

Xavier Didelot

List of Publications by Year in Descending Order

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Version: 2024-04-25

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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.

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	Emergence of methicillin resistance predates the clinical use of antibiotics.. <i>Nature</i> , 2022 ,	50.4	33
164	SARS-CoV-2 transmissibility compared between variants of concern and vaccination status.. <i>Briefings in Bioinformatics</i> , 2022 ,	13.4	2
163	Public health impact and cost-effectiveness of gonorrhoea vaccination: an integrated transmission-dynamic health-economic modelling analysis.. <i>Lancet Infectious Diseases, The</i> , 2022 ,	25.5	2
162	Genomic signatures of pre-resistance in Mycobacterium tuberculosis.. <i>Nature Communications</i> , 2021 , 12, 7312	17.4	3
161	Major genetic discontinuity and novel toxigenic species in taxonomy. <i>ELife</i> , 2021 , 10,	8.9	15
160	Additive Uncorrelated Relaxed Clock Models for the Dating of Genomic Epidemiology Phylogenies. <i>Molecular Biology and Evolution</i> , 2021 , 38, 307-317	8.3	8
159	Phylogenetic Methods for Genome-Wide Association Studies in Bacteria. <i>Methods in Molecular Biology</i> , 2021 , 2242, 205-220	1.4	1
158	Genomic Epidemiology Analysis of Infectious Disease Outbreaks Using TransPhylo. <i>Current Protocols</i> , 2021 , 1, e60		6
157	Assessing the extent of community spread caused by mink-derived SARS-CoV-2 variants. <i>Innovation(China)</i> , 2021 , 2, 100128	17.8	5
156	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> , 2021 , 44, 126165	4.2	8
155	Identification of Hidden Population Structure in Time-Scaled Phylogenies. <i>Systematic Biology</i> , 2020 , 69, 884-896	8.4	5
154	Genomic epidemiology of Vibrio cholerae reveals the regional and global spread of two epidemic non-toxigenic lineages. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008046	4.8	6
153	Comparative genomics of toxinotypes identifies module-based toxin gene evolution. <i>Microbial Genomics</i> , 2020 , 6,	4.4	3
152	Bacterial Microevolution and the Pangenome 2020 , 129-149		1
151	Rapid Detection of Mobilized Colistin Resistance using a Nucleic Acid Based Lab-on-a-Chip Diagnostic System. <i>Scientific Reports</i> , 2020 , 10, 8448	4.9	18
150	Sudden emergence of a clade with reduced susceptibility to extended-spectrum cephalosporins, Norway. <i>Microbial Genomics</i> , 2020 , 6,	4.4	6
149	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> , 2020 , 71, 1912-1919	11.6	2

