Xavier Didelot

List of Publications by Year
in descending order

161 papers	15,443 citations	18436 62 h-index	22102 113 g-index
208 all docs	208 docs citations	208 times ranked	15163 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	Transforming clinical microbiology with bacterial genome sequencing. Nature Reviews Genetics, 2012, 13, 601-612.	7.7	684
3	Inference of Bacterial Microevolution Using Multilocus Sequence Data. Genetics, 2007, 175, 1251-1266.	1.2	616
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	Multilocus Sequence Typing as a Replacement for Serotyping in Salmonella enterica. PLoS Pathogens, 2012, 8, e1002776.	2.1	574
6	A comparison of homologous recombination rates in bacteria and archaea. ISME Journal, 2009, 3, 199-208.	4.4	489
7	The global distribution and spread of the mobilized colistin resistance gene mcr-1. Nature Communications, 2018, 9, 1179.	5.8	464
8	Within-host evolution of bacterial pathogens. Nature Reviews Microbiology, 2016, 14, 150-162.	13.6	373
9	Impact of recombination on bacterial evolution. Trends in Microbiology, 2010, 18, 315-322.	3.5	331
10	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. MBio, 2016, 7, e02162.	1.8	289
11	Effects of control interventions on Clostridium difficile infection in England: an observational study. Lancet Infectious Diseases, The, 2017, 17, 411-421.	4.6	269
12	Genome-wide association study identifies vitamin B$_5$ biosynthesis as a host specificity factor in *Campylobacter*. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11923-11927.	3.3	267
13	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
14	Measurably evolving pathogens in the genomic era. Trends in Ecology and Evolution, 2015, 30, 306-313.	4.2	241
15	*Helicobacter pylori* genome evolution during human infection. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5033-5038.	3.3	235
16	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
17	Patterns of Gene Flow Define Species of Thermophilic Archaea. PLoS Biology, 2012, 10, e1001265.	2.6	214
18	Bayesian Reconstruction of Disease Outbreaks by Combining Epidemiologic and Genomic Data. PLoS Computational Biology, 2014, 10, e1003457.	1.5	207

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19	Microevolutionary analysis of Clostridium difficile genomes to investigate transmission. Genome Biology, 2012, 13, R118.	13.9	199
20	A phylogenetic method to perform genome-wide association studies in microbes that accounts for population structure and recombination. PLoS Computational Biology, 2018, 14, e1005958.	1.5	198
21	Within-Host Evolution of Staphylococcus aureus during Asymptomatic Carriage. PLoS ONE, 2013, 8, e61319.	1.1	194
22	Bayesian Inference of Infectious Disease Transmission from Whole-Genome Sequence Data. Molecular Biology and Evolution, 2014, 31, 1869-1879.	3.5	191
23	Evolutionary History of the Clostridium difficile Pathogenicity Locus. Genome Biology and Evolution, 2014, 6, 36-52.	1.1	190
24	Genomic infectious disease epidemiology in partially sampled and ongoing outbreaks. Molecular Biology and Evolution, 2017, 34, msw075.	3.5	181
25	Maternal high fat diet during pregnancy and lactation alters hepatic expression of insulin like growth factor-2 and key microRNAs in the adult offspring. BMC Genomics, 2009, 10, 478.	1.2	179
26	Bayesian inference of ancestral dates on bacterial phylogenetic trees. Nucleic Acids Research, 2018, 46, e134-e134.	6.5	174
27	Inference of Homologous Recombination in Bacteria Using Whole-Genome Sequences. Genetics, 2010, 186, 1435-1449.	1.2	155
28	Microevolution of Helicobacter pylori during Prolonged Infection of Single Hosts and within Families. PLoS Genetics, 2010, 6, e1001036.	1.5	150
29	Clinical Clostridium difficile: Clonality and Pathogenicity Locus Diversity. PLoS ONE, 2011, 6, e19993.	1.1	150
