

Jeffrey T Foster

List of Publications by Year in Descending Order

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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.

119
papers

4,305
citations

38
h-index

62
g-index

125
ext. papers

5,461
ext. citations

5.7
avg, IF

5.12
L-index

#	Paper	IF	Citations
119	Experimental inoculation trial to determine the effects of temperature and humidity on White-nose Syndrome in hibernating bats.. <i>Scientific Reports</i> , 2022 , 12, 971	4.9	2
118	RESCRIPT: Reproducible sequence taxonomy reference database management. <i>PLoS Computational Biology</i> , 2021 , 17, e1009581	5	30
117	Genetic structure and population history in two critically endangered Kauaʻi honeycreepers. <i>Conservation Genetics</i> , 2021 , 22, 601-614	2.6	1
116	Canine brucellosis in Costa Rica reveals widespread <i>Brucella canis</i> infection and the recent introduction of foreign strains. <i>Veterinary Microbiology</i> , 2021 , 257, 109072	3.3	1
115	First Case of Brucellosis Caused by an Amphibian-type <i>Brucella</i> . <i>Clinical Infectious Diseases</i> , 2021 , 72, e404-e407	11.6	4
114	Ecological correlates of species roles in highly invaded seed dispersal networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	13
113	Mobility and infectiousness in the spatial spread of an emerging fungal pathogen. <i>Journal of Animal Ecology</i> , 2021 , 90, 1134-1141	4.7	2
112	Lord of the Diptera (and Moths and a Spider): Molecular Diet Analyses and Foraging Ecology of Indiana Bats in Illinois. <i>Frontiers in Ecology and Evolution</i> , 2021 , 9,	3.7	4
111	Comprehensive estimation of spatial and temporal migratory connectivity across the annual cycle to direct conservation efforts. <i>Ecography</i> , 2021 , 44, 665-679	6.5	12
110	Emerging diversity and ongoing expansion of the genus <i>Brucella</i> . <i>Infection, Genetics and Evolution</i> , 2021 , 92, 104865	4.5	4
109	Pathogen to commensal? Longitudinal within-host population dynamics, evolution, and adaptation during a chronic >16-year <i>Burkholderia pseudomallei</i> infection. <i>PLoS Pathogens</i> , 2020 , 16, e1008298	7.6	6
108	Environmental reservoir dynamics predict global infection patterns and population impacts for the fungal disease white-nose syndrome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 7255-7262	11.5	26
107	Ambiguities in using telomere length for age determination in two North American bat species. <i>Journal of Mammalogy</i> , 2020 , 101, 958-969	1.8	2
106	Genomic epizootiology of a <i>Brucella abortus</i> outbreak in Northern Ireland (1997-2012). <i>Infection, Genetics and Evolution</i> , 2020 , 81, 104235	4.5	4
105	Evolutionary history and current distribution of the West Mediterranean lineage of in Italy. <i>Microbial Genomics</i> , 2020 , 6,	4.4	4
104	Ricin forensics: comparisons to microbial forensics 2020 , 241-250		
103	Forensic analysis in bacterial pathogens 2020 , 123-140		

