

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
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163
all docs

163
docs citations

163
times ranked

13451
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#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	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
5	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
6	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
7	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
8	Genes Influencing Phage Host Range in <i>Staphylococcus aureus</i> on a Species-Wide Scale. <i>MSphere</i> , 2021, 6, .	2.9	19
9	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
10	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
11	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
12	Shiftwork, functional bowel symptoms, and the microbiome. <i>PeerJ</i> , 2021, 9, e11406.	2.0	5
13	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
14	Generation of Tetracycline and Rifamycin Resistant <i>Chlamydia Suis</i> Recombinants. <i>Frontiers in Microbiology</i> , 2021, 12, 630293.	3.5	3
15	Effect of genetic background on the evolution of Vancomycin-Intermediate <i>Staphylococcus aureus</i> (VISA). <i>PeerJ</i> , 2021, 9, e11764.	2.0	9
16	The whale shark genome reveals patterns of vertebrate gene family evolution. <i>ELife</i> , 2021, 10, .	6.0	19
17	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
18	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

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19	Bactopia: a Flexible Pipeline for Complete Analysis of Bacterial Genomes. <i>MSystems</i> , 2020, 5, .	3.8	82
20	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
21	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
22	Glucocorticoid receptor sensitivity in early pregnancy in an African American cohort. <i>American Journal of Reproductive Immunology</i> , 2020, 84, e13252.	1.2	2
23	Genomic analysis of variability in Delta-toxin levels between <i>Staphylococcus aureus</i> strains. <i>PeerJ</i> , 2020, 8, e8717.	2.0	12
24	Quantitative and qualitative assessment of pollen DNA metabarcoding using constructed species mixtures. <i>Molecular Ecology</i> , 2019, 28, 431-455.	3.9	114
25	Interaction between <i>Streptococcus pneumoniae</i> and <i>Staphylococcus aureus</i> Generates OH^\cdot Radicals That Rapidly Kill <i>Staphylococcus aureus</i> Strains. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	25
26	Determinants of Phage Host Range in <i>Staphylococcus</i> Species. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	59
27	Whole-Genome Sequences of <i>Staphylococcus aureus</i> Isolates from Cystic Fibrosis Lung Infections. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	13
28	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
29	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
30	Genome-Based Prediction of Bacterial Antibiotic Resistance. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	221
31	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
32	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
33	USA300 <i>Staphylococcus aureus</i> persists on multiple body sites following an infection. <i>BMC Microbiology</i> , 2018, 18, 206.	3.3	12
34	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
35	<i>Staphylococcus aureus</i> viewed from the perspective of 40,000+ genomes. <i>PeerJ</i> , 2018, 6, e5261.	2.0	66
36	Lung Tissue Concentrations of Pyrazinamide among Patients with Drug-Resistant Pulmonary Tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	48

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37	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
38	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
39	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
40	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
41	Tet(C) Gene Transfer between <i>Chlamydia suis</i> Strains Occurs by Homologous Recombination after Co-infection: Implications for Spread of Tetracycline-Resistance among Chlamydiaceae. <i>Frontiers in Microbiology</i> , 2017, 8, 156.	3.5	29
42	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
43	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
44	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
45	Antibiotic failure mediated by a resistant subpopulation in <i>Enterobacter cloacae</i> . <i>Nature Microbiology</i> , 2016, 1, 16053.	13.3	169
46	Dynamics of genome change among <i>Legionella</i> species. <i>Scientific Reports</i> , 2016, 6, 33442.	3.3	18
47	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
48	'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
49	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
50	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
51	<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
52	Transmission and Microevolution of USA300 MRSA in U.S. Households: Evidence from Whole-Genome Sequencing. <i>MBio</i> , 2015, 6, e00054.	4.1	97
53	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, fnv125.	1.8	7
54	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

