

Paul Keim

List of Publications by Year in descending order

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162
papers

11,320
citations

26567

56
h-index

37111

96
g-index

180
all docs

180
docs citations

180
times ranked

12166
citing authors

#	ARTICLE	IF	CITATIONS
1	Staphylococcus aureus CC398: Host Adaptation and Emergence of Methicillin Resistance in Livestock. MBio, 2012, 3, .	1.8	638
2	Yersinia pestis genome sequencing identifies patterns of global phylogenetic diversity. Nature Genetics, 2010, 42, 1140-1143.	9.4	504
3	Comparative Genome Sequencing for Discovery of Novel Polymorphisms in Bacillus anthracis. Science, 2002, 296, 2028-2033.	6.0	413
4	The Epidemic of Extended-Spectrum-β-Lactamase-Producing Escherichia coli ST131 Is Driven by a Single Highly Pathogenic Subclone, <i>H</i> 30-Rx. MBio, 2013, 4, e00377-13.	1.8	380
5	Yersinia pestis and the Plague of Justinian 541â€“543 AD: a genomic analysis. Lancet Infectious Diseases, The, 2014, 14, 319-326.	4.6	358
6	Global Genetic Population Structure of Bacillus anthracis. PLoS ONE, 2007, 2, e461.	1.1	317
7	Anthrax molecular epidemiology and forensics: using the appropriate marker for different evolutionary scales. Infection, Genetics and Evolution, 2004, 4, 205-213.	1.0	295
8	Population Genetics of Vibrio cholerae from Nepal in 2010: Evidence on the Origin of the Haitian Outbreak. MBio, 2011, 2, e00157-11.	1.8	268
9	The large-scale blast score ratio (LS-BSR) pipeline: a method to rapidly compare genetic content between bacterial genomes. PeerJ, 2014, 2, e332.	0.9	265
10	Phylogenetic discovery bias in Bacillus anthracis using single-nucleotide polymorphisms from whole-genome sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13536-13541.	3.3	243
11	NASP: an accurate, rapid method for the identification of SNPs in WGS datasets that supports flexible input and output formats. Microbial Genomics, 2016, 2, e000074.	1.0	237
12	Genomic Analysis of the Emergence and Rapid Global Dissemination of the Clonal Group 258 Klebsiella pneumoniae Pandemic. PLoS ONE, 2015, 10, e0133727.	1.1	195
13	Escherichia coli ST131- <i>H</i> 22 as a Foodborne Uropathogen. MBio, 2018, 9, .	1.8	184
14	BactQuant: An enhanced broad-coverage bacterial quantitative real-time PCR assay. BMC Microbiology, 2012, 12, 56.	1.3	172
15	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. Frontiers in Genetics, 2015, 6, 235.	1.1	160
16	Phylogeographic reconstruction of a bacterial species with high levels of lateral gene transfer. BMC Biology, 2009, 7, 78.	1.7	155
17	Valley Fever: Finding New Places for an Old Disease: Coccidioides immitis Found in Washington State Soil Associated With Recent Human Infection. Clinical Infectious Diseases, 2015, 60, e1-e3.	2.9	153
18	Burkholderia stagnalis sp. nov. and Burkholderia territorii sp. nov., two novel Burkholderia cepacia complex species from environmental and human sources. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 2265-2271.	0.8	149

