

# Timothy D Read

## List of Publications by Year in descending order

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136  
papers

13,196  
citations

44069

48  
h-index

24258

110  
g-index

163  
all docs

163  
docs citations

163  
times ranked

13451  
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA sequence of both chromosomes of the cholera pathogen <i>Vibrio cholerae</i> . <i>Nature</i> , 2000, 406, 477-483.	27.8	1,723
2	Complete Genome Sequence of a Virulent Isolate of <i>Streptococcus pneumoniae</i> . <i>Science</i> , 2001, 293, 498-506.	12.6	1,281
3	Genome sequence of the dissimilatory metal ion-reducing bacterium <i>Shewanella oneidensis</i> . <i>Nature Biotechnology</i> , 2002, 20, 1118-1123.	17.5	771
4	The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria. <i>Nature</i> , 2003, 423, 81-86.	27.8	760
5	Complete genome sequence of the Q-fever pathogen <i>Coxiella burnetii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5455-5460.	7.1	506
6	Identification of anthrax toxin genes in a <i>Bacillus cereus</i> associated with an illness resembling inhalation anthrax. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 8449-8454.	7.1	457
7	Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V <i>Streptococcus agalactiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12391-12396.	7.1	447
8	The <i>Brucella suis</i> genome reveals fundamental similarities between animal and plant pathogens and symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13148-13153.	7.1	422
9	Comparative Genome Sequencing for Discovery of Novel Polymorphisms in <i>Bacillus anthracis</i> . <i>Science</i> , 2002, 296, 2028-2033.	12.6	413
10	Direct Comparisons of Illumina vs. Roche 454 Sequencing Technologies on the Same Microbial Community DNA Sample. <i>PLoS ONE</i> , 2012, 7, e30087.	2.5	360
11	The genome sequence of <i>Bacillus cereus</i> ATCC 10987 reveals metabolic adaptations and a large plasmid related to <i>Bacillus anthracis</i> pXO1. <i>Nucleic Acids Research</i> , 2004, 32, 977-988.	14.5	273
12	Phylogenetic discovery bias in <i>Bacillus anthracis</i> using single-nucleotide polymorphisms from whole-genome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13536-13541.	7.1	243
13	Genome-Based Prediction of Bacterial Antibiotic Resistance. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	221
14	Predicting the virulence of MRSA from its genome sequence. <i>Genome Research</i> , 2014, 24, 839-849.	5.5	210
15	Formation and Composition of the <i>Bacillus anthracis</i> Endospore. <i>Journal of Bacteriology</i> , 2004, 186, 164-178.	2.2	187
16	Unity in Variety--The Pan-Genome of the Chlamydiae. <i>Molecular Biology and Evolution</i> , 2011, 28, 3253-3270.	8.9	184
17	Antibiotic failure mediated by a resistant subpopulation in <i>Enterobacter cloacae</i> . <i>Nature Microbiology</i> , 2016, 1, 16053.	13.3	169
18	<i>Bacillus anthracis</i> comparative genome analysis in support of the Amerithrax investigation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5027-5032.	7.1	152

