

# Xavier Didelot

## List of Publications by Citations

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165  
papers

10,777  
citations

57  
h-index

102  
g-index

208  
ext. papers

13,896  
ext. citations

8.8  
avg, IF

6.52  
L-index

#	Paper	IF	Citations
165	Inference of bacterial microevolution using multilocus sequence data. <i>Genetics</i> , <b>2007</b> , 175, 1251-66	4	550
164	Transforming clinical microbiology with bacterial genome sequencing. <i>Nature Reviews Genetics</i> , <b>2012</b> , 13, 601-612	30.1	508
163	Diverse sources of <i>C. difficile</i> infection identified on whole-genome sequencing. <i>New England Journal of Medicine</i> , <b>2013</b> , 369, 1195-205	59.2	471
162	ClonalFrameML: efficient inference of recombination in whole bacterial genomes. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004041	5	458
161	Multilocus sequence typing as a replacement for serotyping in <i>Salmonella enterica</i> . <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1002776	7.6	412
160	A comparison of homologous recombination rates in bacteria and archaea. <i>ISME Journal</i> , <b>2009</b> , 3, 199-208	1.9	394
159	The global distribution and spread of the mobilized colistin resistance gene <i>mcr-1</i> . <i>Nature Communications</i> , <b>2018</b> , 9, 1179	17.4	268
158	Impact of recombination on bacterial evolution. <i>Trends in Microbiology</i> , <b>2010</b> , 18, 315-22	12.4	244
157	Within-host evolution of bacterial pathogens. <i>Nature Reviews Microbiology</i> , <b>2016</b> , 14, 150-62	22.2	239
156	Effects of control interventions on <i>Clostridium difficile</i> infection in England: an observational study. <i>Lancet Infectious Diseases</i> , <b>2017</b> , 17, 411-421	25.5	202
155	Evolutionary History of the Global Emergence of the <i>Escherichia coli</i> Epidemic Clone ST131. <i>MBio</i> , <b>2016</b> , 7, e02162	7.8	200
154	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> , <b>2012</b> , 2,	3	197
153	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> , <b>2012</b> , 109, 4550-5	11.5	195
152	<i>Helicobacter pylori</i> genome evolution during human infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 5033-8	11.5	183
151	Genome-wide association study identifies vitamin B5 biosynthesis as a host specificity factor in <i>Campylobacter</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 11923-7	11.5	178
150	Measurably evolving pathogens in the genomic era. <i>Trends in Ecology and Evolution</i> , <b>2015</b> , 30, 306-13	10.9	168
149	Maternal high fat diet during pregnancy and lactation alters hepatic expression of insulin like growth factor-2 and key microRNAs in the adult offspring. <i>BMC Genomics</i> , <b>2009</b> , 10, 478	4.5	156