30	Whole-genome sequencing to determine transmission of Neisseria gonorrhoeae : an observational study. Lancet Infectious Diseases, The, 2016, 16, 1295-1303.	4.6	149
31	Genomic characterization of the *Bacillus cereus* sensu lato species: Backdrop to the evolution of *Bacillus anthracis*. Genome Research, 2012, 22, 1512-1524.	2.4	148
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	After the bottleneck: Genome-wide diversification of the *Mycobacterium tuberculosis* complex by mutation, recombination, and natural selection. Genome Research, 2012, 22, 721-734.	2.4	141
34	Impact of homologous and non-homologous recombination in the genomic evolution of Escherichia coli. BMC Genomics, 2012, 13, 256.	1.2	141
35	Klebsiella pneumoniae Carbapenemase (KPC)-Producing K. pneumoniae at a Single Institution: Insights into Endemicity from Whole-Genome Sequencing. Antimicrobial Agents and Chemotherapy, 2015, 59, 1656-1663.	1.4	140
36	Emergence of methicillin resistance predates the clinical use of antibiotics. Nature, 2022, 602, 135-141.	13.7	138

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37	Recombination and Population Structure in Salmonella enterica. PLoS Genetics, 2011, 7, e1002191.	1.5	135
38	The ubiquitous nature of <scp><i>L</i></scp><i>isteria monocytogenes</i> clones: a large‐scale <scp>M</scp>ultilocus <scp>S</scp>equence <scp>T</scp>yping study. Environmental Microbiology, 2014, 16, 405-416.	1.8	130
39	Progressive genome‐wide introgression in agricultural <i>Campylobacter coli</i>. Molecular Ecology, 2013, 22, 1051-1064.	2.0	128
40	Mobile elements drive recombination hotspots in the core genome of Staphylococcus aureus. Nature Communications, 2014, 5, 3956.	5.8	128
41	Evolution of pathogenicity in the Bacillus cereus group. Systematic and Applied Microbiology, 2009, 32, 81-90.	1.2	123
42	Mismatch induced speciation in Salmonella : model and data. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 2045-2053.	1.8	116
43	Genomic evolution and transmission of <i>Helicobacter pylori</i> in two South African families. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13880-13885.	3.3	115
44	Disease-associated genotypes of the commensal skin bacterium Staphylococcus epidermidis. Nature Communications, 2018, 9, 5034.	5.8	115
45	A bimodal pattern of relatedness between the Salmonella Paratyphi A and Typhi genomes: Convergence or divergence by homologous recombination?. Genome Research, 2006, 17, 61-68.	2.4	112
46	Evolution and Population Structure of <i>Salmonella enterica</i> Serovar Newport. Journal of Bacteriology, 2010, 192, 6465-6476.	1.0	109
47	Closely related Campylobacter jejuni strains from different sources reveal a generalist rather than a specialist lifestyle. BMC Genomics, 2011, 12, 584.	1.2	101
48	Epidemic Clones, Oceanic Gene Pools, and Eco-LD in the Free Living Marine Pathogen Vibrio parahaemolyticus. Molecular Biology and Evolution, 2015, 32, 1396-1410.	3.5	98
49	Lineage specific recombination rates and microevolution in Listeria monocytogenes. BMC Evolutionary Biology, 2008, 8, 277.	3.2	96
50	Population Genomics of Chlamydia trachomatis: Insights on Drift, Selection, Recombination, and Population Structure. Molecular Biology and Evolution, 2012, 29, 3933-3946.	3.5	94
51	Within-host evolution of Helicobacter pylori shaped by niche-specific adaptation, intragastric migrations and selective sweeps. Nature Communications, 2019, 10, 2273.	5.8	94
52	Recombinational Switching of the Clostridium difficile S-Layer and a Novel Glycosylation Gene Cluster Revealed by Large-Scale Whole-Genome Sequencing. Journal of Infectious Diseases, 2013, 207, 675-686.	1.9	93
53	Simultaneous inference of phylogenetic and transmission trees in infectious disease outbreaks. PLoS Computational Biology, 2017, 13, e1005495.	1.5	93
