7, e02162	7.8	200
83	A pilot study of rapid benchtop sequencing of Staphylococcus aureus and Clostridium difficile for outbreak detection and surveillance. <i>BMJ Open</i> , 2012 , 2,	3	197
82	Evolutionary dynamics of Staphylococcus aureus during progression from carriage to disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 4550-5	11.5	195

81	Nested Russian Doll-Like Genetic Mobility Drives Rapid Dissemination of the Carbapenem Resistance Gene blaKPC. <i>Antimicrobial Agents and Chemotherapy</i> , 2016 , 60, 3767-78	5.9	166
80	Genetic analysis of meningococci carried by children and young adults. <i>Journal of Infectious Diseases</i> , 2005 , 191, 1263-71	7	164
79	Microevolutionary analysis of Clostridium difficile genomes to investigate transmission. <i>Genome Biology</i> , 2012 , 13, R118	18.3	151
78	Assigning the source of human campylobacteriosis in New Zealand: a comparative genetic and epidemiological approach. <i>Infection, Genetics and Evolution</i> , 2009 , 9, 1311-9	4.5	149
77	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. <i>Nature Microbiology</i> , 2016 , 1, 16041	26.6	143
76	Within-host evolution of Staphylococcus aureus during asymptomatic carriage. <i>PLoS ONE</i> , 2013 , 8, e61319	3.7	141
75	Rapid evolution and the importance of recombination to the gastroenteric pathogen Campylobacter jejuni. <i>Molecular Biology and Evolution</i> , 2009 , 26, 385-97	8.3	137
74	New Routes to Phylogeography: A Bayesian Structured Coalescent Approximation. <i>PLoS Genetics</i> , 2015 , 11, e1005421	6	133
73	The influence of mutation, recombination, population history, and selection on patterns of genetic diversity in Neisseria meningitidis. <i>Molecular Biology and Evolution</i> , 2005 , 22, 562-9	8.3	128
72	Predicting the virulence of MRSA from its genome sequence. <i>Genome Research</i> , 2014 , 24, 839-49	9.7	126
71	Whole-genome sequencing to determine transmission of Neisseria gonorrhoeae: an observational study. <i>Lancet Infectious Diseases</i> , 2016 , 16, 1295-1303	25.5	118
70	Transmission of Staphylococcus aureus between health-care workers, the environment, and patients in an intensive care unit: a longitudinal cohort study based on whole-genome sequencing. <i>Lancet Infectious Diseases</i> , 2017 , 17, 207-214	25.5	113
69	Whole-genome sequencing shows that patient-to-patient transmission rarely accounts for acquisition of Staphylococcus aureus in an intensive care unit. <i>Clinical Infectious Diseases</i> , 2014 , 58, 609-18	11.6	112
68	Genome sequencing of an extended series of NDM-producing Klebsiella pneumoniae isolates from neonatal infections in a Nepali hospital characterizes the extent of community- versus hospital-associated transmission in an endemic setting. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 7347-57	5.9	98
67	Mismatch induced speciation in Salmonella: model and data. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006 , 361, 2045-53	5.8	95
66	The harmonic mean κ -value for combining dependent tests. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 1195-1200	11.5	94
65	Mobile elements drive recombination hotspots in the core genome of Staphylococcus aureus. <i>Nature Communications</i> , 2014 , 5, 3956	17.4	90
64	The distribution of bacterial doubling times in the wild. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018 , 285,	4.4	84