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19	Eighteenth century <i>Yersinia pestis</i> genomes reveal the long-term persistence of an historical plague focus. <i>ELife</i> , 2016, 5, e12994.	2.8	139
20	<i>Bacillus anthracis</i> Bioterrorism Incident, Kameido, Tokyo, 1993. <i>Emerging Infectious Diseases</i> , 2004, 10, 117-120.	2.0	127
21	<i>Cryptococcus gattii</i> in North American Pacific Northwest: Whole-Population Genome Analysis Provides Insights into Species Evolution and Dispersal. <i>MBio</i> , 2014, 5, e01464-14.	1.8	126
22	Global and regional dissemination and evolution of <i>Burkholderia pseudomallei</i> . <i>Nature Microbiology</i> , 2017, 2, 16263.	5.9	124
23	Within-Host Evolution of <i>Burkholderia pseudomallei</i> over a Twelve-Year Chronic Carriage Infection. <i>MBio</i> , 2013, 4, .	1.8	121
24	Genomic Epidemiology of the Haitian Cholera Outbreak: a Single Introduction Followed by Rapid, Extensive, and Continued Spread Characterized the Onset of the Epidemic. <i>MBio</i> , 2014, 5, e01721.	1.8	112
25	Comparative Analysis of Subtyping Methods against a Whole-Genome-Sequencing Standard for <i>Salmonella enterica</i> Serotype Enteritidis. <i>Journal of Clinical Microbiology</i> , 2015, 53, 212-218.	1.8	112
26	In Vitro Selection and Characterization of <i>Bacillus anthracis</i> Mutants with High-Level Resistance to Ciprofloxacin. <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 2362-2365.	1.4	111
27	Phylogenetic understanding of clonal populations in an era of whole genome sequencing. <i>Infection, Genetics and Evolution</i> , 2009, 9, 1010-1019.	1.0	106
28	Continuing Evolution of <i>Burkholderia mallei</i> Through Genome Reduction and Large-Scale Rearrangements. <i>Genome Biology and Evolution</i> , 2010, 2, 102-116.	1.1	106
29	Humans and evolutionary and ecological forces shaped the phylogeography of recently emerged diseases. <i>Nature Reviews Microbiology</i> , 2009, 7, 813-821.	13.6	101
30	The 2010 Cholera Outbreak in Haiti: How Science Solved a Controversy. <i>PLoS Pathogens</i> , 2014, 10, e1003967.	2.1	99
31	Detection of Low-Level Mixed-Population Drug Resistance in <i>Mycobacterium tuberculosis</i> Using High Fidelity Amplicon Sequencing. <i>PLoS ONE</i> , 2015, 10, e0126626.	1.1	93
32	Worldwide genotyping of castor bean germplasm (<i>Ricinus communis</i> L.) using AFLPs and SSRs. <i>Genetic Resources and Crop Evolution</i> , 2008, 55, 365-378.	0.8	90
33	Genomic islands from five strains of <i>Burkholderia pseudomallei</i> . <i>BMC Genomics</i> , 2008, 9, 566.	1.2	90
34	The Complete Genome Sequence of <i>Bacillus anthracis</i> Ames "Ancestor". <i>Journal of Bacteriology</i> , 2009, 191, 445-446.	1.0	88
35	Mapping and comparing bacterial microbiota in the sinonasal cavity of healthy, allergic rhinitis, and chronic rhinosinusitis subjects. <i>International Forum of Allergy and Rhinology</i> , 2017, 7, 561-569.	1.5	86
36	<i>Bacillus anthracis</i> in China and its relationship to worldwide lineages. <i>BMC Microbiology</i> , 2009, 9, 71.	1.3	85

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37	Genetic Diversity in the Protective Antigen Gene of <i>Bacillus anthracis</i> . <i>Journal of Bacteriology</i> , 1999, 181, 2358-2362.	1.0	85
38	The K18-Human ACE2 Transgenic Mouse Model Recapitulates Non-severe and Severe COVID-19 in Response to an Infectious Dose of the SARS-CoV-2 Virus. <i>Journal of Virology</i> , 2022, 96, JVI0096421.	1.5	84
39	Comparative integrated omics: identification of key functionalities in microbial community-wide metabolic networks. <i>Npj Biofilms and Microbiomes</i> , 2015, 1, 15007.	2.9	82
40	A Horizontal Gene Transfer Event Defines Two Distinct Groups within <i>Burkholderia pseudomallei</i> That Have Dissimilar Geographic Distributions. <i>Journal of Bacteriology</i> , 2007, 189, 9044-9049.	1.0	81
41	Molecular Epidemiologic Investigation of an Anthrax Outbreak among Heroin Users, Europe. <i>Emerging Infectious Diseases</i> , 2012, 18, 1307-1313.	2.0	77
42	Characterization of Ceftazidime Resistance Mechanisms in Clinical Isolates of <i>Burkholderia pseudomallei</i> from Australia. <i>PLoS ONE</i> , 2012, 7, e30789.	1.1	75
43	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. <i>Nature Communications</i> , 2014, 5, 5603.	5.8	75
44	The genome and variation of <i>Bacillus anthracis</i> . <i>Molecular Aspects of Medicine</i> , 2009, 30, 397-405.	2.7	72
45	<i>Burkholderia pseudomallei</i> Isolates from Sarawak, Malaysian Borneo, Are Predominantly Susceptible to Aminoglycosides and Macrolides. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 162-166.	1.4	72
46	Local Population Structure and Patterns of Western Hemisphere Dispersal for <i>Coccidioides</i> spp., the Fungal Cause of Valley Fever. <i>MBio</i> , 2016, 7, e00550-16.	1.8	71
47	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing <i>Clostridia</i> . <i>BMC Genomics</i> , 2016, 17, 180.	1.2	71
48	Phylogenetics of a Fungal Invasion: Origins and Widespread Dispersal of White-Nose Syndrome. <i>MBio</i> , 2017, 8, .	1.8	70
49	The Genetic and Molecular Basis of O-Antigenic Diversity in <i>Burkholderia pseudomallei</i> Lipopolysaccharide. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1453.	1.3	69
50	Molecular Analysis of Rifampin Resistance in <i>Bacillus anthracis</i> and <i>Bacillus cereus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2002, 46, 511-513.	1.4	67
51	Critical Knowledge Gaps in Our Understanding of Environmental Cycling and Transmission of <i>Leptospira</i> spp. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	67
52	Use of Single Nucleotide Polymorphisms in the <i>plcR</i> Gene for Specific Identification of <i>Bacillus anthracis</i> . <i>Journal of Clinical Microbiology</i> , 2005, 43, 1995-1997.	1.8	66
53	Whole Genome Sequence Typing to Investigate the <i>Apophysomyces</i> Outbreak following a Tornado in Joplin, Missouri, 2011. <i>PLoS ONE</i> , 2012, 7, e49989.	1.1	66
54	More than 50% of <i>Clostridium difficile</i> Isolates from Pet Dogs in Flagstaff, USA, Carry Toxigenic Genotypes. <i>PLoS ONE</i> , 2016, 11, e0164504.	1.1	64

