

Edward J Feil

List of Publications by Year in descending order

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130
papers

16,664
citations

23544

58
h-index

16636

123
g-index

194
all docs

194
docs citations

194
times ranked

16432
citing authors

#	ARTICLE	IF	CITATIONS
1	Co-evolutionary Signals Identify <i>Burkholderia pseudomallei</i> Survival Strategies in a Hostile Environment. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	10
2	Stem Region of tRNA Genes Favors Transition Substitution Towards Keto Bases in Bacteria. <i>Journal of Molecular Evolution</i> , 2022, 90, 114-123.	0.8	6
3	Stereoselective metabolism of chloramphenicol by bacteria isolated from wastewater, and the importance of stereochemistry in environmental risk assessments for antibiotics. <i>Water Research</i> , 2022, 217, 118415.	5.3	3
4	Wastewater Treatment Works: A Last Line of Defense for Preventing Antibiotic Resistance Entry Into the Environment. <i>Frontiers in Water</i> , 2022, 4, .	1.0	2
5	Challenges in realising the potential of wastewater-based epidemiology to quantitatively monitor and predict the spread of disease. <i>Journal of Water and Health</i> , 2022, 20, 1038-1050.	1.1	12
6	Genome of <i>Superficieibacter maynardsmithii</i> , a novel, antibiotic susceptible representative of Enterobacteriaceae. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	3
7	Genome evolution and the emergence of pathogenicity in avian <i>Escherichia coli</i> . <i>Nature Communications</i> , 2021, 12, 765.	5.8	69
8	A high prevalence of bla OXA-48 in <i>Klebsiella (Raoultella) ornithinolytica</i> and related species in hospital wastewater in South West England. <i>Microbial Genomics</i> , 2021, 7, .	1.0	10
9	Stereoselective Bacterial Metabolism of Antibiotics in Environmental Bacteria – A Novel Biochemical Workflow. <i>Frontiers in Microbiology</i> , 2021, 12, 562157.	1.5	4
10	Fatal exudative dermatitis in island populations of red squirrels (<i>Sciurus vulgaris</i>): spillover of a virulent <i>Staphylococcus aureus</i> clone (ST49) from reservoir hosts. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
11	One Health drivers of antibacterial resistance: Quantifying the relative impacts of human, animal and environmental use and transmission. <i>One Health</i> , 2021, 12, 100220.	1.5	67
12	Quantifying bacterial evolution in the wild: A birthday problem for <i>Campylobacter</i> lineages. <i>PLoS Genetics</i> , 2021, 17, e1009829.	1.5	11
13	Spatiotemporal profiling of antibiotics and resistance genes in a river catchment: Human population as the main driver of antibiotic and antibiotic resistance gene presence in the environment. <i>Water Research</i> , 2021, 203, 117533.	5.3	49
14	Phylogeographical Analysis Reveals the Historic Origin, Emergence, and Evolutionary Dynamics of Methicillin-Resistant <i>Staphylococcus aureus</i> ST228. <i>Frontiers in Microbiology</i> , 2020, 11, 2063.	1.5	6
15	A Hopeful Sea-Monster: A Very Large Homologous Recombination Event Impacting the Core Genome of the Marine Pathogen <i>Vibrio anguillarum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 1430.	1.5	7
16	Integrated chromosomal and plasmid sequence analyses reveal diverse modes of carbapenemase gene spread among <i>Klebsiella pneumoniae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25043-25054.	3.3	97
17	(Fluoro)quinolones and quinolone resistance genes in the aquatic environment: A river catchment perspective. <i>Water Research</i> , 2020, 182, 116015.	5.3	48
18	Enantiomeric profiling of quinolones and quinolones resistance gene qnrS in European wastewaters. <i>Water Research</i> , 2020, 175, 115653.	5.3	36

