

Daniel J Wilson

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	The 2021 WHO catalogue of complex mutations associated with drug resistance: A genotypic analysis.. <i>Lancet Microbe, The</i> , 2022 , 3, e265-e273	22.2	3
97	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
96	Machine learning to predict the source of campylobacteriosis using whole genome data. <i>PLoS Genetics</i> , 2021 , 17, e1009436	6	4
95	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
94	Genomic network analysis of environmental and livestock F-type plasmid populations. <i>ISME Journal</i> , 2021 , 15, 2322-2335	11.9	4
93	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
92	Using host genetics to infer the global spread and evolutionary history of HCV subtype 3a. <i>Virus Evolution</i> , 2021 , 7, veab065	3.7	
91	Evolutionary Processes Driving the Rise and Fall of ST239, a Dominant Hybrid Pathogen.. <i>MBio</i> , 2021 , e0216821	7.8	4
90	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
89	Generalized mean κ -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
88	The past, present and future of ancient bacterial DNA. <i>Microbial Genomics</i> , 2020 , 6,	4.4	5
87	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
86	Sequential Monte Carlo with transformations. <i>Statistics and Computing</i> , 2020 , 30, 663-676	1.8	3
85	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019 , 35, 3240-3249	7.2	10
84	Draft Genome Sequences of 64 Type Strains of 50 Species and 25 Subspecies of the Genus <i>Rosenbach 1884</i> . <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	2
83	Reply to Held: When is a harmonic mean κ -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
82	Panton-Valentine leucocidin is the key determinant of pyomyositis in a bacterial GWAS. <i>ELife</i> , 2019 , 8,	8.9	30

81	Combining genomics and epidemiology to analyse bi-directional transmission of in a multi-host system. <i>ELife</i> , 2019 , 8,	8.9	33
80	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
79	Application of machine learning techniques to tuberculosis drug resistance analysis. <i>Bioinformatics</i> , 2019 , 35, 2276-2282	7.2	35
78	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
77	Machine learning for classifying tuberculosis drug-resistance from DNA sequencing data. <i>Bioinformatics</i> , 2018 , 34, 1666-1671	7.2	52
76	Bayesian reconstruction of transmission within outbreaks using genomic variants. <i>PLoS Computational Biology</i> , 2018 , 14, e1006117	5	37
75	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
74	The distribution of bacterial doubling times in the wild. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018 , 285,	4.4	84
73	Bayesian inference of ancestral dates on bacterial phylogenetic trees. <i>Nucleic Acids Research</i> , 2018 , 46, e134	20.1	71
72	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
71	Whole-Genome Sequencing Reveals the Contribution of Long-Term Carriers in Staphylococcus aureus Outbreak Investigation. <i>Journal of Clinical Microbiology</i> , 2017 , 55, 2188-2197	9.7	19
70	The Bacterial Sequential Markov Coalescent. <i>Genetics</i> , 2017 , 206, 333-343	4	17
69	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, The</i> , 2017 , 17, 207-214	25.5	113
68	Severe infections emerge from commensal bacteria by adaptive evolution. <i>ELife</i> , 2017 , 6,	8.9	55
67	Rapid host switching in generalist Campylobacter strains erodes the signal for tracing human infections. <i>ISME Journal</i> , 2016 , 10, 721-9	11.9	77
66	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. <i>Nature Microbiology</i> , 2016 , 1, 16041	26.6	143
65	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
64	Within-host evolution of bacterial pathogens. <i>Nature Reviews Microbiology</i> , 2016 , 14, 150-62	22.2	239

63	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. <i>MBio</i> , 2016 , 7, e02162	7.8	200
62	Evolutionary dynamics of reveals complex genomic relationships between isolates with independent emergence of vancomycin resistance. <i>Microbial Genomics</i> , 2016 , 2,	4.4	37
61	SimBac: simulation of whole bacterial genomes with homologous recombination. <i>Microbial Genomics</i> , 2016 , 2,	4.4	23
60	SCOTTI: Efficient Reconstruction of Transmission within Outbreaks with the Structured Coalescent. <i>PLoS Computational Biology</i> , 2016 , 12, e1005130	5	64
59	Practical Approaches for Detecting Selection in Microbial Genomes. <i>PLoS Computational Biology</i> , 2016 , 12, e1004739	5	17
58	Whole-genome sequencing to determine transmission of Neisseria gonorrhoeae: an observational study. <i>Lancet Infectious Diseases, The</i> , 2016 , 16, 1295-1303	25.5	118
57	Natural mutations in a Staphylococcus aureus 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
56	Global Genomic Epidemiology of Salmonella enterica Serovar Typhimurium DT104. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 2516-26	4.8	69
55	ClonalFrameML: efficient inference of recombination in whole bacterial genomes. <i>PLoS Computational Biology</i> , 2015 , 11, e1004041	5	458
54	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
53	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of Staphylococcus aureus. <i>PLoS Biology</i> , 2015 , 13, e1002229	9.7	76
52	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. <i>Nature Communications</i> , 2015 , 6, 10063	17.4	348
51	New Routes to Phylogeography: A Bayesian Structured Coalescent Approximation. <i>PLoS Genetics</i> , 2015 , 11, e1005421	6	133
50	Predicting the virulence of MRSA from its genome sequence. <i>Genome Research</i> , 2014 , 24, 839-49	9.7	126
49	Healthcare-associated outbreak of methicillin-resistant Staphylococcus aureus bacteraemia: role of a cryptic variant of an epidemic clone. <i>Journal of Hospital Infection</i> , 2014 , 86, 83-9	6.9	25
48	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
47	Reply to Mills and Linkin. <i>Clinical Infectious Diseases</i> , 2014 , 59, 752-3	11.6	
46	Bacterial phylogenetic reconstruction from whole genomes is robust to recombination but demographic inference is not. <i>MBio</i> , 2014 , 5, e02158	7.8	71