148	Patterns of gene flow define species of thermophilic Archaea. <i>PLoS Biology</i> , <b>2012</b> , 10, e1001265	9.7	152
147	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , <b>2012</b> , 13, R118	18.3	151
146	Bayesian reconstruction of disease outbreaks by combining epidemiologic and genomic data. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003457	5	142
145	Within-host evolution of <i>Staphylococcus aureus</i> during asymptomatic carriage. <i>PLoS ONE</i> , <b>2013</b> , 8, e61319	3.7	141
144	Bayesian inference of infectious disease transmission from whole-genome sequence data. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 1869-79	8.3	138
143	Clinical <i>Clostridium difficile</i> : clonality and pathogenicity locus diversity. <i>PLoS ONE</i> , <b>2011</b> , 6, e19993	3.7	131
142	Genomic characterization of the <i>Bacillus cereus</i> sensu lato species: backdrop to the evolution of <i>Bacillus anthracis</i> . <i>Genome Research</i> , <b>2012</b> , 22, 1512-24	9.7	128
141	Evolutionary history of the <i>Clostridium difficile</i> pathogenicity locus. <i>Genome Biology and Evolution</i> , <b>2014</b> , 6, 36-52	3.9	123
140	Inference of homologous recombination in bacteria using whole-genome sequences. <i>Genetics</i> , <b>2010</b> , 186, 1435-49	4	118
139	Microevolution of <i>Helicobacter pylori</i> during prolonged infection of single hosts and within families. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001036	6	118
138	Whole-genome sequencing to determine transmission of <i>Neisseria gonorrhoeae</i> : an observational study. <i>Lancet Infectious Diseases</i> , <b>2016</b> , 16, 1295-1303	25.5	118
137	After the bottleneck: Genome-wide diversification of the <i>Mycobacterium tuberculosis</i> complex by mutation, recombination, and natural selection. <i>Genome Research</i> , <b>2012</b> , 22, 721-34	9.7	115
136	Genomic Infectious Disease Epidemiology in Partially Sampled and Ongoing Outbreaks. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 997-1007	8.3	112
135	<i>Klebsiella pneumoniae</i> carbapenemase (KPC)-producing <i>K. pneumoniae</i> at a single institution: insights into endemicity from whole-genome sequencing. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2015</b> , 59, 1656-63	5.9	107
134	Recombination and population structure in <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002191	6	105
133	Evolution of pathogenicity in the <i>Bacillus cereus</i> group. <i>Systematic and Applied Microbiology</i> , <b>2009</b> , 32, 81-90	4.2	103
132	The ubiquitous nature of <i>Listeria monocytogenes</i> clones: a large-scale Multilocus Sequence Typing study. <i>Environmental Microbiology</i> , <b>2014</b> , 16, 405-16	5.2	102
131	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> , <b>2014</b> , 58, 7317-57	5.9	98

130	Progressive genome-wide introgression in agricultural <i>Campylobacter coli</i> . <i>Molecular Ecology</i> , <b>2013</b> , 22, 1051-64	5.7	98
129	A bimodal pattern of relatedness between the <i>Salmonella Paratyphi A</i> and <i>Typhi</i> genomes: convergence or divergence by homologous recombination?. <i>Genome Research</i> , <b>2007</b> , 17, 61-8	9.7	98
128	A phylogenetic method to perform genome-wide association studies in microbes that accounts for population structure and recombination. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1005958	5	96
127	Impact of homologous and non-homologous recombination in the genomic evolution of <i>Escherichia coli</i> . <i>BMC Genomics</i> , <b>2012</b> , 13, 256	4.5	95
126	Mismatch induced speciation in <i>Salmonella</i> : model and data. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2006</b> , 361, 2045-53	5.8	95
125	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , <b>2014</b> , 5, 3956	17.4	90
124	Evolution and population structure of <i>Salmonella enterica</i> serovar Newport. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 6465-76	3.5	87
123	Closely related <i>Campylobacter jejuni</i> strains from different sources reveal a generalist rather than a specialist lifestyle. <i>BMC Genomics</i> , <b>2011</b> , 12, 584	4.5	86
122	Genomic evolution and transmission of <i>Helicobacter pylori</i> in two South African families. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 13880-5	11.5	80
121	Lineage specific recombination rates and microevolution in <i>Listeria monocytogenes</i> . <i>BMC Evolutionary Biology</i> , <b>2008</b> , 8, 277	3	78
120	Population genomics of <i>Chlamydia trachomatis</i> : insights on drift, selection, recombination, and population structure. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 3933-46	8.3	74
119	Recombinational switching of the <i>Clostridium difficile</i> S-layer and a novel glycosylation gene cluster revealed by large-scale whole-genome sequencing. <i>Journal of Infectious Diseases</i> , <b>2013</b> , 207, 675-86	7.86	72
118	Disease-associated genotypes of the commensal skin bacterium <i>Staphylococcus epidermidis</i> . <i>Nature Communications</i> , <b>2018</b> , 9, 5034	17.4	71
117	Bayesian inference of ancestral dates on bacterial phylogenetic trees. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, e134	20.1	71
116	Comparative analysis of <i>Chlamydia psittaci</i> genomes reveals the recent emergence of a pathogenic lineage with a broad host range. <i>MBio</i> , <b>2013</b> , 4,	7.8	68
115	Epidemic Clones, Oceanic Gene Pools, and Eco-LD in the Free Living Marine Pathogen <i>Vibrio parahaemolyticus</i> . <i>Molecular Biology and Evolution</i> , <b>2015</b> , 32, 1396-410	8.3	63
114	The application of genomics to tracing bacterial pathogen transmission. <i>Current Opinion in Microbiology</i> , <b>2015</b> , 23, 62-7	7.9	63
113	Population structure of the <i>Yersinia pseudotuberculosis</i> complex according to multilocus sequence typing. <i>Environmental Microbiology</i> , <b>2011</b> , 13, 3114-27	5.2	63

