

Jonathan A Eisen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2470831/publications.pdf>

Version: 2024-02-01

430
papers

70,550
citations

2318

98
h-index

693

253
g-index

529
all docs

529
docs citations

529
times ranked

59917
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 796-815.	13.7	8,336
2	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	13.7	3,881
3	Environmental Genome Shotgun Sequencing of the Sargasso Sea. <i>Science</i> , 2004, 304, 66-74.	6.0	3,776
4	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	13.7	2,239
5	Structure, variation, and assembly of the root-associated microbiomes of rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E911-20.	3.3	2,016
6	The Sorcerer II Global Ocean Sampling Expedition: Northwest Atlantic through Eastern Tropical Pacific. <i>PLoS Biology</i> , 2007, 5, e77.	2.6	1,757
7	DNA sequence of both chromosomes of the cholera pathogen <i>Vibrio cholerae</i> . <i>Nature</i> , 2000, 406, 477-483.	13.7	1,723
8	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	9.4	1,512
9	Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of <i>Thermotoga maritima</i> . <i>Nature</i> , 1999, 399, 323-329.	13.7	1,397
10	Complete Genome Sequence of a Virulent Isolate of <i>Streptococcus pneumoniae</i> . <i>Science</i> , 2001, 293, 498-506.	6.0	1,281
11	Complete genome sequence and comparative analysis of the metabolically versatile <i>Pseudomonas putida</i> KT2440. <i>Environmental Microbiology</i> , 2002, 4, 799-808.	1.8	1,218
12	Complete Genome Sequence of <i>Neisseria meningitidis</i> Serogroup B Strain MC58. <i>Science</i> , 2000, 287, 1809-1815.	6.0	1,083
13	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009, 462, 1056-1060.	13.7	924
14	Genome Sequence of the Radioresistant Bacterium <i>Deinococcus radiodurans</i> R1. <i>Science</i> , 1999, 286, 1571-1577.	6.0	879
15	Role of Mobile DNA in the Evolution of Vancomycin-Resistant <i>Enterococcus faecalis</i> . <i>Science</i> , 2003, 299, 2071-2074.	6.0	849
16	Genome sequence of the dissimilatory metal ion-reducing bacterium <i>Shewanella oneidensis</i> . <i>Nature Biotechnology</i> , 2002, 20, 1118-1123.	9.4	771
17	Improving the coverage of the cyanobacterial phylum using diversity-driven genome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1053-1058.	3.3	769
18	The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria. <i>Nature</i> , 2003, 423, 81-86.	13.7	760

#	ARTICLE	IF	CITATIONS
19	The Genome of the Natural Genetic Engineer <i>Agrobacterium tumefaciens</i> C58. <i>Science</i> , 2001, 294, 2317-2323.	6.0	741
20	The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. <i>PLoS Biology</i> , 2007, 5, e16.	2.6	736
21	Sequence and analysis of chromosome 2 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 1999, 402, 761-768.	13.7	724
22	Phylogenomics of the Reproductive Parasite <i>Wolbachia pipientis</i> wMel: A Streamlined Genome Overrun by Mobile Genetic Elements. <i>PLoS Biology</i> , 2004, 2, e69.	2.6	713
23	Drivers of bacterial α -diversity depend on spatial scale. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7850-7854.	3.3	672
24	Macronuclear Genome Sequence of the Ciliate <i>Tetrahymena thermophila</i> , a Model Eukaryote. <i>PLoS Biology</i> , 2006, 4, e286.	2.6	657
25	Evolution of the SNF2 family of proteins: subfamilies with distinct sequences and functions. <i>Nucleic Acids Research</i> , 1995, 23, 2715-2723.	6.5	656
26	Bacterial Communities of Diverse <i>Drosophila</i> Species: Ecological Context of a Host-Microbe Model System. <i>PLoS Genetics</i> , 2011, 7, e1002272.	1.5	650
27	Genome of <i>Geobacter sulfurreducens</i> : Metal Reduction in Subsurface Environments. <i>Science</i> , 2003, 302, 1967-1969.	6.0	648
28	Whole-Genome Comparison of <i>Mycobacterium tuberculosis</i> Clinical and Laboratory Strains. <i>Journal of Bacteriology</i> , 2002, 184, 5479-5490.	1.0	645
29	Research priorities for harnessing plant microbiomes in sustainable agriculture. <i>PLoS Biology</i> , 2017, 15, e2001793.	2.6	640
30	PhyloSift: phylogenetic analysis of genomes and metagenomes. <i>PeerJ</i> , 2014, 2, e243.	0.9	633
31	Phylogenomics: Improving Functional Predictions for Uncharacterized Genes by Evolutionary Analysis. <i>Genome Research</i> , 1998, 8, 163-167.	2.4	571
32	The genome sequence of the anaerobic, sulfate-reducing bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Nature Biotechnology</i> , 2004, 22, 554-559.	9.4	559
33	Patellamide A and C biosynthesis by a microcin-like pathway in <i>Prochloron didemni</i> , the cyanobacterial symbiont of <i>Lissoclinum patella</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7315-7320.	3.3	553
34	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.	3.3	506
35	<i>Acidithiobacillus ferrooxidans</i> metabolism: from genome sequence to industrial applications. <i>BMC Genomics</i> , 2008, 9, 597.	1.2	490
36	Complete genome sequence of <i>Caulobacter crescentus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 4136-4141.	3.3	489

#	ARTICLE	IF	CITATIONS
37	A simple, fast, and accurate method of phylogenomic inference. <i>Genome Biology</i> , 2008, 9, R151.	13.9	482
38	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.	3.3	447
39	TIGRFAMs: a protein family resource for the functional identification of proteins. <i>Nucleic Acids Research</i> , 2001, 29, 41-43.	6.5	445
40	An Integrated Pipeline for de Novo Assembly of Microbial Genomes. <i>PLoS ONE</i> , 2012, 7, e42304.	1.1	436
41	Evolution of sensory complexity recorded in a myxobacterial genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15200-15205.	3.3	424
42	Comparative Genomics of Emerging Human Ehrlichiosis Agents. <i>PLoS Genetics</i> , 2006, 2, e21.	1.5	423
43	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.	3.3	422
44	Genome sequence of <i>Silicibacter pomeroyi</i> reveals adaptations to the marine environment. <i>Nature</i> , 2004, 432, 910-913.	13.7	415
45	Genome Sequence of the PCE-Dechlorinating Bacterium <i>Dehalococcoides ethenogenes</i> . <i>Science</i> , 2005, 307, 105-108.	6.0	402
46	Incorporating 16S Gene Copy Number Information Improves Estimates of Microbial Diversity and Abundance. <i>PLoS Computational Biology</i> , 2012, 8, e1002743.	1.5	400
47	A phylogenomic study of DNA repair genes, proteins, and processes. <i>Mutation Research DNA Repair</i> , 1999, 435, 171-213.	3.8	398
48	Metabolic Complementarity and Genomics of the Dual Bacterial Symbiosis of Sharpshooters. <i>PLoS Biology</i> , 2006, 4, e188.	2.6	391
49	Unsuspected diversity among marine aerobic anoxygenic phototrophs. <i>Nature</i> , 2002, 415, 630-633.	13.7	380
50	Second gene for gonadotropin-releasing hormone in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 305-309.	3.3	367
51	The complete genome sequence of <i>Chlorobium tepidum</i> TLS, a photosynthetic, anaerobic, green-sulfur bacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9509-9514.	3.3	362
52	Complete Genome Sequence of the Oral Pathogenic Bacterium <i>Porphyromonas gingivalis</i> Strain W83. <i>Journal of Bacteriology</i> , 2003, 185, 5591-5601.	1.0	362
53	Assembling the Marine Metagenome, One Cell at a Time. <i>PLoS ONE</i> , 2009, 4, e5299.	1.1	320
54	2019 Novel Coronavirus (COVID-19) Pandemic: Built Environment Considerations To Reduce Transmission. <i>MSystems</i> , 2020, 5, .	1.7	302

#	ARTICLE	IF	CITATIONS
55	Evidence for symmetric chromosomal inversions around the replication origin in bacteria. <i>Genome Biology</i> , 2000, 1, research0011.1.	13.9	287
56	Phylogenomics: Intersection of Evolution and Genomics. <i>Science</i> , 2003, 300, 1706-1707.	6.0	286
57	Microbial Genes in the Human Genome: Lateral Transfer or Gene Loss?. <i>Science</i> , 2001, 292, 1903-1906.	6.0	284
58	Human gut microbiome adopts an alternative state following small bowel transplantation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17187-17192.	3.3	281
59	Genomic Insights into Methanotrophy: The Complete Genome Sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , 2004, 2, e303.	2.6	275
60	Analysis of <i>Deinococcus radiodurans</i> 's Transcriptional Response to Ionizing Radiation and Desiccation Reveals Novel Proteins That Contribute to Extreme Radioresistance. <i>Genetics</i> , 2004, 168, 21-33.	1.2	274
61	Marine probiotics: increasing coral resistance to bleaching through microbiome manipulation. <i>ISME Journal</i> , 2019, 13, 921-936.	4.4	269
62	Comparison of the genome of the oral pathogen <i>Treponema denticola</i> with other spirochete genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 5646-5651.	3.3	251
63	The RecA protein as a model molecule for molecular systematic studies of bacteria: Comparison of trees of RecAs and 16S rRNAs from the same species. <i>Journal of Molecular Evolution</i> , 1995, 41, 1105-23.	0.8	242
64	Horizontal gene transfer among microbial genomes: new insights from complete genome analysis. <i>Current Opinion in Genetics and Development</i> , 2000, 10, 606-611.	1.5	237
65	Nitrogen fixation in a landrace of maize is supported by a mucilage-associated diazotrophic microbiota. <i>PLoS Biology</i> , 2018, 16, e2006352.	2.6	236
66	The Complete Genome Sequence of <i>Haloferax volcanii</i> DS2, a Model Archaeon. <i>PLoS ONE</i> , 2010, 5, e9605.	1.1	234
67	Meeting Report: The Terabase Metagenomics Workshop and the Vision of an Earth Microbiome Project. <i>Standards in Genomic Sciences</i> , 2010, 3, 243-248.	1.5	228
68	Life in Hot Carbon Monoxide: The Complete Genome Sequence of <i>Carboxydothemus hydrogenoformans</i> Z-2901. <i>PLoS Genetics</i> , 2005, 1, e65.	1.5	226
69	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , 2017, 35, 676-683.	9.4	222
70	Environmental Shotgun Sequencing: Its Potential and Challenges for Studying the Hidden World of Microbes. <i>PLoS Biology</i> , 2007, 5, e82.	2.6	218
71	Complete Genome Sequence of the Broad-Host-Range <i>Vibriophage</i> KVP40: Comparative Genomics of a T4-Related Bacteriophage. <i>Journal of Bacteriology</i> , 2003, 185, 5220-5233.	1.0	214
72	Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. <i>Nature Communications</i> , 2013, 4, 2120.	5.8	201

