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	eBURST: Inferring Patterns of Evolutionary Descent among Clusters of Related Bacterial Genotypes from Multilocus Sequence Typing Data. Journal of Bacteriology, 2004, 186, 1518-1530.	1.0	1,697
2	The evolutionary history of methicillin-resistant Staphylococcus aureus (MRSA). Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7687-7692.	3.3	1,354
3	Evolution of MRSA During Hospital Transmission and Intercontinental Spread. Science, 2010, 327, 469-474.	6.0	1,054
4	Re-evaluating prokaryotic species. Nature Reviews Microbiology, 2005, 3, 733-739.	13.6	1,019
5	Complete genomes of two clinical Staphylococcus aureus strains: Evidence for the rapid evolution of virulence and drug resistance. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9786-9791.	3.3	830
6	How Clonal Is Staphylococcus aureus ?. Journal of Bacteriology, 2003, 185, 3307-3316.	1.0	560
7	Epidemic of carbapenem-resistant Klebsiella pneumoniae in Europe is driven by nosocomial spread. Nature Microbiology, 2019, 4, 1919-1929.	5.9	476
8	Microreact: visualizing and sharing data for genomic epidemiology and phylogeography. Microbial Genomics, 2016, 2, e000093.	1.0	470
9	A genomic portrait of the emergence, evolution, and global spread of a methicillin-resistant Staphylococcus aureus pandemic. Genome Research, 2013, 23, 653-664.	2.4	412
10	Comparisons of dN/dS are time dependent for closely related bacterial genomes. Journal of Theoretical Biology, 2006, 239, 226-235.	0.8	400
11	Characterization of Encapsulated and Noncapsulated Haemophilus influenzae and Determination of Phylogenetic Relationships by Multilocus Sequence Typing. Journal of Clinical Microbiology, 2003, 41, 1623-1636.	1.8	329
12	Recombination and the Population Structures of Bacterial Pathogens. Annual Review of Microbiology, 2001, 55, 561-590.	2.9	305
13	MLST of housekeeping genes captures geographic population structure and suggests a European origin ofBorrelia burgdorferi. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8730-8735.	3.3	280
14	Estimating Recombinational Parameters in Streptococcus pneumoniae From Multilocus Sequence Typing Data. Genetics, 2000, 154, 1439-1450.	1.2	235
15	Predicting the virulence of MRSA from its genome sequence. Genome Research, 2014, 24, 839-849.	2.4	210
16	Population structure and evolutionary dynamics of pathogenic bacteria. BioEssays, 2000, 22, 1115-1122.	1.2	202
17	Whole-Genome Sequencing for Routine Pathogen Surveillance in Public Health: a Population Snapshot of Invasive Staphylococcus aureus in Europe. MBio, 2016, 7, .	1.8	192
18	Small change: keeping pace with microevolution. Nature Reviews Microbiology, 2004, 2, 483-495.	13.6	185

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19	The distribution of bacterial doubling times in the wild. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20180789.	1.2	182
20	Displaying the relatedness among isolates of bacterial species Ã¢Â€Â“ the eBURST approach. FEMS Microbiology Letters, 2004, 241, 129-134.	0.7	179
21	Molecular tracing of the emergence, adaptation, and transmission of hospital-associated methicillin-resistant Staphylococcus aureus. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9107-9112.	3.3	174
22	Population biology of Gram-positive pathogens: high-risk clones for dissemination of antibiotic resistance. FEMS Microbiology Reviews, 2011, 35, 872-900.	3.9	173
23	Multilocus sequence typing â€“ what is resolved?. Trends in Microbiology, 2004, 12, 373-377.	3.5	157
24	Gene exchange drives the ecological success of a multi-host bacterial pathogen. Nature Ecology and Evolution, 2018, 2, 1468-1478.	3.4	156
25	A Single Multilocus Sequence Typing (MLST) Scheme for Seven Pathogenic Leptospira Species. PLoS Neglected Tropical Diseases, 2013, 7, e1954.	1.3	153
26	PIRATE: A fast and scalable pangenomics toolbox for clustering diverged orthologues in bacteria. GigaScience, 2019, 8, .	3.3	152
27	A Very Early-Branching Staphylococcus aureus Lineage Lacking the Carotenoid Pigment Staphyloxanthin. Genome Biology and Evolution, 2011, 3, 881-895.	1.1	142
28	Analyses of clonality and the evolution of bacterial pathogens. Current Opinion in Microbiology, 2004, 7, 308-313.	2.3	138