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55	Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. <i>Emerging Infectious Diseases</i> , 2012, 18, e1-e1.	2.0	64
56	Whole Genome Sequence Analysis of <i>Cryptococcus gattii</i> from the Pacific Northwest Reveals Unexpected Diversity. <i>PLoS ONE</i> , 2011, 6, e28550.	1.1	63
57	An Outbreak of Respiratory Tularemia Caused by Diverse Clones of <i>Francisella tularensis</i> . <i>Clinical Infectious Diseases</i> , 2014, 59, 1546-1553.	2.9	61
58	Pre-Columbian Origins for North American Anthrax. <i>PLoS ONE</i> , 2009, 4, e4813.	1.1	60
59	Development of ceftazidime resistance in an acute <i>Burkholderia pseudomallei</i> infection. <i>Infection and Drug Resistance</i> , 2012, 5, 129.	1.1	60
60	Integration of time-series meta-omics data reveals how microbial ecosystems respond to disturbance. <i>Nature Communications</i> , 2020, 11, 5281.	5.8	57
61	Molecular Basis of Rare Aminoglycoside Susceptibility and Pathogenesis of <i>Burkholderia pseudomallei</i> Clinical Isolates from Thailand. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e519.	1.3	55
62	A <i>Bacillus anthracis</i> Genome Sequence from the Sverdlovsk 1979 Autopsy Specimens. <i>MBio</i> , 2016, 7, .	1.8	52
63	The Phylogeny of <i>Bacillus cereus sensu lato</i> . <i>Microbiology Spectrum</i> , 2016, 4, .	1.2	50
64	KlebSeq, a Diagnostic Tool for Surveillance, Detection, and Monitoring of <i>Klebsiella pneumoniae</i> . <i>Journal of Clinical Microbiology</i> , 2016, 54, 2582-2596.	1.8	50
65	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. <i>MBio</i> , 2016, 7, .	1.8	49
66	Mechanisms of Resistance to Folate Pathway Inhibitors in <i>Burkholderia pseudomallei</i> : Deviation from the Norm. <i>MBio</i> , 2017, 8, .	1.8	47
67	Roles of bacteriophages, plasmids and CRISPR immunity in microbial community dynamics revealed using time-series integrated meta-omics. <i>Nature Microbiology</i> , 2021, 6, 123-135.	5.9	47
68	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, 1726-1731.	1.4	46
69	Unprecedented Melioidosis Cases in Northern Australia Caused by an Asian <i>Burkholderia pseudomallei</i> Strain Identified by Using Large-Scale Comparative Genomics. <i>Applied and Environmental Microbiology</i> , 2016, 82, 954-963.	1.4	46
70	When Outgroups Fail; Phylogenomics of Rooting the Emerging Pathogen, <i>Coxiella burnetii</i> . <i>Systematic Biology</i> , 2013, 62, 752-762.	2.7	45
71	<i>Burkholderia humptydoensis</i> sp. nov., a New Species Related to <i>Burkholderia thailandensis</i> and the Fifth Member of the <i>Burkholderia pseudomallei</i> Complex. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	45
72	High <i>Leptospira</i> Diversity in Animals and Humans Complicates the Search for Common Reservoirs of Human Disease in Rural Ecuador. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004990.	1.3	44