#	ARTICLE	IF	CITATIONS
73	Metagenomic Sequencing of an In Vitro-Simulated Microbial Community. <i>PLoS ONE</i> , 2010, 5, e10209.	1.1	200
74	The <i>Calyptogenia magnifica</i> Chemoautotrophic Symbiont Genome. <i>Science</i> , 2007, 315, 998-1000.	6.0	194
75	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	2.6	190
76	Comparative studies of resistin expression and phylogenomics in human and mouse. <i>Biochemical and Biophysical Research Communications</i> , 2003, 310, 927-935.	1.0	187
77	A phylogenomic study of the MutS family of proteins. <i>Nucleic Acids Research</i> , 1998, 26, 4291-4300.	6.5	183
78	Systematic Identification of Gene Families for Use as "Markers" for Phylogenetic and Phylogeny-Driven Ecological Studies of Bacteria and Archaea and Their Major Subgroups. <i>PLoS ONE</i> , 2013, 8, e77033.	1.1	171
79	Microbial genome sequencing. <i>Nature</i> , 2000, 406, 799-803.	13.7	164
80	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	13.5	164
81	Accounting For Alignment Uncertainty in Phylogenomics. <i>PLoS ONE</i> , 2012, 7, e30288.	1.1	163
82	Yeast Communities of Diverse <i>Drosophila</i> Species: Comparison of Two Symbiont Groups in the Same Hosts. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7327-7336.	1.4	160
83	Global-Scale Structure of the Eelgrass Microbiome. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	147
84	Ten questions concerning the microbiomes of buildings. <i>Building and Environment</i> , 2016, 109, 224-234.	3.0	143
85	Rokubacteria: Genomic Giants among the Uncultured Bacterial Phyla. <i>Frontiers in Microbiology</i> , 2017, 8, 2264.	1.5	142
86	Forensic analysis of the microbiome of phones and shoes. <i>Microbiome</i> , 2015, 3, 21.	4.9	140
87	Phylogeny of Bacterial and Archaeal Genomes Using Conserved Genes: Supertrees and Supermatrices. <i>PLoS ONE</i> , 2013, 8, e62510.	1.1	138
88	Phylogenetically Driven Sequencing of Extremely Halophilic Archaea Reveals Strategies for Static and Dynamic Osmo-response. <i>PLoS Genetics</i> , 2014, 10, e1004784.	1.5	136
89	MlxS-BE: a MlxS extension defining a minimum information standard for sequence data from the built environment. <i>ISME Journal</i> , 2014, 8, 1-3.	4.4	127
90	Adaptations to Submarine Hydrothermal Environments Exemplified by the Genome of <i>Nautilia profundicola</i> . <i>PLoS Genetics</i> , 2009, 5, e1000362.	1.5	126

#	ARTICLE	IF	CITATIONS
91	Genetic and Physical Mapping of DNA Replication Origins in <i>Haloferax volcanii</i> . <i>PLoS Genetics</i> , 2007, 3, e77.	1.5	118
92	The age of the <i>Arabidopsis thaliana</i> genome duplication. <i>Plant Molecular Biology</i> , 2003, 51, 859-866.	2.0	115
93	Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium <i>Ktedonobacter racemifer</i> type strain (SOSP1-21T). <i>Standards in Genomic Sciences</i> , 2011, 5, 97-111.	1.5	115
94	Microbial communities in sediment from <i>Zostera marina</i> patches, but not the <i>Z. Âmarina</i> leaf or root microbiomes, vary in relation to distance from patch edge. <i>PeerJ</i> , 2017, 5, e3246.	0.9	115
95	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	5.9	115
96	Root-hair endophyte stacking in finger millet creates a physicochemical barrier to trap the fungal pathogen <i>Fusarium graminearum</i> . <i>Nature Microbiology</i> , 2016, 1, 16167.	5.9	113
97	Complete Genome Sequence of the Aerobic CO-Oxidizing Thermophile <i>Thermomicrobium roseum</i> . <i>PLoS ONE</i> , 2009, 4, e4207.	1.1	113
98	Strain- and plasmid-level deconvolution of a synthetic metagenome by sequencing proximity ligation products. <i>PeerJ</i> , 2014, 2, e415.	0.9	111
99	Mauve Assembly Metrics. <i>Bioinformatics</i> , 2011, 27, 2756-2757.	1.8	108
100	Sequence similarity of putative transposases links the maize <i>Mutator</i> autonomous element and a group of bacterial insertion sequences. <i>Nucleic Acids Research</i> , 1994, 22, 2634-2636.	6.5	107
101	Microscale sulfur cycling in the phototrophic pink berry consortia of the <i>S</i> <i>ippewissett</i> <i>S</i> <i>M</i> <i>arsh</i> . <i>Environmental Microbiology</i> , 2014, 16, 3398-3415.	1.8	106
102	A genomic analysis of the archaeal system <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> . <i>Genome Biology</i> , 2008, 9, R158.	3.8	104
103	Host-associated microbiomes drive structure and function of marine ecosystems. <i>PLoS Biology</i> , 2019, 17, e3000533.	2.6	103
104	The Value of Complete Microbial Genome Sequencing (You Get What You Pay For). <i>Journal of Bacteriology</i> , 2002, 184, 6403-6405.	1.0	101
105	Modeling Bacterial Evolution with Comparative-Genome-Based Marker Systems: Application to <i>Mycobacterium tuberculosis</i> Evolution and Pathogenesis. <i>Journal of Bacteriology</i> , 2003, 185, 3392-3399.	1.0	101
106	Characterization of Bacterial Communities Associated with Deep-Sea Corals on Gulf of Alaska Seamounts. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1680-1683.	1.4	101
107	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541T). <i>Standards in Genomic Sciences</i> , 2009, 1, 12-20.	1.5	100
108	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6T). <i>Standards in Genomic Sciences</i> , 2011, 4, 200-209.	1.5	96

#	ARTICLE	IF	CITATIONS
109	Stalking the Fourth Domain in Metagenomic Data: Searching for, Discovering, and Interpreting Novel, Deep Branches in Marker Gene Phylogenetic Trees. <i>PLoS ONE</i> , 2011, 6, e18011.	1.1	95
110	Assessing evolutionary relationships among microbes from whole-genome analysis. <i>Current Opinion in Microbiology</i> , 2000, 3, 475-480.	2.3	94
111	The Complete Genome of <i>Teredinibacter turnerae</i> T7901: An Intracellular Endosymbiont of Marine Wood-Boring Bivalves (Shipworms). <i>PLoS ONE</i> , 2009, 4, e6085.	1.1	93
112	Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 183-191.	0.5	92
113	Phylogenetic Analysis and Gene Functional Predictions: Phylogenomics in Action. <i>Theoretical Population Biology</i> , 2002, 61, 481-487.	0.5	87
114	CompostBin: A DNA Composition-Based Algorithm for Binning Environmental Shotgun Reads. <i>Lecture Notes in Computer Science</i> , 2008, , 17-28.	1.0	85
115	The microbes we eat: abundance and taxonomy of microbes consumed in a day's worth of meals for three diet types. <i>PeerJ</i> , 2014, 2, e659.	0.9	85
116	Refined annotation and assembly of the <i>Tetrahymena thermophila</i> genome sequence through EST analysis, comparative genomic hybridization, and targeted gap closure. <i>BMC Genomics</i> , 2008, 9, 562.	1.2	84
117	The Phylogenetic Diversity of Metagenomes. <i>PLoS ONE</i> , 2011, 6, e23214.	1.1	83
118	Identification of a fourth family of lycopene cyclases in photosynthetic bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11784-11789.	3.3	82
119	Genomic Encyclopedia of Type Strains, Phase I: The one thousand microbial genomes (KMG-I) project. <i>Standards in Genomic Sciences</i> , 2013, 9, 1278-1284.	1.5	79
120	Taking the First Steps towards a Standard for Reporting on Phylogenies: Minimum Information about a Phylogenetic Analysis (MIAPA). <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 231-237.	1.0	76
121	Complete genome sequence of <i>Planctomyces brasiliensis</i> type strain (DSM 5305T), phylogenomic analysis and reclassification of <i>Planctomycetes</i> including the descriptions of <i>Gimesia</i> gen. nov., <i>Planctopirus</i> gen. nov. and <i>Rubinisphaera</i> gen. nov. and emended descriptions of the order <i>Planctomycetales</i> and the family <i>Planctomycetaceae</i> . <i>Standards in Genomic Sciences</i> , 2014, 9, 10.	1.5	76
122	Complete genome sequence of <i>Chitinophaga pinensis</i> type strain (UQM 2034T). <i>Standards in Genomic Sciences</i> , 2010, 2, 87-95.	1.5	74
123	Genomic Encyclopedia of Bacterial and Archaeal Type Strains, Phase III: the genomes of soil and plant-associated and newly described type strains. <i>Standards in Genomic Sciences</i> , 2015, 10, 26.	1.5	74
124	PhyLOTU: A High-Throughput Procedure Quantifies Microbial Community Diversity and Resolves Novel Taxa from Metagenomic Data. <i>PLoS Computational Biology</i> , 2011, 7, e1001061.	1.5	73
125	Comparative Genomics and Understanding of Microbial Biology. <i>Emerging Infectious Diseases</i> , 2000, 6, 505-512.	2.0	72
126	Complete genome sequence of <i>Haliangium ochraceum</i> type strain (SMP-2T). <i>Standards in Genomic Sciences</i> , 2010, 2, 96-106.	1.5	70