29	The Carriage Population of Staphylococcus aureus from Mali Is Composed of a Combination of Pandemic Clones and the Divergent Panton-Valentine Leukocidin-Positive Genotype ST152. Journal of Bacteriology, 2008, 190, 3962-3968.	1.0	130
30	Ecological Overlap and Horizontal Gene Transfer in Staphylococcus aureus and Staphylococcus epidermidis. Genome Biology and Evolution, 2015, 7, 1313-1328.	1.1	130
31	Global expansion of Mycobacterium tuberculosis lineage 4 shaped by colonial migration and local adaptation. Science Advances, 2018, 4, eaat5869.	4.7	130
32	Searching for species in haloarchaea. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 14092-14097.	3.3	128
33	The secret life of the multilocus sequence type. International Journal of Antimicrobial Agents, 2007, 29, 129-135.	1.1	121
34	Evolutionary Trade-Offs Underlie the Multi-faceted Virulence of Staphylococcus aureus. PLoS Biology, 2015, 13, e1002229.	2.6	120
35	Phylogeographic variation in recombination rates within a global clone of methicillin-resistant Staphylococcus aureus. Genome Biology, 2012, 13, R126.	13.9	118
36	Disease-associated genotypes of the commensal skin bacterium Staphylococcus epidermidis. Nature Communications, 2018, 9, 5034.	5.8	115

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37	Molecular genetic typing reveals further insights into the diversity of animal-associated Staphylococcus aureus. Journal of Medical Microbiology, 2009, 58, 1343-1353.	0.7	112
38	Evolutionary Genetics of the Accessory Gene Regulator (agr) Locus in Staphylococcus aureus. Journal of Bacteriology, 2005, 187, 8312-8321.	1.0	108
39	Determining the Genetic Structure of the Natural Population of Staphylococcus aureus : a Comparison of Multilocus Sequence Typing with Pulsed-Field Gel Electrophoresis, Randomly Amplified Polymorphic DNA Analysis, and Phage Typing. Journal of Clinical Microbiology, 2002, 40, 4544-4546.	1.8	105
40	The Impact of Recombination on dN/dS within Recently Emerged Bacterial Clones. PLoS Pathogens, 2011, 7, e1002129.	2.1	105
41	A Link Between Virulence and Ecological Abundance in Natural Populations of Staphylococcus aureus. Science, 2001, 292, 114-116.	6.0	100
42	Estimating the relative contributions of mutation and recombination to clonal diversification: a comparison between Neisseria meningitidisand Streptococcus pneumoniae. Research in Microbiology, 2000, 151, 465-469.	1.0	98
43	Host migration impacts on the phylogeography of Lyme Borreliosis spirochaete species in Europe. Environmental Microbiology, 2011, 13, 184-192.	1.8	97
44	Integrated chromosomal and plasmid sequence analyses reveal diverse modes of carbapenemase gene spread among Klebsiella pneumoniae. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25043-25054.	3.3	97
45	Mutational Patterns Cannot Explain Genome Composition: Are There Any Neutral Sites in the Genomes of Bacteria?. PLoS Genetics, 2010, 6, e1001104.	1.5	92
46	Comparisons between Geographically Diverse Samples of Carried Staphylococcus aureus. Journal of Bacteriology, 2009, 191, 5577-5583.	1.0	91
47	The Stealthy Superbug: the Role of Asymptomatic Enteric Carriage in Maintaining a Long-Term Hospital Outbreak of ST228 Methicillin-Resistant Staphylococcus aureus. MBio, 2016, 7, e02039-15.	1.8	90
48	Similar compositional biases are caused by very different mutational effects. Genome Research, 2006, 16, 1537-1547.	2.4	87
49	The Persistence of Parasitic Plasmids. Genetics, 2007, 177, 399-405.	1.2	83
50	Emergence of a Virulent Clade of Vibrio vulnificus and Correlation with the Presence of a 33-Kilobase Genomic Island. Applied and Environmental Microbiology, 2007, 73, 5553-5565.	1.4	83
51	The Promise of Whole Genome Pathogen Sequencing for the Molecular Epidemiology of Emerging Aquaculture Pathogens. Frontiers in Microbiology, 2017, 8, 121.	1.5	80
52	A comparison of the nucleotide sequences of theadk andrecA genes of pathogenic and commensalNeisseria species: Evidence for extensive interspecies recombination withinadk. Journal of Molecular Evolution, 1996, 43, 631-640.	0.8	76