148	Inference of person-to-person transmission of COVID-19 reveals hidden super-spreading events during the early outbreak phase. <i>Nature Communications</i> , 2020 , 11, 5006	17.4	49
147	Population genomics and antimicrobial resistance in <i>Corynebacterium diphtheriae</i> . <i>Genome Medicine</i> , 2020 , 12, 107	14.4	11
146	Emerging phylogenetic structure of the SARS-CoV-2 pandemic. <i>Virus Evolution</i> , 2020 , 6, veaa082	3.7	11
145	Genomic epidemiology of <i>Vibrio cholerae</i> reveals the regional and global spread of two epidemic non-toxigenic lineages 2020 , 14, e0008046		
144	Genomic epidemiology of <i>Vibrio cholerae</i> reveals the regional and global spread of two epidemic non-toxigenic lineages 2020 , 14, e0008046		
143	Genomic epidemiology of <i>Vibrio cholerae</i> reveals the regional and global spread of two epidemic non-toxigenic lineages 2020 , 14, e0008046		
142	Genomic epidemiology of <i>Vibrio cholerae</i> reveals the regional and global spread of two epidemic non-toxigenic lineages 2020 , 14, e0008046		
141	Genomic epidemiology of <i>Vibrio cholerae</i> reveals the regional and global spread of two epidemic non-toxigenic lineages 2020 , 14, e0008046		
140	Genomic epidemiology of <i>Vibrio cholerae</i> reveals the regional and global spread of two epidemic non-toxigenic lineages 2020 , 14, e0008046		
139	Within-host evolution of <i>Helicobacter pylori</i> shaped by niche-specific adaptation, intragastric migrations and selective sweeps. <i>Nature Communications</i> , 2019 , 10, 2273	17.4	43
138	Framework for DNA Quantification and Outlier Detection Using Multidimensional Standard Curves. <i>Analytical Chemistry</i> , 2019 , 91, 7426-7434	7.8	10
137	<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> , 2019 , 43, 347-355	8.8	18
136	A dynamic power-law sexual network model of gonorrhoea outbreaks. <i>PLoS Computational Biology</i> , 2019 , 15, e1006748	5	7
135	A Role for Tetracycline Selection in Recent Evolution of Agriculture-Associated PCR Ribotype 078. <i>MBio</i> , 2019 , 10,	7.8	32
134	Rapid phenotypic evolution in multidrug-resistant <i>Klebsiella pneumoniae</i> hospital outbreak strains. <i>Microbial Genomics</i> , 2019 , 5,	4.4	13
133	The Population Structure of <i>Pseudomonas aeruginosa</i> Is Characterized by Genetic Isolation of exoU+ and exoS+ Lineages. <i>Genome Biology and Evolution</i> , 2019 , 11, 1780-1796	3.9	29
132	Machine-learning-assisted selection of antibiotic prescription. <i>Nature Medicine</i> , 2019 , 25, 1033-1034	50.5	4
131	The speciation and hybridization history of the genus. <i>Microbial Genomics</i> , 2019 , 5,	4.4	9

130	Modeling the Growth and Decline of Pathogen Effective Population Size Provides Insight into Epidemic Dynamics and Drivers of Antimicrobial Resistance. <i>Systematic Biology</i> , 2018 , 67, 719-728	8.4	38
129	Range Expansion and the Origin of USA300 North American Epidemic Methicillin-Resistant. <i>MBio</i> , 2018 , 9,	7.8	26
128	The global distribution and spread of the mobilized colistin resistance gene mcr-1. <i>Nature Communications</i> , 2018 , 9, 1179	17.4	268
127	Whole genome sequencing of reveals transmission clusters involving patients of mixed HIV serostatus. <i>Sexually Transmitted Infections</i> , 2018 , 94, 138-143	2.8	15
126	Epidemiological Trends of Antibiotic Resistant Gonorrhoea in the United Kingdom. <i>Antibiotics</i> , 2018 , 7,	4.9	19
125	A phylogenetic method to perform genome-wide association studies in microbes that accounts for population structure and recombination. <i>PLoS Computational Biology</i> , 2018 , 14, e1005958	5	96
124	Genomic Investigation of a Outbreak Involving Prison and Community Cases in Florida, United States. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018 , 99, 867-874	3.2	8
123	Genomic surveillance of Neisseria gonorrhoeae to investigate the distribution and evolution of antimicrobial-resistance determinants and lineages. <i>Microbial Genomics</i> , 2018 , 4,	4.4	32
122	Disease-associated genotypes of the commensal skin bacterium Staphylococcus epidermidis. <i>Nature Communications</i> , 2018 , 9, 5034	17.4	71
121	Microevolution of Neisseria lactamica during nasopharyngeal colonisation induced by controlled human infection. <i>Nature Communications</i> , 2018 , 9, 4753	17.4	18
120	outbreaker2: a modular platform for outbreak reconstruction. <i>BMC Bioinformatics</i> , 2018 , 19, 363	3.6	30
119	Bayesian inference of ancestral dates on bacterial phylogenetic trees. <i>Nucleic Acids Research</i> , 2018 , 46, e134	20.1	71
118	Testing for gonorrhoea should routinely include the pharynx. <i>Lancet Infectious Diseases, The</i> , 2018 , 18, 716-717	25.5	10
117	Genomic Infectious Disease Epidemiology in Partially Sampled and Ongoing Outbreaks. <i>Molecular Biology and Evolution</i> , 2017 , 34, 997-1007	8.3	112
116	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
115	Re-emergence of methicillin susceptibility in a resistant lineage of Staphylococcus aureus. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 1285-1288	5.1	13
114	Local genes for local bacteria: Evidence of allopatry in the genomes of transatlantic Campylobacter populations. <i>Molecular Ecology</i> , 2017 , 26, 4497-4508	5.7	20
113	Clostridium difficile in England: can we stop washing our hands? - AuthorsSreply. <i>Lancet Infectious Diseases, The</i> , 2017 , 17, 478-479	25.5	1