#	ARTICLE	IF	CITATIONS
127	Phosphate transporters in marine phytoplankton and their viruses: cross-domain commonalities in viral-host gene exchanges. <i>Environmental Microbiology</i> , 2012, 14, 162-176.	1.8	70
128	Microbial Mat Communities along an Oxygen Gradient in a Perennially Ice-Covered Antarctic Lake. <i>Applied and Environmental Microbiology</i> , 2016, 82, 620-630.	1.4	69
129	Genome-Scale Analysis of Programmed DNA Elimination Sites in <i>Tetrahymena thermophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 515-522.	0.8	68
130	Sequence and analysis of the Arabidopsis genome. <i>Current Opinion in Plant Biology</i> , 2001, 4, 105-110.	3.5	66
131	Cloning and Characterization of HARP/SMARCAL1: A Prokaryotic HepA-Related SNF2 Helicase Protein from Human and Mouse. <i>Genomics</i> , 2000, 65, 274-282.	1.3	65
132	A Case for Evolutionary Genomics and the Comprehensive Examination of Sequence Biodiversity. <i>Molecular Biology and Evolution</i> , 2000, 17, 1776-1788.	3.5	63
133	Deep-sea hydrothermal vent bacteria related to human pathogenic <i>Vibrio</i> species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2813-9.	3.3	63
134	Metagenome-assembled genomes provide new insight into the microbial diversity of two thermal pools in Kamchatka, Russia. <i>Scientific Reports</i> , 2019, 9, 3059.	1.6	63
135	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. <i>Frontiers in Microbiology</i> , 2020, 11, 1848.	1.5	62
136	Functional Biogeography of Ocean Microbes Revealed through Non-Negative Matrix Factorization. <i>PLoS ONE</i> , 2012, 7, e43866.	1.1	60
137	Complete genome sequence of the termite hindgut bacterium <i>Spirochaeta coccoides</i> type strain (SPN1T), reclassification in the genus <i>Sphaerochaeta</i> as <i>Sphaerochaeta coccoides</i> comb. nov. and emendations of the family Spirochaetaceae and the genus <i>Sphaerochaeta</i> . <i>Standards in Genomic Sciences</i> , 2012, 6, 194-209.	1.5	58
138	Gene Conservation among Endospore-Forming Bacteria Reveals Additional Sporulation Genes in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2013, 195, 253-260.	1.0	57
139	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20T). <i>Standards in Genomic Sciences</i> , 2010, 2, 158-167.	1.5	56
140	In silico-initiated cloning and molecular characterization of a novel human member of the L1 gene family of neural cell adhesion molecules. <i>Human Genetics</i> , 1998, 103, 355-364.	1.8	55
141	Automated and Accurate Estimation of Gene Family Abundance from Shotgun Metagenomes. <i>PLoS Computational Biology</i> , 2015, 11, e1004573.	1.5	55
142	Genomic perspective on the photobiology of <i>Halobacterium</i> species NRC-1, a phototrophic, phototactic, and UV-tolerant haloarchaeon. <i>Photosynthesis Research</i> , 2001, 70, 3-17.	1.6	54
143	Phylogenetic relationships of chemoautotrophic bacterial symbionts of <i>Solemya velum</i> say (Mollusca: Tj ETQq1 1 0.784314 ggBT /Overl	1.0	52
144	A microbial survey of the International Space Station (ISS). <i>PeerJ</i> , 2017, 5, e4029.	0.9	52

#	ARTICLE	IF	CITATIONS
145	Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3T). <i>Standards in Genomic Sciences</i> , 2011, 4, 100-110.	1.5	51
146	Complete genome sequence of the thermophilic, hydrogen-oxidizing <i>Bacillus tusciae</i> type strain (T2T) and reclassification in the new genus, <i>Kyrpidia</i> gen. nov. as <i>Kyrpidia tusciae</i> comb. nov. and emendation of the family <i>Alicyclobacillaceae</i> da Costa and Rainey, 2010.. <i>Standards in Genomic Sciences</i> , 2011, 5, 121-134.	1.5	51
147	Complete genome sequence of <i>Truepera radiovictrix</i> type strain (RQ-24T). <i>Standards in Genomic Sciences</i> , 2011, 4, 91-99.	1.5	46
148	Complete genome sequence of <i>Isosphaera pallida</i> type strain (IS1BT). <i>Standards in Genomic Sciences</i> , 2011, 4, 63-71.	1.5	46
149	The Impact of <i>Helicobacter pylori</i> Infection on the Gastric Microbiota of the Rhesus Macaque. <i>PLoS ONE</i> , 2013, 8, e76375.	1.1	46
150	Complete genome sequence of <i>Rhodothermus marinus</i> type strain (R-10T). <i>Standards in Genomic Sciences</i> , 2009, 1, 283-290.	1.5	45
151	A phylogenetically novel cyanobacterium most closely related to <i>Gloeobacter</i> . <i>ISME Journal</i> , 2020, 14, 2142-2152.	4.4	45
152	Complete genome sequence of <i>Veillonella parvula</i> type strain (Te3T). <i>Standards in Genomic Sciences</i> , 2010, 2, 57-65.	1.5	44
153	Genome sequence of the thermophilic fresh-water bacterium <i>Spirochaeta caldaria</i> type strain (H11), reclassification of <i>Spirochaeta caldaria</i> , <i>Spirochaeta stenostrepta</i> , and <i>Spirochaeta zuelzeriae</i> in the genus <i>Treponema</i> as <i>Treponema caldaria</i> comb. nov., <i>Treponema stenostrepta</i> comb. nov., and <i>Treponema zuelzeriae</i> comb. nov., and emendation of the genus <i>Treponema</i> . <i>Standards in Genomic Sciences</i> , 2013, 8, 88-105.	1.5	44
154	An Automated Phylogenetic Tree-Based Small Subunit rRNA Taxonomy and Alignment Pipeline (STAP). <i>PLoS ONE</i> , 2008, 3, e2566.	1.1	44
155	Complete genome sequence of <i>Olsenella uli</i> type strain (VPI D76D-27CT). <i>Standards in Genomic Sciences</i> , 2010, 3, 76-84.	1.5	43
156	A cut above: Discovery of an alternative excision repair pathway in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 2581-2583.	3.3	42
157	Sequencing of Seven Haloarchaeal Genomes Reveals Patterns of Genomic Flux. <i>PLoS ONE</i> , 2012, 7, e41389.	1.1	42
158	Complete genome sequence of <i>Treponema succinifaciens</i> type strain (6091T). <i>Standards in Genomic Sciences</i> , 2011, 4, 361-370.	1.5	41
159	Community-Level Differences in the Microbiome of Healthy Wild Mallards and Those Infected by Influenza A Viruses. <i>MSystems</i> , 2017, 2, .	1.7	41
160	Gastrogenomic delights: A movable feast. <i>Nature Medicine</i> , 1997, 3, 1076-1078.	15.2	40
161	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1T). <i>Standards in Genomic Sciences</i> , 2010, 2, 176-184.	1.5	40
162	Complete genome sequence of <i>Arcobacter nitrofigilis</i> type strain (CIT). <i>Standards in Genomic Sciences</i> , 2010, 2, 300-308.	1.5	40