53	Nonrandom Distribution of Burkholderia pseudomallei Clones in Relation to Geographical Location and Virulence. Journal of Clinical Microbiology, 2006, 44, 2553-2557.	1.8	73
54	The Core and Accessory Genomes of Burkholderia pseudomallei: Implications for Human Melioidosis. PLoS Pathogens, 2008, 4, e1000178.	2.1	71

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55	Genome evolution and the emergence of pathogenicity in avian Escherichia coli. Nature Communications, 2021, 12, 765.	5.8	69
56	Rapid Detection of the Pandemic Methicillin-Resistant Staphylococcus aureus Clone ST 239, a Dominant Strain in Asian Hospitals. Journal of Clinical Microbiology, 2008, 46, 1520-1522.	1.8	67
57	The Temporal Dynamics of Slightly Deleterious Mutations in Escherichia coli and Shigella spp.. Molecular Biology and Evolution, 2009, 26, 345-355.	3.5	67
58	One Health drivers of antibacterial resistance: Quantifying the relative impacts of human, animal and environmental use and transmission. One Health, 2021, 12, 100220.	1.5	67
59	Burkholderia pseudomallei genome plasticity associated with genomic island variation. BMC Genomics, 2008, 9, 190.	1.2	66
60	Comparative Analyses of Selection Operating on Nontranslated Intergenic Regions of Diverse Bacterial Species. Genetics, 2017, 206, 363-376.	1.2	65
61	Building a genomic framework for prospective MRSA surveillance in the United Kingdom and the Republic of Ireland. Genome Research, 2016, 26, 263-270.	2.4	63
62	High rates of recombination in otitis media isolates of non-typeable Haemophilus influenzae1. Infection, Genetics and Evolution, 2003, 3, 57-66.	1.0	61
63	Piggy: a rapid, large-scale pan-genome analysis tool for intergenic regions in bacteria. GigaScience, 2018, 7, 1-11.	3.3	59
64	The phylogeny of Staphylococcus aureus â€“ which genes make the best intra-species markers?. Microbiology (United Kingdom), 2006, 152, 1297-1305.	0.7	58
65	Historical Zoonoses and Other Changes in Host Tropism of Staphylococcus aureus, Identified by Phylogenetic Analysis of a Population Dataset. PLoS ONE, 2013, 8, e62369.	1.1	55
66	Genetic Relationships of Vibrio parahaemolyticus Isolates from Clinical, Human Carrier, and Environmental Sources in Thailand, Determined by Multilocus Sequence Analysis. Applied and Environmental Microbiology, 2013, 79, 2358-2370.	1.4	53
67	Biogeography and Virulence of Staphylococcus aureus. PLoS ONE, 2009, 4, e6216.	1.1	51
68	Diversity and recombination in Wolbachia and Cardinium from Bryobia spider mites. BMC Microbiology, 2012, 12, S13.	1.3	51
69	Phylogeny of Vibrio vulnificus from the Analysis of the Core-Genome: Implications for Intra-Species Taxonomy. Frontiers in Microbiology, 2017, 8, 2613.	1.5	50
70	Molecular epidemiology and population structure of the honey bee brood pathogen Melissococcus plutonius. ISME Journal, 2014, 8, 1588-1597.	4.4	49
71	Description of Klebsiella spallanzanii sp. nov. and of Klebsiella pasteurii sp. nov.. Frontiers in Microbiology, 2019, 10, 2360.	1.5	49
72	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. Water Research, 2021, 203, 117533.	5.3	49

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73	(Fluoro)quinolones and quinolone resistance genes in the aquatic environment: A river catchment perspective. Water Research, 2020, 182, 116015.	5.3	48
74	Causes of trends in amino-acid gain and loss. Nature, 2006, 442, E11-E12.	13.7	47
75	Multi-Locus Sequence Typing of Bartonella henselae Isolates from Three Continents Reveals Hypervirulent and Feline-Associated Clones. PLoS ONE, 2007, 2, e1346.	1.1	47
76	Evidence for Host-Genotype Associations of Borrelia burgdorferi Sensu Stricto. PLoS ONE, 2016, 11, e0149345.	1.1	44
77	WGS of 1058 Enterococcus faecium 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. Journal of Antimicrobial Chemotherapy, 2019, 74, 1776-1785.	1.3	43
78	Recent mixing of Vibrio parahaemolyticus populations. ISME Journal, 2019, 13, 2578-2588.	4.4	41
79	Genomic analysis of 495 vancomycin-resistantEnterococcus faeciumreveals broad dissemination of avanAplasmid in more than 19 clones from Copenhagen, Denmark. Journal of Antimicrobial Chemotherapy, 2017, 72, 40-47.	1.3	40
80	Atypical AT Skew in Firmicute Genomes Results from Selection and Not from Mutation. PLoS Genetics, 2011, 7, e1002283.	1.5	36