102	A total crapshoot? Evaluating bioinformatic decisions in animal diet metabarcoding analyses. <i>Ecology and Evolution</i> , 2020 , 10, 9721-9739	2.8	10
101	Mating type determination within a microsatellite multiplex for the fungal pathogen <i>Pseudogymnoascus destructans</i> , the causative agent of white-nose disease in bats. <i>Conservation Genetics Resources</i> , 2020 , 12, 45-48	0.8	2
100	Persistence of <i>Brucella abortus</i> lineages revealed by genomic characterization and phylodynamic analysis. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008235	4.8	6
99	Detection of on Wisconsin Bats During Summer. <i>Journal of Wildlife Diseases</i> , 2019 , 55, 673-677	1.3	6
98	Structure, spatial dynamics, and stability of novel seed dispersal mutualistic networks in Hawaii. <i>Science</i> , 2019 , 364, 78-82	33.3	45
97	Field trial of a probiotic bacteria to protect bats from white-nose syndrome. <i>Scientific Reports</i> , 2019 , 9, 9158	4.9	26
96	Population genetics of an island invasion by Japanese Bush-Warblers in Hawaii, USA Genética poblacional de una invasión de islas por <i>Cettia diphone</i> en Hawái Bush-warbler invasion genetics in Hawaii. <i>Auk</i> , 2018 , 135, 171-180	2.1	3
95	Extreme sensitivity to ultraviolet light in the fungal pathogen causing white-nose syndrome of bats. <i>Nature Communications</i> , 2018 , 9, 35	17.4	31
94	Energy conserving thermoregulatory patterns and lower disease severity in a bat resistant to the impacts of white-nose syndrome. <i>Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology</i> , 2018 , 188, 163-176	2.2	32
93	Whole genome SNP analysis suggests unique virulence factor differences of the Beijing and Manila families of <i>Mycobacterium tuberculosis</i> found in Hawaii. <i>PLoS ONE</i> , 2018 , 13, e0201146	3.7	7
92	Genomic sequencing is required for identification of tuberculosis transmission in Hawaii. <i>BMC Infectious Diseases</i> , 2018 , 18, 608	4	5
91	Cryptic connections illuminate pathogen transmission within community networks. <i>Nature</i> , 2018 , 563, 710-713	50.4	33
90	Characterization of Microsatellites in <i>Pseudogymnoascus destructans</i> for White-nose Syndrome Genetic Analysis. <i>Journal of Wildlife Diseases</i> , 2017 , 53, 869-874	1.3	4
89	Similar dietary but different numerical responses to nonnative tamarisk (<i>Tamarix</i> spp.) by two native warblers. <i>Biological Invasions</i> , 2017 , 19, 1935-1950	2.7	8
88	<i>Brucella</i> spp. of amphibians comprise genomically diverse motile strains competent for replication in macrophages and survival in mammalian hosts. <i>Scientific Reports</i> , 2017 , 7, 44420	4.9	41
87	Resistance in persisting bat populations after white-nose syndrome invasion. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017 , 372,	5.8	64
86	Pathogen dynamics during invasion and establishment of white-nose syndrome explain mechanisms of host persistence. <i>Ecology</i> , 2017 , 98, 624-631	4.6	71
85	AOAC SMPR 2016.009. <i>Journal of AOAC INTERNATIONAL</i> , 2017 , 100, 255-260	1.7	

84	White-nose syndrome fungus, <i>Pseudogymnoascus destructans</i> , on bats captured emerging from caves during winter in the southeastern United States. <i>BMC Zoology</i> , 2017 , 2,	1.8	10
83	African Lineage Isolates from Omani Livestock. <i>Frontiers in Microbiology</i> , 2017 , 8, 2702	5.7	15
82	Origins and global context of <i>Brucella abortus</i> in Italy. <i>BMC Microbiology</i> , 2017 , 17, 28	4.5	18
81	Efficacy of a probiotic bacterium to treat bats affected by the disease white-nose syndrome. <i>Journal of Applied Ecology</i> , 2017 , 54, 701-708	5.8	40
80	Phylogenetics of a Fungal Invasion: Origins and Widespread Dispersal of White-Nose Syndrome. <i>MBio</i> , 2017 , 8,	7.8	45
79	White-Nose Syndrome Fungus in a 1918 Bat Specimen from France. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1611-1612	10.2	21
78	Connecting Resource Tracking by Frugivores to Temporal Variation in Seed Dispersal Networks. <i>Frontiers in Ecology and Evolution</i> , 2017 , 5,	3.7	6
77	Drivers of variation in species impacts for a multi-host fungal disease of bats. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016 , 371,	5.8	63
76	Genomics reveals historic and contemporary transmission dynamics of a bacterial disease among wildlife and livestock. <i>Nature Communications</i> , 2016 , 7, 11448	17.4	65
75	First Detection of Bat White-Nose Syndrome in Western North America. <i>MSphere</i> , 2016 , 1,	5	55
74	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing <i>Clostridia</i> . <i>BMC Genomics</i> , 2016 , 17, 180	4.5	56
73	Host persistence or extinction from emerging infectious disease: insights from white-nose syndrome in endemic and invading regions. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016 , 283, 20152861	4.4	33
72	White-Nose Syndrome Disease Severity and a Comparison of Diagnostic Methods. <i>EcoHealth</i> , 2016 , 13, 60-71	3.1	24
71	Genomics in Conservation: Case Studies and Bridging the Gap between Data and Application. <i>Trends in Ecology and Evolution</i> , 2016 , 31, 81-83	10.9	115
70	Widespread Bat White-Nose Syndrome Fungus, Northeastern China. <i>Emerging Infectious Diseases</i> , 2016 , 22, 140-2	10.2	40
69	Deconstructing the Bat Skin Microbiome: Influences of the Host and the Environment. <i>Frontiers in Microbiology</i> , 2016 , 7, 1753	5.7	50
68	Nesting success of native and introduced forest birds on the island of Kauaʻi. <i>Journal of Avian Biology</i> , 2016 , 47, 252-262	1.9	2
67	Application of genetics and genomics to wildlife epidemiology. <i>Journal of Wildlife Management</i> , 2016 , 80, 593-608	1.9	33