63	Rapid host switching in generalist <i>Campylobacter</i> strains erodes the signal for tracing human infections. <i>ISME Journal</i> , 2016 , 10, 721-9	11.9	77
62	Broad-scale recombination patterns underlying proper disjunction in humans. <i>PLoS Genetics</i> , 2009 , 5, e1000658	6	77
61	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of <i>Staphylococcus aureus</i> . <i>PLoS Biology</i> , 2015 , 13, e1002229	9.7	76
60	Dynamic linkage of COVID-19 test results between Public Health England's Second Generation Surveillance System and UK Biobank. <i>Microbial Genomics</i> , 2020 , 6,	4.4	73
59	A population genetics-phylogenetics approach to inferring natural selection in coding sequences. <i>PLoS Genetics</i> , 2011 , 7, e1002395	6	72
58	Bacterial phylogenetic reconstruction from whole genomes is robust to recombination but demographic inference is not. <i>MBio</i> , 2014 , 5, e02158	7.8	71
57	Bayesian inference of ancestral dates on bacterial phylogenetic trees. <i>Nucleic Acids Research</i> , 2018 , 46, e134	20.1	71
56	Global Genomic Epidemiology of <i>Salmonella enterica</i> Serovar Typhimurium DT104. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 2516-26	4.8	69
55	Variation of the factor H-binding protein of <i>Neisseria meningitidis</i> . <i>Microbiology (United Kingdom)</i> , 2009 , 155, 4155-4169	2.9	67
54	Insights from genomics into bacterial pathogen populations. <i>PLoS Pathogens</i> , 2012 , 8, e1002874	7.6	66
53	Detection of mixed infection from bacterial whole genome sequence data allows assessment of its role in <i>Clostridium difficile</i> transmission. <i>PLoS Computational Biology</i> , 2013 , 9, e1003059	5	65
52	SCOTTI: Efficient Reconstruction of Transmission within Outbreaks with the Structured Coalescent. <i>PLoS Computational Biology</i> , 2016 , 12, e1005130	5	64
51	Molecular and spatial epidemiology of human campylobacteriosis: source association and genotype-related risk factors. <i>Epidemiology and Infection</i> , 2010 , 138, 1372-83	4.3	62
50	Natural mutations in a <i>Staphylococcus aureus</i> virulence regulator attenuate cytotoxicity but permit bacteremia and abscess formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E3101-10	11.5	61
49	Evolution of the human immunodeficiency virus envelope gene is dominated by purifying selection. <i>Genetics</i> , 2006 , 174, 1441-53	4	58
48	Evolution of an agriculture-associated disease causing <i>Campylobacter coli</i> clade: evidence from national surveillance data in Scotland. <i>PLoS ONE</i> , 2010 , 5, e15708	3.7	56
47	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017 , 6,	8.9	55
46	Population genetic estimation of the loss of genetic diversity during horizontal transmission of HIV-1. <i>BMC Evolutionary Biology</i> , 2006 , 6, 28	3	55

45	Machine learning for classifying tuberculosis drug-resistance from DNA sequencing data. <i>Bioinformatics</i> , 2018 , 34, 1666-1671	7.2	52
44	A modified RNA-Seq approach for whole genome sequencing of RNA viruses from faecal and blood samples. <i>PLoS ONE</i> , 2013 , 8, e66129	3.7	52
43	Different selective pressures shape the evolution of Toll-like receptors in human and African great ape populations. <i>Human Molecular Genetics</i> , 2013 , 22, 4829-40	5.6	38
42	Bayesian reconstruction of transmission within outbreaks using genomic variants. <i>PLoS Computational Biology</i> , 2018 , 14, e1006117	5	37
41	Evolutionary dynamics of reveals complex genomic relationships between isolates with independent emergence of vancomycin resistance. <i>Microbial Genomics</i> , 2016 , 2,	4.4	37
40	Application of machine learning techniques to tuberculosis drug resistance analysis. <i>Bioinformatics</i> , 2019 , 35, 2276-2282	7.2	35
39	Germs, genomes and genealogies. <i>Trends in Ecology and Evolution</i> , 2005 , 20, 39-45	10.9	33
38	Combining genomics and epidemiology to analyse bi-directional transmission of in a multi-host system. <i>ELife</i> , 2019 , 8,	8.9	33
37	Whole genome sequencing and de novo assembly identifies Sydney-like variant noroviruses and recombinants during the winter 2012/2013 outbreak in England. <i>Virology Journal</i> , 2013 , 10, 335	6.1	31
36	Panton-Valentine leucocidin is the key determinant of pyomyositis in a bacterial GWAS. <i>ELife</i> , 2019 , 8,	8.9	30
35	Coalescent inference for infectious disease: meta-analysis of hepatitis C. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013 , 368, 20120314	5.8	29
34	Healthcare-associated outbreak of methicillin-resistant <i>Staphylococcus aureus</i> bacteraemia: role of a cryptic variant of an epidemic clone. <i>Journal of Hospital Infection</i> , 2014 , 86, 83-9	6.9	25
33	Genetic variability and natural selection at the ligand domain of the Duffy binding protein in Brazilian <i>Plasmodium vivax</i> populations. <i>Malaria Journal</i> , 2010 , 9, 334	3.6	24
32	SimBac: simulation of whole bacterial genomes with homologous recombination. <i>Microbial Genomics</i> , 2016 , 2,	4.4	23
31	Utilizing a combination of molecular and spatial tools to assess the effect of a public health intervention. <i>Preventive Veterinary Medicine</i> , 2011 , 102, 242-53	3.1	21
30	Whole-Genome Sequencing Reveals the Contribution of Long-Term Carriers in <i>Staphylococcus aureus</i> Outbreak Investigation. <i>Journal of Clinical Microbiology</i> , 2017 , 55, 2188-2197	9.7	19
29	The Bacterial Sequential Markov Coalescent. <i>Genetics</i> , 2017 , 206, 333-343	4	17
28	Practical Approaches for Detecting Selection in Microbial Genomes. <i>PLoS Computational Biology</i> , 2016 , 12, e1004739	5	17

