

Jeffrey T Foster

List of Publications by Citations

Source: <https://exaly.com/author-pdf/1550172/jeffrey-t-foster-publications-by-citations.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Staphylococcus aureus CC398: host adaptation and emergence of methicillin resistance in livestock. <i>MBio</i> , 2012 , 3,	7.8	504
118	Multidrug-Resistant Staphylococcus aureus in US Meat and Poultry. <i>Clinical Infectious Diseases</i> , 2011 , 52, 1227-30	11.6	171
117	Disease alters macroecological patterns of North American bats. <i>Global Ecology and Biogeography</i> , 2015 , 24, 741-749	6.1	148
116	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
115	Phylogeographic reconstruction of a bacterial species with high levels of lateral gene transfer. <i>BMC Biology</i> , 2009 , 7, 78	7.3	129
114	Whole-genome-based phylogeny and divergence of the genus Brucella. <i>Journal of Bacteriology</i> , 2009 , 191, 2864-70	3.5	119
113	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
112	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. <i>Frontiers in Genetics</i> , 2015 , 6, 235	4.5	109
111	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
110	Introduced birds and the fate of hawaiian rainforests. <i>Conservation Biology</i> , 2007 , 21, 1248-57	6	81
109	Worldwide phylogenetic relationship of avian poxviruses. <i>Journal of Virology</i> , 2013 , 87, 4938-51	6.6	79
108	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
107	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
106	Castor bean organelle genome sequencing and worldwide genetic diversity analysis. <i>PLoS ONE</i> , 2011 , 6, e21743	3.7	77
105	Genetic structure and evolved malaria resistance in Hawaiian honeycreepers. <i>Molecular Ecology</i> , 2007 , 16, 4738-46	5.7	74
104	Comparative phylogenomics and evolution of the Brucellae reveal a path to virulence. <i>Journal of Bacteriology</i> , 2014 , 196, 920-30	3.5	73
103	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

102	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
101	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
100	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
99	Invasion dynamics of white-nose syndrome fungus, midwestern United States, 2012-2014. <i>Emerging Infectious Diseases</i> , 2015 , 21, 1023-6	10.2	63
98	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
97	Molecular epidemiologic investigation of an anthrax outbreak among heroin users, Europe. <i>Emerging Infectious Diseases</i> , 2012 , 18, 1307-13	10.2	58
96	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing Clostridia. <i>BMC Genomics</i> , 2016 , 17, 180	4.5	56
95	First Detection of Bat White-Nose Syndrome in Western North America. <i>MSphere</i> , 2016 , 1,	5	55
94	Pre-Columbian origins for North American anthrax. <i>PLoS ONE</i> , 2009 , 4, e4813	3.7	51
93	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
92	Deconstructing the Bat Skin Microbiome: Influences of the Host and the Environment. <i>Frontiers in Microbiology</i> , 2016 , 7, 1753	5.7	50
91	Survival, dispersal, and home-range establishment of reintroduced captive-bred puaiuhi, <i>Myadestes palmeri</i> . <i>Biological Conservation</i> , 2003 , 111, 1-9	6.2	49
90	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
89	Structure, spatial dynamics, and stability of novel seed dispersal mutualistic networks in Hawaii. <i>Science</i> , 2019 , 364, 78-82	33.3	45
88	Phylogenetics of a Fungal Invasion: Origins and Widespread Dispersal of White-Nose Syndrome. <i>MBio</i> , 2017 , 8,	7.8	45
87	Within-host evolution of <i>Burkholderia pseudomallei</i> in four cases of acute melioidosis. <i>PLoS Pathogens</i> , 2010 , 6, e1000725	7.6	45
86	<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
85	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

84	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
83	Widespread Bat White-Nose Syndrome Fungus, Northeastern China. <i>Emerging Infectious Diseases</i> , 2016 , 22, 140-2	10.2	40
82	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
81	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
80	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
79	<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
78	Phylogeography of <i>Francisella tularensis</i> subspecies <i>holarctica</i> from the country of Georgia. <i>BMC Microbiology</i> , 2011 , 11, 139	4.5	33
77	Development and validation of <i>Burkholderia pseudomallei</i> -specific real-time PCR assays for clinical, environmental or forensic detection applications. <i>PLoS ONE</i> , 2012 , 7, e37723	3.7	33
76	Application of genetics and genomics to wildlife epidemiology. <i>Journal of Wildlife Management</i> , 2016 , 80, 593-608	1.9	33
75	Cryptic connections illuminate pathogen transmission within community networks. <i>Nature</i> , 2018 , 563, 710-713	50.4	33
74	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
73	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
72	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
71	RESCRIPT: Reproducible sequence taxonomy reference database management. <i>PLoS Computational Biology</i> , 2021 , 17, e1009581	5	30
70	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
69	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
68	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
67	Field trial of a probiotic bacteria to protect bats from white-nose syndrome. <i>Scientific Reports</i> , 2019 , 9, 9158	4.9	26

