

# Daniel J Wilson

## List of Publications by Year in descending order

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95  
papers

13,468  
citations

26630

56  
h-index

42399

92  
g-index

119  
all docs

119  
docs citations

119  
times ranked

14189  
citing authors

#	ARTICLE	IF	CITATIONS
1	The 2021 WHO catalogue of Mycobacterium tuberculosis complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273.	7.3	114
2	Targeted control of pneumolysin production by a mobile genetic element in <i>Streptococcus pneumoniae</i> . <i>Microbial Genomics</i> , 2022, 8, .	2.0	5
3	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.	3.2	9
4	Genomic network analysis of environmental and livestock F-type plasmid populations. <i>ISME Journal</i> , 2021, 15, 2322-2335.	9.8	24
5	Using host genetics to infer the global spread and evolutionary history of HCV subtype 3a. <i>Virus Evolution</i> , 2021, 7, veab065.	4.9	0
6	Machine learning to predict the source of campylobacteriosis using whole genome data. <i>PLoS Genetics</i> , 2021, 17, e1009436.	3.5	21
7	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.	4.7	15
8	Antimicrobial resistance determinants are associated with <i>Staphylococcus aureus</i> bacteraemia and adaptation to the healthcare environment: a bacterial genome-wide association study. <i>Microbial Genomics</i> , 2021, 7, .	2.0	15
9	Evolutionary Processes Driving the Rise and Fall of <i>Staphylococcus aureus</i> ST239, a Dominant Hybrid Pathogen. <i>MBio</i> , 2021, 12, e0216821.	4.1	9
10	Sequential Monte Carlo with transformations. <i>Statistics and Computing</i> , 2020, 30, 663-676.	1.5	7
11	GenomeMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 2450-2460.	8.9	25
12	The past, present and future of ancient bacterial DNA. <i>Microbial Genomics</i> , 2020, 6, .	2.0	12
13	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, .	2.0	120
14	Generalized mean p-values for combining dependent tests: comparison of generalized central limit theorem and robust risk analysis. <i>Wellcome Open Research</i> , 2020, 5, 55.	1.8	4
15	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019, 35, 3240-3249.	4.1	38
16	Draft Genome Sequences of 64 Type Strains of 50 Species and 25 Subspecies of the Genus <i>Staphylococcus</i> Rosenbach 1884. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	7
17	Reply to Held: When is a harmonic mean $p$ -value a Bayes factor?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5857-5858.	7.1	4
18	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.	7.1	2

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19	Application of machine learning techniques to tuberculosis drug resistance analysis. <i>Bioinformatics</i> , 2019, 35, 2276-2282.	4.1	71
20	The harmonic mean $\langle i \rangle_p$ -value for combining dependent tests. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1195-1200.	7.1	223
21	Pantonâ€“Valentine leucocidin is the key determinant of <i>Staphylococcus aureus</i> pyomyositis in a bacterial GWAS. <i>ELife</i> , 2019, 8, .	6.0	56
22	Combining genomics and epidemiology to analyse bi-directional transmission of <i>Mycobacterium bovis</i> in a multi-host system. <i>ELife</i> , 2019, 8, .	6.0	63
23	Machine learning for classifying tuberculosis drug-resistance from DNA sequencing data. <i>Bioinformatics</i> , 2018, 34, 1666-1671.	4.1	100
24	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415.	27.0	405
25	The distribution of bacterial doubling times in the wild. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180789.	2.6	182
26	Bayesian inference of ancestral dates on bacterial phylogenetic trees. <i>Nucleic Acids Research</i> , 2018, 46, e134-e134.	14.5	174
27	Bayesian reconstruction of transmission within outbreaks using genomic variants. <i>PLoS Computational Biology</i> , 2018, 14, e1006117.	3.2	69
28	Effects of control interventions on <i>Clostridium difficile</i> infection in England: an observational study. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 411-421.	9.1	269
29	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.	3.9	26
30	The Bacterial Sequential Markov Coalescent. <i>Genetics</i> , 2017, 206, 333-343.	2.9	28
31	Transmission of <i>Staphylococcus aureus</i> 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> , The, 2017, 17, 207-214.	9.1	155
32	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017, 6, .	6.0	93
33	Promiscuous bacteria have staying power. <i>ELife</i> , 2017, 6, .	6.0	2
34	SimBac: simulation of whole bacterial genomes with homologous recombination. <i>Microbial Genomics</i> , 2016, 2, .	2.0	33
35	SCOTTI: Efficient Reconstruction of Transmission within Outbreaks with the Structured Coalescent. <i>PLoS Computational Biology</i> , 2016, 12, e1005130.	3.2	104
36	Practical Approaches for Detecting Selection in Microbial Genomes. <i>PLoS Computational Biology</i> , 2016, 12, e1004739.	3.2	21