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19	Genomic characterization of the <i>Bacillus cereus</i> sensu lato species: Backdrop to the evolution of <i>Bacillus anthracis</i> . <i>Genome Research</i> , 2012, 22, 1512-1524.	5.5	148
20	Dissecting Vancomycin-Intermediate Resistance in <i>Staphylococcus aureus</i> Using Genome-Wide Association. <i>Genome Biology and Evolution</i> , 2014, 6, 1174-1185.	2.5	132
21	Strain-Specific Single-Nucleotide Polymorphism Assays for the <i>Bacillus anthracis</i> Ames Strain. <i>Journal of Clinical Microbiology</i> , 2007, 45, 47-53.	3.9	126
22	Quantitative and qualitative assessment of pollen DNA metabarcoding using constructed species mixtures. <i>Molecular Ecology</i> , 2019, 28, 431-455.	3.9	114
23	Characterizing the genetic basis of bacterial phenotypes using genome-wide association studies: a new direction for bacteriology. <i>Genome Medicine</i> , 2014, 6, 109.	8.2	105
24	Genomic characterization of the <i>Yersinia</i> genus. <i>Genome Biology</i> , 2010, 11, R1.	9.6	103
25	Hypervirulent <i>Chlamydia trachomatis</i> Clinical Strain Is a Recombinant between Lymphogranuloma Venereum (L <sub>2</sub> ) and D Lineages. <i>MBio</i> , 2011, 2, e00045-11.	4.1	100
26	Transmission and Microevolution of USA300 MRSA in U.S. Households: Evidence from Whole-Genome Sequencing. <i>MBio</i> , 2015, 6, e00054.	4.1	97
27	<i>Bacillus anthracis</i> , a bug with attitude!. <i>Current Opinion in Microbiology</i> , 2001, 4, 78-81.	5.1	94
28	Population Genomics of <i>Chlamydia trachomatis</i> : Insights on Drift, Selection, Recombination, and Population Structure. <i>Molecular Biology and Evolution</i> , 2012, 29, 3933-3946.	8.9	94
29	Draft sequencing and assembly of the genome of the world's largest fish, the whale shark: <i>Rhincodon typus</i> Smith 1828. <i>BMC Genomics</i> , 2017, 18, 532.	2.8	91
30	Comparative Analysis of <i>Chlamydia psittaci</i> Genomes Reveals the Recent Emergence of a Pathogenic Lineage with a Broad Host Range. <i>MBio</i> , 2013, 4, .	4.1	90
31	The Complete Genome Sequence of <i>Bacillus anthracis</i> Ames "Ancestor". <i>Journal of Bacteriology</i> , 2009, 191, 445-446.	2.2	88
32	IsdB-dependent Hemoglobin Binding Is Required for Acquisition of Heme by <i>Staphylococcus aureus</i> . <i>Journal of Infectious Diseases</i> , 2014, 209, 1764-1772.	4.0	88
33	Predicting Phenotype and Emerging Strains among <i>Chlamydia trachomatis</i> Infections. <i>Emerging Infectious Diseases</i> , 2009, 15, 1385-1394.	4.3	87
34	USA300 and USA500 Clonal Lineages of <i>Staphylococcus aureus</i> Do Not Produce a Capsular Polysaccharide Due to Conserved Mutations in the <i>cap5</i> Locus. <i>MBio</i> , 2015, 6, .	4.1	82
35	Bactopia: a Flexible Pipeline for Complete Analysis of Bacterial Genomes. <i>MSystems</i> , 2020, 5, .	3.8	82
36	Emergence of a new <i>Neisseria meningitidis</i> clonal complex 11 lineage 11.2 clade as an effective urogenital pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4237-4242.	7.1	79

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37	DIYA: a bacterial annotation pipeline for any genomics lab. <i>Bioinformatics</i> , 2009, 25, 962-963.	4.1	73
38	Characterization of <i>Aeromonas hydrophila</i> Wound Pathotypes by Comparative Genomic and Functional Analyses of Virulence Genes. <i>MBio</i> , 2013, 4, e00064-13.	4.1	71
39	Identification and Characterization of the <i>gerH</i> Operon of <i>Bacillus anthracis</i> Endospores: a Differential Role for Purine Nucleosides in Germination. <i>Journal of Bacteriology</i> , 2003, 185, 1462-1464.	2.2	70
40	Interplay of recombination and selection in the genomes of <i>Chlamydia trachomatis</i> . <i>Biology Direct</i> , 2011, 6, 28.	4.6	70
41	Genome Sequence of a Clinical Isolate of <i>Campylobacter jejuni</i> from Thailand. <i>Infection and Immunity</i> , 2007, 75, 3425-3433.	2.2	68
42	Population structure of <i>Neisseria gonorrhoeae</i> based on whole genome data and its relationship with antibiotic resistance. <i>PeerJ</i> , 2015, 3, e806.	2.0	67
43	<i>Staphylococcus aureus</i> viewed from the perspective of 40,000+ genomes. <i>PeerJ</i> , 2018, 6, e5261.	2.0	66
44	Microarray-based resequencing of multiple <i>Bacillus anthracis</i> isolates. <i>Genome Biology</i> , 2004, 6, R10.	9.6	64
45	Molecular Analysis of the Multiple GroEL Proteins of <i>Chlamydiae</i> . <i>Journal of Bacteriology</i> , 2003, 185, 1958-1966.	2.2	63
46	Determinants of Phage Host Range in <i>Staphylococcus</i> Species. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	59
47	Protocol for the Emory University African American Vaginal, Oral, and Gut Microbiome in Pregnancy Cohort Study. <i>BMC Pregnancy and Childbirth</i> , 2017, 17, 161.	2.4	58
48	Molecular Characterization of a Variant of <i>Bacillus anthracis</i> -Specific Phage AP50 with Improved Bacteriolytic Activity. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6792-6796.	3.1	56
49	Functional Genomic Characterization of Virulence Factors from Necrotizing Fasciitis-Causing Strains of <i>Aeromonas hydrophila</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 4162-4183.	3.1	54
50	Arbovirus Detection in Insect Vectors by Rapid, High-Throughput Pyrosequencing. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e878.	3.0	53
51	The <i>Bacillus anthracis</i> chromosome contains four conserved, excision-proficient, putative prophages. <i>BMC Microbiology</i> , 2006, 6, 34.	3.3	50
52	Global mRNA decay analysis at single nucleotide resolution reveals segmental and positional degradation patterns in a Gram-positive bacterium. <i>Genome Biology</i> , 2012, 13, R30.	9.6	50
53	A Mutation in the PP2C Phosphatase Gene in a <i>Staphylococcus aureus</i> USA300 Clinical Isolate with Reduced Susceptibility to Vancomycin and Daptomycin. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 5212-5223.	3.2	50
54	Sequencing <i>Bacillus anthracis</i> Typing Phages Gamma and Cherry Reveals a Common Ancestry. <i>Journal of Bacteriology</i> , 2006, 188, 3402-3408.	2.2	49