112	Reconstructing the Ancestral Relationships Between Bacterial Pathogen Genomes. <i>Methods in Molecular Biology</i> , 2017 , 1535, 109-137	1.4	5
111	Pneumococcal Capsule Synthesis Locus cps as Evolutionary Hotspot with Potential to Generate Novel Serotypes by Recombination. <i>Molecular Biology and Evolution</i> , 2017 , 34, 2537-2554	8.3	42
110	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. <i>Molecular Biology and Evolution</i> , 2017 , 34, 185-203	8.3	41
109	Evolution and Transmission of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Expressing the blaOXA-232 Gene During an Institutional Outbreak Associated With Endoscopic Retrograde Cholangiopancreatography. <i>Clinical Infectious Diseases</i> , 2017 , 64, 894-901	11.6	28
108	A combined case-control and molecular source attribution study of human <i>Campylobacter</i> infections in Germany, 2011-2014. <i>Scientific Reports</i> , 2017 , 7, 5139	4.9	54
107	Genome-wide association of functional traits linked with <i>Campylobacter jejuni</i> survival from farm to fork. <i>Environmental Microbiology</i> , 2017 , 19, 361-380	5.2	61
106	Model-based analysis of an outbreak of bubonic plague in Cairo in 1801. <i>Journal of the Royal Society Interface</i> , 2017 , 14,	4.1	8
105	Computational Methods in Microbial Population Genomics. <i>Population Genomics</i> , 2017 , 3-29	1.4	2
104	Y92-1009 complete genome sequence. <i>Standards in Genomic Sciences</i> , 2017 , 12, 41		5
103	Simultaneous inference of phylogenetic and transmission trees in infectious disease outbreaks. <i>PLoS Computational Biology</i> , 2017 , 13, e1005495	5	55
102	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> , 2017 , 14, e1002416	11.6	30
101	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> , 2016 , 8, 2613-23	3.9	20
100	Bayesian Inference of the Evolution of a Phenotype Distribution on a Phylogenetic Tree. <i>Genetics</i> , 2016 , 204, 89-98	4	21
99	Dynamics of genome change among <i>Legionella</i> species. <i>Scientific Reports</i> , 2016 , 6, 33442	4.9	14
98	Within-host evolution of bacterial pathogens. <i>Nature Reviews Microbiology</i> , 2016 , 14, 150-62	22.2	239
97	Evolutionary History of the Global Emergence of the <i>Escherichia coli</i> Epidemic Clone ST131. <i>MBio</i> , 2016 , 7, e02162	7.8	200
96	The Landscape of Realized Homologous Recombination in Pathogenic Bacteria. <i>Molecular Biology and Evolution</i> , 2016 , 33, 456-71	8.3	40
95	Impact of HIV co-infection on the evolution and transmission of multidrug-resistant tuberculosis. <i>ELife</i> , 2016 , 5,	8.9	39