45	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2014 , 5, 3956	17.4	90
44	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, 7347-57	5.9	98
43	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, 609-18	11.6	112
42	Prediction of <i>Staphylococcus aureus</i> antimicrobial resistance by whole-genome sequencing. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 1182-91	9.7	218
41	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
40	Diverse sources of <i>C. difficile</i> infection identified on whole-genome sequencing. <i>New England Journal of Medicine</i> , 2013 , 369, 1195-205	59.2	471
39	Whole-genome sequencing to delineate <i>Mycobacterium tuberculosis</i> outbreaks: a retrospective observational study. <i>Lancet Infectious Diseases</i> , 2013 , 13, 137-46	25.5	615
38	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
37	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
36	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
35	Within-host evolution of <i>Staphylococcus aureus</i> during asymptomatic carriage. <i>PLoS ONE</i> , 2013 , 8, e613197	19.7	141
34	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
33	Transforming clinical microbiology with bacterial genome sequencing. <i>Nature Reviews Genetics</i> , 2012 , 13, 601-612	30.1	508
32	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,	3	197
31	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , 2012 , 13, R118	18.3	151
30	Insights from genomics into bacterial pathogen populations. <i>PLoS Pathogens</i> , 2012 , 8, e1002874	7.6	66
29	On the evolution of virulence during <i>Staphylococcus aureus</i> nasal carriage. <i>Virulence</i> , 2012 , 3, 454-6	4.7	6
28	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, 4550-5	11.5	195

27	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
26	A population genetics-phylogenetics approach to inferring natural selection in coding sequences. <i>PLoS Genetics</i> , 2011 , 7, e1002395	6	72
25	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
24	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
23	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
22	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
21	Rapid evolution and the importance of recombination to the gastroenteric pathogen <i>Campylobacter jejuni</i> . <i>Molecular Biology and Evolution</i> , 2009 , 26, 385-97	8.3	137
20	Broad-scale recombination patterns underlying proper disjunction in humans. <i>PLoS Genetics</i> , 2009 , 5, e1000658	6	77
19	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
18	<i>Campylobacter</i> genotyping to determine the source of human infection. <i>Clinical Infectious Diseases</i> , 2009 , 48, 1072-8	11.6	281
17	Variation of the factor H-binding protein of <i>Neisseria meningitidis</i> . <i>Microbiology (United Kingdom)</i> , 2009 , 155, 4155-4169	2.9	67
16	Tracing the source of campylobacteriosis. <i>PLoS Genetics</i> , 2008 , 4, e1000203	6	309
15	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
14	Evolution of the human immunodeficiency virus envelope gene is dominated by purifying selection. <i>Genetics</i> , 2006 , 174, 1441-53	4	58
13	Mismatch induced speciation in <i>Salmonella</i> : model and data. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006 , 361, 2045-53	5.8	95
12	Estimating diversifying selection and functional constraint in the presence of recombination. <i>Genetics</i> , 2006 , 172, 1411-25	4	210
11	Germs, genomes and genealogies. <i>Trends in Ecology and Evolution</i> , 2005 , 20, 39-45	10.9	33
10	Genetic analysis of meningococci carried by children and young adults. <i>Journal of Infectious Diseases</i> , 2005 , 191, 1263-71	7	164

9	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, 562-9	8.3	128
8	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, 5146-53	9.7	203
7	The Distribution of Bacterial Doubling Times in the Wild		1
6	Severe infections emerge from the microbiome by adaptive evolution		4
5	Incidence of Microbial Infections in English UK Biobank Participants: Comparison with the General Population	3	
4	GenomeMap: within-species genome-wide dN/dS estimation from over 10,000 genomes		1
3	The harmonic mean p-value for combining dependent tests		1
2	Genome-wide association studies of global <i>Mycobacterium tuberculosis</i> resistance to thirteen antimicrobials in 10,228 genomes		1
1	Evolutionary processes driving the rise and fall of <i>Staphylococcus aureus</i> ST239, a dominant hybrid pathogen		1