#	ARTICLE	IF	CITATIONS
163	Recent Outbreaks of Shigellosis in California Caused by Two Distinct Populations of <i>Shigella sonnei</i> with either Increased Virulence or Fluoroquinolone Resistance. <i>MSphere</i> , 2016, 1, .	1.3	40
164	Complete genome sequence of <i>Actinosynnema mirum</i> type strain (101T). <i>Standards in Genomic Sciences</i> , 2009, 1, 46-53.	1.5	38
165	Complete genome sequence of <i>Cellulomonas flavigena</i> type strain (134T). <i>Standards in Genomic Sciences</i> , 2010, 3, 15-25.	1.5	38
166	Insights into the evolution of Darwin's finches from comparative analysis of the <i>Geospiza magnirostris</i> genome sequence. <i>BMC Genomics</i> , 2013, 14, 95.	1.2	38
167	Complete genome sequence of <i>Eggerthella lenta</i> type strain (VPI 0255T). <i>Standards in Genomic Sciences</i> , 2009, 1, 174-182.	1.5	37
168	Complete genome sequence of <i>Desulfarculus baarsii</i> type strain (2st14T). <i>Standards in Genomic Sciences</i> , 2010, 3, 276-284.	1.5	37
169	Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph <i>Sulfuricurvum kujiense</i> type strain (YK-1T). <i>Standards in Genomic Sciences</i> , 2012, 6, 94-103.	1.5	37
170	SARS-CoV-2 detection and genomic sequencing from hospital surface samples collected at UC Davis. <i>PLoS ONE</i> , 2021, 16, e0253578.	1.1	37
171	Complete genome sequence of <i>Sulfurimonas autotrophica</i> type strain (OK10T). <i>Standards in Genomic Sciences</i> , 2010, 3, 194-202.	1.5	37
172	Growth of 48 built environment bacterial isolates on board the International Space Station (ISS). <i>PeerJ</i> , 2016, 4, e1842.	0.9	37
173	Swabs to genomes: a comprehensive workflow. <i>PeerJ</i> , 2015, 3, e960.	0.9	37
174	Complete genome sequence of <i>Desulfomicrobium baculatum</i> type strain (XT). <i>Standards in Genomic Sciences</i> , 2009, 1, 29-37.	1.5	36
175	Complete genome sequence of the extremely halophilic <i>Halanaerobium praevalens</i> type strain (GSLT). <i>Standards in Genomic Sciences</i> , 2011, 4, 312-321.	1.5	36
176	Complete genome sequence of <i>Desulfotomaculum acetoxidans</i> type strain (5575T). <i>Standards in Genomic Sciences</i> , 2009, 1, 242-253.	1.5	35
177	Complete genome sequence of <i>Nakamurella multipartita</i> type strain (Y-104T). <i>Standards in Genomic Sciences</i> , 2010, 2, 168-175.	1.5	35
178	The Genome Sequence of <i>Methanohalophilus mahii</i> SLP ^T Reveals Differences in the Energy Metabolism among Members of the <i>Methanosarcinaceae</i> Inhabiting Freshwater and Saline Environments. <i>Archaea</i> , 2010, 2010, 1-16.	2.3	35
179	Complete genome sequence of <i>Thermomonospora curvata</i> type strain (B9T). <i>Standards in Genomic Sciences</i> , 2011, 4, 13-22.	1.5	35
180	Fungi, bacteria and oomycota opportunistically isolated from the seagrass, <i>Zostera marina</i> . <i>PLoS ONE</i> , 2020, 15, e0236135.	1.1	35

#	ARTICLE	IF	CITATIONS
181	Complete genome sequence of <i>Pirellula staleyii</i> type strain (ATCC 27377T). <i>Standards in Genomic Sciences</i> , 2009, 1, 308-316.	1.5	34
182	Complete genome sequence of <i>Sebaldella termitidis</i> type strain (NCTC 11300T). <i>Standards in Genomic Sciences</i> , 2010, 2, 220-227.	1.5	34
183	Characterization of the Mycobiome of the Seagrass, <i>Zostera marina</i> , Reveals Putative Associations With Marine Chytrids. <i>Frontiers in Microbiology</i> , 2019, 10, 2476.	1.5	34
184	Genomic analysis of <i>Hyphomonas neptunium</i> contradicts 16S rRNA gene-based phylogenetic analysis: implications for the taxonomy of the orders "Rhodobacterales"™ and Caulobacterales. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005, 55, 1021-1026.	0.8	33
185	Complete genome sequence of <i>Meiothermus ruber</i> type strain (21T). <i>Standards in Genomic Sciences</i> , 2010, 3, 26-36.	1.5	33
186	Complete genome sequence of <i>Cellulophaga lytica</i> type strain (LIM-21T). <i>Standards in Genomic Sciences</i> , 2011, 4, 221-232.	1.5	33
187	Complete genome sequence of <i>Riemerella anatipestifer</i> type strain (ATCC 11845T). <i>Standards in Genomic Sciences</i> , 2011, 4, 144-153.	1.5	33
188	The United States Culture Collection Network (USCCN): Enhancing Microbial Genomics Research through Living Microbe Culture Collections. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5671-5674.	1.4	33
189	Complete genome sequence of <i>Acidimicrobium ferrooxidans</i> type strain (ICPT). <i>Standards in Genomic Sciences</i> , 2009, 1, 38-45.	1.5	32
190	Complete genome sequence of <i>Nocardiopsis dassonvillei</i> type strain (IMRU 509T). <i>Standards in Genomic Sciences</i> , 2010, 3, 325-336.	1.5	32
191	Complete genome sequence of <i>Haloterrigena turkmenica</i> type strain (4kT). <i>Standards in Genomic Sciences</i> , 2010, 2, 107-116.	1.5	32
192	Complete genome sequence of <i>Aminobacterium colombiense</i> type strain (ALA-1T). <i>Standards in Genomic Sciences</i> , 2010, 2, 280-289.	1.5	32
193	Complete genome sequence of <i>Halomicrobium mukohataei</i> type strain (arg-2T). <i>Standards in Genomic Sciences</i> , 2009, 1, 270-277.	1.5	31
194	Complete genome sequence of <i>Planctomyces limnophilus</i> type strain (M ¹ 4 290T). <i>Standards in Genomic Sciences</i> , 2010, 3, 47-56.	1.5	31
195	Complete genome sequence of <i>Acidaminococcus fermentans</i> type strain (VR4T). <i>Standards in Genomic Sciences</i> , 2010, 3, 1-14.	1.5	31
196	Gut Check: The evolution of an educational board game. <i>PLoS Biology</i> , 2017, 15, e2001984.	2.6	31
197	Complete genome sequence of <i>Atopobium parvulum</i> type strain (IPP 1246T). <i>Standards in Genomic Sciences</i> , 2009, 1, 166-173.	1.5	30
198	Complete genome sequence of <i>Paludibacter propionicigenes</i> type strain (WB4T). <i>Standards in Genomic Sciences</i> , 2011, 4, 36-44.	1.5	30

#	ARTICLE	IF	CITATIONS
199	Characterization of shifts of koala (<i>Phascolarctos cinereus</i>) intestinal microbial communities associated with antibiotic treatment. PeerJ, 2018, 6, e4452.	0.9	30
200	Gastrogenomics. Nature, 2001, 409, 463-465.	13.7	29
201	Complete genome sequence of <i>Sulfurospirillum deleyianum</i> type strain (5175T). Standards in Genomic Sciences, 2010, 2, 149-157.	1.5	29
202	Introducing W.A.T.E.R.S.: a Workflow for the Alignment, Taxonomy, and Ecology of Ribosomal Sequences. BMC Bioinformatics, 2010, 11, 317.	1.2	29
203	BioTorrents: A File Sharing Service for Scientific Data. PLoS ONE, 2010, 5, e10071.	1.1	29
204	Complete genome sequence of <i>Kangiella koreensis</i> type strain (SW-125T). Standards in Genomic Sciences, 2009, 1, 226-233.	1.5	28
205	Complete genome sequence of <i>Coralimargarita akajimensis</i> type strain (04OKA010-24T). Standards in Genomic Sciences, 2010, 2, 290-299.	1.5	28
206	Complete genome sequence of <i>Cellulophaga algicola</i> type strain (IC166T). Standards in Genomic Sciences, 2011, 4, 72-80.	1.5	28
207	The Cloacal Microbiome of Five Wild Duck Species Varies by Species and Influenza A Virus Infection Status. MSphere, 2018, 3, .	1.3	28
208	Complete genome sequence of <i>Sphaerobacter thermophilus</i> type strain (S 6022T). Standards in Genomic Sciences, 2010, 2, 49-56.	1.5	27
209	Complete genome sequence of <i>Streptosporangium roseum</i> type strain (NI 9100T). Standards in Genomic Sciences, 2010, 2, 29-37.	1.5	27
210	Complete genome sequence of <i>Archaeoglobus profundus</i> type strain (AV18T). Standards in Genomic Sciences, 2010, 2, 327-346.	1.5	26
211	Complete genome sequence of <i>Gordonia bronchialis</i> type strain (3410T). Standards in Genomic Sciences, 2010, 2, 19-28.	1.5	26
212	Complete genome sequence of <i>Haliscomenobacter hydrossis</i> type strain (OT). Standards in Genomic Sciences, 2011, 4, 352-360.	1.5	26
213	Genome sequence of the moderately thermophilic, amino-acid-degrading and sulfur-reducing bacterium <i>Thermovirga lienii</i> type strain (Cas60314T). Standards in Genomic Sciences, 2012, 6, 230-239.	1.5	26
214	Genome sequence of the homoacetogenic bacterium <i>Holophaga foetida</i> type strain (TMBS4T). Standards in Genomic Sciences, 2012, 6, 174-184.	1.5	26
215	The genome of the intracellular bacterium of the coastal bivalve, <i>Solemya velum</i> : a blueprint for thriving in and out of symbiosis. BMC Genomics, 2014, 15, 924.	1.2	26
216	Genome of <i>Thermotoga maritima</i> MSB8. Methods in Enzymology, 2001, 330, 169-180.	0.4	25