94	Declaring a tuberculosis outbreak over with genomic epidemiology. <i>Microbial Genomics</i> , 2016 , 2, e0000604	4.4	19
93	SimBac: simulation of whole bacterial genomes with homologous recombination. <i>Microbial Genomics</i> , 2016 , 2,	4.4	23
92	Whole-genome sequencing to determine transmission of <i>Neisseria gonorrhoeae</i> : an observational study. <i>Lancet Infectious Diseases</i> , 2016 , 16, 1295-1303	25.5	118
91	Genomic Analysis and Comparison of Two Gonorrhea Outbreaks. <i>MBio</i> , 2016 , 7,	7.8	39
90	Genome-wide analysis of chromosomal import patterns after natural transformation of <i>Helicobacter pylori</i> . <i>Nature Communications</i> , 2016 , 7, 11995	17.4	35
89	A barrier to homologous recombination between sympatric strains of the cooperative soil bacterium <i>Myxococcus xanthus</i> . <i>ISME Journal</i> , 2016 , 10, 2468-77	11.9	31
88	Epidemiological analysis of the Eyam plague outbreak of 1665-1666. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016 , 283,	4.4	43
87	Heroic sacrifice or tragic mistake? Revisiting the Eyam plague, 350 years on. <i>Significance</i> , 2016 , 13, 20-25	0.5	0
86	ClonalFrameML: efficient inference of recombination in whole bacterial genomes. <i>PLoS Computational Biology</i> , 2015 , 11, e1004041	5	458
85	The role of China in the global spread of the current cholera pandemic. <i>PLoS Genetics</i> , 2015 , 11, e1005072	2	58
84	Worldwide Population Structure, Long-Term Demography, and Local Adaptation of <i>Helicobacter pylori</i> . <i>Genetics</i> , 2015 , 200, 947-63	4	50
83	Progressive genomic convergence of two <i>Helicobacter pylori</i> strains during mixed infection of a patient with chronic gastritis. <i>Gut</i> , 2015 , 64, 554-61	19.2	38
82	Measurably evolving pathogens in the genomic era. <i>Trends in Ecology and Evolution</i> , 2015 , 30, 306-13	10.9	168
81	Epidemic Clones, Oceanic Gene Pools, and Eco-LD in the Free Living Marine Pathogen <i>Vibrio parahaemolyticus</i> . <i>Molecular Biology and Evolution</i> , 2015 , 32, 1396-410	8.3	63
80	<i>Burkholderia pseudomallei</i> sequencing identifies genomic clades with distinct recombination, accessory, and epigenetic profiles. <i>Genome Research</i> , 2015 , 25, 129-41	9.7	43
79	The application of genomics to tracing bacterial pathogen transmission. <i>Current Opinion in Microbiology</i> , 2015 , 23, 62-7	7.9	63
78	Formal Comment to Pettengill: The Time to Most Recent Common Ancestor Does Not (Usually) Approximate the Date of Divergence. <i>PLoS ONE</i> , 2015 , 10, e0134435	3.7	2
77	Population structure of <i>Neisseria gonorrhoeae</i> based on whole genome data and its relationship with antibiotic resistance. <i>PeerJ</i> , 2015 , 3, e806	3.1	58

76	Chlamydiaceae Genomics Reveals Interspecies Admixture and the Recent Evolution of Chlamydia abortus Infecting Lower Mammalian Species and Humans. <i>Genome Biology and Evolution</i> , 2015 , 7, 3070-84 ^{3,9}		21
75	Klebsiella pneumoniae carbapenemase (KPC)-producing K. pneumoniae at a single institution: insights into endemicity from whole-genome sequencing. <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 1656-63	5.9	107
74	The ubiquitous nature of Listeria monocytogenes clones: a large-scale Multilocus Sequence Typing study. <i>Environmental Microbiology</i> , 2014 , 16, 405-16	5.2	102
73	OutbreakTools: a new platform for disease outbreak analysis using the R software. <i>Epidemics</i> , 2014 , 7, 28-34	5.1	32
72	Bidirectional genomic exchange between Helicobacter pylori strains from a family in Coventry, United Kingdom. <i>International Journal of Medical Microbiology</i> , 2014 , 304, 1135-46	3.7	17
71	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
70	Inference of the properties of the recombination process from whole bacterial genomes. <i>Genetics</i> , 2014 , 196, 253-65	4	29
69	A Bayesian approach to inferring the phylogenetic structure of communities from metagenomic data. <i>Genetics</i> , 2014 , 197, 925-37	4	18
68	Bayesian reconstruction of disease outbreaks by combining epidemiologic and genomic data. <i>PLoS Computational Biology</i> , 2014 , 10, e1003457	5	142
67	Efficient inference of recombination hot regions in bacterial genomes. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1593-605	8.3	49
66	Mobile elements drive recombination hotspots in the core genome of Staphylococcus aureus. <i>Nature Communications</i> , 2014 , 5, 3956	17.4	90
65	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, 7247-57	5.9	98
64	Recombination shapes genome architecture in an organism from the archaeal domain. <i>Genome Biology and Evolution</i> , 2014 , 6, 170-8	3.9	9
63	The complexity and diversity of the Pathogenicity Locus in Clostridium difficile clade 5. <i>Genome Biology and Evolution</i> , 2014 , 6, 3159-70	3.9	27
62	Evolutionary history of the Clostridium difficile pathogenicity locus. <i>Genome Biology and Evolution</i> , 2014 , 6, 36-52	3.9	123
61	Bayesian inference of infectious disease transmission from whole-genome sequence data. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1869-79	8.3	138
60	Comparisons of infant Escherichia coli isolates link genomic profiles with adaptation to the ecological niche. <i>BMC Genomics</i> , 2013 , 14, 81	4.5	10
59	Recombinational switching of the Clostridium difficile S-layer and a novel glycosylation gene cluster revealed by large-scale whole-genome sequencing. <i>Journal of Infectious Diseases</i> , 2013 , 207, 675-86 ⁷		72