112	Genome-wide association of functional traits linked with <i>Campylobacter jejuni</i> survival from farm to fork. <i>Environmental Microbiology</i> , <b>2017</b> , 19, 361-380	5.2	61
111	Likelihood-free estimation of model evidence. <i>Bayesian Analysis</i> , <b>2011</b> , 6,	2.3	60
110	The role of China in the global spread of the current cholera pandemic. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005072		58
109	Population structure of <i>Neisseria gonorrhoeae</i> based on whole genome data and its relationship with antibiotic resistance. <i>PeerJ</i> , <b>2015</b> , 3, e806	3.1	58
108	Interplay of recombination and selection in the genomes of <i>Chlamydia trachomatis</i> . <i>Biology Direct</i> , <b>2011</b> , 6, 28	7.2	57
107	Simultaneous inference of phylogenetic and transmission trees in infectious disease outbreaks. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005495	5	55
106	A combined case-control and molecular source attribution study of human <i>Campylobacter</i> infections in Germany, 2011-2014. <i>Scientific Reports</i> , <b>2017</b> , 7, 5139	4.9	54
105	Worldwide Population Structure, Long-Term Demography, and Local Adaptation of <i>Helicobacter pylori</i> . <i>Genetics</i> , <b>2015</b> , 200, 947-63	4	50
104	Efficient inference of recombination hot regions in bacterial genomes. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 1593-605	8.3	49
103	Inference of person-to-person transmission of COVID-19 reveals hidden super-spreading events during the early outbreak phase. <i>Nature Communications</i> , <b>2020</b> , 11, 5006	17.4	49
102	Whole genome sequencing in the prevention and control of <i>Staphylococcus aureus</i> infection. <i>Journal of Hospital Infection</i> , <b>2013</b> , 83, 14-21	6.9	46
101	Within-host evolution of <i>Helicobacter pylori</i> shaped by niche-specific adaptation, intragastric migrations and selective sweeps. <i>Nature Communications</i> , <b>2019</b> , 10, 2273	17.4	43
100	<i>Burkholderia pseudomallei</i> sequencing identifies genomic clades with distinct recombination, accessory, and epigenetic profiles. <i>Genome Research</i> , <b>2015</b> , 25, 129-41	9.7	43
99	Epidemiological analysis of the Eyam plague outbreak of 1665-1666. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2016</b> , 283,	4.4	43
98	Pneumococcal Capsule Synthesis Locus <i>cps</i> as Evolutionary Hotspot with Potential to Generate Novel Serotypes by Recombination. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 2537-2554	8.3	42
97	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 185-203	8.3	41
96	The Landscape of Realized Homologous Recombination in Pathogenic Bacteria. <i>Molecular Biology and Evolution</i> , <b>2016</b> , 33, 456-71	8.3	40
95	Impact of HIV co-infection on the evolution and transmission of multidrug-resistant tuberculosis. <i>ELife</i> , <b>2016</b> , 5,	8.9	39