#	ARTICLE	IF	CITATIONS
217	On the taxonomic status of the intracellular bacterium <i>Wolbachia pipientis</i> ; should this species name include the intracellular bacteria of filarial nematodes?. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 1677-1678.	0.8	25
218	Complete genome sequence of <i>Pedobacter heparinus</i> type strain (HIM 762-3T). <i>Standards in Genomic Sciences</i> , 2009, 1, 54-62.	1.5	25
219	Complete genome sequence of <i>Anaerococcus prevotii</i> type strain (PC1T). <i>Standards in Genomic Sciences</i> , 2009, 1, 159-165.	1.5	25
220	Complete genome sequence of <i>Brachybacterium faecium</i> type strain (Scheffeler 6-10T). <i>Standards in Genomic Sciences</i> , 2009, 1, 3-11.	1.5	25
221	Complete genome sequence of <i>Dyadobacter fermentans</i> type strain (NS114T). <i>Standards in Genomic Sciences</i> , 2009, 1, 133-140.	1.5	25
222	Complete genome sequence of the acetate-degrading sulfate reducer <i>Desulfobacca acetoxidans</i> type strain (ASRB2T). <i>Standards in Genomic Sciences</i> , 2011, 4, 393-401.	1.5	25
223	Sequence Characterization and Comparative Analysis of Three Plasmids Isolated from Environmental <i>Vibrio</i> spp. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7703-7710.	1.4	24
224	Complete genome sequence of <i>Catenulispora acidiphila</i> type strain (ID 139908T). <i>Standards in Genomic Sciences</i> , 2009, 1, 119-125.	1.5	24
225	Complete genome sequence of <i>Leptotrichia buccalis</i> type strain (C-1013-bT). <i>Standards in Genomic Sciences</i> , 2009, 1, 126-132.	1.5	24
226	Complete genome sequence of <i>Saccharomonospora viridis</i> type strain (P101T). <i>Standards in Genomic Sciences</i> , 2009, 1, 141-149.	1.5	24
227	Complete genome sequence of <i>Conexibacter woesei</i> type strain (ID131577T). <i>Standards in Genomic Sciences</i> , 2010, 2, 212-219.	1.5	24
228	Complete genome sequence of <i>Acetohalobium arabaticum</i> type strain (Z-7288T). <i>Standards in Genomic Sciences</i> , 2010, 3, 57-65.	1.5	24
229	Complete genome sequence of <i>Alicyclobacillus acidocaldarius</i> type strain (104-IAT). <i>Standards in Genomic Sciences</i> , 2010, 2, 9-18.	1.5	24
230	Complete genome sequence of the aquatic bacterium <i>Runella slithyformis</i> type strain (LSU 4T). <i>Standards in Genomic Sciences</i> , 2012, 6, 145-154.	1.5	24
231	Microbiome succession during ammonification in eelgrass bed sediments. <i>PeerJ</i> , 2017, 5, e3674.	0.9	24
232	recA mutations that reduce the constitutive coprotease activity of the RecA1202(Prtc) protein: possible involvement of interfilament association in proteolytic and recombination activities. <i>Journal of Bacteriology</i> , 1993, 175, 6518-6529.	1.0	23
233	Complete genome sequence of <i>Halogeometricum borinquense</i> type strain (PR3T). <i>Standards in Genomic Sciences</i> , 2009, 1, 150-158.	1.5	23
234	Complete genome sequence of <i>Thermanaerovibrio acidaminovorans</i> type strain (Su883T). <i>Standards in Genomic Sciences</i> , 2009, 1, 254-261.	1.5	23

#	ARTICLE	IF	CITATIONS
235	Complete genome sequence of <i>Stackebrandtia nassauensis</i> type strain (LLR-40K-21T). <i>Standards in Genomic Sciences</i> , 2009, 1, 292-299.	1.5	23
236	Complete genome sequence of <i>Thermobispora bispora</i> type strain (R51T). <i>Standards in Genomic Sciences</i> , 2010, 2, 318-326.	1.5	23
237	Complete genome sequence of the gliding freshwater bacterium <i>Fluviicola taffensis</i> type strain (RW262T). <i>Standards in Genomic Sciences</i> , 2011, 5, 21-29.	1.5	23
238	Complete genome sequence of the moderately thermophilic mineral-sulfide-oxidizing firmicute <i>Sulfobacillus acidophilus</i> type strain (NALT). <i>Standards in Genomic Sciences</i> , 2012, 6, 293-303.	1.5	23
239	Comparative Genomics of the Genus <i>Porphyromonas</i> Identifies Adaptations for Heme Synthesis within the Prevalent Canine Oral Species <i>Porphyromonas gingivalis</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 3397-3413.	1.1	23
240	Complete genome sequence of <i>Halorhabdus utahensis</i> type strain (AX-2T). <i>Standards in Genomic Sciences</i> , 2009, 1, 218-225.	1.5	22
241	Complete genome sequence of <i>Desulfohalobium retbaense</i> type strain (HR100T). <i>Standards in Genomic Sciences</i> , 2010, 2, 38-48.	1.5	22
242	Complete genome sequence of <i>Leadbetterella byssophila</i> type strain (4M15T). <i>Standards in Genomic Sciences</i> , 2011, 4, 2-12.	1.5	22
243	Genome sequence of the filamentous, gliding <i>Thiothrix nivea</i> neotype strain (JP2T). <i>Standards in Genomic Sciences</i> , 2011, 5, 398-406.	1.5	22
244	Genome sequence of the mud-dwelling archaeon <i>Methanoplanus limicola</i> type strain (DSM 2279T), reclassification of <i>Methanoplanus petrolearius</i> as <i>Methanolacinia petrolearia</i> and emended descriptions of the genera <i>Methanoplanus</i> and <i>Methanolacinia</i> . <i>Standards in Genomic Sciences</i> , 2014, 9, 1076-1088.	1.5	22
245	Genes Required for the Anti-fungal Activity of a Bacterial Endophyte Isolated from a Corn Landrace Grown Continuously by Subsistence Farmers Since 1000 BC. <i>Frontiers in Microbiology</i> , 2016, 7, 1548.	1.5	22
246	Sequenced strains must be saved from extinction. <i>Nature</i> , 2001, 414, 148-148.	13.7	21
247	New evolutionary frontiers from unusual virus genomes. <i>Genome Biology</i> , 2005, 6, 212.	13.9	21
248	Complete genome sequence of <i>Streptobacillus moniliformis</i> type strain (9901T). <i>Standards in Genomic Sciences</i> , 2009, 1, 300-307.	1.5	21
249	Open Science and Reporting Animal Studies: Who's Accountable?. <i>PLoS Biology</i> , 2014, 12, e1001757.	2.6	21
250	Transcriptomes of post-mitotic neurons identify the usage of alternative pathways during adult and embryonic neuronal differentiation. <i>BMC Genomics</i> , 2015, 16, 1100.	1.2	21
251	Brouhaha over the other yeast. <i>Nature</i> , 2002, 415, 845-847.	13.7	20
252	Complete genome sequence of <i>Slackia heliotrinireducens</i> type strain (RHS 1T). <i>Standards in Genomic Sciences</i> , 2009, 1, 234-241.	1.5	20

#	ARTICLE	IF	CITATIONS
253	Complete genome sequence of <i>Brachyspira murdochii</i> type strain (56-150T). <i>Standards in Genomic Sciences</i> , 2010, 2, 260-269.	1.5	20
254	Sifting through genomes with iterative-sequence clustering produces a large, phylogenetically diverse protein-family resource. <i>BMC Bioinformatics</i> , 2012, 13, 264.	1.2	20
255	Whole genome sequencing of extended-spectrum β -lactamase producing <i>Klebsiella pneumoniae</i> isolated from a patient in Lebanon. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 32.	1.8	20
256	<i>Teredinibacter haidensis</i> sp. nov., <i>Teredinibacter purpureus</i> sp. nov. and <i>Teredinibacter frankisiae</i> sp. nov., marine, cellulolytic endosymbiotic bacteria isolated from the gills of the wood-boring mollusc <i>Bankia setacea</i> (Bivalvia: Teredinidae) and emended description of the genus <i>Teredinibacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	20
257	Genome Analysis of <i>Streptococcus pyogenes</i> Associated with Pharyngitis and Skin Infections. <i>PLoS ONE</i> , 2016, 11, e0168177.	1.1	20
258	Complete genome sequence of <i>Riemerella anatipestifer</i> type strain (ATCC 11845). <i>Standards in Genomic Sciences</i> , 2011, 4, 144-53.	1.5	20
259	Complete genome sequence of <i>Meiothermus silvanus</i> type strain (VI-R2T). <i>Standards in Genomic Sciences</i> , 2010, 3, 37-46.	1.5	19
260	Global Diversity and Biogeography of the <i>Zostera marina</i> Mycobiome. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0279520.	1.4	19
261	Complete genome sequence of <i>Thermocrinis albus</i> type strain (HI 11/12T). <i>Standards in Genomic Sciences</i> , 2010, 2, 194-202.	1.5	18
262	Complete genome sequence of <i>Candidatus Ruthia magnifica</i> . <i>Standards in Genomic Sciences</i> , 2010, 3, 163-173.	1.5	18
263	Complete genome sequence of <i>Spirochaeta smaragdinae</i> type strain (SEBR 4228T). <i>Standards in Genomic Sciences</i> , 2010, 3, 1-9.	1.5	18
264	Complete genome sequence of <i>Marivirga tractuosa</i> type strain (H-43T). <i>Standards in Genomic Sciences</i> , 2011, 4, 154-162.	1.5	18
265	Draft Genome Sequence of <i>Tenacibaculum soleae</i> UCD-KL19. <i>Genome Announcements</i> , 2016, 4, .	0.8	18
266	<i>Teredinibacter waterburyi</i> sp. nov., a marine, cellulolytic endosymbiotic bacterium isolated from the gills of the wood-boring mollusc <i>Bankia setacea</i> (Bivalvia: Teredinidae) and emended description of the genus <i>Teredinibacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2388-2394.	0.8	18
267	Effects of preservation method on canine (<i>Canis lupus familiaris</i>) fecal microbiota. <i>PeerJ</i> , 2018, 6, e4827.	0.9	18
268	Microbial genome sequencing 2000: new insights into physiology, evolution and expression analysis. <i>Research in Microbiology</i> , 2000, 151, 79-84.	1.0	17
269	Complete genome sequence of <i>Cryptobacterium curtum</i> type strain (12-3T). <i>Standards in Genomic Sciences</i> , 2009, 1, 93-100.	1.5	17
270	Complete genome sequence of <i>Methanothermus fervidus</i> type strain (V24ST). <i>Standards in Genomic Sciences</i> , 2010, 3, 315-324.	1.5	17