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55	Lung Tissue Concentrations of Pyrazinamide among Patients with Drug-Resistant Pulmonary Tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	48
56	Finishing genomes with limited resources: lessons from an ensemble of microbial genomes. <i>BMC Genomics</i> , 2010, 11, 242.	2.8	46
57	Genotypic and Phenotypic Diversity of <i>Staphylococcus aureus</i> Isolates from Cystic Fibrosis Patient Lung Infections and Their Interactions with <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2020, 11, .	4.1	45
58	Quantitative characterization of quantum dot- $\alpha$ -labeled lambda phage for <i>Escherichia coli</i> detection. <i>Biotechnology and Bioengineering</i> , 2009, 104, 1059-1067.	3.3	44
59	Bacterial population genomics and infectious disease diagnostics. <i>Trends in Biotechnology</i> , 2010, 28, 611-618.	9.3	44
60	Characterization of Two <i>Campylobacter jejuni</i> Strains for Use in Volunteer Experimental-Infection Studies. <i>Infection and Immunity</i> , 2008, 76, 5655-5667.	2.2	43
61	Evasion of type I and type II DNA restriction systems by Inc11 plasmid Collb-P9 during transfer by bacterial conjugation. <i>Molecular Microbiology</i> , 1992, 6, 1933-1941.	2.5	41
62	Genomic Signatures of Strain Selection and Enhancement in <i>Bacillus atrophaeus</i> var. <i>globigii</i> , a Historical Biowarfare Simulant. <i>PLoS ONE</i> , 2011, 6, e17836.	2.5	41
63	Vaginal Microbiome Composition in Early Pregnancy and Risk of Spontaneous Preterm and Early Term Birth Among African American Women. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 641005.	3.9	41
64	Genome Sequence of the Obligate Intracellular Animal Pathogen <i>Chlamydia pecorum</i> E58. <i>Journal of Bacteriology</i> , 2011, 193, 3690-3690.	2.2	36
65	Finding drug targets in microbial genomes. <i>Drug Discovery Today</i> , 2001, 6, 887-892.	6.4	35
66	Tetracycline Selective Pressure and Homologous Recombination Shape the Evolution of <i>Chlamydia suis</i> : A Recently Identified Zoonotic Pathogen. <i>Genome Biology and Evolution</i> , 2016, 8, 2613-2623.	2.5	35
67	The complete mitochondrial genome sequence of the world's largest fish, the whale shark ( <i>Rhincodon typus</i> ), and its comparison with those of related shark species. <i>Gene</i> , 2014, 539, 44-49.	2.2	34
68	A <i>Bacillus thuringiensis</i> strain producing a polyglutamate capsule resembling that of <i>Bacillus anthracis</i> . <i>FEMS Microbiology Letters</i> , 2008, 285, 220-226.	1.8	33
69	Stability of the vaginal, oral, and gut microbiota across pregnancy among African American women: the effect of socioeconomic status and antibiotic exposure. <i>PeerJ</i> , 2019, 7, e8004.	2.0	31
70	<i>Chlamydiaceae</i> Genomics Reveals Interspecies Admixture and the Recent Evolution of <i>Chlamydia abortus</i> Infecting Lower Mammalian Species and Humans. <i>Genome Biology and Evolution</i> , 2015, 7, 3070-3084.	2.5	30
71	Strand-Specific RNA-Seq Reveals Ordered Patterns of Sense and Antisense Transcription in <i>Bacillus anthracis</i> . <i>PLoS ONE</i> , 2012, 7, e43350.	2.5	30
72	Tet(C) Gene Transfer between <i>Chlamydia suis</i> Strains Occurs by Homologous Recombination after Co-infection: Implications for Spread of Tetracycline-Resistance among <i>Chlamydiaceae</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 156.	3.5	29