66	Use of Multiple Sequencing Technologies To Produce a High-Quality Genome of the Fungus <i>Pseudogymnoascus destructans</i> , the Causative Agent of Bat White-Nose Syndrome. <i>Genome Announcements</i> , 2016 , 4,		16
65	VNTR diversity in <i>Yersinia pestis</i> isolates from an animal challenge study reveals the potential for in vitro mutations during laboratory cultivation. <i>Infection, Genetics and Evolution</i> , 2016 , 45, 297-302	4.5	
64	Whole-genome sequencing of <i>Burkholderia pseudomallei</i> isolates from an unusual melioidosis case identifies a polyclonal infection with the same multilocus sequence type. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 282-6	9.7	23
63	First isolation and characterization of <i>Brucella microti</i> from wild boar. <i>BMC Veterinary Research</i> , 2015 , 11, 147	2.7	20
62	Invasion dynamics of white-nose syndrome fungus, midwestern United States, 2012-2014. <i>Emerging Infectious Diseases</i> , 2015 , 21, 1023-6	10.2	63
61	Molecular detection of the causative agent of white-nose syndrome on Rafinesque's big-eared bats (<i>Corynorhinus rafinesquii</i>) and two species of migratory bats in the southeastern USA. <i>Journal of Wildlife Diseases</i> , 2015 , 51, 519-22	1.3	28
60	First confirmation of <i>Pseudogymnoascus destructans</i> in British bats and hibernacula. <i>Veterinary Record</i> , 2015 , 177, 73	0.9	9
59	Host and pathogen ecology drive the seasonal dynamics of a fungal disease, white-nose syndrome. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015 , 282, 20142335	4.4	139
58	Phylogenetically typing bacterial strains from partial SNP genotypes observed from direct sequencing of clinical specimen metagenomic data. <i>Genome Medicine</i> , 2015 , 7, 52	14.4	32
57	Genome Sequences of 11 <i>Brucella abortus</i> Isolates from Persistently Infected Italian Regions. <i>Genome Announcements</i> , 2015 , 3,		6
56	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. <i>Frontiers in Genetics</i> , 2015 , 6, 235	4.5	109
55	Efficacy of Visual Surveys for White-Nose Syndrome at Bat Hibernacula. <i>PLoS ONE</i> , 2015 , 10, e0133390	3.7	26
54	Investigation of <i>Yersinia pestis</i> Laboratory Adaptation through a Combined Genomics and Proteomics Approach. <i>PLoS ONE</i> , 2015 , 10, e0142997	3.7	14
53	Genomic sequences of six botulinum neurotoxin-producing strains representing three clostridial species illustrate the mobility and diversity of botulinum neurotoxin genes. <i>Infection, Genetics and Evolution</i> , 2015 , 30, 102-113	4.5	47
52	Disease alters macroecological patterns of North American bats. <i>Global Ecology and Biogeography</i> , 2015 , 24, 741-749	6.1	148
51	Breeding biology of two endangered forest birds on the island of Kauai, Hawaii. <i>Condor</i> , 2015 , 117, 31-40.	4.1	8
50	Comparative phylogenomics and evolution of the Brucellae reveal a path to virulence. <i>Journal of Bacteriology</i> , 2014 , 196, 920-30	3.5	73
49	Changing climate and the altitudinal range of avian malaria in the Hawaiian Islands - an ongoing conservation crisis on the island of Kauai. <i>Global Change Biology</i> , 2014 , 20, 2426-36	11.4	64