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19	The role of stereochemistry of antibiotic agents in the development of antibiotic resistance in the environment. <i>Environment International</i> , 2020, 139, 105681.	4.8	21
20	High-resolution sweep metagenomics using fast probabilistic inference. <i>Wellcome Open Research</i> , 2020, 5, 14.	0.9	13
21	Epidemic of carbapenem-resistant <i>Klebsiella pneumoniae</i> in Europe is driven by nosocomial spread. <i>Nature Microbiology</i> , 2019, 4, 1919-1929.	5.9	476
22	PIRATE: A fast and scalable pangenomics toolbox for clustering diverged orthologues in bacteria. <i>GigaScience</i> , 2019, 8, .	3.3	152
23	Gene Composition as a Potential Barrier to Large Recombinations in the Bacterial Pathogen <i>Klebsiella pneumoniae</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 3240-3251.	1.1	18
24	Description of <i>Klebsiella spallanzanii</i> sp. nov. and of <i>Klebsiella pasteurii</i> sp. nov.. <i>Frontiers in Microbiology</i> , 2019, 10, 2360.	1.5	49
25	Using the wax moth larva <i>Galleria mellonella</i> infection model to detect emerging bacterial pathogens. <i>PeerJ</i> , 2019, 6, e6150.	0.9	24
26	Recent mixing of <i>Vibrio parahaemolyticus</i> populations. <i>ISME Journal</i> , 2019, 13, 2578-2588.	4.4	41
27	High tech research reveals preferential feeding in honey bees. <i>Journal of Apicultural Research</i> , 2019, 58, 471-477.	0.7	2
28	WGS of 1058 <i>Enterococcus faecium</i> from Copenhagen, Denmark, reveals rapid clonal expansion of vancomycin-resistant clone ST80 combined with widespread dissemination of a vanA-containing plasmid and acquisition of a heterogeneous accessory genome. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1776-1785.	1.3	43
29	Multi-locus sequence typing of <i>Ixodes ricinus</i> and its symbiont <i>Candidatus Midichloria mitochondrii</i> across Europe reveals evidence of local co-cladogenesis in Scotland. <i>Ticks and Tick-borne Diseases</i> , 2019, 10, 52-62.	1.1	22
30	Real time monitoring of <i>Aeromonas salmonicida</i> evolution in response to successive antibiotic therapies in a commercial fish farm. <i>Environmental Microbiology</i> , 2019, 21, 1113-1123.	1.8	16
31	Closed genome sequences of <i>Staphylococcus lloydii</i> sp. nov. and <i>Staphylococcus durrellii</i> sp. nov. isolated from captive fruit bats (<i>Pteropus livingstonii</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	18
32	Piggy: a rapid, large-scale pan-genome analysis tool for intergenic regions in bacteria. <i>GigaScience</i> , 2018, 7, 1-11.	3.3	59
33	Genomic epidemiology of the commercially important pathogen <i>Renibacterium salmoninarum</i> within the Chilean salmon industry. <i>Microbial Genomics</i> , 2018, 4, .	1.0	12
34	Disease-associated genotypes of the commensal skin bacterium <i>Staphylococcus epidermidis</i> . <i>Nature Communications</i> , 2018, 9, 5034.	5.8	115
35	The distribution of bacterial doubling times in the wild. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180789.	1.2	182
36	Global expansion of <i>Mycobacterium tuberculosis</i> lineage 4 shaped by colonial migration and local adaptation. <i>Science Advances</i> , 2018, 4, eaat5869.	4.7	130