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73	Combined proteomic and transcriptomic analysis of the response of <i>Bacillus anthracis</i> to oxidative stress. <i>Proteomics</i> , 2011, 11, 3036-3055.	2.2	28
74	Whole genome sequencing of phage resistant <i>Bacillus anthracis</i> mutants reveals an essential role for cell surface anchoring protein CsaB in phage AP50c adsorption. <i>Virology Journal</i> , 2012, 9, 246.	3.4	28
75	Genetic Evidence for the Involvement of the S-Layer Protein Gene <i>sap</i> and the Sporulation Genes <i>spo0A</i> , <i>spo0B</i> , and <i>spo0F</i> in Phage AP50c Infection of <i>Bacillus anthracis</i> . <i>Journal of Bacteriology</i> , 2014, 196, 1143-1154.	2.2	28
76	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
77	Comprehensive bioinformatics analysis of <i>Mycoplasma pneumoniae</i> genomes to investigate underlying population structure and type-specific determinants. <i>PLoS ONE</i> , 2017, 12, e0174701.	2.5	27
78	Genome Sequences of the Zoonotic Pathogens <i>Chlamydia psittaci</i> 6BC and Cal10. <i>Journal of Bacteriology</i> , 2011, 193, 4039-4040.	2.2	26
79	Interaction between <i>Streptococcus pneumoniae</i> and <i>Staphylococcus aureus</i> Generates $\text{OH}^\cdot$ Radicals That Rapidly Kill <i>Staphylococcus aureus</i> Strains. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	25
80	'SEEDY' (Simulation of Evolutionary and Epidemiological Dynamics): An R Package to Follow Accumulation of Within-Host Mutation in Pathogens. <i>PLoS ONE</i> , 2015, 10, e0129745.	2.5	24
81	Direct Amplification, Sequencing and Profiling of <i>Chlamydia trachomatis</i> Strains in Single and Mixed Infection Clinical Samples. <i>PLoS ONE</i> , 2014, 9, e99290.	2.5	24
82	The Female Genital Tract Microbiome Is Associated With Vaginal Antiretroviral Drug Concentrations in Human Immunodeficiency Virus-Infected Women on Antiretroviral Therapy. <i>Journal of Infectious Diseases</i> , 2017, 216, 990-999.	4.0	23
83	Comparative Analysis of <i>Chlamydia</i> Bacteriophages Reveals Variation Localized to a Putative Receptor Binding Domain. <i>Microbial &amp; Comparative Genomics</i> , 2000, 5, 223-231.	0.4	21
84	Phase-Variable Expression of <i>lptA</i> Modulates the Resistance of <i>Neisseria gonorrhoeae</i> to Cationic Antimicrobial Peptides. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 4230-4233.	3.2	21
85	Genome-wide recombination in <i>Chlamydia trachomatis</i> . <i>Nature Genetics</i> , 2012, 44, 364-366.	21.4	20
86	Whole genome sequencing for investigations of meningococcal outbreaks in the United States: a retrospective analysis. <i>Scientific Reports</i> , 2018, 8, 15803.	3.3	20
87	Human mAbs to <i>Staphylococcus aureus</i> IsdA Provide Protection Through Both Heme-Blocking and Fc-Mediated Mechanisms. <i>Journal of Infectious Diseases</i> , 2019, 219, 1264-1273.	4.0	20
88	Genotyping of <i>Bacillus cereus</i> Strains by Microarray-Based Resequencing. <i>PLoS ONE</i> , 2008, 3, e2513.	2.5	20
89	The <i>bcr1</i> DNA Repeat Element Is Specific to the <i>Bacillus cereus</i> Group and Exhibits Mobile Element Characteristics. <i>Journal of Bacteriology</i> , 2004, 186, 7714-7725.	2.2	19
90	Genes Influencing Phage Host Range in <i>Staphylococcus aureus</i> on a Species-Wide Scale. <i>MSphere</i> , 2021, 6, .	2.9	19