54	Comparative Analysis of Chlamydia psittaci Genomes Reveals the Recent Emergence of a Pathogenic Lineage with a Broad Host Range. MBio, 2013, 4, .	1.8	90

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55	A combined case-control and molecular source attribution study of human Campylobacter infections in Germany, 2011–2014. Scientific Reports, 2017, 7, 5139.	1.6	89
56	Genome-wide association of functional traits linked with *Campylobacter jejuni* survival from farm to fork. Environmental Microbiology, 2017, 19, 361-380.	1.8	88
57	Population structure of the *Yersinia pseudotuberculosis* complex according to multilocus sequence typing. Environmental Microbiology, 2011, 13, 3114-3127.	1.8	84
58	The application of genomics to tracing bacterial pathogen transmission. Current Opinion in Microbiology, 2015, 23, 62-67.	2.3	84
59	Inference of person-to-person transmission of COVID-19 reveals hidden super-spreading events during the early outbreak phase. Nature Communications, 2020, 11, 5006.	5.8	80
60	Modeling the Growth and Decline of Pathogen Effective Population Size Provides Insight into Epidemic Dynamics and Drivers of Antimicrobial Resistance. Systematic Biology, 2018, 67, 719-728.	2.7	78
61	Likelihood-free estimation of model evidence. Bayesian Analysis, 2011, 6, .	1.6	74
62	The Population Structure of Pseudomonas aeruginosa Is Characterized by Genetic Isolation of exoU+ and exoS+ Lineages. Genome Biology and Evolution, 2019, 11, 1780-1796.	1.1	74
63	The Role of China in the Global Spread of the Current Cholera Pandemic. PLoS Genetics, 2015, 11, e1005072.	1.5	73
64	The Landscape of Realized Homologous Recombination in Pathogenic Bacteria. Molecular Biology and Evolution, 2016, 33, 456-471.	3.5	72
65	Interplay of recombination and selection in the genomes of Chlamydia trachomatis. Biology Direct, 2011, 6, 28.	1.9	70
66	Population structure of *Neisseria gonorrhoeae* based on whole genome data and its relationship with antibiotic resistance. PeerJ, 2015, 3, e806.	0.9	67
67	Worldwide Population Structure, Long-Term Demography, and Local Adaptation of *Helicobacter pylori*. Genetics, 2015, 200, 947-963.	1.2	65
68	Pneumococcal Capsule Synthesis Locus cps as Evolutionary Hotspot with Potential to Generate Novel Serotypes by Recombination. Molecular Biology and Evolution, 2017, 34, 2537-2554.	3.5	65
69	Efficient Inference of Recombination Hot Regions in Bacterial Genomes. Molecular Biology and Evolution, 2014, 31, 1593-1605.	3.5	62
70	*Burkholderia pseudomallei* sequencing identifies genomic clades with distinct recombination, accessory, and epigenetic profiles. Genome Research, 2015, 25, 129-141.	2.4	61
71	outbreaker2: a modular platform for outbreak reconstruction. BMC Bioinformatics, 2018, 19, 363.	1.2	60
72	Whole genome sequencing in the prevention and control of Staphylococcus aureus infection. Journal of Hospital Infection, 2013, 83, 14-21.	1.4	59

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73	Genome-wide analysis of chromosomal import patterns after natural transformation of Helicobacter pylori. Nature Communications, 2016, 7, 11995.	5.8	59
74	Epidemiological analysis of the Eyam plague outbreak of 1665â€"1666. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20160618.	1.2	56
75	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. Molecular Biology and Evolution, 2017, 34, 185-203.	3.5	53
76	A barrier to homologous recombination between sympatric strains of the cooperative soil bacterium <i>Myxococcus xanthus</i>. ISME Journal, 2016, 10, 2468-2477.	4.4	52
77	Genomic Analysis and Comparison of Two Gonorrhea Outbreaks. MBio, 2016, 7, .	1.8	51
78	Impact of HIV co-infection on the evolution and transmission of multidrug-resistant tuberculosis. ELife, 2016, 5, .	2.8	51
79	Major genetic discontinuity and novel toxigenic species in Clostridioides difficile taxonomy. ELife, 2021, 10, .	2.8	50