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37	Evidence for an effect of landscape connectivity on <i>Borrelia burgdorferi</i> sensu stricto dispersion in a zone of range expansion. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 1407-1415.	1.1	11
38	Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , 2018, 2, 1468-1478.	3.4	156
39	Whole genome sequencing and phylogenetic analysis of strains of the agent of Lyme disease <i>Borrelia burgdorferi</i> from Canadian emergence zones. <i>Scientific Reports</i> , 2018, 8, 10552.	1.6	34
40	Enantioselective fractionation of fluoroquinolones in the aqueous environment using chiral liquid chromatography coupled with tandem mass spectrometry. <i>Chemosphere</i> , 2018, 206, 376-386.	4.2	31
41	The importance of cross-disciplinary research to combat antimicrobial resistance: introducing a new pop-up journal, <i>X-AMR</i> . <i>Microbial Genomics</i> , 2018, 4, .	1.0	2
42	Comparative Analyses of Selection Operating on Nontranslated Intergenic Regions of Diverse Bacterial Species. <i>Genetics</i> , 2017, 206, 363-376.	1.2	65
43	Draft Genome Sequences of <i>Salinivibrio proteolyticus</i> , <i>Salinivibrio sharmensis</i> , <i>Salinivibrio siamensis</i> , <i>Salinivibrio costicola</i> subsp. <i>alcaliphilus</i> , <i>Salinivibrio costicola</i> subsp. <i>vallismortis</i> , and 29 New Isolates Belonging to the Genus <i>Salinivibrio</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	7
44	Genomic analysis of 495 vancomycin-resistant <i>Enterococcus faecium</i> reveals broad dissemination of a <i>vanA</i> plasmid in more than 19 clones from Copenhagen, Denmark. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 40-47.	1.3	40
45	<i>Enterobacteriaceae</i> : joining the dots with pan-European epidemiology. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 118-119.	4.6	14
46	The Promise of Whole Genome Pathogen Sequencing for the Molecular Epidemiology of Emerging Aquaculture Pathogens. <i>Frontiers in Microbiology</i> , 2017, 8, 121.	1.5	80
47	Phylogeny of <i>Vibrio vulnificus</i> from the Analysis of the Core-Genome: Implications for Intra-Species Taxonomy. <i>Frontiers in Microbiology</i> , 2017, 8, 2613.	1.5	50
48	Population genetic structuring of methicillin-resistant <i>Staphylococcus aureus</i> clone EMRSA-15 within UK reflects patient referral patterns. <i>Microbial Genomics</i> , 2017, 3, e000113.	1.0	19
49	Microreact: visualizing and sharing data for genomic epidemiology and phylogeography. <i>Microbial Genomics</i> , 2016, 2, e000093.	1.0	470
50	Evidence for Host-Genotype Associations of <i>Borrelia burgdorferi</i> Sensu Stricto. <i>PLoS ONE</i> , 2016, 11, e0149345.	1.1	44
51	The Stealthy Superbug: the Role of Asymptomatic Enteric Carriage in Maintaining a Long-Term Hospital Outbreak of ST228 Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2016, 7, e02039-15.	1.8	90
52	Building a genomic framework for prospective MRSA surveillance in the United Kingdom and the Republic of Ireland. <i>Genome Research</i> , 2016, 26, 263-270.	2.4	63
53	Whole-Genome Sequencing for Routine Pathogen Surveillance in Public Health: a Population Snapshot of Invasive <i>Staphylococcus aureus</i> in Europe. <i>MBio</i> , 2016, 7, .	1.8	192
54	Transmission of <i>Staphylococcus aureus</i> from Humans to Green Monkeys in The Gambia as Revealed by Whole-Genome Sequencing. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5910-5917.	1.4	30