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37	Whole-genome sequencing to determine transmission of <i>Neisseria gonorrhoeae</i> : an observational study. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 1295-1303.	9.1	149
38	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.	7.1	103
39	Global Genomic Epidemiology of <i>Salmonella enterica</i> Serovar Typhimurium DT104. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2516-2526.	3.1	105
40	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. <i>Nature Microbiology</i> , 2016, 1, 16041.	13.3	247
41	Nested Russian Doll-Like Genetic Mobility Drives Rapid Dissemination of the Carbapenem Resistance Gene <i>bla</i> <sub>KPC</sub> . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3767-3778.	3.2	255
42	Within-host evolution of bacterial pathogens. <i>Nature Reviews Microbiology</i> , 2016, 14, 150-162.	28.6	373
43	Evolutionary History of the Global Emergence of the <i>Escherichia coli</i> Epidemic Clone ST131. <i>MBio</i> , 2016, 7, e02162.	4.1	289
44	Rapid host switching in generalist <i>Campylobacter</i> strains erodes the signal for tracing human infections. <i>ISME Journal</i> , 2016, 10, 721-729.	9.8	123
45	Evolutionary dynamics of <i>Enterococcus faecium</i> reveals complex genomic relationships between isolates with independent emergence of vancomycin resistance. <i>Microbial Genomics</i> , 2016, 2, .	2.0	50
46	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of <i>Staphylococcus aureus</i> . <i>PLoS Biology</i> , 2015, 13, e1002229.	5.6	120
47	Rapid antibiotic-resistance predictions from genome sequence data for <i>Staphylococcus aureus</i> and <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2015, 6, 10063.	12.8	479
48	ClonalFrameML: Efficient Inference of Recombination in Whole Bacterial Genomes. <i>PLoS Computational Biology</i> , 2015, 11, e1004041.	3.2	841
49	Whole-genome sequencing for prediction of <i>Mycobacterium tuberculosis</i> drug susceptibility and resistance: a retrospective cohort study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 1193-1202.	9.1	553
50	New Routes to Phylogeography: A Bayesian Structured Coalescent Approximation. <i>PLoS Genetics</i> , 2015, 11, e1005421.	3.5	216
51	Reply to Mills and Linkin. <i>Clinical Infectious Diseases</i> , 2014, 59, 752-753.	5.8	0
52	Bacterial Phylogenetic Reconstruction from Whole Genomes Is Robust to Recombination but Demographic Inference Is Not. <i>MBio</i> , 2014, 5, e02158.	4.1	107
53	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2014, 5, 3956.	12.8	128
54	Genome Sequencing of an Extended Series of NDM-Producing <i>Klebsiella pneumoniae</i> 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, 7347-7357.	3.2	142

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55	Whole-Genome Sequencing Shows That Patient-to-Patient Transmission Rarely Accounts for Acquisition of <i>Staphylococcus aureus</i> in an Intensive Care Unit. <i>Clinical Infectious Diseases</i> , 2014, 58, 609-618.	5.8	142
56	Prediction of <i>Staphylococcus aureus</i> Antimicrobial Resistance by Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1182-1191.	3.9	303
57	Predicting the virulence of MRSA from its genome sequence. <i>Genome Research</i> , 2014, 24, 839-849.	5.5	210
58	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, 83-89.	2.9	31
59	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, .	1.5	6
60	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.	3.4	37
61	Diverse Sources of <i>C. difficile</i> Infection Identified on Whole-Genome Sequencing. <i>New England Journal of Medicine</i> , 2013, 369, 1195-1205.	27.0	595
62	Whole-genome sequencing to delineate <i>Mycobacterium tuberculosis</i> outbreaks: a retrospective observational study. <i>Lancet Infectious Diseases</i> , The, 2013, 13, 137-146.	9.1	786
63	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.	3.2	75
64	Coalescent inference for infectious disease: meta-analysis of hepatitis C. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120314.	4.0	43
65	Different selective pressures shape the evolution of Toll-like receptors in human and African great ape populations. <i>Human Molecular Genetics</i> , 2013, 22, 4829-4840.	2.9	49
66	Within-Host Evolution of <i>Staphylococcus aureus</i> during Asymptomatic Carriage. <i>PLoS ONE</i> , 2013, 8, e61319.	2.5	194
67	A Modified RNA-Seq Approach for Whole Genome Sequencing of RNA Viruses from Faecal and Blood Samples. <i>PLoS ONE</i> , 2013, 8, e66129.	2.5	62
68	Insights from Genomics into Bacterial Pathogen Populations. <i>PLoS Pathogens</i> , 2012, 8, e1002874.	4.7	87
69	On the evolution of virulence during <i>Staphylococcus aureus</i> nasal carriage. <i>Virulence</i> , 2012, 3, 454-456.	4.4	8
70	Evolutionary dynamics of <i>Staphylococcus aureus</i> during progression from carriage to disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4550-4555.	7.1	244
71	Transforming clinical microbiology with bacterial genome sequencing. <i>Nature Reviews Genetics</i> , 2012, 13, 601-612.	16.3	684
72	A pilot study of rapid benchtop sequencing of <i>Staphylococcus aureus</i> and <i>Clostridium difficile</i> for outbreak detection and surveillance. <i>BMJ Open</i> , 2012, 2, e001124.	1.9	228

