Daniel J Wilson

List of Publications by Year
in descending order

95 papers	13,468 citations	26610 56 h-index	42364 92 g-index
119 all docs	119 docs citations	119 times ranked	14189 citing authors

#	Article	IF	Citations
1	ClonalFrameML: Efficient Inference of Recombination in Whole Bacterial Genomes. PLoS Computational Biology, 2015, 11, e1004041.	1.5	841
2	Whole-genome sequencing to delineate Mycobacterium tuberculosis outbreaks: a retrospective observational study. Lancet Infectious Diseases, The, 2013, 13, 137-146.	4.6	786
3	Transforming clinical microbiology with bacterial genome sequencing. Nature Reviews Genetics, 2012, 13, 601-612.	7.7	684
4	Diverse Sources of *C. difficile* Infection Identified on Whole-Genome Sequencing. New England Journal of Medicine, 2013, 369, 1195-1205.	13.9	595
5	Whole-genome sequencing for prediction of Mycobacterium tuberculosis drug susceptibility and resistance: a retrospective cohort study. Lancet Infectious Diseases, The, 2015, 15, 1193-1202.	4.6	553
6	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. Nature Communications, 2015, 6, 10063.	5.8	479
7	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. New England Journal of Medicine, 2018, 379, 1403-1415.	13.9	405
8	Within-host evolution of bacterial pathogens. Nature Reviews Microbiology, 2016, 14, 150-162.	13.6	373
9	Tracing the Source of Campylobacteriosis. PLoS Genetics, 2008, 4, e1000203.	1.5	365
10	*Campylobacter* Genotyping to Determine the Source of Human Infection. Clinical Infectious Diseases, 2009, 48, 1072-1078.	2.9	358
11	Prediction of Staphylococcus aureus Antimicrobial Resistance by Whole-Genome Sequencing. Journal of Clinical Microbiology, 2014, 52, 1182-1191.	1.8	303
12	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. MBio, 2016, 7, e02162.	1.8	289
13	Estimating Diversifying Selection and Functional Constraint in the Presence of Recombination. Genetics, 2006, 172, 1411-1425.	1.2	269
14	Effects of control interventions on Clostridium difficile infection in England: an observational study. Lancet Infectious Diseases, The, 2017, 17, 411-421.	4.6	269
15	Nested Russian Doll-Like Genetic Mobility Drives Rapid Dissemination of the Carbapenem Resistance Gene *bla*$_{KPC}$. Antimicrobial Agents and Chemotherapy, 2016, 60, 3767-3778.	1.4	255
16	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. Nature Microbiology, 2016, 1, 16041.	5.9	247
17	Evolutionary dynamics of *Staphylococcus aureus* during progression from carriage to disease. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4550-4555.	3.3	244
18	A pilot study of rapid benchtop sequencing of *Staphylococcus aureus* and *Clostridium difficile* for outbreak detection and surveillance. BMJ Open, 2012, 2, e001124.	0.8	228

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19	The harmonic mean <i>p</i> -value for combining dependent tests. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1195-1200.	3.3	223
20	Distribution of Serogroups and Genotypes among Disease-Associated and Carried Isolates of Neisseria meningitidis from the Czech Republic, Greece, and Norway. Journal of Clinical Microbiology, 2004, 42, 5146-5153.	1.8	222
21	New Routes to Phylogeography: A Bayesian Structured Coalescent Approximation. PLoS Genetics, 2015, 11, e1005421.	1.5	216
22	Predicting the virulence of MRSA from its genome sequence. Genome Research, 2014, 24, 839-849.	2.4	210
23	Microevolutionary analysis of Clostridium difficile genomes to investigate transmission. Genome Biology, 2012, 13, R118.	13.9	199
24	Within-Host Evolution of Staphylococcus aureus during Asymptomatic Carriage. PLoS ONE, 2013, 8, e61319.	1.1	194
25	The distribution of bacterial doubling times in the wild. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20180789.	1.2	182
26	Genetic Analysis of Meningococci Carried by Children and Young Adults. Journal of Infectious Diseases, 2005, 191, 1263-1271.	1.9	178
27	Bayesian inference of ancestral dates on bacterial phylogenetic trees. Nucleic Acids Research, 2018, 46, e134-e134.	6.5	174
28	Assigning the source of human campylobacteriosis in New Zealand: A comparative genetic and epidemiological approach. Infection, Genetics and Evolution, 2009, 9, 1311-1319.	1.0	170
29	Rapid Evolution and the Importance of Recombination to the Gastroenteric Pathogen Campylobacter jejuni. Molecular Biology and Evolution, 2009, 26, 385-397.	3.5	160
30	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. Lancet Infectious Diseases, The, 2017, 17, 207-214.	4.6	155
31	Whole-genome sequencing to determine transmission of Neisseria gonorrhoeae : an observational study. Lancet Infectious Diseases, The, 2016, 16, 1295-1303.	4.6	149
32	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. Antimicrobial Agents and Chemotherapy, 2014, 58, 7347-7357.	1.4	142
33	Whole-Genome Sequencing Shows That Patient-to-Patient Transmission Rarely Accounts for Acquisition of Staphylococcus aureus in an Intensive Care Unit. Clinical Infectious Diseases, 2014, 58, 609-618.	2.9	142
34	The Influence of Mutation, Recombination, Population History, and Selection on Patterns of Genetic Diversity in Neisseria meningitidis. Molecular Biology and Evolution, 2005, 22, 562-569.	3.5	138
35	Mobile elements drive recombination hotspots in the core genome of Staphylococcus aureus. Nature Communications, 2014, 5, 3956.	5.8	128
36	Rapid host switching in generalist <i>Campylobacter</i> strains erodes the signal for tracing human infections. ISME Journal, 2016, 10, 721-729.	4.4	123