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55	Identifying the effect of patient sharing on between-hospital genetic differentiation of methicillin-resistant <i>Staphylococcus aureus</i> . <i>Genome Medicine</i> , 2016, 8, 18.	3.6	20
56	The impact of host metapopulation structure on the population genetics of colonizing bacteria. <i>Journal of Theoretical Biology</i> , 2016, 396, 53-62.	0.8	13
57	Identifying copy number variation of the dominant virulence factors <i>msa</i> and <i>p22</i> within genomes of the fish pathogen <i>Renibacterium salmoninarum</i> . <i>Microbial Genomics</i> , 2016, 2, e000055.	1.0	14
58	Bayesian identification of bacterial strains from sequencing data. <i>Microbial Genomics</i> , 2016, 2, e000075.	1.0	19
59	Alternative Splice in Alternative Lice. <i>Molecular Biology and Evolution</i> , 2015, 32, 2749-2759.	3.5	29
60	Toward a synthesis of genotypic typing and phenotypic inference in the genomics era. <i>Future Microbiology</i> , 2015, 10, 1897-1899.	1.0	5
61	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of <i>Staphylococcus aureus</i> . <i>PLoS Biology</i> , 2015, 13, e1002229.	2.6	120
62	The Diversity and Geographical Structure of <i>Orientia tsutsugamushi</i> Strains from Scrub Typhus Patients in Laos. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004024.	1.3	25
63	Towards a Synthesis of Population Genomics and Epidemiology. , 2015, , 337-345.		0
64	Ecological Overlap and Horizontal Gene Transfer in <i>Staphylococcus aureus</i> and <i>Staphylococcus epidermidis</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 1313-1328.	1.1	130
65	Molecular epidemiology and population structure of the honey bee brood pathogen <i>Melissococcus plutonius</i> . <i>ISME Journal</i> , 2014, 8, 1588-1597.	4.4	49
66	Microevolution of <i>Renibacterium salmoninarum</i> : evidence for intercontinental dissemination associated with fish movements. <i>ISME Journal</i> , 2014, 8, 746-756.	4.4	32
67	Multilocus sequence typing using mitochondrial genes (mtMLST) reveals geographic population structure of <i>Ixodes ricinus</i> ticks. <i>Ticks and Tick-borne Diseases</i> , 2014, 5, 152-160.	1.1	25
68	Predicting the virulence of MRSA from its genome sequence. <i>Genome Research</i> , 2014, 24, 839-849.	2.4	210
69	Multilocus variable-number tandem-repeat genotyping of <i>Renibacterium salmoninarum</i> , a bacterium causing bacterial kidney disease in salmonid fish. <i>BMC Microbiology</i> , 2013, 13, 285.	1.3	7
70	A genomic portrait of the emergence, evolution, and global spread of a methicillin-resistant <i>Staphylococcus aureus</i> pandemic. <i>Genome Research</i> , 2013, 23, 653-664.	2.4	412
71	A Single Multilocus Sequence Typing (MLST) Scheme for Seven Pathogenic <i>Leptospira</i> Species. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e1954.	1.3	153
72	Genetic Relationships of <i>Vibrio parahaemolyticus</i> Isolates from Clinical, Human Carrier, and Environmental Sources in Thailand, Determined by Multilocus Sequence Analysis. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2358-2370.	1.4	53

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73	Historical Zoonoses and Other Changes in Host Tropism of <i>Staphylococcus aureus</i> , Identified by Phylogenetic Analysis of a Population Dataset. <i>PLoS ONE</i> , 2013, 8, e62369.	1.1	55
74	Covering All the Bases: The Promise of Genome-Wide Sequence Data for Large Population Samples of Bacteria. <i>Social and Ecological Interactions in the Galapagos Islands</i> , 2013, , 41-62.	0.4	2
75	Sugar concentration influences decision making in <i>Apis mellifera</i> L. workers during early-stage honey storage behaviour. <i>Open Journal of Animal Sciences</i> , 2013, 03, 210-218.	0.2	7
76	The emergence and spread of dysentery. <i>Nature Genetics</i> , 2012, 44, 964-965.	9.4	6
77	Molecular tracing of the emergence, adaptation, and transmission of hospital-associated methicillin-resistant <i>Staphylococcus aureus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9107-9112.	3.3	174
78	Phylogeographic variation in recombination rates within a global clone of methicillin-resistant <i>Staphylococcus aureus</i> . <i>Genome Biology</i> , 2012, 13, R126.	13.9	118
79	Diversity and recombination in <i>Wolbachia</i> and <i>Cardinium</i> from <i>Bryobia</i> spider mites. <i>BMC Microbiology</i> , 2012, 12, S13.	1.3	51
80	The Evolution and Dynamics of Methicillin-Resistant <i>Staphylococcus aureus</i> . , 2011, , 669-688.		1
81	A Very Early-Branching <i>Staphylococcus aureus</i> Lineage Lacking the Carotenoid Pigment Staphyloxanthin. <i>Genome Biology and Evolution</i> , 2011, 3, 881-895.	1.1	142
82	Host migration impacts on the phylogeography of Lyme Borreliosis spirochaete species in Europe. <i>Environmental Microbiology</i> , 2011, 13, 184-192.	1.8	97
83	Population biology of Gram-positive pathogens: high-risk clones for dissemination of antibiotic resistance. <i>FEMS Microbiology Reviews</i> , 2011, 35, 872-900.	3.9	173
84	Atypical AT Skew in Firmicute Genomes Results from Selection and Not from Mutation. <i>PLoS Genetics</i> , 2011, 7, e1002283.	1.5	36
85	The Impact of Recombination on dN/dS within Recently Emerged Bacterial Clones. <i>PLoS Pathogens</i> , 2011, 7, e1002129.	2.1	105
86	Evolution of MRSA During Hospital Transmission and Intercontinental Spread. <i>Science</i> , 2010, 327, 469-474.	6.0	1,054
87	Mutational Patterns Cannot Explain Genome Composition: Are There Any Neutral Sites in the Genomes of Bacteria?. <i>PLoS Genetics</i> , 2010, 6, e1001104.	1.5	92
88	Biogeography and Virulence of <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2009, 4, e6216.	1.1	51
89	Comparisons between Geographically Diverse Samples of Carried <i>Staphylococcus aureus</i> . <i>Journal of Bacteriology</i> , 2009, 191, 5577-5583.	1.0	91
90	The Temporal Dynamics of Slightly Deleterious Mutations in <i>Escherichia coli</i> and <i>Shigella</i> spp.. <i>Molecular Biology and Evolution</i> , 2009, 26, 345-355.	3.5	67

