

# Paul Keim

## List of Publications by Year in descending order

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162  
papers

11,320  
citations

26630

56  
h-index

37204

96  
g-index

180  
all docs

180  
docs citations

180  
times ranked

12166  
citing authors

#	ARTICLE	IF	CITATIONS
1	Expanding the <i>Burkholderia pseudomallei</i> Complex with the Addition of Two Novel Species: <i>Burkholderia mayonis</i> sp. nov. and <i>Burkholderia savannae</i> sp. nov.. Applied and Environmental Microbiology, 2022, 88, AEM0158321.	3.1	11
2	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. Journal of Virology, 2022, 96, JVI0096421.	3.4	84
3	Multiple phylogenetically-diverse, differentially-virulent <i>Burkholderia pseudomallei</i> isolated from a single soil sample collected in Thailand. PLoS Neglected Tropical Diseases, 2022, 16, e0010172.	3.0	3
4	A chromosomal-level reference genome of the widely utilized <i>Coccidioides posadasii</i> laboratory strain "Silveira" G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	10
5	Identification of novel, cryptic <i>Clostridioides</i> species isolates from environmental samples collected from diverse geographical locations. Microbial Genomics, 2022, 8, .	2.0	11
6	Off-the-shelf CAR natural killer cells secreting IL-15 target spike in treating COVID-19. Nature Communications, 2022, 13, 2576.	12.8	21
7	Roles of bacteriophages, plasmids and CRISPR immunity in microbial community dynamics revealed using time-series integrated meta-omics. Nature Microbiology, 2021, 6, 123-135.	13.3	47
8	<i>Burkholderia ubonensis</i> High-Level Tetracycline Resistance Is Due to Efflux Pump Synergy Involving a Novel TetA(64) Resistance Determinant. Antimicrobial Agents and Chemotherapy, 2021, 65, .	3.2	5
9	<i>Burkholderia pseudomallei</i> OMVs derived from infection mimicking conditions elicit similar protection to a live-attenuated vaccine. Npj Vaccines, 2021, 6, 18.	6.0	26
10	<i>Leptospira</i> in river and soil in a highly endemic area of Ecuador. BMC Microbiology, 2021, 21, 17.	3.3	16
11	Stenoparib, an Inhibitor of Cellular Poly(ADP-Ribose) Polymerase, Blocks Replication of the SARS-CoV-2 and HCoV-NL63 Human Coronaviruses In Vitro. MBio, 2021, 12, .	4.1	16
12	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. Frontiers in Microbiology, 2021, 12, 566908.	3.5	11
13	Conservation of Resistance-Nodulation-Cell Division Efflux Pump-Mediated Antibiotic Resistance in <i>Burkholderia cepacia</i> Complex and <i>Burkholderia pseudomallei</i> Complex Species. Antimicrobial Agents and Chemotherapy, 2021, 65, e0092021.	3.2	6
14	Forensic analysis in bacterial pathogens. , 2020, , 123-140.		0
15	Integration of time-series meta-omics data reveals how microbial ecosystems respond to disturbance. Nature Communications, 2020, 11, 5281.	12.8	57
16	Differential Thermotolerance Adaptation between Species of <i>Coccidioides</i> . Journal of Fungi (Basel,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.5	13
17	An Early Pandemic Analysis of SARS-CoV-2 Population Structure and Dynamics in Arizona. MBio, 2020, 11, .	4.1	29
18	Pathogen to commensal? Longitudinal within-host population dynamics, evolution, and adaptation during a chronic >16-year <i>Burkholderia pseudomallei</i> infection. PLoS Pathogens, 2020, 16, e1008298.	4.7	12