58	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> , 2013 , 110, 13880-5	11.5	80
57	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
56	Whole genome sequencing in the prevention and control of <i>Staphylococcus aureus</i> infection. <i>Journal of Hospital Infection</i> , 2013 , 83, 14-21	6.9	46
55	Comparative analysis of <i>Chlamydia psittaci</i> genomes reveals the recent emergence of a pathogenic lineage with a broad host range. <i>MBio</i> , 2013 , 4,	7.8	68
54	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> , 2013 , 110, 11923-7	11.5	178
53	Progressive genome-wide introgression in agricultural <i>Campylobacter coli</i> . <i>Molecular Ecology</i> , 2013 , 22, 1051-64	5.7	98
52	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> , 2013 , 81, 3534-51	3.7	26
51	Within-host evolution of <i>Staphylococcus aureus</i> during asymptomatic carriage. <i>PLoS ONE</i> , 2013 , 8, e61319	19.7	141
50	Transforming clinical microbiology with bacterial genome sequencing. <i>Nature Reviews Genetics</i> , 2012 , 13, 601-612	30.1	508
49	Population genomics of <i>Chlamydia trachomatis</i> : insights on drift, selection, recombination, and population structure. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3933-46	8.3	74
48	Impact of homologous and non-homologous recombination in the genomic evolution of <i>Escherichia coli</i> . <i>BMC Genomics</i> , 2012 , 13, 256	4.5	95
47	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> , 2012 , 12, 67	4.5	15
46	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
45	Molecular signatures identify a candidate target of balancing selection in an <i>arcD</i> -like gene of <i>Staphylococcus epidermidis</i> . <i>Journal of Molecular Evolution</i> , 2012 , 75, 43-54	3.1	9
44	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , 2012 , 13, R118	18.3	151
43	Multilocus sequence typing as a replacement for serotyping in <i>Salmonella enterica</i> . <i>PLoS Pathogens</i> , 2012 , 8, e1002776	7.6	412
42	Patterns of gene flow define species of thermophilic Archaea. <i>PLoS Biology</i> , 2012 , 10, e1001265	9.7	152
41	After the bottleneck: Genome-wide diversification of the <i>Mycobacterium tuberculosis</i> complex by mutation, recombination, and natural selection. <i>Genome Research</i> , 2012 , 22, 721-34	9.7	115