#	ARTICLE	IF	CITATIONS
271	Genome Sequence of the Sulfate-Reducing Thermophilic Bacterium <i>Thermodesulfovibrio yellowstonii</i> Strain DSM 11347 (Phylum Nitrospirae). <i>Genome Announcements</i> , 2015, 3, .	0.8	17
272	Natural experiments and long-term monitoring are critical to understand and predict marine host-microbe ecology and evolution. <i>PLoS Biology</i> , 2021, 19, e3001322.	2.6	17
273	The phylogenetic relationships of <i>Chlorobium tepidum</i> and <i>Chloroflexus aurantiacus</i> based upon their RecA sequences. <i>FEMS Microbiology Letters</i> , 1998, 162, 53-60.	0.7	16
274	Complete genome sequence of <i>Sanguibacter keddieii</i> type strain (ST-74T). <i>Standards in Genomic Sciences</i> , 2009, 1, 110-118.	1.5	16
275	Complete genome sequence of <i>Denitrovibrio acetiphilus</i> type strain (N2460T). <i>Standards in Genomic Sciences</i> , 2010, 2, 270-279.	1.5	16
276	Complete genome sequence of the gliding, heparinolytic <i>Pedobacter saltans</i> type strain (113T). <i>Standards in Genomic Sciences</i> , 2011, 5, 30-40.	1.5	16
277	Genome sequence of the Antarctic rhodopsins-containing flavobacterium <i>Gillisia limnaea</i> type strain (R-8282T). <i>Standards in Genomic Sciences</i> , 2012, 7, 107-119.	1.5	16
278	Complete Genome Sequence of the Extreme Thermophile <i>Dictyoglomus thermophilum</i> H-6-12. <i>Genome Announcements</i> , 2014, 2, .	0.8	16
279	<i>Porphyrobacter mercurialis</i> sp. nov., isolated from a stadium seat and emended description of the genus <i>Porphyrobacter</i> . <i>PeerJ</i> , 2015, 3, e1400.	0.9	16
280	Genome data: what do we learn?. <i>Current Opinion in Structural Biology</i> , 2000, 10, 343-348.	2.6	15
281	Complete genome sequence of <i>Ignisphaera aggregans</i> type strain (AQ1.S1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 66-75.	1.5	15
282	Complete genome sequence of <i>Weeksella virosa</i> type strain (9751T). <i>Standards in Genomic Sciences</i> , 2011, 4, 81-90.	1.5	15
283	MicrobeDB: a locally maintainable database of microbial genomic sequences. <i>Bioinformatics</i> , 2012, 28, 1947-1948.	1.8	15
284	Global biogeography of chemosynthetic symbionts reveals both localized and globally distributed symbiont groups. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	15
285	Use of HAPPY mapping for the higher order assembly of the <i>Tetrahymena</i> genome. <i>Genomics</i> , 2006, 88, 443-451.	1.3	14
286	Complete genome sequence of <i>Capnocytophaga ochracea</i> type strain (VPI 2845T). <i>Standards in Genomic Sciences</i> , 2009, 1, 101-109.	1.5	14
287	Genomics of Emerging Infectious Disease: A PLoS Collection. <i>PLoS Biology</i> , 2009, 7, e1000224.	2.6	14
288	Complete genome sequence of <i>Jonesia denitrificans</i> type strain (Prevot 55134T). <i>Standards in Genomic Sciences</i> , 2009, 1, 262-269.	1.5	14

#	ARTICLE	IF	CITATIONS
289	Complete genome sequence of <i>Ferrimonas balearica</i> type strain (PATT). Standards in Genomic Sciences, 2010, 3, 174-182.	1.5	14
290	Complete genome sequence of <i>Thermosphaera aggregans</i> type strain (M11TLT). Standards in Genomic Sciences, 2010, 2, 245-259.	1.5	14
291	Complete genome sequence of <i>Bacteroides helcogenes</i> type strain (P 36-108T). Standards in Genomic Sciences, 2011, 4, 45-53.	1.5	14
292	Complete genome sequence of <i>Deinococcus maricopensis</i> type strain (LB-34T). Standards in Genomic Sciences, 2011, 4, 163-172.	1.5	14
293	Complete genome sequence of the thermophilic sulfate-reducing ocean bacterium <i>Thermodesulfator indicus</i> type strain (CIR29812T). Standards in Genomic Sciences, 2012, 6, 155-164.	1.5	14
294	Complete genome sequence of the orange-red pigmented, radioresistant <i>Deinococcus proteolyticus</i> type strain (MRPT). Standards in Genomic Sciences, 2012, 6, 240-250.	1.5	14
295	Comparison of Whole-Genome Sequences of <i>Legionella pneumophila</i> in Tap Water and in Clinical Strains, Flint, Michigan, USA, 2016. Emerging Infectious Diseases, 2019, 25, 2013-2020.	2.0	14
296	Microbial Community Succession and Nutrient Cycling Responses following Perturbations of Experimental Saltwater Aquaria. MSphere, 2019, 4, .	1.3	14
297	Complete genome sequence of <i>Methanoplanus petrolearius</i> type strain (SEBR 4847T). Standards in Genomic Sciences, 2010, 3, 203-211.	1.5	14
298	Complete genome sequence of <i>Syntrophothermus lipocalidus</i> type strain (TGB-C1T). Standards in Genomic Sciences, 2010, 3, 268-275.	1.5	13
299	Complete genome sequence of <i>Nitratifactor salsuginis</i> type strain (E9137-1T). Standards in Genomic Sciences, 2011, 4, 322-330.	1.5	13
300	Complete genome sequence of the hyperthermophilic chemolithoautotroph <i>Pyrolobus fumarii</i> type strain (1AT). Standards in Genomic Sciences, 2011, 4, 381-392.	1.5	13
301	Energetic and Environmental Constraints on the Community Structure of Benthic Microbial Mats in Lake Fryxell, Antarctica. FEMS Microbiology Ecology, 2020, 96, .	1.3	13
302	The emergence of microbiome centres. Nature Microbiology, 2020, 5, 2-3.	5.9	13
303	Environmental control on the distribution of metabolic strategies of benthic microbial mats in Lake Fryxell, Antarctica. PLoS ONE, 2020, 15, e0231053.	1.1	13
304	Sequencing and analysis of a 63 kb bacterial artificial chromosome insert from the <i>Wolbachia</i> endosymbiont of the human filarial parasite <i>Brugia malayi</i> . International Journal for Parasitology, 2002, 32, 159-166.	1.3	12
305	Complete genome sequence of <i>Beutenbergia cavernae</i> type strain (HK1 0122T). Standards in Genomic Sciences, 2009, 1, 21-28.	1.5	12
306	Complete genome sequence of <i>Thermosediminibacter oceani</i> type strain (JW/IW-1228PT). Standards in Genomic Sciences, 2010, 3, 108-116.	1.5	12