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19	Genomic Characterization of Newly Completed Genomes of Botulinum Neurotoxin-Producing Species from Argentina, Australia, and Africa. <i>Genome Biology and Evolution</i> , 2020, 12, 229-242.	2.5	8
20	Draft Whole-Genome Sequences of Ciprofloxacin-Resistant Derivatives of a <i>Bacillus anthracis</i> Î”ANR Strain Lacking pXO1 and pXO2 Plasmids. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
21	<i>Burkholderia ubonensis</i> Meropenem Resistance: Insights into Distinct Properties of Class A Î²-Lactamases in <i>Burkholderia cepacia</i> Complex and <i>Burkholderia pseudomallei</i> Complex Bacteria. <i>MBio</i> , 2020, 11, .	4.1	7
22	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. <i>F1000Research</i> , 2020, 9, 657.	1.6	14
23	<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.	3.0	26
24	Genomic Analyses of Acute Flaccid Myelitis Cases among a Cluster in Arizona Provide Further Evidence of Enterovirus D68 Role. <i>MBio</i> , 2019, 10, .	4.1	15
25	Caprine humoral response to <i>Burkholderia pseudomallei</i> antigens during acute melioidosis from aerosol exposure. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0006851.	3.0	9
26	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.	2.1	20
27	Population Structure and Genetic Diversity among Isolates of <i>Coccidioides posadasii</i> in Venezuela and Surrounding Regions. <i>MBio</i> , 2019, 10, .	4.1	28
28	Persistence of <i>Burkholderia thailandensis</i> E264 in lung tissue after a single binge alcohol episode. <i>PLoS ONE</i> , 2019, 14, e0218147.	2.5	5
29	A global to local genomics analysis of <i>Clostridioides difficile</i> ST1/RT027 identifies cryptic transmission events in a northern Arizona healthcare network. <i>Microbial Genomics</i> , 2019, 5, .	2.0	7
30	Complete Genome Sequence of the Environmental <i>Burkholderia pseudomallei</i> Sequence Type 131 Isolate MSHR1435, Associated with a Chronic Melioidosis Infection. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
31	Improved Subtyping of <i>Staphylococcus aureus</i> Clonal Complex 8 Strains Based on Whole-Genome Phylogenetic Analysis. <i>MSphere</i> , 2018, 3, .	2.9	32
32	Developing Inclusivity and Exclusivity Panels for Testing Diagnostic and Detection Tools Targeting <i>Burkholderia pseudomallei</i> , the Causative Agent of Melioidosis. <i>Journal of AOAC INTERNATIONAL</i> , 2018, 101, 1920-1926.	1.5	5
33	A mouse model of binge alcohol consumption and <i>Burkholderia</i> infection. <i>PLoS ONE</i> , 2018, 13, e0208061.	2.5	4
34	Botulinum Neurotoxin-Producing Bacteria. Isnâ€™t It Time that We Called a Species a Species?. <i>MBio</i> , 2018, 9, .	4.1	40
35	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.	2.5	8
36	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.	2.5	27

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37	Escherichia coli ST131- <i>H</i> 22 as a Foodborne Uropathogen. MBio, 2018, 9, .	4.1	184
38	Global and regional dissemination and evolution of Burkholderia pseudomallei. Nature Microbiology, 2017, 2, 16263.	13.3	124
39	Meta-analysis to estimate the load of Leptospira excreted in urine: beyond rats as important sources of transmission in low-income rural communities. BMC Research Notes, 2017, 10, 71.	1.4	36
40	Mapping and comparing bacterial microbiota in the sinonasal cavity of healthy, allergic rhinitis, and chronic rhinosinusitis subjects. International Forum of Allergy and Rhinology, 2017, 7, 561-569.	2.8	86
41	Characterization of Microsatellites in Pseudogymnoascus destructans for White-nose Syndrome Genetic Analysis. Journal of Wildlife Diseases, 2017, 53, 869.	0.8	10
42	Unexpected Relations of Historical Anthrax Strain. MBio, 2017, 8, .	4.1	7
43	Burkholderia humptydoensis sp. nov., a New Species Related to Burkholderia thailandensis and the Fifth Member of the Burkholderia pseudomallei Complex. Applied and Environmental Microbiology, 2017, 83, .	3.1	45
44	Mechanisms of Resistance to Folate Pathway Inhibitors in Burkholderia pseudomallei : Deviation from the Norm. MBio, 2017, 8, .	4.1	47
45	Effects of binge alcohol exposure on Burkholderia thailandensis-alveolar macrophage interaction. Alcohol, 2017, 64, 55-63.	1.7	8
46	Differentiating Botulinum Neurotoxin-Producing Clostridia with a Simple, Multiplex PCR Assay. Applied and Environmental Microbiology, 2017, 83, .	3.1	18
47	Critical Knowledge Gaps in Our Understanding of Environmental Cycling and Transmission of Leptospira spp. Applied and Environmental Microbiology, 2017, 83, .	3.1	67
48	Non-Toxin-Producing Bacillus cereus Strains Belonging to the B. anthracis Clade Isolated from the International Space Station. MSystems, 2017, 2, .	3.8	28
49	Phylogenetics of a Fungal Invasion: Origins and Widespread Dispersal of White-Nose Syndrome. MBio, 2017, 8, .	4.1	70
50	First draft genome sequence of a strain belonging to the Zoogloea genus and its gene expression in situ. Standards in Genomic Sciences, 2017, 12, 64.	1.5	8
51	Phylogeographic, genomic, and meropenem susceptibility analysis of Burkholderia ubonensis. PLoS Neglected Tropical Diseases, 2017, 11, e0005928.	3.0	16
52	Hypervirulent emm59 Clone in Invasive Group A Streptococcus Outbreak, Southwestern United States. Emerging Infectious Diseases, 2016, 22, 734-738.	4.3	25
53	Eighteenth century Yersinia pestis genomes reveal the long-term persistence of an historical plague focus. ELife, 2016, 5, e12994.	6.0	139
54	Local Population Structure and Patterns of Western Hemisphere Dispersal for Coccidioides spp., the Fungal Cause of Valley Fever. MBio, 2016, 7, e00550-16.	4.1	71