40	Genomic characterization of the <i>Bacillus cereus</i> sensu lato species: backdrop to the evolution of <i>Bacillus anthracis</i> . <i>Genome Research</i> , 2012 , 22, 1512-24	9.7	128
39	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
38	Likelihood-free estimation of model evidence. <i>Bayesian Analysis</i> , 2011 , 6,	2.3	60
37	Clinical <i>Clostridium difficile</i> : clonality and pathogenicity locus diversity. <i>PLoS ONE</i> , 2011 , 6, e19993	3.7	131
36	Population structure of the <i>Yersinia pseudotuberculosis</i> complex according to multilocus sequence typing. <i>Environmental Microbiology</i> , 2011 , 13, 3114-27	5.2	63
35	Closely related <i>Campylobacter jejuni</i> strains from different sources reveal a generalist rather than a specialist lifestyle. <i>BMC Genomics</i> , 2011 , 12, 584	4.5	86
34	Interplay of recombination and selection in the genomes of <i>Chlamydia trachomatis</i> . <i>Biology Direct</i> , 2011 , 6, 28	7.2	57
33	<i>Helicobacter pylori</i> genome evolution during human infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 5033-8	11.5	183
32	Recombination and population structure in <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , 2011 , 7, e1002191	6	105
31	Inference of homologous recombination in bacteria using whole-genome sequences. <i>Genetics</i> , 2010 , 186, 1435-49	4	118
30	Sequence-Based Analysis of Bacterial Population Structures 2010 , 37-60		5
29	Evolution and population structure of <i>Salmonella enterica</i> serovar Newport. <i>Journal of Bacteriology</i> , 2010 , 192, 6465-76	3.5	87
28	Microevolution of <i>Helicobacter pylori</i> during prolonged infection of single hosts and within families. <i>PLoS Genetics</i> , 2010 , 6, e1001036	6	118
27	Impact of recombination on bacterial evolution. <i>Trends in Microbiology</i> , 2010 , 18, 315-22	12.4	244
26	SimMLST: simulation of multi-locus sequence typing data under a neutral model. <i>Bioinformatics</i> , 2009 , 25, 1442-4	7.2	15
25	Evolution of pathogenicity in the <i>Bacillus cereus</i> group. <i>Systematic and Applied Microbiology</i> , 2009 , 32, 81-90	4.2	103
24	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> , 2009 , 10, 478	4.5	156
23	A comparison of homologous recombination rates in bacteria and archaea. <i>ISME Journal</i> , 2009 , 3, 199-208	1.9	394

22	Inferring genomic flux in bacteria. <i>Genome Research</i> , 2009 , 19, 306-17	9.7	26
21	Genealogical typing of <i>Neisseria meningitidis</i> . <i>Microbiology (United Kingdom)</i> , 2009 , 155, 3176-3186	2.9	31
20	Lineage specific recombination rates and microevolution in <i>Listeria monocytogenes</i> . <i>BMC Evolutionary Biology</i> , 2008 , 8, 277	3	78
19	A Duality Identity between a Model of Bacterial Recombination and the Wright-Fisher Diffusion. <i>Institute of Mathematical Statistics Collections</i> , 2008 , 315-324		1
18	Mosaic DNA imports with interspersions of recipient sequence after natural transformation of <i>Helicobacter pylori</i> . <i>PLoS ONE</i> , 2008 , 3, e3797	3.7	30
17	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> , 2007 , 17, 61-8	9.7	98
16	Inference of bacterial microevolution using multilocus sequence data. <i>Genetics</i> , 2007 , 175, 1251-66	4	550
15	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
14	Bacterial Recombination in vivo	23-46	
13	Detection of a bedaquiline / clofazimine resistance reservoir in <i>Mycobacterium tuberculosis</i> predating the antibiotic era		1
12	The global distribution and spread of the mobilized colistin resistance gene <i>mcr-1</i>		1
11	Emerging phylogenetic structure of the SARS-CoV-2 pandemic		5
10	New method to reconstruct phylogenetic and transmission trees with sequence data from infectious disease outbreaks		3
9	Quantifying the fitness benefit and cost of cefixime resistance in <i>Neisseria gonorrhoeae</i> to inform prescription policy		1
8	A phylogenetic method to perform genome-wide association studies in microbes that accounts for population structure and recombination		3
7	The sudden emergence of a <i>Neisseria gonorrhoeae</i> strain with reduced susceptibility to extended-spectrum cephalosporins, Norway		1
6	Hospital outbreak of carbapenem-resistant Enterobacteriales associated with an OXA-48 plasmid carried mostly by <i>Escherichia coli</i> ST399		5
5	The <i>Clostridioides difficile</i> species problem: global phylogenomic analysis uncovers three ancient, toxigenic, genomospecies		2

- 4 A role for tetracycline selection in the evolution of *Clostridium difficile* PCR-ribotype 078 6
- 3 Why panmictic bacteria are rare 10
- 2 Automated reconstruction of all gene histories in large bacterial pangenome datasets and search for co-evolved gene modules with Pantagruel 4
- 1 Phylogenomic analysis reveals the basis of adaptation of *Pseudorhizobium* species to extreme environments 1