48	Genetic relatedness of <i>Brucella suis</i> biovar 2 isolates from hares, wild boars and domestic pigs. <i>Veterinary Microbiology</i> , 2014 , 172, 492-8	3.3	25
47	Genome Sequence of <i>Bacillus anthracis</i> ST1, a Sterne-Like Georgian/Soviet Vaccine Strain. <i>Genome Announcements</i> , 2014 , 2,		5
46	Incongruence between multi-locus sequence analysis (MLSA) and whole-genome-based phylogenies: <i>Pseudomonas syringae</i> pathovar pisi as a cautionary tale. <i>Molecular Plant Pathology</i> , 2014 , 15, 461-5	5.7	19
45	No selection on immunological markers in response to a highly virulent pathogen in an Arctic breeding bird. <i>Evolutionary Applications</i> , 2014 , 7, 765-73	4.8	10
44	Complete Genome Sequences of Beijing and Manila Family Strains of <i>Mycobacterium tuberculosis</i> . <i>Genome Announcements</i> , 2014 , 2,		4
43	Development and assessment of multiplex high resolution melting assay as a tool for rapid single-tube identification of five <i>Brucella</i> species. <i>BMC Research Notes</i> , 2014 , 7, 903	2.3	15
42	MetaGeniE: characterizing human clinical samples using deep metagenomic sequencing. <i>PLoS ONE</i> , 2014 , 9, e110915	3.7	12
41	Highly sensitive quantitative PCR for the detection and differentiation of <i>Pseudogymnoascus destructans</i> and other <i>Pseudogymnoascus</i> species. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 1726-31	4.8	35
40	Spotted bat (<i>Euderma maculatum</i>) microsatellite discovery using illumina sequencing. <i>Conservation Genetics Resources</i> , 2014 , 6, 457-459	0.8	1
39	Investigating genetic diversity of <i>Brucella abortus</i> and <i>Brucella melitensis</i> in Italy with MLVA-16. <i>Infection, Genetics and Evolution</i> , 2013 , 19, 59-70	4.5	41
38	Within-host evolution of <i>Brucella canis</i> during a canine brucellosis outbreak in a kennel. <i>BMC Veterinary Research</i> , 2013 , 9, 76	2.7	14
37	Feral swine brucellosis in the United States and prospective genomic techniques for disease epidemiology. <i>Veterinary Microbiology</i> , 2013 , 166, 1-10	3.3	27
36	<i>Francisella guangzhouensis</i> sp. nov., isolated from air-conditioning systems. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013 , 63, 3628-3635	2.2	33
35	Worldwide phylogenetic relationship of avian poxviruses. <i>Journal of Virology</i> , 2013 , 87, 4938-51	6.6	79
34	Draft Genome Sequences of Two Bulgarian <i>Bacillus anthracis</i> Strains. <i>Genome Announcements</i> , 2013 , 1, e0015213		2
33	<i>Staphylococcus aureus</i> CC398: Host Adaptation and Emergence of Methicillin Resistance in Livestock. <i>MBio</i> , 2013 , 4,	7.8	11
32	The innate immune response may be important for surviving plague in wild Gunnison [®] prairie dogs. <i>Journal of Wildlife Diseases</i> , 2013 , 49, 920-31	1.3	11
31	Accurate and rapid identification of the <i>Burkholderia pseudomallei</i> near-neighbour, <i>Burkholderia ubonensis</i> , using real-time PCR. <i>PLoS ONE</i> , 2013 , 8, e71647	3.7	17