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91	Molecular genetic typing reveals further insights into the diversity of animal-associated <i>Staphylococcus aureus</i> . <i>Journal of Medical Microbiology</i> , 2009, 58, 1343-1353.	0.7	112
92	<i>Burkholderia pseudomallei</i> genome plasticity associated with genomic island variation. <i>BMC Genomics</i> , 2008, 9, 190.	1.2	66
93	MLST of housekeeping genes captures geographic population structure and suggests a European origin of <i>Borrelia burgdorferi</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8730-8735.	3.3	280
94	The Carriage Population of <i>Staphylococcus aureus</i> from Mali Is Composed of a Combination of Pandemic Clones and the Divergent Panton-Valentine Leukocidin-Positive Genotype ST152. <i>Journal of Bacteriology</i> , 2008, 190, 3962-3968.	1.0	130
95	The Core and Accessory Genomes of <i>Burkholderia pseudomallei</i> : Implications for Human Melioidosis. <i>PLoS Pathogens</i> , 2008, 4, e1000178.	2.1	71
96	Rapid Detection of the Pandemic Methicillin-Resistant <i>Staphylococcus aureus</i> Clone ST 239, a Dominant Strain in Asian Hospitals. <i>Journal of Clinical Microbiology</i> , 2008, 46, 1520-1522.	1.8	67
97	Searching for species in haloarchaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14092-14097.	3.3	128
98	The Persistence of Parasitic Plasmids. <i>Genetics</i> , 2007, 177, 399-405.	1.2	83
99	Emergence of a Virulent Clade of <i>Vibrio vulnificus</i> and Correlation with the Presence of a 33-Kilobase Genomic Island. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5553-5565.	1.4	83
100	The rise and fall of deleterious mutation. <i>Research in Microbiology</i> , 2007, 158, 779-786.	1.0	23
101	The secret life of the multilocus sequence type. <i>International Journal of Antimicrobial Agents</i> , 2007, 29, 129-135.	1.1	121
102	Large-Scale Comparative Genomic Ranking of Taxonomically Restricted Genes (TRGs) in Bacterial and Archaeal Genomes. <i>PLoS ONE</i> , 2007, 2, e324.	1.1	28
103	Multi-Locus Sequence Typing of <i>Bartonella henselae</i> Isolates from Three Continents Reveals Hypervirulent and Feline-Associated Clones. <i>PLoS ONE</i> , 2007, 2, e1346.	1.1	47
104	Causes of trends in amino-acid gain and loss. <i>Nature</i> , 2006, 442, E11-E12.	13.7	47
105	Comparisons of dN/dS are time dependent for closely related bacterial genomes. <i>Journal of Theoretical Biology</i> , 2006, 239, 226-235.	0.8	400
106	Nonrandom Distribution of <i>Burkholderia pseudomallei</i> Clones in Relation to Geographical Location and Virulence. <i>Journal of Clinical Microbiology</i> , 2006, 44, 2553-2557.	1.8	73
107	Similar compositional biases are caused by very different mutational effects. <i>Genome Research</i> , 2006, 16, 1537-1547.	2.4	87
108	The phylogeny of <i>Staphylococcus aureus</i> – which genes make the best intra-species markers?. <i>Microbiology (United Kingdom)</i> , 2006, 152, 1297-1305.	0.7	58