80	Progressive genomic convergence of two<i>Helicobacter pylori</i>strains during mixed infection of a patient with chronic gastritis. Gut, 2015, 64, 554-561.	6.1	47
81	Genomic surveillance of Neisseria gonorrhoeae to investigate the distribution and evolution of antimicrobial-resistance determinants and lineages. Microbial Genomics, 2018, 4, .	1.0	47
82	Population genomics and antimicrobial resistance in Corynebacterium diphtheriae. Genome Medicine, 2020, 12, 107.	3.6	47
83	Estimating the fitness cost and benefit of cefixime resistance in Neisseria gonorrhoeae to inform prescription policy: A modelling study. PLoS Medicine, 2017, 14, e1002416.	3.9	47
84	A Role for Tetracycline Selection in Recent Evolution of Agriculture-Associated <i>Clostridium difficile</i> PCR Ribotype 078. MBio, 2019, 10, .	1.8	46
85	Range Expansion and the Origin of USA300 North American Epidemic Methicillin-Resistant <i>Staphylococcus aureus</i>. MBio, 2018, 9, .	1.8	42
86	Inference of the Properties of the Recombination Process from Whole Bacterial Genomes. Genetics, 2014, 196, 253-265.	1.2	41
87	Bayesian Inference of the Evolution of a Phenotype Distribution on a Phylogenetic Tree. Genetics, 2016, 204, 89-98.	1.2	40
88	Evolution and Transmission of Carbapenem-Resistant Klebsiella pneumoniae Expressing the blaOXA-232 Gene During an Institutional Outbreak Associated With Endoscopic Retrograde Cholangiopancreatography. Clinical Infectious Diseases, 2017, 64, 894-901.	2.9	39
89	OutbreakTools: A new platform for disease outbreak analysis using the R software. Epidemics, 2014, 7, 28-34.	1.5	37
90	Local genes for local bacteria: Evidence of allopatry in the genomes of transatlantic <i>Campylobacter</i> populations. Molecular Ecology, 2017, 26, 4497-4508.	2.0	36

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91	Mosaic DNA Imports with Interspersions of Recipient Sequence after Natural Transformation of Helicobacter pylori. PLoS ONE, 2008, 3, e3797.	1.1	36
92	Inferring genomic flux in bacteria. Genome Research, 2009, 19, 306-317.	2.4	35
93	Tetracycline Selective Pressure and Homologous Recombination Shape the Evolution ofChlamydia suis: A Recently Identified Zoonotic Pathogen. Genome Biology and Evolution, 2016, 8, 2613-2623.	1.1	35
94	Clostridium difficile trehalose metabolism variants are common and not associated with adverse patient outcomes when variably present in the same lineage. EBioMedicine, 2019, 43, 347-355.	2.7	35
95	Genomic Epidemiology Analysis of Infectious Disease Outbreaks Using TransPhylo. Current Protocols, 2021, 1, e60.	1.3	34
96	SimBac: simulation of whole bacterial genomes with homologous recombination. Microbial Genomics, 2016, 2, .	1.0	33
97	Phylogenomics reveals the basis of adaptation of Pseudorhizobium species to extreme environments and supports a taxonomic revision of the genus. Systematic and Applied Microbiology, 2021, 44, 126165.	1.2	33
98	Rapid Detection of Mobilized Colistin Resistance using a Nucleic Acid Based Lab-on-a-Chip Diagnostic System. Scientific Reports, 2020, 10, 8448.	1.6	33
99	Genomic signatures of pre-resistance in Mycobacterium tuberculosis. Nature Communications, 2021, 12, 7312.	5.8	33
100	The Complexity and Diversity of the Pathogenicity Locus in Clostridium difficile Clade 5. Genome Biology and Evolution, 2014, 6, 3159-3170.	1.1	31
101	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
102	Genealogical typing of Neisseria meningitidis. Microbiology (United Kingdom), 2009, 155, 3176-3186.	0.7	31
103	Role of Energy Sensor TlpD of Helicobacter pylori in Gerbil Colonization and Genome Analyses after Adaptation in the Gerbil. Infection and Immunity, 2013, 81, 3534-3551.	1.0	30
104	<i>Chlamydiaceae</i>Genomics Reveals Interspecies Admixture and the Recent Evolution of<i>Chlamydia abortus</i>Infecting Lower Mammalian Species and Humans. Genome Biology and Evolution, 2015, 7, 3070-3084.	1.1	30