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55	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.	1.4	10
56	The Phylogeny of <i>Bacillus cereus sensu lato</i> . <i>Microbiology Spectrum</i> , 2016, 4, .	3.0	50
57	A <i>Bacillus anthracis</i> Genome Sequence from the Sverdlovsk 1979 Autopsy Specimens. <i>MBio</i> , 2016, 7, .	4.1	52
58	KlebSeq, a Diagnostic Tool for Surveillance, Detection, and Monitoring of <i>Klebsiella pneumoniae</i> . <i>Journal of Clinical Microbiology</i> , 2016, 54, 2582-2596.	3.9	50
59	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.	2.3	1
60	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.	1.5	24
61	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. <i>MBio</i> , 2016, 7, .	4.1	49
62	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing <i>Clostridia</i> . <i>BMC Genomics</i> , 2016, 17, 180.	2.8	71
63	False detection of <i>Coxiella burnetii</i> "what is the risk?. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw088.	1.8	7
64	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.	3.1	46
65	A Novel Botulinum Neurotoxin and How It Tested Our Scientific Institutions. <i>Journal of Infectious Diseases</i> , 2016, 213, 332-334.	4.0	5
66	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.	2.3	19
67	NASP: an accurate, rapid method for the identification of SNPs in WGS datasets that supports flexible input and output formats. <i>Microbial Genomics</i> , 2016, 2, e000074.	2.0	237
68	Long-range dispersal moved <i>Francisella tularensis</i> into Western Europe from the East. <i>Microbial Genomics</i> , 2016, 2, e000100.	2.0	32
69	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.	3.0	44
70	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.	2.5	64
71	Comparative integrated omics: identification of key functionalities in microbial community-wide metabolic networks. <i>Npj Biofilms and Microbiomes</i> , 2015, 1, 15007.	6.4	82
72	Phylogenetically typing bacterial strains from partial SNP genotypes observed from direct sequencing of clinical specimen metagenomic data. <i>Genome Medicine</i> , 2015, 7, 52.	8.2	38

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73	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. <i>Frontiers in Genetics</i> , 2015, 6, 235.	2.3	160
74	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.	2.5	93
75	Identification of <i>Burkholderia pseudomallei</i> Near-Neighbor Species in the Northern Territory of Australia. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003892.	3.0	34
76	Genomic Analysis of the Emergence and Rapid Global Dissemination of the Clonal Group 258 <i>Klebsiella pneumoniae</i> Pandemic. <i>PLoS ONE</i> , 2015, 10, e0133727.	2.5	195
77	Pangenome Analysis of <i>Burkholderia pseudomallei</i> : Genome Evolution Preserves Gene Order despite High Recombination Rates. <i>PLoS ONE</i> , 2015, 10, e0140274.	2.5	37
78	Investigation of <i>Yersinia pestis</i> Laboratory Adaptation through a Combined Genomics and Proteomics Approach. <i>PLoS ONE</i> , 2015, 10, e0142997.	2.5	17
79	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.	1.9	19
80	Whole Genome Analysis of Injectional Anthrax Identifies Two Disease Clusters Spanning More Than 13 Years. <i>EBioMedicine</i> , 2015, 2, 1613-1618.	6.1	27
81	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, 282-286.	3.9	32
82	<i>Burkholderia stagnalis</i> sp. nov. and <i>Burkholderia territorii</i> sp. nov., two novel <i>Burkholderia cepacia</i> complex species from environmental and human sources. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 2265-2271.	1.7	149
83	Tracing Melioidosis Back to the Source: Using Whole-Genome Sequencing To Investigate an Outbreak Originating from a Contaminated Domestic Water Supply. <i>Journal of Clinical Microbiology</i> , 2015, 53, 1144-1148.	3.9	35
84	Valley Fever: Finding New Places for an Old Disease: <i>Coccidioides immitis</i> Found in Washington State Soil Associated With Recent Human Infection. <i>Clinical Infectious Diseases</i> , 2015, 60, e1-e3.	5.8	153
85	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.	3.9	112
86	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.	2.0	9
87	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.	2.0	9
88	Diverse Genotypes of <i>Yersinia pestis</i> Caused Plague in Madagascar in 2007. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003844.	3.0	16
89	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.	2.5	25
90	Using Whole Genome Analysis to Examine Recombination across Diverse Sequence Types of <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2015, 10, e0130955.	2.5	40