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73	Molecular Epidemiology of Anthrax Cases Associated with Recreational Use of Animal Hides and Yarn in the United States. PLoS ONE, 2011, 6, e28274.	1.1	42
74	Complete Genome Sequence of the Epidemic and Highly Virulent CTX-M-15-Producing <i>H30-Rx</i> Subclone of <i>Escherichia coli</i> ST131. Genome Announcements, 2013, 1, .	0.8	42
75	Genotyping of <i>Burkholderia mallei</i> from an Outbreak of Glanders in Bahrain Suggests Multiple Introduction Events. PLoS Neglected Tropical Diseases, 2014, 8, e3195.	1.3	41
76	Botulinum Neurotoxin-Producing Bacteria. Isn't It Time that We Called a Species a Species?. MBio, 2018, 9, .	1.8	40
77	Using Whole Genome Analysis to Examine Recombination across Diverse Sequence Types of <i>Staphylococcus aureus</i> . PLoS ONE, 2015, 10, e0130955.	1.1	40
78	Phylogenetically typing bacterial strains from partial SNP genotypes observed from direct sequencing of clinical specimen metagenomic data. Genome Medicine, 2015, 7, 52.	3.6	38
79	Tetranucleotide microsatellites for aquila and haliaeetus eagles. Molecular Ecology Notes, 2005, 5, 39-41.	1.7	37
80	Knockout and pullout recombineering for naturally transformable <i>Burkholderia thailandensis</i> and <i>Burkholderia pseudomallei</i> . Nature Protocols, 2011, 6, 1085-1104.	5.5	37
81	Pangenome Analysis of <i>Burkholderia pseudomallei</i> : Genome Evolution Preserves Gene Order despite High Recombination Rates. PLoS ONE, 2015, 10, e0140274.	1.1	37
82	Anthrax, but Not <i>Bacillus anthracis</i> ?. PLoS Pathogens, 2006, 2, e122.	2.1	36
83	Development of a rapid, cost-effective TaqMan Real-Time PCR Assay for identification and differentiation of <i>Coccidioides immitis</i> and <i>Coccidioides posadasii</i> . Medical Mycology, 2010, 48, 466-469.	0.3	36
84	Meta-analysis to estimate the load of <i>Leptospira</i> excreted in urine: beyond rats as important sources of transmission in low-income rural communities. BMC Research Notes, 2017, 10, 71.	0.6	36
85	Tracing Melioidosis Back to the Source: Using Whole-Genome Sequencing To Investigate an Outbreak Originating from a Contaminated Domestic Water Supply. Journal of Clinical Microbiology, 2015, 53, 1144-1148.	1.8	35
86	Identification of <i>Burkholderia pseudomallei</i> Near-Neighbor Species in the Northern Territory of Australia. PLoS Neglected Tropical Diseases, 2015, 9, e0003892.	1.3	34
87	VNTR analysis of selected outbreaks of <i>Burkholderia pseudomallei</i> in Australia. Infection, Genetics and Evolution, 2007, 7, 416-423.	1.0	32
88	Whole-Genome Sequencing of <i>Burkholderia pseudomallei</i> Isolates from an Unusual Melioidosis Case Identifies a Polyclonal Infection with the Same Multilocus Sequence Type. Journal of Clinical Microbiology, 2015, 53, 282-286.	1.8	32
89	Improved Subtyping of <i>Staphylococcus aureus</i> Clonal Complex 8 Strains Based on Whole-Genome Phylogenetic Analysis. MSphere, 2018, 3, .	1.3	32
90	Long-range dispersal moved <i>Francisella tularensis</i> into Western Europe from the East. Microbial Genomics, 2016, 2, e000100.	1.0	32