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109	Re-evaluating prokaryotic species. <i>Nature Reviews Microbiology</i> , 2005, 3, 733-739.	13.6	1,019
110	Evolutionary Genetics of the Accessory Gene Regulator (agr) Locus in <i>Staphylococcus aureus</i> . <i>Journal of Bacteriology</i> , 2005, 187, 8312-8321.	1.0	108
111	Databases and software for the comparison of prokaryotic genomes. <i>Microbiology (United Kingdom)</i> , 2005, 151, 2125-2132.	0.7	29
112	Complete genomes of two clinical <i>Staphylococcus aureus</i> strains: Evidence for the rapid evolution of virulence and drug resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9786-9791.	3.3	830
113	eBURST: Inferring Patterns of Evolutionary Descent among Clusters of Related Bacterial Genotypes from Multilocus Sequence Typing Data. <i>Journal of Bacteriology</i> , 2004, 186, 1518-1530.	1.0	1,697
114	Small change: keeping pace with microevolution. <i>Nature Reviews Microbiology</i> , 2004, 2, 483-495.	13.6	185
115	Displaying the relatedness among isolates of bacterial species " the eBURST approach. <i>FEMS Microbiology Letters</i> , 2004, 241, 129-134.	0.7	179
116	Multilocus sequence typing " what is resolved?. <i>Trends in Microbiology</i> , 2004, 12, 373-377.	3.5	157
117	Analyses of clonality and the evolution of bacterial pathogens. <i>Current Opinion in Microbiology</i> , 2004, 7, 308-313.	2.3	138
118	High rates of recombination in otitis media isolates of non-typeable <i>Haemophilus influenzae</i> 1. <i>Infection, Genetics and Evolution</i> , 2003, 3, 57-66.	1.0	61
119	Characterization of Encapsulated and Noncapsulated <i>Haemophilus influenzae</i> and Determination of Phylogenetic Relationships by Multilocus Sequence Typing. <i>Journal of Clinical Microbiology</i> , 2003, 41, 1623-1636.	1.8	329
120	How Clonal Is <i>Staphylococcus aureus</i> ?. <i>Journal of Bacteriology</i> , 2003, 185, 3307-3316.	1.0	560
121	Determining the Genetic Structure of the Natural Population of <i>Staphylococcus aureus</i> : a Comparison of Multilocus Sequence Typing with Pulsed-Field Gel Electrophoresis, Randomly Amplified Polymorphic DNA Analysis, and Phage Typing. <i>Journal of Clinical Microbiology</i> , 2002, 40, 4544-4546.	1.8	105
122	The evolutionary history of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 7687-7692.	3.3	1,354
123	Population Genetics of Bacterial Pathogens. , 2002, , 445-484.		1
124	Recombination and the Population Structures of Bacterial Pathogens. <i>Annual Review of Microbiology</i> , 2001, 55, 561-590.	2.9	305
125	A Link Between Virulence and Ecological Abundance in Natural Populations of <i>Staphylococcus aureus</i> . <i>Science</i> , 2001, 292, 114-116.	6.0	100
126	Population structure and evolutionary dynamics of pathogenic bacteria. <i>BioEssays</i> , 2000, 22, 1115-1122.	1.2	202

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127	Estimating the relative contributions of mutation and recombination to clonal diversification: a comparison between <i>Neisseria meningitidis</i> and <i>Streptococcus pneumoniae</i> . <i>Research in Microbiology</i> , 2000, 151, 465-469.	1.0	98
128	Population structure and evolutionary dynamics of pathogenic bacteria. <i>BioEssays</i> , 2000, 22, 1115-1122.	1.2	4
129	Estimating Recombinational Parameters in <i>Streptococcus pneumoniae</i> From Multilocus Sequence Typing Data. <i>Genetics</i> , 2000, 154, 1439-1450.	1.2	235
130	A comparison of the nucleotide sequences of the <i>adk</i> and <i>recA</i> genes of pathogenic and commensal <i>Neisseria</i> species: Evidence for extensive interspecies recombination within <i>adk</i> . <i>Journal of Molecular Evolution</i> , 1996, 43, 631-640.	0.8	76