94	Genomic Analysis and Comparison of Two Gonorrhea Outbreaks. <i>MBio</i> , <b>2016</b> , 7,	7.8	39
93	Progressive genomic convergence of two <i>Helicobacter pylori</i> strains during mixed infection of a patient with chronic gastritis. <i>Gut</i> , <b>2015</b> , 64, 554-61	19.2	38
92	Modeling the Growth and Decline of Pathogen Effective Population Size Provides Insight into Epidemic Dynamics and Drivers of Antimicrobial Resistance. <i>Systematic Biology</i> , <b>2018</b> , 67, 719-728	8.4	38
91	Genome-wide analysis of chromosomal import patterns after natural transformation of <i>Helicobacter pylori</i> . <i>Nature Communications</i> , <b>2016</b> , 7, 11995	17.4	35
90	Emergence of methicillin resistance predates the clinical use of antibiotics.. <i>Nature</i> , <b>2022</b> ,	50.4	33
89	A Role for Tetracycline Selection in Recent Evolution of Agriculture-Associated PCR Ribotype 078. <i>MBio</i> , <b>2019</b> , 10,	7.8	32
88	OutbreakTools: a new platform for disease outbreak analysis using the R software. <i>Epidemics</i> , <b>2014</b> , 7, 28-34	5.1	32
87	Genomic surveillance of <i>Neisseria gonorrhoeae</i> to investigate the distribution and evolution of antimicrobial-resistance determinants and lineages. <i>Microbial Genomics</i> , <b>2018</b> , 4,	4.4	32
86	Genealogical typing of <i>Neisseria meningitidis</i> . <i>Microbiology (United Kingdom)</i> , <b>2009</b> , 155, 3176-3186	2.9	31
85	A barrier to homologous recombination between sympatric strains of the cooperative soil bacterium <i>Myxococcus xanthus</i> . <i>ISME Journal</i> , <b>2016</b> , 10, 2468-77	11.9	31
84	Estimating the fitness cost and benefit of cefixime resistance in <i>Neisseria gonorrhoeae</i> to inform prescription policy: A modelling study. <i>PLoS Medicine</i> , <b>2017</b> , 14, e1002416	11.6	30
83	Mosaic DNA imports with interspersions of recipient sequence after natural transformation of <i>Helicobacter pylori</i> . <i>PLoS ONE</i> , <b>2008</b> , 3, e3797	3.7	30
82	outbreaker2: a modular platform for outbreak reconstruction. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 363	3.6	30
81	The Population Structure of <i>Pseudomonas aeruginosa</i> Is Characterized by Genetic Isolation of <i>exoU+</i> and <i>exoS+</i> Lineages. <i>Genome Biology and Evolution</i> , <b>2019</b> , 11, 1780-1796	3.9	29
80	Inference of the properties of the recombination process from whole bacterial genomes. <i>Genetics</i> , <b>2014</b> , 196, 253-65	4	29
79	Evolution and Transmission of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Expressing the <i>blaOXA-232</i> Gene During an Institutional Outbreak Associated With Endoscopic Retrograde Cholangiopancreatography. <i>Clinical Infectious Diseases</i> , <b>2017</b> , 64, 894-901	11.6	28
78	The complexity and diversity of the Pathogenicity Locus in <i>Clostridium difficile</i> clade 5. <i>Genome Biology and Evolution</i> , <b>2014</b> , 6, 3159-70	3.9	27
77	Range Expansion and the Origin of USA300 North American Epidemic Methicillin-Resistant. <i>MBio</i> , <b>2018</b> , 9,	7.8	26