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91	Diverse Burkholderia Species Isolated from Soils in the Southern United States with No Evidence of <i>B. pseudomallei</i> . PLoS ONE, 2015, 10, e0143254.	2.5	20
92	TaqMan Real-Time PCR Assays for Single-Nucleotide Polymorphisms Which Identify <i>Francisella tularensis</i> and Its Subspecies and Subpopulations. PLoS ONE, 2014, 9, e107964.	2.5	25
93	Genotyping of <i>Burkholderia mallei</i> from an Outbreak of Glanders in Bahrain Suggests Multiple Introduction Events. PLoS Neglected Tropical Diseases, 2014, 8, e3195.	3.0	41
94	The 2010 Cholera Outbreak in Haiti: How Science Solved a Controversy. PLoS Pathogens, 2014, 10, e1003967.	4.7	99
95	Genomic Epidemiology of the Haitian Cholera Outbreak: a Single Introduction Followed by Rapid, Extensive, and Continued Spread Characterized the Onset of the Epidemic. MBio, 2014, 5, e01721.	4.1	112
96	<i>Cryptococcus gattii</i> in North American Pacific Northwest: Whole-Population Genome Analysis Provides Insights into Species Evolution and Dispersal. MBio, 2014, 5, e01464-14.	4.1	126
97	<i>Burkholderia pseudomallei</i> Isolates from Sarawak, Malaysian Borneo, Are Predominantly Susceptible to Aminoglycosides and Macrolides. Antimicrobial Agents and Chemotherapy, 2014, 58, 162-166.	3.2	72
98	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. Nature Communications, 2014, 5, 5603.	12.8	75
99	MetaGeniE: Characterizing Human Clinical Samples Using Deep Metagenomic Sequencing. PLoS ONE, 2014, 9, e110915.	2.5	14
100	Highly Sensitive Quantitative PCR for the Detection and Differentiation of <i>Pseudogymnoascus destructans</i> and Other <i>Pseudogymnoascus</i> Species. Applied and Environmental Microbiology, 2014, 80, 1726-1731.	3.1	46
101	<i>Yersinia pestis</i> and the Plague of Justinian 541â€“543 AD: a genomic analysis. Lancet Infectious Diseases, The, 2014, 14, 319-326.	9.1	358
102	An Outbreak of Respiratory Tularemia Caused by Diverse Clones of <i>Francisella tularensis</i> . Clinical Infectious Diseases, 2014, 59, 1546-1553.	5.8	61
103	<i>Yersinia pestis</i> and the three plague pandemicsâ€™ Authors' reply. Lancet Infectious Diseases, The, 2014, 14, 919.	9.1	4
104	Phylogeography of <i>Bacillus anthracis</i> in the Country of Georgia Shows Evidence of Population Structuring and Is Dissimilar to Other Regional Genotypes. PLoS ONE, 2014, 9, e102651.	2.5	20
105	Insights to Genetic Characterization Tools for Epidemiological Tracking of <i>Francisella tularensis</i> in Sweden. PLoS ONE, 2014, 9, e112167.	2.5	7
106	The large-scale blast score ratio (LS-BSR) pipeline: a method to rapidly compare genetic content between bacterial genomes. PeerJ, 2014, 2, e332.	2.0	265
107	Rapid and robust phylotyping of <i>spa</i> t003, a dominant MRSA clone in Luxembourg and other European countries. BMC Infectious Diseases, 2013, 13, 339.	2.9	11
108	Contrasting rRNA gene abundance patterns for aquatic fungi and bacteria in response to leaf-litter chemistry. Freshwater Science, 2013, 32, 663-672.	1.8	26