#	ARTICLE	IF	CITATIONS
307	Complete genome sequence of <i>Hydrogenobacter thermophilus</i> type strain (TK-6T). <i>Standards in Genomic Sciences</i> , 2011, 4, 131-143.	1.5	12
308	Genome sequence of the moderately thermophilic halophile <i>Flexistipes sinusarabici</i> strain (MAS10T). <i>Standards in Genomic Sciences</i> , 2011, 5, 86-96.	1.5	12
309	Badomics words and the power and peril of the ome-meme. <i>GigaScience</i> , 2012, 1, 6.	3.3	12
310	Complete genome sequence of the bile-resistant pigment-producing anaerobe <i>Alistipes finegoldii</i> type strain (AHN2437T). <i>Standards in Genomic Sciences</i> , 2013, 8, 26-36.	1.5	12
311	Complete genome sequence of <i>Kribbella flavida</i> type strain (IFO 14399T). <i>Standards in Genomic Sciences</i> , 2010, 2, 185-192.	1.5	11
312	Complete genome sequence of <i>Thermobaculum terrenum</i> ™ type strain (YNP1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 153-162.	1.5	11
313	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FIGlyRT). <i>Standards in Genomic Sciences</i> , 2011, 4, 371-380.	1.5	11
314	Complete genome sequence of the thermophilic sulfur-reducer <i>Desulfurobacterium thermolithotrophum</i> type strain (BSAT) from a deep-sea hydrothermal vent. <i>Standards in Genomic Sciences</i> , 2011, 5, 407-415.	1.5	11
315	Complete genome sequence of <i>Bacteroides salanitronis</i> type strain (BL78T). <i>Standards in Genomic Sciences</i> , 2011, 4, 191-199.	1.5	11
316	Genome sequence of the orange-pigmented seawater bacterium <i>Owenweeksia hongkongensis</i> type strain (UST20020801T). <i>Standards in Genomic Sciences</i> , 2012, 7, 120-130.	1.5	11
317	Expert Failure: Re-evaluating Research Assessment. <i>PLoS Biology</i> , 2013, 11, e1001677.	2.6	11
318	High-quality-draft genome sequence of the yellow-pigmented flavobacterium <i>Joostella marina</i> type strain (En5T). <i>Standards in Genomic Sciences</i> , 2013, 8, 37-46.	1.5	11
319	Complete genome sequence of the moderate thermophile <i>Anaerobaculum mobile</i> type strain (NGAT). <i>Standards in Genomic Sciences</i> , 2013, 8, 47-57.	1.5	11
320	Genome sequence of the free-living aerobic spirochete <i>Turneriella parva</i> type strain (HT), and emendation of the species <i>Turneriella parva</i> . <i>Standards in Genomic Sciences</i> , 2013, 8, 228-238.	1.5	11
321	Bacteria isolated from Bengal cat (<i>Felis catus</i> Æ <i>Prionailurus bengalensis</i>) anal sac secretions produce volatile compounds potentially associated with animal signaling. <i>PLoS ONE</i> , 2019, 14, e0216846.	1.1	11
322	Metagenomic methylation patterns resolve bacterial genomes of unusual size and structural complexity. <i>ISME Journal</i> , 2022, 16, 1921-1931.	4.4	11
323	Complete genome sequence of <i>Ilyobacter polytropus</i> type strain (CuHbu1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 304-314.	1.5	10
324	Complete genome sequence of <i>Vulcanisaeta distributa</i> type strain (IC-017T). <i>Standards in Genomic Sciences</i> , 2010, 3, 117-125.	1.5	10

#	ARTICLE	IF	CITATIONS
325	Complete genome sequence of <i>Thermaerobacter marianensis</i> type strain (7p75aT). Standards in Genomic Sciences, 2010, 3, 337-345.	1.5	10
326	Complete genome sequence of <i>Xylanimonas cellulositytica</i> type strain (XIL07T). Standards in Genomic Sciences, 2010, 2, 1-8.	1.5	10
327	Complete genome sequence of <i>Segniliparus rotundus</i> type strain (CDC 1076T). Standards in Genomic Sciences, 2010, 2, 203-211.	1.5	10
328	Complete genome sequence of <i>Desulfurococcus mucosus</i> type strain (O7/1T). Standards in Genomic Sciences, 2011, 4, 173-182.	1.5	10
329	Complete genome sequence of <i>Calditerrivibrio nitroreducens</i> type strain (Yu37-1T). Standards in Genomic Sciences, 2011, 4, 54-62.	1.5	10
330	Complete genome sequence of <i>Tsakamurella paurometabola</i> type strain (no. 33T). Standards in Genomic Sciences, 2011, 4, 342-351.	1.5	10
331	Complete genome sequence of the facultatively anaerobic, appendaged bacterium <i>Muricauda ruestringensis</i> type strain (B1T). Standards in Genomic Sciences, 2012, 6, 185-193.	1.5	10
332	Genomic attributes of extended-spectrum β -lactamase-producing <i>Escherichia coli</i> isolated from patients in Lebanon. Future Microbiology, 2017, 12, 213-226.	1.0	10
333	Draft Genome Sequences of <i>Pseudomonas moraviensis</i> UCD-KL30, <i>Vibrio ostreicida</i> UCD-KL16, <i>Colwellia</i> sp. Strain UCD-KL20, <i>Shewanella</i> sp. Strain UCD-KL12, and <i>Shewanella</i> sp. Strain UCD-KL21, Isolated from Seagrass. Genome Announcements, 2017, 5, .	0.8	10
334	What does the term microbiome mean? And where did it come from? A bit of a surprise ... The Winnower, 2015, , .	0.0	10
335	Permanent draft genome sequence of <i>Dethiosulfovibrio peptidovorans</i> type strain (SEBR 4207T). Standards in Genomic Sciences, 2010, 3, 85-92.	1.5	9
336	Non-contiguous finished genome sequence of <i>Aminomonas paucivorans</i> type strain (GLU-3T). Standards in Genomic Sciences, 2010, 3, 285-293.	1.5	9
337	Non-contiguous finished genome sequence of <i>Bacteroides coprosuis</i> type strain (PC139T). Standards in Genomic Sciences, 2011, 4, 233-243.	1.5	9
338	Draft Genome Sequence of an Actinobacterium, <i>Brachybacterium muris</i> Strain UCD-AY4. Genome Announcements, 2013, 1, e0008613.	0.8	9
339	Draft Genome Sequences of 26 <i>Porphyromonas</i> Strains Isolated from the Canine Oral Microbiome. Genome Announcements, 2015, 3, .	0.8	9
340	Complete genome sequence of <i>Jiangella gansuensis</i> strain YIM 002T (DSM 44835T), the type species of the genus <i>Jiangella</i> and source of new antibiotic compounds. Standards in Genomic Sciences, 2017, 12, 21.	1.5	9
341	Draft genome sequences of eight bacteria isolated from the indoor environment: <i>Staphylococcus capitis</i> strain H36, <i>S. capitis</i> strain H65, <i>S. cohnii</i> strain H62, <i>S. hominis</i> strain H69, <i>Microbacterium</i> sp. strain H83, <i>Mycobacterium iranicum</i> strain H39, <i>Plantibacter</i> sp. strain H53, and <i>Pseudomonas oryzihabitans</i> strain H72. Standards in Genomic Sciences. 2017. 12. 17.	1.5	9
342	Complete genome sequence of <i>Arcanobacterium haemolyticum</i> type strain (11018T). Standards in Genomic Sciences, 2010, 3, 126-135.	1.5	8

#	ARTICLE	IF	CITATIONS
343	Complete genome sequence of the thermophilic sulfur-reducer <i>Hipaea maritima</i> type strain (MH2T). Standards in Genomic Sciences, 2011, 4, 303-311.	1.5	8
344	Complete genome sequence of the aerobic, heterotroph <i>Marinithermus hydrothermalis</i> type strain (T1T) from a deep-sea hydrothermal vent chimney. Standards in Genomic Sciences, 2012, 6, 21-30.	1.5	8
345	Complete genome sequence of <i>Coriobacterium glomerans</i> type strain (PW2T) from the midgut of <i>Pyrrhocoris apterus</i> L. (red soldier bug). Standards in Genomic Sciences, 2013, 8, 15-25.	1.5	8
346	Genome sequence of the moderately thermophilic sulfur-reducing bacterium <i>Thermanaerovibrio velox</i> type strain (Z-9701T) and emended description of the genus <i>Thermanaerovibrio</i> . Standards in Genomic Sciences, 2013, 9, 57-70.	1.5	8
347	Complete Genome Sequence of <i>Coprothermobacter proteolyticus</i> DSM 5265. Genome Announcements, 2014, 2, .	0.8	8
348	Draft Genome Sequence of <i>Bacillus safensis</i> JPL-MERTA-8-2, Isolated from a Mars-Bound Spacecraft. Genome Announcements, 2015, 3, .	0.8	8
349	Complete genome sequence of <i>Intrasporangium calvum</i> type strain (7 KIPT). Standards in Genomic Sciences, 2010, 3, 294-303.	1.5	7
350	Complete genome sequence of <i>Mahella australiensis</i> type strain (50-1 BONT). Standards in Genomic Sciences, 2011, 4, 331-341.	1.5	7
351	Non-contiguous finished genome sequence of the opportunistic oral pathogen <i>Prevotella multisaccharivorax</i> type strain (PPPA20T). Standards in Genomic Sciences, 2011, 5, 41-49.	1.5	7
352	Draft Genome Sequence of <i>Curtobacterium flaccumfaciens</i> Strain UCD-AKU (Phylum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 Td (<i>A	0.8	7
353	Genome sequence of the <i>Thermotoga thermarum</i> type strain (LA3T) from an African solfataric spring. Standards in Genomic Sciences, 2014, 9, 1105-1117.	1.5	7
354	Draft Genome Sequences of <i>Acinetobacter baumannii</i> Strains Harboring the <i>bla</i>_{NDM-1} Gene Isolated in Lebanon from Civilians Wounded during the Syrian Civil War. Genome Announcements, 2016, 4, .	0.8	7
355	The Green Berry Consortia of the Sippewissett Salt Marsh: Millimeter-Sized Aggregates of Diazotrophic Unicellular Cyanobacteria. Frontiers in Microbiology, 2017, 8, 1623.	1.5	7
356	Prospecting Microbial Strains for Bioremediation and Probiotics Development for Metaorganism Research and Preservation. Journal of Visualized Experiments, 2019, , .	0.2	7
357	Genomes from bacteria associated with the canine oral cavity: A test case for automated genome-based taxonomic assignment. PLoS ONE, 2019, 14, e0214354.	1.1	7
358	Draft Genome Sequence of <i>Burkholderia gladioli</i> Strain UCD-UG_CHAPALOTE (Phylum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142 Td (<i>A	0.8	6
359	Bacterial communities associated with cell phones and shoes. PeerJ, 2020, 8, e9235.	0.9	6
360	Draft Genome Sequence of <i>Microbacterium</i> sp. Strain UCD-TDU (Phylum <i>Actinobacteria</i>). Genome Announcements, 2013, 1, e0012013.	0.8	5