76	Role of energy sensor TlpD of <i>Helicobacter pylori</i> in gerbil colonization and genome analyses after adaptation in the gerbil. <i>Infection and Immunity</i> , <b>2013</b> , 81, 3534-51	3.7	26
75	Inferring genomic flux in bacteria. <i>Genome Research</i> , <b>2009</b> , 19, 306-17	9.7	26
74	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> , <b>2014</b> , 86, 83-9	6.9	25
73	SimBac: simulation of whole bacterial genomes with homologous recombination. <i>Microbial Genomics</i> , <b>2016</b> , 2,	4.4	23
72	Bayesian Inference of the Evolution of a Phenotype Distribution on a Phylogenetic Tree. <i>Genetics</i> , <b>2016</b> , 204, 89-98	4	21
71	Chlamydiaceae Genomics Reveals Interspecies Admixture and the Recent Evolution of <i>Chlamydia abortus</i> Infecting Lower Mammalian Species and Humans. <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 3070-84	3.9	21
70	Local genes for local bacteria: Evidence of allopatry in the genomes of transatlantic <i>Campylobacter</i> populations. <i>Molecular Ecology</i> , <b>2017</b> , 26, 4497-4508	5.7	20
69	Tetracycline Selective Pressure and Homologous Recombination Shape the Evolution of <i>Chlamydia suis</i> : A Recently Identified Zoonotic Pathogen. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 2613-23	3.9	20
68	Epidemiological Trends of Antibiotic Resistant Gonorrhoea in the United Kingdom. <i>Antibiotics</i> , <b>2018</b> , 7,	4.9	19
67	Declaring a tuberculosis outbreak over with genomic epidemiology. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000060	4.4	19
66	<i>Clostridium difficile</i> trehalose metabolism variants are common and not associated with adverse patient outcomes when variably present in the same lineage. <i>EBioMedicine</i> , <b>2019</b> , 43, 347-355	8.8	18
65	A Bayesian approach to inferring the phylogenetic structure of communities from metagenomic data. <i>Genetics</i> , <b>2014</b> , 197, 925-37	4	18
64	Rapid Detection of Mobilized Colistin Resistance using a Nucleic Acid Based Lab-on-a-Chip Diagnostic System. <i>Scientific Reports</i> , <b>2020</b> , 10, 8448	4.9	18
63	Microevolution of <i>Neisseria lactamica</i> during nasopharyngeal colonisation induced by controlled human infection. <i>Nature Communications</i> , <b>2018</b> , 9, 4753	17.4	18
62	Bidirectional genomic exchange between <i>Helicobacter pylori</i> strains from a family in Coventry, United Kingdom. <i>International Journal of Medical Microbiology</i> , <b>2014</b> , 304, 1135-46	3.7	17
61	Whole genome sequencing of reveals transmission clusters involving patients of mixed HIV serostatus. <i>Sexually Transmitted Infections</i> , <b>2018</b> , 94, 138-143	2.8	15
60	The nucleotide excision repair (NER) system of <i>Helicobacter pylori</i> : role in mutation prevention and chromosomal import patterns after natural transformation. <i>BMC Microbiology</i> , <b>2012</b> , 12, 67	4.5	15
59	SimMLST: simulation of multi-locus sequence typing data under a neutral model. <i>Bioinformatics</i> , <b>2009</b> , 25, 1442-4	7.2	15