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91	Genetic Variation in The Endangered Southwestern Willow Flycatcher. <i>Auk</i> , 2000, 117, 586-595.	0.7	31
92	Single Nucleotide Polymorphism Typing of <i>Bacillus anthracis</i> from Sverdlovsk Tissue. <i>Emerging Infectious Diseases</i> , 2008, 14, 653-656.	2.0	30
93	An Early Pandemic Analysis of SARS-CoV-2 Population Structure and Dynamics in Arizona. <i>MBio</i> , 2020, 11, .	1.8	29
94	Non-Toxin-Producing <i>Bacillus cereus</i> Strains Belonging to the <i>B. anthracis</i> Clade Isolated from the International Space Station. <i>MSystems</i> , 2017, 2, .	1.7	28
95	Population Structure and Genetic Diversity among Isolates of <i>Coccidioides posadasii</i> in Venezuela and Surrounding Regions. <i>MBio</i> , 2019, 10, .	1.8	28
96	Rapid Identification of Genetic Modifications in <i>Bacillus anthracis</i> Using Whole Genome Draft Sequences Generated by 454 Pyrosequencing. <i>PLoS ONE</i> , 2010, 5, e12397.	1.1	27
97	Genome Sequence of <i>Candidatus Microthrix parvicella</i> -Bio17-1, a Long-Chain-Fatty-Acid-Accumulating Filamentous Actinobacterium from a Biological Wastewater Treatment Plant. <i>Journal of Bacteriology</i> , 2012, 194, 6670-6671.	1.0	27
98	Whole Genome Analysis of Injectional Anthrax Identifies Two Disease Clusters Spanning More Than 13 Years. <i>EBioMedicine</i> , 2015, 2, 1613-1618.	2.7	27
99	Phenotypic characterization and whole genome analysis of extended-spectrum beta-lactamase-producing bacteria isolated from dogs in Germany. <i>PLoS ONE</i> , 2018, 13, e0206252.	1.1	27
100	Contrasting rRNA gene abundance patterns for aquatic fungi and bacteria in response to leaf-litter chemistry. <i>Freshwater Science</i> , 2013, 32, 663-672.	0.9	26
101	<i>Burkholderia pseudomallei</i> , the causative agent of melioidosis, is rare but ecologically established and widely dispersed in the environment in Puerto Rico. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007727.	1.3	26
102	<i>Burkholderia pseudomallei</i> OMVs derived from infection mimicking conditions elicit similar protection to a live-attenuated vaccine. <i>Npj Vaccines</i> , 2021, 6, 18.	2.9	26
103	TaqMan Real-Time PCR Assays for Single-Nucleotide Polymorphisms Which Identify <i>Francisella tularensis</i> and Its Subspecies and Subpopulations. <i>PLoS ONE</i> , 2014, 9, e107964.	1.1	25
104	Hypervirulent <i>emm</i> 59 Clone in Invasive Group A <i>Streptococcus</i> Outbreak, Southwestern United States. <i>Emerging Infectious Diseases</i> , 2016, 22, 734-738.	2.0	25
105	Genomic Characterization of <i>Burkholderia pseudomallei</i> Isolates Selected for Medical Countermeasures Testing: Comparative Genomics Associated with Differential Virulence. <i>PLoS ONE</i> , 2015, 10, e0121052.	1.1	25
106	Genotyping and Axenic Growth of <i>Coxiella burnetii</i> Isolates Found in the United States Environment. <i>Vector-Borne and Zoonotic Diseases</i> , 2016, 16, 588-594.	0.6	24
107	Detection of <i>Burkholderia pseudomallei</i> O-antigen serotypes in near-neighbor species. <i>BMC Microbiology</i> , 2012, 12, 250.	1.3	21
108	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.	1.1	21