81	Enantiomeric profiling of quinolones and quinolones resistance gene qnrS in European wastewaters. Water Research, 2020, 175, 115653.	5.3	36
82	Whole genome sequencing and phylogenetic analysis of strains of the agent of Lyme disease Borrelia burgdorferi from Canadian emergence zones. Scientific Reports, 2018, 8, 10552.	1.6	34
83	Microevolution of Renibacterium salmoninarum: evidence for intercontinental dissemination associated with fish movements. ISME Journal, 2014, 8, 746-756.	4.4	32
84	Enantioselective fractionation of fluoroquinolones in the aqueous environment using chiral liquid chromatography coupled with tandem mass spectrometry. Chemosphere, 2018, 206, 376-386.	4.2	31
85	Transmission of Staphylococcus aureus from Humans to Green Monkeys in The Gambia as Revealed by Whole-Genome Sequencing. Applied and Environmental Microbiology, 2016, 82, 5910-5917.	1.4	30
86	Databases and software for the comparison of prokaryotic genomes. Microbiology (United Kingdom), 2005, 151, 2125-2132.	0.7	29
87	Alternative Splice in Alternative Lice. Molecular Biology and Evolution, 2015, 32, 2749-2759.	3.5	29
88	Large-Scale Comparative Genomic Ranking of Taxonomically Restricted Genes (TRGs) in Bacterial and Archaeal Genomes. PLoS ONE, 2007, 2, e324.	1.1	28
89	Multilocus sequence typing using mitochondrial genes (mtMLST) reveals geographic population structure of Ixodes ricinus ticks. Ticks and Tick-borne Diseases, 2014, 5, 152-160.	1.1	25
90	The Diversity and Geographical Structure of Orientia tsutsugamushi Strains from Scrub Typhus Patients in Laos. PLoS Neglected Tropical Diseases, 2015, 9, e0004024.	1.3	25

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91	Using the wax moth larvaGalleria mellonellainfection model to detect emerging bacterial pathogens. PeerJ, 2019, 6, e6150.	0.9	24
92	The rise and fall of deleterious mutation. Research in Microbiology, 2007, 158, 779-786.	1.0	23
93	Multi-locus sequence typing of Ixodes ricinus and its symbiont Candidatus Midichloria mitochondrii across Europe reveals evidence of local co-cladogenesis in Scotland. Ticks and Tick-borne Diseases, 2019, 10, 52-62.	1.1	22
94	The role of stereochemistry of antibiotic agents in the development of antibiotic resistance in the environment. Environment International, 2020, 139, 105681.	4.8	21
95	Identifying the effect of patient sharing on between-hospital genetic differentiation of methicillin-resistant Staphylococcus aureus. Genome Medicine, 2016, 8, 18.	3.6	20
96	Bayesian identification of bacterial strains from sequencing data. Microbial Genomics, 2016, 2, e000075.	1.0	19
97	Population genetic structuring of methicillin-resistant Staphylococcus aureus clone EMRSA-15 within UK reflects patient referral patterns. Microbial Genomics, 2017, 3, e000113.	1.0	19
98	Gene Composition as a Potential Barrier to Large Recombinations in the Bacterial Pathogen Klebsiella pneumoniae. Genome Biology and Evolution, 2019, 11, 3240-3251.	1.1	18
99	Closed genome sequences of Staphylococcus lloydii sp. nov. and Staphylococcus durrellii sp. nov. isolated from captive fruit bats (Pteropus livingstonii). International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	18
100	Real time monitoring of <scp>Aeromonas salmonicida</scp> evolution in response to successive antibiotic therapies in a commercial fish farm. Environmental Microbiology, 2019, 21, 1113-1123.	1.8	16
101	Enterobacteriaceae: joining the dots with pan-European epidemiology. Lancet Infectious Diseases, The, 2017, 17, 118-119.	4.6	14
102	Identifying copy number variation of the dominant virulence factors msa and p22 within genomes of the fish pathogen Renibacterium salmoninarum. Microbial Genomics, 2016, 2, e000055.	1.0	14
103	The impact of host metapopulation structure on the population genetics of colonizing bacteria. Journal of Theoretical Biology, 2016, 396, 53-62.	0.8	13
104	High-resolution sweep metagenomics using fast probabilistic inference. Wellcome Open Research, 2020, 5, 14.	0.9	13
105	Genomic epidemiology of the commercially important pathogen Renibacterium salmoninarum within the Chilean salmon industry. Microbial Genomics, 2018, 4, .	1.0	12