66	Efficacy of Visual Surveys for White-Nose Syndrome at Bat Hibernacula. <i>PLoS ONE</i> , 2015 , 10, e0133390	3.7	26
65	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
64	White-Nose Syndrome Disease Severity and a Comparison of Diagnostic Methods. <i>EcoHealth</i> , 2016 , 13, 60-71	3.1	24
63	RESCRIPT: Reproducible sequence taxonomy reference database management for the masses		24
62	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
61	Long-Term Population Changes of Native and Introduced Birds in the Alakaʻi Swamp, Kauaʻi	6	23
60	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
59	Convergent evolution of <i>Reepers</i> in the Hawaiian honeycreeper radiation. <i>Biology Letters</i> , 2009 , 5, 221-46	3.46	22
58	White-Nose Syndrome Fungus in a 1918 Bat Specimen from France. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1611-1612	10.2	21
57	First isolation and characterization of <i>Brucella microti</i> from wild boar. <i>BMC Veterinary Research</i> , 2015 , 11, 147	2.7	20
56	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
55	Genotyping of <i>Brucella</i> species using clade specific SNPs. <i>BMC Microbiology</i> , 2012 , 12, 110	4.5	19
54	Origins and global context of <i>Brucella abortus</i> in Italy. <i>BMC Microbiology</i> , 2017 , 17, 28	4.5	18
53	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
52	BREEDING BIOLOGY AND SUCCESS OF A REINTRODUCED POPULATION OF THE CRITICALLY ENDANGERED PUAIOHI (MYADESTES PALMERI). <i>Auk</i> , 2006 , 123, 753	2.1	16
51	Breeding Biology and Success of a Reintroduced Population of the Critically Endangered Puaiohi (<i>Myadestes Palmeri</i>). <i>Auk</i> , 2006 , 123, 753-763	2.1	16
50	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
49	African Lineage Isolates from Omani Livestock. <i>Frontiers in Microbiology</i> , 2017 , 8, 2702	5.7	15

48	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
47	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
46	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
45	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
44	MetaGeniE: characterizing human clinical samples using deep metagenomic sequencing. <i>PLoS ONE</i> , 2014 , 9, e110915	3.7	12
43	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
42	<i>Staphylococcus aureus</i> CC398: Host Adaptation and Emergence of Methicillin Resistance in Livestock. <i>MBio</i> , 2013 , 4,	7.8	11
41	The innate immune response may be important for surviving plague in wild Gunnison's prairie dogs. <i>Journal of Wildlife Diseases</i> , 2013 , 49, 920-31	1.3	11
40	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
39	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
38	A total crapshoot? Evaluating bioinformatic decisions in animal diet metabarcoding analyses. <i>Ecology and Evolution</i> , 2020 , 10, 9721-9739	2.8	10
37	First confirmation of <i>Pseudogymnoascus destructans</i> in British bats and hibernacula. <i>Veterinary Record</i> , 2015 , 177, 73	0.9	9
36	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
35	Breeding biology of two endangered forest birds on the island of Kauai, Hawaii. <i>Condor</i> , 2015 , 117, 31-40.	0.1	8
34	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
33	Detection of on Wisconsin Bats During Summer. <i>Journal of Wildlife Diseases</i> , 2019 , 55, 673-677	1.3	6
32	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
31	Connecting Resource Tracking by Frugivores to Temporal Variation in Seed Dispersal Networks. <i>Frontiers in Ecology and Evolution</i> , 2017 , 5,	3.7	6

30	Genome Sequences of 11 <i>Brucella abortus</i> Isolates from Persistently Infected Italian Regions. <i>Genome Announcements</i> , 2015 , 3,		6
29	Ground-based rodent control in a remote Hawaiian rainforest on Maui. <i>Pacific Conservation Biology</i> , 2008 , 14, 206	1.2	6
28	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
27	Genome Sequence of <i>Bacillus anthracis</i> ST1, a Sterne-Like Georgian/Soviet Vaccine Strain. <i>Genome Announcements</i> , 2014 , 2,		5
26	Genomic sequencing is required for identification of tuberculosis transmission in Hawaii. <i>BMC Infectious Diseases</i> , 2018 , 18, 608	4	5
25	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
24	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
23	Complete Genome Sequences of Beijing and Manila Family Strains of <i>Mycobacterium tuberculosis</i> . <i>Genome Announcements</i> , 2014 , 2,		4
22	Evolutionary history and current distribution of the West Mediterranean lineage of in Italy. <i>Microbial Genomics</i> , 2020 , 6,	4.4	4
21	White-nose syndrome restructures bat skin microbiomes		4
20	First Case of Brucellosis Caused by an Amphibian-type <i>Brucella</i> . <i>Clinical Infectious Diseases</i> , 2021 , 72, e404-e407	11.6	4
19	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
18	Emerging diversity and ongoing expansion of the genus <i>Brucella</i> . <i>Infection, Genetics and Evolution</i> , 2021 , 92, 104865	4.5	4
17	Population genetics of an island invasion by Japanese Bush-Warblers in Hawaii, USA <i>Genética poblacional de una invasión de islas por <i>Cettia diphone</i> en Hawái</i> Bush-warbler invasion genetics in Hawaii. <i>Auk</i> , 2018 , 135, 171-180	2.1	3
16	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
15	Draft Genome Sequences of Two Bulgarian <i>Bacillus anthracis</i> Strains. <i>Genome Announcements</i> , 2013 , 1, e0015213		2
14	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
13	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

12	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
11	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
10	Spotted bat (<i>Euderma maculatum</i>) microsatellite discovery using illumina sequencing. <i>Conservation Genetics Resources</i> , 2014 , 6, 457-459	0.8	1
9	Ricin Forensics: Comparisons to Microbial Forensics 2011 , 315-326		1
8	Mobility and infectiousness in the spatial spread of an emerging fungal pathogen		1
7	Genetic structure and population history in two critically endangered Kauaʻi honeycreepers. <i>Conservation Genetics</i> , 2021 , 22, 601-614	2.6	1
6	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
5	AOAC SMPR 2016.009. <i>Journal of AOAC INTERNATIONAL</i> , 2017 , 100, 255-260	1.7	
4	Forensic Analysis in Bacterial Pathogens 2011 , 259-276		
3	Ricin forensics: comparisons to microbial forensics 2020 , 241-250		
2	Forensic analysis in bacterial pathogens 2020 , 123-140		
1	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	