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37	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of Staphylococcus aureus. PLoS Biology, 2015, 13, e1002229.	2.6	120
38	Dynamic linkage of COVID-19 test results between Public Health England's Second Generation Surveillance System and UK Biobank. Microbial Genomics, 2020, 6, .	1.0	120
39	Mismatch induced speciation in Salmonella : model and data. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 2045-2053.	1.8	116
40	The 2021 WHO catalogue of Mycobacterium tuberculosis complex mutations associated with drug resistance: a genotypic analysis. Lancet Microbe, The, 2022, 3, e265-e273.	3.4	114
41	Broad-Scale Recombination Patterns Underlying Proper Disjunction in Humans. PLoS Genetics, 2009, 5, e1000658.	1.5	107
42	Bacterial Phylogenetic Reconstruction from Whole Genomes Is Robust to Recombination but Demographic Inference Is Not. MBio, 2014, 5, e02158.	1.8	107
43	Global Genomic Epidemiology of Salmonella enterica Serovar Typhimurium DT104. Applied and Environmental Microbiology, 2016, 82, 2516-2526.	1.4	105
44	SCOTTI: Efficient Reconstruction of Transmission within Outbreaks with the Structured Coalescent. PLoS Computational Biology, 2016, 12, e1005130.	1.5	104
45	Natural mutations in a <i>Staphylococcus aureus</i> virulence regulator attenuate cytotoxicity but permit bacteremia and abscess formation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3101-10.	3.3	103
46	Machine learning for classifying tuberculosis drug-resistance from DNA sequencing data. Bioinformatics, 2018, 34, 1666-1671.	1.8	100
47	Severe infections emerge from commensal bacteria by adaptive evolution. ELife, 2017, 6, .	2.8	93
48	Insights from Genomics into Bacterial Pathogen Populations. PLoS Pathogens, 2012, 8, e1002874.	2.1	87
49	Variation of the factor H-binding protein of Neisseria meningitidis. Microbiology (United Kingdom), 2009, 155, 4155-4169.	0.7	79
50	A Population Genetics-Phylogenetics Approach to Inferring Natural Selection in Coding Sequences. PLoS Genetics, 2011, 7, e1002395.	1.5	78
51	Evolution of an Agriculture-Associated Disease Causing Campylobacter coli Clade: Evidence from National Surveillance Data in Scotland. PLoS ONE, 2010, 5, e15708.	1.1	75
52	Detection of Mixed Infection from Bacterial Whole Genome Sequence Data Allows Assessment of Its Role in Clostridium difficile Transmission. PLoS Computational Biology, 2013, 9, e1003059.	1.5	75
53	Molecular and spatial epidemiology of human campylobacteriosis: source association and genotype-related risk factors. Epidemiology and Infection, 2010, 138, 1372-1383.	1.0	71
54	Application of machine learning techniques to tuberculosis drug resistance analysis. Bioinformatics, 2019, 35, 2276-2282.	1.8	71

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55	Bayesian reconstruction of transmission within outbreaks using genomic variants. PLoS Computational Biology, 2018, 14, e1006117.	1.5	69
56	Population genetic estimation of the loss of genetic diversity during horizontal transmission of HIV-1. BMC Evolutionary Biology, 2006, 6, 28.	3.2	67
57	Evolution of the Human Immunodeficiency Virus Envelope Gene Is Dominated by Purifying Selection. Genetics, 2006, 174, 1441-1453.	1.2	64
58	Combining genomics and epidemiology to analyse bi-directional transmission of Mycobacterium bovis in a multi-host system. ELife, 2019, 8, .	2.8	63
59	A Modified RNA-Seq Approach for Whole Genome Sequencing of RNA Viruses from Faecal and Blood Samples. PLoS ONE, 2013, 8, e66129.	1.1	62
60	Panton–Valentine leucocidin is the key determinant of Staphylococcus aureus pyomyositis in a bacterial GWAS. ELife, 2019, 8, .	2.8	56
61	Evolutionary dynamics of Enterococcus faecium reveals complex genomic relationships between isolates with independent emergence of vancomycin resistance. Microbial Genomics, 2016, 2, .	1.0	50
62	Different selective pressures shape the evolution of Toll-like receptors in human and African great ape populations. Human Molecular Genetics, 2013, 22, 4829-4840.	1.4	49
63	Coalescent inference for infectious disease: meta-analysis of hepatitis C. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120314.	1.8	43
64	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i>. Bioinformatics, 2019, 35, 3240-3249.	1.8	38
65	Germs, genomes and genealogies. Trends in Ecology and Evolution, 2005, 20, 39-45.	4.2	37
66	Whole genome sequencing and de novo assembly identifies Sydney-like variant noroviruses and recombinants during the winter 2012/2013 outbreak in England. Virology Journal, 2013, 10, 335.	1.4	37
67	SimBac: simulation of whole bacterial genomes with homologous recombination. Microbial Genomics, 2016, 2, .	1.0	33
68	Genetic variability and natural selection at the ligand domain of the Duffy binding protein in brazilian Plasmodium vivax populations. Malaria Journal, 2010, 9, 334.	0.8	31
69	Healthcare-associated outbreak of meticillin-resistant Staphylococcus aureus bacteraemia: role of a cryptic variant of an epidemic clone. Journal of Hospital Infection, 2014, 86, 83-89.	1.4	31
70	The Bacterial Sequential Markov Coalescent. Genetics, 2017, 206, 333-343.	1.2	28
71	Whole-Genome Sequencing Reveals the Contribution of Long-Term Carriers in Staphylococcus aureus Outbreak Investigation. Journal of Clinical Microbiology, 2017, 55, 2188-2197.	1.8	26
72	GenomegaMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. Molecular Biology and Evolution, 2020, 37, 2450-2460.	3.5	25