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109	Off-the-shelf CAR natural killer cells secreting IL-15 target spike in treating COVID-19. <i>Nature Communications</i> , 2022, 13, 2576.	5.8	21
110	Domestic canines do not display evidence of gut microbial dysbiosis in the presence of <i>Clostridioides (Clostridium) difficile</i> , despite cellular susceptibility to its toxins. <i>Anaerobe</i> , 2019, 58, 53-72.	1.0	20
111	Phylogeography of <i>Bacillus anthracis</i> in the Country of Georgia Shows Evidence of Population Structuring and Is Dissimilar to Other Regional Genotypes. <i>PLoS ONE</i> , 2014, 9, e102651.	1.1	20
112	Diverse <i>Burkholderia</i> Species Isolated from Soils in the Southern United States with No Evidence of <i>B. pseudomallei</i> . <i>PLoS ONE</i> , 2015, 10, e0143254.	1.1	20
113	Estimated herd prevalence and sequence types of <i>Coxiella burnetii</i> in bulk tank milk samples from commercial dairies in Indiana. <i>BMC Veterinary Research</i> , 2015, 11, 186.	0.7	19
114	A review of methods for subtyping <i>Yersinia pestis</i> : From phenotypes to whole genome sequencing. <i>Infection, Genetics and Evolution</i> , 2016, 37, 21-36.	1.0	19
115	Differentiating <i>Botulinum Neurotoxin</i> -Producing <i>Clostridia</i> with a Simple, Multiplex PCR Assay. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	18
116	Investigation of <i>Yersinia pestis</i> Laboratory Adaptation through a Combined Genomics and Proteomics Approach. <i>PLoS ONE</i> , 2015, 10, e0142997.	1.1	17
117	<i>Leptospira</i> in river and soil in a highly endemic area of Ecuador. <i>BMC Microbiology</i> , 2021, 21, 17.	1.3	16
118	Stenoparib, an Inhibitor of Cellular Poly(ADP-Ribose) Polymerase, Blocks Replication of the SARS-CoV-2 and HCoV-NL63 Human Coronaviruses In Vitro. <i>MBio</i> , 2021, 12, .	1.8	16
119	Diverse Genotypes of <i>Yersinia pestis</i> Caused Plague in Madagascar in 2007. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003844.	1.3	16
120	Phylogeographic, genomic, and meropenem susceptibility analysis of <i>Burkholderia ubonensis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005928.	1.3	16
121	Genomic Analyses of Acute Flaccid Myelitis Cases among a Cluster in Arizona Provide Further Evidence of Enterovirus D68 Role. <i>MBio</i> , 2019, 10, .	1.8	15
122	MetaGeniE: Characterizing Human Clinical Samples Using Deep Metagenomic Sequencing. <i>PLoS ONE</i> , 2014, 9, e110915.	1.1	14
123	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. <i>F1000Research</i> , 2020, 9, 657.	0.8	14
124	Differential Thermotolerance Adaptation between Species of <i>Coccidioides</i> . <i>Journal of Fungi (Basel)</i> , Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.5	13
125	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.	2.1	12
126	Rapid and robust phylotyping of spa t003, a dominant MRSA clone in Luxembourg and other European countries. <i>BMC Infectious Diseases</i> , 2013, 13, 339.	1.3	11

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127	The Distinctive Evolution of orfX <i>Clostridium parbotulinum</i> Strains and Their Botulinum Neurotoxin Type A and F Gene Clusters Is Influenced by Environmental Factors and Gene Interactions via Mobile Genetic Elements. <i>Frontiers in Microbiology</i> , 2021, 12, 566908.	1.5	11
128	Expanding the <i>Burkholderia pseudomallei</i> Complex with the Addition of Two Novel Species: <i>Burkholderia mayonis</i> sp. nov. and <i>Burkholderia savanna</i> sp. nov.. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0158321.	1.4	11
129	Identification of novel, cryptic <i>Clostridioides</i> species isolates from environmental samples collected from diverse geographical locations. <i>Microbial Genomics</i> , 2022, 8, .	1.0	11
130	Whole genome SNP typing to investigate methicillin-resistant <i>Staphylococcus aureus</i> carriage in a health-care provider as the source of multiple surgical site infections. <i>Hereditas</i> , 2016, 153, 11.	0.5	10
131	Characterization of Microsatellites in <i>Pseudogymnoascus destructans</i> for White-nose Syndrome Genetic Analysis. <i>Journal of Wildlife Diseases</i> , 2017, 53, 869.	0.3	10
132	A chromosomal-level reference genome of the widely utilized <i>Coccidioides posadasii</i> laboratory strain "Silveira" G3: <i>Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	10
133	Caprine humoral response to <i>Burkholderia pseudomallei</i> antigens during acute melioidosis from aerosol exposure. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0006851.	1.3	9
134	Redefining the differences in gene content between <i>Yersinia pestis</i> and <i>Yersinia pseudotuberculosis</i> using large-scale comparative genomics. <i>Microbial Genomics</i> , 2015, 1, e000028.	1.0	9
135	Whole-genome sequencing investigation of animal-skin-drum-associated UK anthrax cases reveals evidence of mixed populations and relatedness to a US case. <i>Microbial Genomics</i> , 2015, 1, e000039.	1.0	9
136	Effects of binge alcohol exposure on <i>Burkholderia thailandensis</i> "alveolar macrophage interaction. <i>Alcohol</i> , 2017, 64, 55-63.	0.8	8
137	First draft genome sequence of a strain belonging to the <i>Zoogloea</i> genus and its gene expression in situ. <i>Standards in Genomic Sciences</i> , 2017, 12, 64.	1.5	8
138	Proteomic analysis of four <i>Clostridium botulinum</i> strains identifies proteins that link biological responses to proteomic signatures. <i>PLoS ONE</i> , 2018, 13, e0205586.	1.1	8
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