58	Major genetic discontinuity and novel toxigenic species in taxonomy. <i>ELife</i> , <b>2021</b> , 10,	8.9	15
57	Dynamics of genome change among Legionella species. <i>Scientific Reports</i> , <b>2016</b> , 6, 33442	4.9	14
56	Re-emergence of methicillin susceptibility in a resistant lineage of Staphylococcus aureus. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2017</b> , 72, 1285-1288	5.1	13
55	Rapid phenotypic evolution in multidrug-resistant Klebsiella pneumoniae hospital outbreak strains. <i>Microbial Genomics</i> , <b>2019</b> , 5,	4.4	13
54	Population genomics and antimicrobial resistance in Corynebacterium diphtheriae. <i>Genome Medicine</i> , <b>2020</b> , 12, 107	14.4	11
53	Emerging phylogenetic structure of the SARS-CoV-2 pandemic. <i>Virus Evolution</i> , <b>2020</b> , 6, veaa082	3.7	11
52	Framework for DNA Quantification and Outlier Detection Using Multidimensional Standard Curves. <i>Analytical Chemistry</i> , <b>2019</b> , 91, 7426-7434	7.8	10
51	Comparisons of infant Escherichia coli isolates link genomic profiles with adaptation to the ecological niche. <i>BMC Genomics</i> , <b>2013</b> , 14, 81	4.5	10
50	Why panmictic bacteria are rare		10
49	Testing for gonorrhoea should routinely include the pharynx. <i>Lancet Infectious Diseases</i> , <b>2018</b> , 18, 716-717	25.5	10
48	Recombination shapes genome architecture in an organism from the archaeal domain. <i>Genome Biology and Evolution</i> , <b>2014</b> , 6, 170-8	3.9	9
47	Molecular signatures identify a candidate target of balancing selection in an arcD-like gene of Staphylococcus epidermidis. <i>Journal of Molecular Evolution</i> , <b>2012</b> , 75, 43-54	3.1	9
46	The speciation and hybridization history of the genus. <i>Microbial Genomics</i> , <b>2019</b> , 5,	4.4	9
45	Model-based analysis of an outbreak of bubonic plague in Cairo in 1801. <i>Journal of the Royal Society Interface</i> , <b>2017</b> , 14,	4.1	8
44	Genomic Investigation of a Outbreak Involving Prison and Community Cases in Florida, United States. <i>American Journal of Tropical Medicine and Hygiene</i> , <b>2018</b> , 99, 867-874	3.2	8
43	Additive Uncorrelated Relaxed Clock Models for the Dating of Genomic Epidemiology Phylogenies. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 307-317	8.3	8
42	Phylogenomics reveals the basis of adaptation of Pseudorhizobium species to extreme environments and supports a taxonomic revision of the genus. <i>Systematic and Applied Microbiology</i> , <b>2021</b> , 44, 126165	4.2	8
41	A dynamic power-law sexual network model of gonorrhoea outbreaks. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1006748	5	7



40	Genomic epidemiology of <i>Vibrio cholerae</i> reveals the regional and global spread of two epidemic non-toxicogenic lineages. <i>PLoS Neglected Tropical Diseases</i> , <b>2020</b> , 14, e0008046	4.8	6
39	Sudden emergence of a clade with reduced susceptibility to extended-spectrum cephalosporins, Norway. <i>Microbial Genomics</i> , <b>2020</b> , 6,	4.4	6
38	A role for tetracycline selection in the evolution of <i>Clostridium difficile</i> PCR-ribotype 078		6
37	Genomic Epidemiology Analysis of Infectious Disease Outbreaks Using TransPhylo. <i>Current Protocols</i> , <b>2021</b> , 1, e60		6
36	Reconstructing the Ancestral Relationships Between Bacterial Pathogen Genomes. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1535, 109-137	1.4	5
35	Identification of Hidden Population Structure in Time-Scaled Phylogenies. <i>Systematic Biology</i> , <b>2020</b> , 69, 884-896	8.4	5
34	Y92-1009 complete genome sequence. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 41		5
33	Sequence-Based Analysis of Bacterial Population Structures <b>2010</b> , 37-60		5
32	Emerging phylogenetic structure of the SARS-CoV-2 pandemic		5
31	Hospital outbreak of carbapenem-resistant Enterobacteriales associated with an OXA-48 plasmid carried mostly by <i>Escherichia coli</i> ST399		5
30	Assessing the extent of community spread caused by mink-derived SARS-CoV-2 variants. <i>Innovation(China)</i> , <b>2021</b> , 2, 100128	17.8	5
29	Machine-learning-assisted selection of antibiotic prescription. <i>Nature Medicine</i> , <b>2019</b> , 25, 1033-1034	50.5	4
28	Automated reconstruction of all gene histories in large bacterial pangenome datasets and search for co-evolved gene modules with Pantagruel		4
27	Genomic signatures of pre-resistance in <i>Mycobacterium tuberculosis</i> .. <i>Nature Communications</i> , <b>2021</b> , 12, 7312	17.4	3
26	Comparative genomics of toxinotypes identifies module-based toxin gene evolution. <i>Microbial Genomics</i> , <b>2020</b> , 6,	4.4	3
25	New method to reconstruct phylogenetic and transmission trees with sequence data from infectious disease outbreaks		3
24	A phylogenetic method to perform genome-wide association studies in microbes that accounts for population structure and recombination		3
23	Computational Methods in Microbial Population Genomics. <i>Population Genomics</i> , <b>2017</b> , 3-29	1.4	2