30	Genotyping of Brucella species using clade specific SNPs. <i>BMC Microbiology</i> , 2012 , 12, 110	4.5	19
29	Molecular epidemiologic investigation of an anthrax outbreak among heroin users, Europe. <i>Emerging Infectious Diseases</i> , 2012 , 18, 1307-13	10.2	58
28	Staphylococcus aureus CC398: host adaptation and emergence of methicillin resistance in livestock. <i>MBio</i> , 2012 , 3,	7.8	504
27	Development and validation of Burkholderia pseudomallei-specific real-time PCR assays for clinical, environmental or forensic detection applications. <i>PLoS ONE</i> , 2012 , 7, e37723	3.7	33
26	Ricin Forensics: Comparisons to Microbial Forensics 2011 , 315-326		1
25	Forensic Analysis in Bacterial Pathogens 2011 , 259-276		
24	Castor bean organelle genome sequencing and worldwide genetic diversity analysis. <i>PLoS ONE</i> , 2011 , 6, e21743	3.7	77
23	Interactions between the yeast <i>Ogataea pini</i> and filamentous fungi associated with the western pine beetle. <i>Microbial Ecology</i> , 2011 , 61, 626-34	4.4	40
22	Phylogeography of <i>Francisella tularensis</i> subspecies holarctica from the country of Georgia. <i>BMC Microbiology</i> , 2011 , 11, 139	4.5	33
21	Multidrug-Resistant <i>Staphylococcus aureus</i> in US Meat and Poultry. <i>Clinical Infectious Diseases</i> , 2011 , 52, 1227-30	11.6	171
20	Epidemiological tracking and population assignment of the non-clonal bacterium, <i>Burkholderia pseudomallei</i> . <i>PLoS Neglected Tropical Diseases</i> , 2011 , 5, e1381	4.8	22
19	Within-host evolution of <i>Burkholderia pseudomallei</i> in four cases of acute melioidosis. <i>PLoS Pathogens</i> , 2010 , 6, e1000725	7.6	45
18	Single nucleotide polymorphisms for assessing genetic diversity in castor bean (<i>Ricinus communis</i>). <i>BMC Plant Biology</i> , 2010 , 10, 13	5.3	78
17	Pre-Columbian origins for North American anthrax. <i>PLoS ONE</i> , 2009 , 4, e4813	3.7	51
16	Whole-genome-based phylogeny and divergence of the genus <i>Brucella</i> . <i>Journal of Bacteriology</i> , 2009 , 191, 2864-70	3.5	119
15	Phylogeographic reconstruction of a bacterial species with high levels of lateral gene transfer. <i>BMC Biology</i> , 2009 , 7, 78	7.3	129
14	Phylogenetic understanding of clonal populations in an era of whole genome sequencing. <i>Infection, Genetics and Evolution</i> , 2009 , 9, 1010-9	4.5	91
13	Convergent evolution of <i>RreepersRin</i> the Hawaiian honeycreeper radiation. <i>Biology Letters</i> , 2009 , 5, 221-46	3.6	22

12	Real-time PCR assays of single-nucleotide polymorphisms defining the major Brucella clades. <i>Journal of Clinical Microbiology</i> , 2008 , 46, 296-301	9.7	50
11	Real-Time PCR Assays of Single-Nucleotide Polymorphisms Defining the Major Brucella Clades. <i>Journal of Clinical Microbiology</i> , 2008 , 46, 2474-2474	9.7	78
10	Ground-based rodent control in a remote Hawaiian rainforest on Maui. <i>Pacific Conservation Biology</i> , 2008 , 14, 206	1.2	6
9	Genetic structure and evolved malaria resistance in Hawaiian honeycreepers. <i>Molecular Ecology</i> , 2007 , 16, 4738-46	5.7	74
8	Introduced birds and the fate of hawaiian rainforests. <i>Conservation Biology</i> , 2007 , 21, 1248-57	6	81
7	BREEDING BIOLOGY AND SUCCESS OF A REINTRODUCED POPULATION OF THE CRITICALLY ENDANGERED PUAIOHI (MYADESTES PALMERI). <i>Auk</i> , 2006 , 123, 753	2.1	16
6	Breeding Biology and Success of a Reintroduced Population of the Critically Endangered Puaiohi (Myadestes Palmeri). <i>Auk</i> , 2006 , 123, 753-763	2.1	16
5	Long-Term Population Changes of Native and Introduced Birds in the Alakaʻi Swamp, Kauaʻi <i>Conservation Biology</i> , 2004 , 18, 716-725	6	23
4	Survival, dispersal, and home-range establishment of reintroduced captive-bred puaiohi, Myadestes palmeri. <i>Biological Conservation</i> , 2003 , 111, 1-9	6.2	49
3	Mobility and infectiousness in the spatial spread of an emerging fungal pathogen		1
2	RESCRIPT: Reproducible sequence taxonomy reference database management for the masses		24
1	White-nose syndrome restructures bat skin microbiomes		4