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91	The whale shark genome reveals patterns of vertebrate gene family evolution. <i>ELife</i> , 2021, 10, .	6.0	19
92	Using Crude Whole-Genome Assemblies of <i>Neisseria gonorrhoeae</i> as a Platform for Strain Analysis: Clonal Spread of Gonorrhoea Infection in Saskatchewan, Canada. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3772-3776.	3.9	18
93	Dynamics of genome change among <i>Legionella</i> species. <i>Scientific Reports</i> , 2016, 6, 33442.	3.3	18
94	Comparing whole-genome shotgun sequencing and DNA metabarcoding approaches for species identification and quantification of pollen species mixtures. <i>Ecology and Evolution</i> , 2021, 11, 16082-16098.	1.9	17
95	Copy Number of Pilus Gene Clusters in <i>Haemophilus influenzae</i> and Variation in the <i>hifE</i> Pilin Gene. <i>Infection and Immunity</i> , 1998, 66, 1622-1631.	2.2	16
96	Dynamic PET-facilitated modeling and high-dose rifampin regimens for <i>Staphylococcus aureus</i> orthopedic implant-associated infections. <i>Science Translational Medicine</i> , 2021, 13, eabl6851.	12.4	16
97	Identification of <i>Bacillus anthracis</i> Spore Component Antigens Conserved across Diverse <i>Bacillus cereus sensu lato</i> Strains. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1174-1191.	3.8	15
98	A Multiplexed Microfluidic PCR Assay for Sensitive and Specific Point-of-Care Detection of <i>Chlamydia trachomatis</i> . <i>PLoS ONE</i> , 2012, 7, e51685.	2.5	14
99	Overproduction of the MtrCDE Efflux Pump in <i>Neisseria gonorrhoeae</i> Produces Unexpected Changes in Cellular Transcription Patterns. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 724-726.	3.2	13
100	Whole-Genome Sequences of <i>Staphylococcus aureus</i> Isolates from Cystic Fibrosis Lung Infections. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	13
101	A Comparison of the Bacterial Nasal Microbiome in Allergic Rhinitis Patients Before and After Immunotherapy. <i>Laryngoscope</i> , 2020, 130, E882-E888.	2.0	13
102	Structures of <i>Neisseria gonorrhoeae</i> MtrR-operator complexes reveal molecular mechanisms of DNA recognition and antibiotic resistance-conferring clinical mutations. <i>Nucleic Acids Research</i> , 2021, 49, 4155-4170.	14.5	13
103	Species-Wide Phylogenomics of the <i>Staphylococcus aureus</i> <i>Agr</i> Operon Revealed Convergent Evolution of Frameshift Mutations. <i>Microbiology Spectrum</i> , 2022, 10, e0133421.	3.0	13
104	Rapid Multi-Locus Sequence Typing Using Microfluidic Biochips. <i>PLoS ONE</i> , 2010, 5, e10595.	2.5	12
105	USA300 <i>Staphylococcus aureus</i> persists on multiple body sites following an infection. <i>BMC Microbiology</i> , 2018, 18, 206.	3.3	12
106	Genomic analysis of variability in Delta-toxin levels between <i>Staphylococcus aureus</i> strains. <i>PeerJ</i> , 2020, 8, e8717.	2.0	12
107	High-Redundancy Draft Sequencing of 15 Clinical and Environmental <i>Burkholderia</i> Strains. <i>Journal of Bacteriology</i> , 2010, 192, 6313-6314.	2.2	11
108	Nucleotide Sequence Analysis of Hypervariable Junctions of <i>Haemophilus influenzae</i> Pilus Gene Clusters. <i>Infection and Immunity</i> , 2000, 68, 6896-6902.	2.2	9