105	Additive Uncorrelated Relaxed Clock Models for the Dating of Genomic Epidemiology Phylogenies. Molecular Biology and Evolution, 2021, 38, 307-317.	3.5	28
106	Declaring a tuberculosis outbreak over with genomic epidemiology. Microbial Genomics, 2016, 2, e000060.	1.0	27
107	Epidemiological Trends of Antibiotic Resistant Gonorrhoea in the United Kingdom. Antibiotics, 2018, 7, 60.	1.5	26
108	Identification of Hidden Population Structure in Time-Scaled Phylogenies. Systematic Biology, 2020, 69, 884-896.	2.7	26

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109	Rapid phenotypic evolution in multidrug-resistant Klebsiella pneumoniae hospital outbreak strains. Microbial Genomics, 2019, 5, .	1.0	25
110	A dynamic power-law sexual network model of gonorrhoea outbreaks. PLoS Computational Biology, 2019, 15, e1006748.	1.5	25
111	Microevolution of Neisseria lactamica during nasopharyngeal colonisation induced by controlled human infection. Nature Communications, 2018, 9, 4753.	5.8	24
112	Bidirectional genomic exchange between Helicobacter pylori strains from a family in Coventry, United Kingdom. International Journal of Medical Microbiology, 2014, 304, 1135-1146.	1.5	22
113	Re-emergence of methicillin susceptibility in a resistant lineage ofStaphylococcus aureus. Journal of Antimicrobial Chemotherapy, 2017, 72, dkw570.	1.3	22
114	Assessment of the Potential of Vaccination to Combat Antibiotic Resistance in Gonorrhea: A Modeling Analysis to Determine Preferred Product Characteristics. Clinical Infectious Diseases, 2020, 71, 1912-1919.	2.9	22
115	SimMLST: simulation of multi-locus sequence typing data under a neutral model. Bioinformatics, 2009, 25, 1442-1444.	1.8	21
116	Framework for DNA Quantification and Outlier Detection Using Multidimensional Standard Curves. Analytical Chemistry, 2019, 91, 7426-7434.	3.2	21
117	Emerging phylogenetic structure of the SARS-CoV-2 pandemic. Virus Evolution, 2020, 6, veaa082.	2.2	21
118	The nucleotide excision repair (NER) system of Helicobacter pylori: Role in mutation prevention and chromosomal import patterns after natural transformation. BMC Microbiology, 2012, 12, 67.	1.3	20
119	A Bayesian Approach to Inferring the Phylogenetic Structure of Communities from Metagenomic Data. Genetics, 2014, 197, 925-937.	1.2	20
120	Whole genome sequencing of <i>Neisseria gonorrhoeae</i> reveals transmission clusters involving patients of mixed HIV serostatus. Sexually Transmitted Infections, 2018, 94, 138-143.	0.8	19
121	Dynamics of genome change among Legionella species. Scientific Reports, 2016, 6, 33442.	1.6	18
122	Genomic Investigation of a Mycobacterium tuberculosis Outbreak Involving Prison and Community Cases in Florida, United States. American Journal of Tropical Medicine and Hygiene, 2018, 99, 867-874.	0.6	17
123	Public health impact and cost-effectiveness of gonorrhoea vaccination: an integrated transmission-dynamic health-economic modelling analysis. Lancet Infectious Diseases, The, 2022, 22, 1030-1041.	4.6	17
124	Genomic epidemiology of Vibrio cholerae reveals the regional and global spread of two epidemic non-toxigenic lineages. PLoS Neglected Tropical Diseases, 2020, 14, e0008046.	1.3	16
125	Assessing the extent of community spread caused by mink-derived SARS-CoV-2 variants. Innovation(China), 2021, 2, 100128.	5.2	16
126	Recombination Shapes Genome Architecture in an Organism from the Archaeal Domain. Genome Biology and Evolution, 2014, 6, 170-178.	1.1	14

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127	Testing for gonorrhoea should routinely include the pharynx. Lancet Infectious Diseases, The, 2018, 18, 716-717.	4.6	13
128	The speciation and hybridization history of the genus Salmonella. Microbial Genomics, 2019, 5, .	1.0	13