27	Spatio-temporal epidemiology of <i>Campylobacter jejuni</i> enteritis, in an area of Northwest England, 2000-2002. <i>Epidemiology and Infection</i> , 2010 , 138, 1384-90	4.3	13
26	GenomeMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. <i>Molecular Biology and Evolution</i> , 2020 , 37, 2450-2460	8.3	11
25	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019 , 35, 3240-3249	7.2	10
24	On the evolution of virulence during <i>Staphylococcus aureus</i> nasal carriage. <i>Virulence</i> , 2012 , 3, 454-6	4.7	6
23	The hospital microbiome project: meeting report for the UK science and innovation network UK-USA workshop Beating the superbugs: hospital microbiome studies for tackling antimicrobial resistance October 14th 2013. <i>Standards in Genomic Sciences</i> , 2014 , 9, 12		5
22	The past, present and future of ancient bacterial DNA. <i>Microbial Genomics</i> , 2020 , 6,	4.4	5
21	Machine learning to predict the source of campylobacteriosis using whole genome data. <i>PLoS Genetics</i> , 2021 , 17, e1009436	6	4
20	Severe infections emerge from the microbiome by adaptive evolution		4
19	Genomic network analysis of environmental and livestock F-type plasmid populations. <i>ISME Journal</i> , 2021 , 15, 2322-2335	11.9	4
18	Probabilistic transmission models incorporating sequencing data for healthcare-associated <i>Clostridioides difficile</i> outperform heuristic rules and identify strain-specific differences in transmission. <i>PLoS Computational Biology</i> , 2021 , 17, e1008417	5	4
17	Evolutionary Processes Driving the Rise and Fall of ST239, a Dominant Hybrid Pathogen.. <i>MBio</i> , 2021 , e0216821	7.8	4
16	Antimicrobial resistance determinants are associated with bacteraemia and adaptation to the healthcare environment: a bacterial genome-wide association study. <i>Microbial Genomics</i> , 2021 , 7,	4.4	3
15	Incidence of Microbial Infections in English UK Biobank Participants: Comparison with the General Population		3
14	Sequential Monte Carlo with transformations. <i>Statistics and Computing</i> , 2020 , 30, 663-676	1.8	3
13	The 2021 WHO catalogue of complex mutations associated with drug resistance: A genotypic analysis.. <i>Lancet Microbe</i> , 2022 , 3, e265-e273	22.2	3
12	Draft Genome Sequences of 64 Type Strains of 50 Species and 25 Subspecies of the Genus <i>Rosenbach</i> 1884. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	2
11	Reply to Held: When is a harmonic mean ϕ -value a Bayes factor?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 5857-5858	11.5	2
10	Genome-wide association studies reveal the role of polymorphisms affecting factor H binding protein expression in host invasion by <i>Neisseria meningitidis</i> . <i>PLoS Pathogens</i> , 2021 , 17, e1009992	7.6	1

9	The Distribution of Bacterial Doubling Times in the Wild		1
8	GenomeMap: within-species genome-wide dN/dS estimation from over 10,000 genomes		1
7	The harmonic mean p-value for combining dependent tests		1
6	Reply to Goeman et al.: Trade-offs in model averaging using multilevel tests. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 23384-23385	11.5	1
5	Genome-wide association studies of global Mycobacterium tuberculosis resistance to thirteen antimicrobials in 10,228 genomes		1
4	Evolutionary processes driving the rise and fall of Staphylococcus aureus ST239, a dominant hybrid pathogen		1
3	Generalized mean ϕ -values for combining dependent tests: comparison of generalized central limit theorem and robust risk analysis. <i>Wellcome Open Research</i> , 2020 , 5, 55	4.8	0
2	Reply to Mills and Linkin. <i>Clinical Infectious Diseases</i> , 2014 , 59, 752-3	11.6	
1	Using host genetics to infer the global spread and evolutionary history of HCV subtype 3a. <i>Virus Evolution</i> , 2021 , 7, veab065	3.7	