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109	Horizontal Transfer of CS1 Pilin Genes of Enterotoxigenic <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2004, 186, 3230-3237.	2.2	9
110	Whole-Genome Enrichment and Sequencing of <i>Chlamydia trachomatis</i> Directly from Patient Clinical Vaginal and Rectal Swabs. <i>MSphere</i> , 2021, 6, .	2.9	9
111	Effect of genetic background on the evolution of Vancomycin-Intermediate <i>Staphylococcus aureus</i> (VISA). <i>PeerJ</i> , 2021, 9, e11764.	2.0	9
112	Rapid detection and strain typing of <i>Chlamydia trachomatis</i> using a highly multiplexed microfluidic PCR assay. <i>PLoS ONE</i> , 2017, 12, e0178653.	2.5	8
113	The single-species metagenome: subtyping <i>Staphylococcus aureus</i> core genome sequences from shotgun metagenomic data. <i>PeerJ</i> , 2016, 4, e2571.	2.0	8
114	Metagenomic Shotgun Sequencing of Endocervical, Vaginal, and Rectal Samples among Fijian Women with and without <i>Chlamydia trachomatis</i> Reveals Disparate Microbial Populations and Function across Anatomic Sites: a Pilot Study. <i>Microbiology Spectrum</i> , 2022, 10, e0010522.	3.0	8
115	Conserved extragenic DNA elements in <i>Haemophilus influenzae</i> . <i>Molecular Microbiology</i> , 1997, 23, 627-628.	2.5	7
116	Genomic Plasticity of the <i>rrn-nqrF</i> Intergenic Segment in the <i>Chlamydiaceae</i> . <i>Journal of Bacteriology</i> , 2007, 189, 2128-2132.	2.2	7
117	Genetic variation and linkage disequilibrium in <i>Bacillus anthracis</i> . <i>Scientific Reports</i> , 2011, 1, 169.	3.3	7
118	PheMaDB: A solution for storage, retrieval, and analysis of high throughput phenotype data. <i>BMC Bioinformatics</i> , 2011, 12, 109.	2.6	7
119	Development of Oxacillin Resistance in a Patient with Recurrent <i>Staphylococcus aureus</i> Bacteremia. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3114-3117.	3.9	7
120	Characterization of a spermine/spermidine transport system reveals a novel DNA sequence duplication in <i>Neisseria gonorrhoeae</i> . <i>FEMS Microbiology Letters</i> , 2015, 362, fmv125.	1.8	7
121	Invasive Nontypeable <i>Haemophilus influenzae</i> Infection Among Adults With HIV in Metropolitan Atlanta, Georgia, 2008-2018. <i>JAMA - Journal of the American Medical Association</i> , 2019, 322, 2399.	7.4	7
122	Symbiont Genomic Features and Localization in the Bean Beetle <i>Callosobruchus maculatus</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0021221.	3.1	7
123	The evolution of infectious agents in relation to sex in animals and humans: brief discussions of some individual organisms. <i>Annals of the New York Academy of Sciences</i> , 2011, 1230, 74-107.	3.8	5
124	Fine-scale differentiation between <i>Bacillus anthracis</i> and <i>Bacillus cereus</i> group signatures in metagenome shotgun data. <i>PeerJ</i> , 2018, 6, e5515.	2.0	5
125	Shiftwork, functional bowel symptoms, and the microbiome. <i>PeerJ</i> , 2021, 9, e11406.	2.0	5
126	Unsuspected clonal spread of Methicillin-resistant <i>Staphylococcus aureus</i> causing bloodstream infections in hospitalized adults detected using whole genome sequencing. <i>Clinical Infectious Diseases</i> , 2022, , .	5.8	5



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127	Species-Scale Genomic Analysis of <i>Staphylococcus aureus</i> Genes Influencing Phage Host Range and Their Relationships to Virulence and Antibiotic Resistance Genes. <i>MSystems</i> , 2022, 7, e0108321.	3.8	4
128	A Single Amino Acid Substitution in Elongation Factor G Can Confer Low-Level Gentamicin Resistance in <i>Neisseria gonorrhoeae</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, e0025122.	3.2	4
129	Generation of Tetracycline and Rifamycin Resistant <i>Chlamydia Suis</i> Recombinants. <i>Frontiers in Microbiology</i> , 2021, 12, 630293.	3.5	3
130	Using Genomics To Standardize Population Analysis Profile-Area under the Curve Ratio for Vancomycin-Intermediate <i>Staphylococcus aureus</i> . <i>Journal of Clinical Microbiology</i> , 2014, 52, 3824-3826.	3.9	2
131	Glucocorticoid receptor sensitivity in early pregnancy in an African American cohort. <i>American Journal of Reproductive Immunology</i> , 2020, 84, e13252.	1.2	2
132	Unrecognized introductions of SARS-CoV-2 into the US state of Georgia shaped the early epidemic. <i>Virus Evolution</i> , 2022, 8, veac011.	4.9	2
133	<i>Chlamydiae</i> . , 2005, , .		0
134	Genome Sequence of a Clinical Isolate of <i>Campylobacter jejuni</i> from Thailand. <i>Infection and Immunity</i> , 2007, 75, 4671-4671.	2.2	0
135	Pathogenomics of Bacterial Biothreat Agents. , 0, , 232-266.		0
136	Association of secretor status and recent norovirus infection with gut microbiome diversity metrics in a Veterans Affairs population. <i>Open Forum Infectious Diseases</i> , 2022, 9, ofac125.	0.9	0