129	Transmission history of SARS-CoV-2 in humans and white-tailed deer. Scientific Reports, 2022, 12, .	1.6	13
130	Comparisons of infant Escherichia coli isolates link genomic profiles with adaptation to the ecological niche. BMC Genomics, 2013, 14, 81.	1.2	12
131	Machine-learning-assisted selection of antibiotic prescription. Nature Medicine, 2019, 25, 1033-1034.	15.2	12
132	Model-based analysis of an outbreak of bubonic plague in Cairo in 1801. Journal of the Royal Society Interface, 2017, 14, 20170160.	1.5	11
133	Sudden emergence of a Neisseria gonorrhoeae clade with reduced susceptibility to extended-spectrum cephalosporins, Norway. Microbial Genomics, 2020, 6, .	1.0	11
134	Molecular Signatures Identify a Candidate Target of Balancing Selection in an arcD-Like Gene of Staphylococcus epidermidis. Journal of Molecular Evolution, 2012, 75, 43-54.	0.8	10
135	Using rapid point-of-care tests to inform antibiotic choice to mitigate drug resistance in gonorrhoea. Eurosurveillance, 2020, 25, .	3.9	8
136	Comparative genomics of Clostridioides difficile toxinotypes identifies module-based toxin gene evolution. Microbial Genomics, 2020, 6, .	1.0	8
137	Bayesian Inference of Clonal Expansions in a Dated Phylogeny. Systematic Biology, 2022, 71, 1073-1087.	2.7	8
138	Neisseria lactamica Y92–1009 complete genome sequence. Standards in Genomic Sciences, 2017, 12, 41.	1.5	6
139	Genomic analysis to improve the management of outbreaks of bacterial infection. Expert Review of Anti-Infective Therapy, 2013, 11, 335-337.	2.0	5
140	Reconstructing the Ancestral Relationships Between Bacterial Pathogen Genomes. Methods in Molecular Biology, 2017, 1535, 109-137.	0.4	5
141	Phylogenetic Methods for Genome-Wide Association Studies in Bacteria. Methods in Molecular Biology, 2021, 2242, 205-220.	0.4	5
142	Hunting alters viral transmission and evolution in a large carnivore. Nature Ecology and Evolution, 2022, 6, 174-182.	3.4	5
143	The bounded coalescent model: Conditioning a genealogy on a minimum root date. Journal of Theoretical Biology, 2022, 548, 111186.	0.8	4
144	Hospital outbreak of carbapenem-resistant Enterobacterales associated with a bla OXA-48 plasmid carried mostly by Escherichia coli ST399. Microbial Genomics, 2022, 8, .	1.0	3

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145	Formal Comment to Pettengill: The Time to Most Recent Common Ancestor Does Not (Usually) Approximate the Date of Divergence. PLoS ONE, 2015, 10, e0134435.	1.1	2
146	Computational Methods in Microbial Population Genomics. Population Genomics, 2017, , 3-29.	0.2	2
147	OUP accepted manuscript. Briefings in Bioinformatics, 2022, , .	3.2	2
148	Bacterial Recombination in vivo. , 0, , 23-46.		1
149	A Duality Identity between a Model of Bacterial Recombination and the Wright–Fisher Diffusion. Institute of Mathematical Statistics Collections, 2008, , 315-324.	0.3	1
150	Heroic sacrifice or tragic mistake? Revisiting the Eyam plague, 350 years on. Significance, 2016, 13, 20-25.	0.3	1
151	Clostridium difficile in England: can we stop washing our hands? – Authors' reply. Lancet Infectious Diseases, The, 2017, 17, 478-479.	4.6	1
152	Co-existence of multiple distinct lineages in Vibrio parahaemolyticus serotype O4:K12. Microbial Genomics, 2020, 6, .	1.0	1
153	Bacterial Microevolution and the Pangenome. , 2020, , 129-149.		1
154	P3.134…Modelling the dynamics of antibiotic resistance in gonorrhoea to determine fitness benefits and costs. , 2017, , .		0
155	Title is missing!. , 2020, 14, e0008046.		0
156	Title is missing!. , 2020, 14, e0008046.		0
157	Title is missing!. , 2020, 14, e0008046.		0
158	Title is missing!. , 2020, 14, e0008046.		0
159	Title is missing!. , 2020, 14, e0008046.		0
160	Title is missing!. , 2020, 14, e0008046.		0
161	Catwalk: identifying closely related sequences in large microbial sequence databases. Microbial Genomics, 2022, 8, .	1.0	0