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55	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
56	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
57	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
58	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
59	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
60	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
61	Using Crude Whole-Genome Assemblies of <i>Neisseria gonorrhoeae</i> as a Platform for Strain Analysis: Clonal Spread of Gonorrhea Infection in Saskatchewan, Canada. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3772-3776.	3.9	18
62	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
63	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
64	Predicting the virulence of MRSA from its genome sequence. <i>Genome Research</i> , 2014, 24, 839-849.	5.5	210
65	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
66	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
67	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
68	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
69	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
70	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
71	Genome-wide recombination in <i>Chlamydia trachomatis</i> . <i>Nature Genetics</i> , 2012, 44, 364-366.	21.4	20
72	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

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73	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
74	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
75	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
76	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
77	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
78	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
79	Genetic variation and linkage disequilibrium in <i>Bacillus anthracis</i> . <i>Scientific Reports</i> , 2011, 1, 169.	3.3	7
80	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
81	Interplay of recombination and selection in the genomes of <i>Chlamydia trachomatis</i> . <i>Biology Direct</i> , 2011, 6, 28.	4.6	70
82	PheMaDB: A solution for storage, retrieval, and analysis of high throughput phenotype data. <i>BMC Bioinformatics</i> , 2011, 12, 109.	2.6	7
83	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
84	Hypervirulent <i>Chlamydia trachomatis</i> Clinical Strain Is a Recombinant between Lymphogranuloma Venereum (L ₂) and D Lineages. <i>MBio</i> , 2011, 2, e00045-11.	4.1	100
85	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
86	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
87	<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
88	Unity in Variety--The Pan-Genome of the Chlamydiae. <i>Molecular Biology and Evolution</i> , 2011, 28, 3253-3270.	8.9	184
89	Bacterial population genomics and infectious disease diagnostics. <i>Trends in Biotechnology</i> , 2010, 28, 611-618.	9.3	44
90	Finishing genomes with limited resources: lessons from an ensemble of microbial genomes. <i>BMC Genomics</i> , 2010, 11, 242.	2.8	46

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91	Rapid Multi-Locus Sequence Typing Using Microfluidic Biochips. PLoS ONE, 2010, 5, e10595.	2.5	12
92	High-Redundancy Draft Sequencing of 15 Clinical and Environmental Burkholderia Strains. Journal of Bacteriology, 2010, 192, 6313-6314.	2.2	11
93	Arbovirus Detection in Insect Vectors by Rapid, High-Throughput Pyrosequencing. PLoS Neglected Tropical Diseases, 2010, 4, e878.	3.0	53
94	Rapid Identification of Genetic Modifications in Bacillus anthracis Using Whole Genome Draft Sequences Generated by 454 Pyrosequencing. PLoS ONE, 2010, 5, e12397.	2.5	27
95	Genomic characterization of the Yersinia genus. Genome Biology, 2010, 11, R1.	9.6	103
96	Predicting Phenotype and Emerging Strains among <i>Chlamydia trachomatis</i> Infections. Emerging Infectious Diseases, 2009, 15, 1385-1394.	4.3	87
97	DIYA: a bacterial annotation pipeline for any genomics lab. Bioinformatics, 2009, 25, 962-963.	4.1	73
98	Identification of Bacillus anthracis Spore Component Antigens Conserved across Diverse Bacillus cereus sensu lato Strains. Molecular and Cellular Proteomics, 2009, 8, 1174-1191.	3.8	15
99	The Complete Genome Sequence of Bacillus anthracis Ames Ancestor. Journal of Bacteriology, 2009, 191, 445-446.	2.2	88
100	Quantitative characterization of quantum dot-labeled lambda phage for <i>Escherichia coli</i> detection. Biotechnology and Bioengineering, 2009, 104, 1059-1067.	3.3	44
101	A <i>Bacillus thuringiensis</i> strain producing a polyglutamate capsule resembling that of <i>Bacillus anthracis</i> . FEMS Microbiology Letters, 2008, 285, 220-226.	1.8	33
102	Characterization of Two <i>Campylobacter jejuni</i> Strains for Use in Volunteer Experimental-Infection Studies. Infection and Immunity, 2008, 76, 5655-5667.	2.2	43
103	Molecular Characterization of a Variant of <i>Bacillus anthracis</i> -Specific Phage AP50 with Improved Bacteriolytic Activity. Applied and Environmental Microbiology, 2008, 74, 6792-6796.	3.1	56
104	Genotyping of Bacillus cereus Strains by Microarray-Based Resequencing. PLoS ONE, 2008, 3, e2513.	2.5	20
105	Genome Sequence of a Clinical Isolate of Campylobacter jejuni from Thailand. Infection and Immunity, 2007, 75, 3425-3433.	2.2	68
106	Strain-Specific Single-Nucleotide Polymorphism Assays for the Bacillus anthracis Ames Strain. Journal of Clinical Microbiology, 2007, 45, 47-53.	3.9	126
107	Genomic Plasticity of the rrn-nqrF Intergenic Segment in the Chlamydiaceae. Journal of Bacteriology, 2007, 189, 2128-2132.	2.2	7
108	Genome Sequence of a Clinical Isolate of <i>Campylobacter jejuni</i> from Thailand. Infection and Immunity, 2007, 75, 4671-4671.	2.2	0