22	Formal Comment to Pettengill: The Time to Most Recent Common Ancestor Does Not (Usually) Approximate the Date of Divergence. <i>PLoS ONE</i> , <b>2015</b> , 10, e0134435	3.7	2
21	SARS-CoV-2 transmissibility compared between variants of concern and vaccination status.. <i>Briefings in Bioinformatics</i> , <b>2022</b> ,	13.4	2
20	The <i>Clostridioides difficile</i> species problem: global phylogenomic analysis uncovers three ancient, toxigenic, genomospecies		2
19	Assessment of the Potential of Vaccination to Combat Antibiotic Resistance in Gonorrhoea: A Modeling Analysis to Determine Preferred Product Characteristics. <i>Clinical Infectious Diseases</i> , <b>2020</b> , 71, 1912-1919	11.6	2
18	Public health impact and cost-effectiveness of gonorrhoea vaccination: an integrated transmission-dynamic health-economic modelling analysis.. <i>Lancet Infectious Diseases, The</i> , <b>2022</b> ,	25.5	2
17	<i>Clostridium difficile</i> in England: can we stop washing our hands? - AuthorsSreply. <i>Lancet Infectious Diseases, The</i> , <b>2017</b> , 17, 478-479	25.5	1
16	A Duality Identity between a Model of Bacterial Recombination and the WrightFisher Diffusion. <i>Institute of Mathematical Statistics Collections</i> , <b>2008</b> , 315-324		1
15	Detection of a bedaquiline / clofazimine resistance reservoir in <i>Mycobacterium tuberculosis</i> predating the antibiotic era		1
14	The global distribution and spread of the mobilized colistin resistance gene <i>mcr-1</i>		1
13	Bacterial Microevolution and the Pangenome <b>2020</b> , 129-149		1
12	Quantifying the fitness benefit and cost of cefixime resistance in <i>Neisseria gonorrhoeae</i> to inform prescription policy		1
11	The sudden emergence of a <i>Neisseria gonorrhoeae</i> strain with reduced susceptibility to extended-spectrum cephalosporins, Norway		1
10	Phylogenomic analysis reveals the basis of adaptation of <i>Pseudorhizobium</i> species to extreme environments		1
9	Phylogenetic Methods for Genome-Wide Association Studies in Bacteria. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2242, 205-220	1.4	1
8	Heroic sacrifice or tragic mistake? Revisiting the Eyam plague, 350 years on. <i>Significance</i> , <b>2016</b> , 13, 20-25	0.5	0
7	Bacterial Recombination in vivo	23-46	
6	Genomic epidemiology of <i>Vibrio cholerae</i> reveals the regional and global spread of two epidemic non-toxigenic lineages <b>2020</b> , 14, e0008046		
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- 3 Genomic epidemiology of *Vibrio cholerae* reveals the regional and global spread of two epidemic non-toxigenic lineages **2020**, 14, e0008046
- 2 Genomic epidemiology of *Vibrio cholerae* reveals the regional and global spread of two epidemic non-toxigenic lineages **2020**, 14, e0008046
- 1 Genomic epidemiology of *Vibrio cholerae* reveals the regional and global spread of two epidemic non-toxigenic lineages **2020**, 14, e0008046