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73	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , 2012, 13, R118.	9.6	199
74	Utilizing a combination of molecular and spatial tools to assess the effect of a public health intervention. <i>Preventive Veterinary Medicine</i> , 2011, 102, 242-253.	1.9	22
75	A Population Genetics-Phylogenetics Approach to Inferring Natural Selection in Coding Sequences. <i>PLoS Genetics</i> , 2011, 7, e1002395.	3.5	78
76	Molecular and spatial epidemiology of human campylobacteriosis: source association and genotype-related risk factors. <i>Epidemiology and Infection</i> , 2010, 138, 1372-1383.	2.1	71
77	Spatio-temporal epidemiology of <i>Campylobacter jejuni</i> enteritis, in an area of Northwest England, 2000-2002. <i>Epidemiology and Infection</i> , 2010, 138, 1384-1390.	2.1	18
78	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.	2.5	75
79	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.	2.3	31
80	Rapid Evolution and the Importance of Recombination to the Gastroenteric Pathogen <i>Campylobacter jejuni</i> . <i>Molecular Biology and Evolution</i> , 2009, 26, 385-397.	8.9	160
81	Broad-Scale Recombination Patterns Underlying Proper Disjunction in Humans. <i>PLoS Genetics</i> , 2009, 5, e1000658.	3.5	107
82	Assigning the source of human campylobacteriosis in New Zealand: A comparative genetic and epidemiological approach. <i>Infection, Genetics and Evolution</i> , 2009, 9, 1311-1319.	2.3	170
83	<i>Campylobacter</i> Genotyping to Determine the Source of Human Infection. <i>Clinical Infectious Diseases</i> , 2009, 48, 1072-1078.	5.8	358
84	Variation of the factor H-binding protein of <i>Neisseria meningitidis</i> . <i>Microbiology (United Kingdom)</i> , 2009, 155, 4155-4169.	1.8	79
85	Tracing the Source of Campylobacteriosis. <i>PLoS Genetics</i> , 2008, 4, e1000203.	3.5	365
86	Population genetic estimation of the loss of genetic diversity during horizontal transmission of HIV-1. <i>BMC Evolutionary Biology</i> , 2006, 6, 28.	3.2	67
87	Evolution of the Human Immunodeficiency Virus Envelope Gene Is Dominated by Purifying Selection. <i>Genetics</i> , 2006, 174, 1441-1453.	2.9	64
88	Mismatch induced speciation in <i>Salmonella</i> : model and data. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 2045-2053.	4.0	116
89	Estimating Diversifying Selection and Functional Constraint in the Presence of Recombination. <i>Genetics</i> , 2006, 172, 1411-1425.	2.9	269
90	The genetic structure of human pathogens. , 2005, , .		0

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91	Genetic Analysis of Meningococci Carried by Children and Young Adults. <i>Journal of Infectious Diseases</i> , 2005, 191, 1263-1271.	4.0	178
92	The Influence of Mutation, Recombination, Population History, and Selection on Patterns of Genetic Diversity in <i>Neisseria meningitidis</i> . <i>Molecular Biology and Evolution</i> , 2005, 22, 562-569.	8.9	138
93	Germs, genomes and genealogies. <i>Trends in Ecology and Evolution</i> , 2005, 20, 39-45.	8.7	37
94	Distribution of Serogroups and Genotypes among Disease-Associated and Carried Isolates of <i>Neisseria meningitidis</i> from the Czech Republic, Greece, and Norway. <i>Journal of Clinical Microbiology</i> , 2004, 42, 5146-5153.	3.9	222
95	Niche-specific genome degradation and convergent evolution shaping <i>Staphylococcus aureus</i> adaptation during severe infections. <i>ELife</i> , 0, 11, .	6.0	18