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73	Genomic network analysis of environmental and livestock F-type plasmid populations. ISME Journal, 2021, 15, 2322-2335.	4.4	24
74	Utilizing a combination of molecular and spatial tools to assess the effect of a public health intervention. Preventive Veterinary Medicine, 2011, 102, 242-253.	0.7	22
75	Practical Approaches for Detecting Selection in Microbial Genomes. PLoS Computational Biology, 2016, 12, e1004739.	1.5	21
76	Machine learning to predict the source of campylobacteriosis using whole genome data. PLoS Genetics, 2021, 17, e1009436.	1.5	21
77	Spatio-temporal epidemiology of Campylobacter jejuni enteritis, in an area of Northwest England, 2000â€"2002. Epidemiology and Infection, 2010, 138, 1384-1390.	1.0	18
78	Niche-specific genome degradation and convergent evolution shaping Staphylococcus aureus adaptation during severe infections. ELife, 0, 11, .	2.8	18
79	Genome-wide association studies reveal the role of polymorphisms affecting factor H binding protein expression in host invasion by Neisseria meningitidis. PLoS Pathogens, 2021, 17, e1009992.	2.1	15
80	Antimicrobial resistance determinants are associated with Staphylococcus aureus bacteraemia and adaptation to the healthcare environment: a bacterial genome-wide association study. Microbial Genomics, 2021, 7, .	1.0	15
81	The past, present and future of ancient bacterial DNA. Microbial Genomics, 2020, 6, .	1.0	12
82	Probabilistic transmission models incorporating sequencing data for healthcare-associated Clostridioides difficile outperform heuristic rules and identify strain-specific differences in transmission. PLoS Computational Biology, 2021, 17, e1008417.	1.5	9
83	Evolutionary Processes Driving the Rise and Fall of <i>Staphylococcus aureus</i> ST239, a Dominant Hybrid Pathogen. MBio, 2021, 12, e0216821.	1.8	9
84	On the evolution of virulence during <i>Staphylococcus aureus</i> nasal carriage. Virulence, 2012, 3, 454-456.	1.8	8
85	Draft Genome Sequences of 64 Type Strains of 50 Species and 25 Subspecies of the Genus Staphylococcus Rosenbach 1884. Microbiology Resource Announcements, 2019, 8, .	0.3	7
86	Sequential Monte Carlo with transformations. Statistics and Computing, 2020, 30, 663-676.	0.8	7
87	The hospital microbiome project: meeting report for the UK science and innovation network UK-USA workshop â€˜beating the superbugs: hospital microbiome studies for tackling antimicrobial resistanceâ€™, October 14th 2013. Standards in Genomic Sciences, 2014, 9, .	1.5	6
88	Targeted control of pneumolysin production by a mobile genetic element in Streptococcus pneumoniae. Microbial Genomics, 2022, 8, .	1.0	5
89	Reply to Held: When is a harmonic mean <i>p</i>-value a Bayes factor?. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5857-5858.	3.3	4
90	Generalized mean p-values for combining dependent tests: comparison of generalized central limit theorem and robust risk analysis. Wellcome Open Research, 2020, 5, 55.	0.9	4

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91	Reply to Goeman et al.: Trade-offs in model averaging using multilevel tests. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23384-23385.	3.3	2
92	Promiscuous bacteria have staying power. ELife, 2017, 6, .	2.8	2
93	The genetic structure of human pathogens. , 2005, , .		0
94	Reply to Mills and Linkin. Clinical Infectious Diseases, 2014, 59, 752-753.	2.9	0
95	Using host genetics to infer the global spread and evolutionary history of HCV subtype 3a. Virus Evolution, 2021, 7, veab065.	2.2	0