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109	Within-Host Evolution of <i>Burkholderia pseudomallei</i> over a Twelve-Year Chronic Carriage Infection. <i>MBio</i> , 2013, 4, .	4.1	121
110	The Epidemic of Extended-Spectrum- $\beta$ -Lactamase-Producing <i>Escherichia coli</i> ST131 Is Driven by a Single Highly Pathogenic Subclone, <i>H30-Rx</i> . <i>MBio</i> , 2013, 4, e00377-13.	4.1	380
111	Complete Genome Sequence of the Epidemic and Highly Virulent CTX-M-15-Producing <i>H30-Rx</i> Subclone of <i>Escherichia coli</i> ST131. <i>Genome Announcements</i> , 2013, 1, .	0.8	42
112	When Outgroups Fail; Phylogenomics of Rooting the Emerging Pathogen, <i>Coxiella burnetii</i> . <i>Systematic Biology</i> , 2013, 62, 752-762.	5.6	45
113	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.	2.5	21
114	The Genetic and Molecular Basis of O-Antigenic Diversity in <i>Burkholderia pseudomallei</i> Lipopolysaccharide. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1453.	3.0	69
115	<i>Staphylococcus aureus</i> CC398: Host Adaptation and Emergence of Methicillin Resistance in Livestock. <i>MBio</i> , 2012, 3, .	4.1	638
116	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.	2.2	27
117	Characterization of Ceftazidime Resistance Mechanisms in Clinical Isolates of <i>Burkholderia pseudomallei</i> from Australia. <i>PLoS ONE</i> , 2012, 7, e30789.	2.5	75
118	Detection of <i>Burkholderia pseudomallei</i> O-antigen serotypes in near-neighbor species. <i>BMC Microbiology</i> , 2012, 12, 250.	3.3	21
119	BactQuant: An enhanced broad-coverage bacterial quantitative real-time PCR assay. <i>BMC Microbiology</i> , 2012, 12, 56.	3.3	172
120	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.	2.5	66
121	Molecular Epidemiologic Investigation of an Anthrax Outbreak among Heroin Users, Europe. <i>Emerging Infectious Diseases</i> , 2012, 18, 1307-1313.	4.3	77
122	Development of ceftazidime resistance in an acute <i>Burkholderia pseudomallei</i> infection. <i>Infection and Drug Resistance</i> , 2012, 5, 129.	2.7	60
123	Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. <i>Emerging Infectious Diseases</i> , 2012, 18, e1-e1.	4.3	64
124	Microbial Forensic Investigations in the Context of Bacterial Population Genetics. , 2011, , 545-559.		3
125	Molecular Epidemiology of Anthrax Cases Associated with Recreational Use of Animal Hides and Yarn in the United States. <i>PLoS ONE</i> , 2011, 6, e28274.	2.5	42
126	Population Genetics of <i>Vibrio cholerae</i> from Nepal in 2010: Evidence on the Origin of the Haitian Outbreak. <i>MBio</i> , 2011, 2, e00157-11.	4.1	268



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127	Knockout and pullout recombineering for naturally transformable <i>Burkholderia thailandensis</i> and <i>Burkholderia pseudomallei</i> . <i>Nature Protocols</i> , 2011, 6, 1085-1104.	12.0	37
128	Whole Genome Sequence Analysis of <i>Cryptococcus gattii</i> from the Pacific Northwest Reveals Unexpected Diversity. <i>PLoS ONE</i> , 2011, 6, e28550.	2.5	63
129	Continuing Evolution of <i>Burkholderia mallei</i> Through Genome Reduction and Large-Scale Rearrangements. <i>Genome Biology and Evolution</i> , 2010, 2, 102-116.	2.5	106
130	<i>Yersinia pestis</i> genome sequencing identifies patterns of global phylogenetic diversity. <i>Nature Genetics</i> , 2010, 42, 1140-1143.	21.4	504
131	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> . <i>Medical Mycology</i> , 2010, 48, 466-469.	0.7	36
132	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.	2.5	27
133	Pre-Columbian Origins for North American Anthrax. <i>PLoS ONE</i> , 2009, 4, e4813.	2.5	60
134	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.	3.0	55
135	The Complete Genome Sequence of <i>Bacillus anthracis</i> Ames Ancestor. <i>Journal of Bacteriology</i> , 2009, 191, 445-446.	2.2	88
136	<i>Bacillus anthracis</i> in China and its relationship to worldwide lineages. <i>BMC Microbiology</i> , 2009, 9, 71.	3.3	85
137	Development of polymorphic tetranucleotide microsatellites for pinyon jays ( <i>Gymnorhinus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 5 1.5 6	1.5	6
138	Phylogeographic reconstruction of a bacterial species with high levels of lateral gene transfer. <i>BMC Biology</i> , 2009, 7, 78.	3.8	155
139	Humans and evolutionary and ecological forces shaped the phylogeography of recently emerged diseases. <i>Nature Reviews Microbiology</i> , 2009, 7, 813-821.	28.6	101
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