106	Challenges in realising the potential of wastewater-based epidemiology to quantitatively monitor and predict the spread of disease. Journal of Water and Health, 2022, 20, 1038-1050.	1.1	12
107	Evidence for an effect of landscape connectivity on Borrelia burgdorferi sensu stricto dispersion in a zone of range expansion. Ticks and Tick-borne Diseases, 2018, 9, 1407-1415.	1.1	11
108	Quantifying bacterial evolution in the wild: A birthday problem for Campylobacter lineages. PLoS Genetics, 2021, 17, e1009829.	1.5	11

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109	A high prevalence of bla OXA-48 in Klebsiella (Raoultella) ornithinolytica and related species in hospital wastewater in South West England. Microbial Genomics, 2021, 7, .	1.0	10
110	Co-evolutionary Signals IdentifyBurkholderia pseudomalleiSurvival Strategies in a Hostile Environment. Molecular Biology and Evolution, 2022, 39, .	3.5	10
111	Multilocus variable-number tandem-repeat genotyping of Renibacterium salmoninarum, a bacterium causing bacterial kidney disease in salmonid fish. BMC Microbiology, 2013, 13, 285.	1.3	7
112	Draft Genome Sequences of Salinivibrio proteolyticus, Salinivibrio sharmensis, Salinivibrio siamensis, Salinivibrio costicola subsp. alcaliphilus , Salinivibrio costicola subsp. vallismortis , and 29 New Isolates Belonging to the Genus Salinivibrio. Genome Announcements, 2017, 5, .	0.8	7
113	A Hopeful Sea-Monster: A Very Large Homologous Recombination Event Impacting the Core Genome of the Marine Pathogen Vibrio anguillarum. Frontiers in Microbiology, 2020, 11, 1430.	1.5	7
114	Fatal exudative dermatitis in island populations of red squirrels (Sciurus vulgaris): spillover of a virulent Staphylococcus aureus clone (ST49) from reservoir hosts. Microbial Genomics, 2021, 7, .	1.0	7
115	Sugar concentration influences decision making in <i>Apis mellifera</i> L. workers during early-stage honey storage behaviour. Open Journal of Animal Sciences, 2013, 03, 210-218.	0.2	7
116	The emergence and spread of dysentery. Nature Genetics, 2012, 44, 964-965.	9.4	6
117	Phylogeographical Analysis Reveals the Historic Origin, Emergence, and Evolutionary Dynamics of Methicillin-Resistant Staphylococcus aureus ST228. Frontiers in Microbiology, 2020, 11, 2063.	1.5	6
118	Stem Region of tRNA Genes Favors Transition Substitution Towards Keto Bases in Bacteria. Journal of Molecular Evolution, 2022, 90, 114-123.	0.8	6
119	Toward a synthesis of genotypic typing and phenotypic inference in the genomics era. Future Microbiology, 2015, 10, 1897-1899.	1.0	5
120	Stereoselective Bacterial Metabolism of Antibiotics in Environmental Bacteria â€“ A Novel Biochemical Workflow. Frontiers in Microbiology, 2021, 12, 562157.	1.5	4
121	Population structure and evolutionary dynamics of pathogenic bacteria. BioEssays, 2000, 22, 1115-1122.	1.2	4
122	Genome of Superficieibacter maynardsmithii, a novel, antibiotic susceptible representative of Enterobacteriaceae. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	3
123	Stereoselective metabolism of chloramphenicol by bacteria isolated from wastewater, and the importance of stereochemistry in environmental risk assessments for antibiotics. Water Research, 2022, 217, 118415.	5.3	3
124	High tech research reveals preferential feeding in honey bees. Journal of Apicultural Research, 2019, 58, 471-477.	0.7	2
125	Covering All the Bases: The Promise of Genome-Wide Sequence Data for Large Population Samples of Bacteria. Social and Ecological Interactions in the Galapagos Islands, 2013, , 41-62.	0.4	2
126	The importance of cross-disciplinary research to combat antimicrobial resistance: introducing a new pop-up journal, X-AMR. Microbial Genomics, 2018, 4, .	1.0	2

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127	Wastewater Treatment Works: A Last Line of Defense for Preventing Antibiotic Resistance Entry Into the Environment. Frontiers in Water, 2022, 4, .	1.0	2
128	Population Genetics of Bacterial Pathogens. , 2002, , 445-484.		1
129	The Evolution and Dynamics of Methicillin-Resistant Staphylococcus aureus. , 2011, , 669-688.		1
130	Towards a Synthesis of Population Genomics and Epidemiology. , 2015, , 337-345.		0