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109	The <i>Bacillus anthracis</i> chromosome contains four conserved, excision-proficient, putative prophages. <i>BMC Microbiology</i> , 2006, 6, 34.	3.3	50
110	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
111	<i>Chlamydiae</i> . , 2005, , .		0
112	Formation and Composition of the <i>Bacillus anthracis</i> Endospore. <i>Journal of Bacteriology</i> , 2004, 186, 164-178.	2.2	187
113	Horizontal Transfer of CS1 Pilin Genes of Enterotoxigenic <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2004, 186, 3230-3237.	2.2	9
114	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
115	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
116	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
117	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
118	Microarray-based resequencing of multiple <i>Bacillus anthracis</i> isolates. <i>Genome Biology</i> , 2004, 6, R10.	9.6	64
119	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
120	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
121	Molecular Analysis of the Multiple GroEL Proteins of <i>Chlamydiae</i> . <i>Journal of Bacteriology</i> , 2003, 185, 1958-1966.	2.2	63
122	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
123	Comparative Genome Sequencing for Discovery of Novel Polymorphisms in <i>Bacillus anthracis</i> . <i>Science</i> , 2002, 296, 2028-2033.	12.6	413
124	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
125	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
126	Genome sequence of the dissimilatory metal ion-reducing bacterium <i>Shewanella oneidensis</i> . <i>Nature Biotechnology</i> , 2002, 20, 1118-1123.	17.5	771

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127	Bacillus anthracis, a bug with attitude!. Current Opinion in Microbiology, 2001, 4, 78-81.	5.1	94
128	Complete Genome Sequence of a Virulent Isolate of <i>Streptococcus pneumoniae</i> . Science, 2001, 293, 498-506.	12.6	1,281
129	Finding drug targets in microbial genomes. Drug Discovery Today, 2001, 6, 887-892.	6.4	35
130	DNA sequence of both chromosomes of the cholera pathogen <i>Vibrio cholerae</i> . Nature, 2000, 406, 477-483.	27.8	1,723
131	Comparative Analysis of <i>Chlamydia</i> Bacteriophages Reveals Variation Localized to a Putative Receptor Binding Domain. Microbial & Comparative Genomics, 2000, 5, 223-231.	0.4	21
132	Nucleotide Sequence Analysis of Hypervariable Junctions of <i>Haemophilus influenzae</i> Pilus Gene Clusters. Infection and Immunity, 2000, 68, 6896-6902.	2.2	9
133	Copy Number of Pilus Gene Clusters in <i>Haemophilus influenzae</i> and Variation in the <i>hifE</i> Pilin Gene. Infection and Immunity, 1998, 66, 1622-1631.	2.2	16
134	Conserved extragenic DNA elements in <i>Haemophilus influenzae</i> . Molecular Microbiology, 1997, 23, 627-628.	2.5	7
135	Evasion of type I and type II DNA restriction systems by Inc11 plasmid Collb-P9 during transfer by bacterial conjugation. Molecular Microbiology, 1992, 6, 1933-1941.	2.5	41
136	Pathogenomics of Bacterial Biothreat Agents. , 0, , 232-266.		0