#	ARTICLE	IF	CITATIONS
361	Draft Genome Sequence of <i>Kocuria</i> sp. Strain UCD-OTCP (Phylum <i>Actinobacteria</i>). Genome Announcements, 2013, 1, .	0.8	5
362	Prokaryotic Super Program Advisory Committee DOE Joint Genome Institute, Walnut Creek, CA, March 27, 2013. Standards in Genomic Sciences, 2013, 8, 561-570.	1.5	5
363	Genome sequence of the phylogenetically isolated spirochete <i>Leptonema illini</i> type strain (3055T). Standards in Genomic Sciences, 2013, 8, 177-187.	1.5	5
364	Draft Genome Sequence of <i>Leucobacter</i> sp. Strain UCD-THU (Phylum <i>Actinobacteria</i>). Genome Announcements, 2013, 1, .	0.8	5
365	Draft Genome Sequence of <i>Dietzia</i> sp. Strain UCD-THP (Phylum <i>Actinobacteria</i>). Genome Announcements, 2013, 1, .	0.8	5
366	Draft Genome Sequences of <i>Streptococcus pyogenes</i> Strains Associated with Throat and Skin Infections in Lebanon. Genome Announcements, 2014, 2, .	0.8	5
367	Draft Genome Sequence of <i>Porphyrobacter mercurialis</i> (sp. nov.) Strain Coronado. Genome Announcements, 2015, 3, .	0.8	5
368	Draft Genome Sequence of <i>Curtobacterium</i> sp. Strain UCD-KPL2560 (Phylum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462 Td (<i>A	0.8	5
369	Draft Genome Sequence of <i>Cobetia</i> sp. UCD-24C, Isolated from Roots and Leaves of the Seagrass <i>Zostera marina. Genome Announcements, 2016, 4, .	0.8	5
370	Draft Genome Sequences of Two <i>Pseudoalteromonas porphyrae</i> Strains Isolated from Seagrass Sediment. Genome Announcements, 2016, 4, .	0.8	5
371	Draft Genome Analysis of <i>Christensenella minuta</i> DSM 22607, exhibiting an unusual expansion of transporter homologs of unknown function. Journal of Genomics, 2020, 8, 25-29.	0.6	5
372	Whole genome sequence analysis reveals the broad distribution of the RtxA type 1 secretion system and four novel putative type 1 secretion systems throughout the <i>Legionella</i> genus. PLoS ONE, 2020, 15, e0223033.	1.1	5
373	Isolation and sequence-based characterization of a koala symbiont: <i>Lonepinella koalarum</i> . PeerJ, 2020, 8, e10177.	0.9	5
374	Complete genome sequence of <i>Oceanithermus profundus</i> type strain (506T). Standards in Genomic Sciences, 2011, 4, 210-220.	1.5	4
375	microBEnet: Lessons Learned from Building an Interdisciplinary Scientific Community in the Online Sphere. PLoS Biology, 2014, 12, e1001884.	2.6	4
376	Draft Genome Sequence of <i>Tatumella</i> sp. Strain UCD-D_suzukii (Phylum <i>Proteobacteria</i>) Isolated from <i>Drosophila suzukii</i> Larvae. Genome Announcements, 2014, 2, .	0.8	4
377	Draft Genome Sequences of <i>Escherichia coli</i> Strains Isolated from Septic Patients. Genome Announcements, 2014, 2, .	0.8	4
378	Draft Genome Sequence of <i>Pseudoalteromonas tetraodonis</i> Strain UCD-SED8 (Phylum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462 Td (<i>A	0.8	4

#	ARTICLE	IF	CITATIONS
379	Draft Genome Sequence of <i>Bacillus vietnamensis</i> Strain UCD-SED5 (Phylum Firmicutes). <i>Genome Announcements</i> , 2015, 3, .	0.8	4
380	Genome Sequence of a Sulfate-Reducing Thermophilic Bacterium, <i>Thermodesulfobacterium commune</i> DSM 2178 T (Phylum Thermodesulfobacteria). <i>Genome Announcements</i> , 2015, 3, .	0.8	4
381	Draft Genome Sequence of <i>Gordonia</i> sp. Strain UCD-TK1 (Phylum Actinobacteria). <i>Genome Announcements</i> , 2016, 4, .	0.8	4
382	Draft Genome Sequence of <i>Klebsiella pneumoniae</i> KGM-IMP216 Harboring <i>bla</i> _{CTX-M-15} , <i>bla</i> _{DHA-1} , <i>bla</i> _{TEM-1B} , <i>bla</i> _{NDM-1} , <i>bla</i> _{SHV-28} , and <i>bla</i> _{OXA-1} , Isolated from a Patient in Lebanon. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
383	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FLGlyR). <i>Standards in Genomic Sciences</i> , 2011, 4, 371-80.	1.5	4
384	Aggregating, Tagging and Integrating Biodiversity Research. <i>PLoS ONE</i> , 2011, 6, e19491.	1.1	3
385	Permanent draft genome sequence of the gliding predator <i>Saprospira grandis</i> strain Sa g1 (= HR1). <i>Standards in Genomic Sciences</i> , 2012, 6, 210-219.	1.5	3
386	Genome sequence of <i>Frateuria aurantia</i> type strain (KondÅ´67T), a xanthomonade isolated from <i>Lilium auratum</i> Lindl.. <i>Standards in Genomic Sciences</i> , 2013, 9, 83-92.	1.5	3
387	Complete genome sequence of the halophilic bacterium <i>Spirochaeta africana</i> type strain (Z-7692T) from the alkaline Lake Magadi in the East African Rift. <i>Standards in Genomic Sciences</i> , 2013, 8, 165-176.	1.5	3
388	Draft Genome Sequences of Two <i>Pseudoalteromonas</i> Strains Isolated from Roots and Leaf Blades of the Seagrass <i>Zostera marina</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	3
389	Complete Genome Sequence of a <i>Paenalcaligenes hominis</i> Strain Isolated from a Paraplegic Patient with Neurogenic Bladder Using Single-Molecule Real-Time Sequencing Technology. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
390	Draft Genome Sequence of <i>Propionibacterium avidum</i> Strain UCD-PD2 Isolated from a Feline Anal Sac. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
391	Draft Genome Sequence of <i>Arthrobacter</i> sp. Strain UCD-GKA (Phylum Actinobacteria). <i>Genome Announcements</i> , 2017, 5, .	0.8	3
392	Genome sequence of the flexirubin-pigmented soil bacterium <i>Niabella soli</i> type strain (JS13-8T). <i>Standards in Genomic Sciences</i> , 2012, 7, 210-220.	1.5	2
393	Draft Genome Sequence of the Arsenate-Respiring Bacterium <i>Chrysiogenes arsenatis</i> Strain DSM 11915. <i>Genome Announcements</i> , 2013, 1, .	0.8	2
394	Draft Genome Sequence of <i>Planomicrobium glaciei</i> UCD-HAM (Phylum <i>Firmicutes</i>). <i>Genome Announcements</i> , 2015, 3, .	0.8	2
395	Draft Genome Sequences of Two <i>Vibrio splendidus</i> Strains, Isolated from Seagrass Sediment. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
396	Draft Genome Sequences of <i>Dermacoccus nishinomiyaensis</i> Strains UCD-KPL2534 and UCD-KPL2528 Isolated from an Indoor Track Facility. <i>Genome Announcements</i> , 2017, 5, .	0.8	2

#	ARTICLE	IF	CITATIONS
397	Draft Genome Sequences and Genomic Analysis for Pigment Production in Bacteria Isolated from Blue Discolored Soymilk and Tofu. <i>Journal of Genomics</i> , 2021, 9, 55-67.	0.6	2
398	A science renga. <i>Nature</i> , 1998, 393, 512-513.	13.7	1
399	PLoS Biology 2.0. <i>PLoS Biology</i> , 2008, 6, e48.	2.6	1
400	Draft Genome Sequence of the Pyridinediol-Fermenting Bacterium <i>Synergistes jonesii</i> 78-1. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
401	Draft Genome Sequence of Extended-Spectrum β -Lactamase-Producing <i>Klebsiella pneumoniae</i> Isolated from a Patient in Lebanon. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
402	Draft Genome Sequence of <i>Enterobacter</i> sp. Strain UCD-UG_FMILLET (Phylum Proteobacteria). <i>Genome Announcements</i> , 2015, 3, .	0.8	1
403	Genome Sequence of a Multidrug-Resistant Strain of <i>Bacillus pumilus</i> , CB01, Isolated from the Feces of an American Crow, <i>Corvus brachyrhynchos</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	1
404	Complete Genome Sequence of <i>Dolosigranulum pigrum</i> from a Patient with Interstitial Lung Disease Using Single-Molecule Real-Time Sequencing Technology. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
405	Combining Microbial Culturing With Mathematical Modeling in an Introductory Course-Based Undergraduate Research Experience. <i>Frontiers in Microbiology</i> , 2020, 11, 581903.	1.5	1
406	Reconstruction of Metagenome-Assembled Genomes from Aquaria. <i>Microbiology Resource Announcements</i> , 2021, 10, e0055721.	0.3	1
407	The phylogenetic relationships of <i>Chlorobium tepidum</i> and <i>Chloroflexus aurantiacus</i> based upon their RecA sequences. <i>FEMS Microbiology Letters</i> , 1998, 162, 53-60.	0.7	1
408	Life in Hot Carbon Monoxide: the Complete Genome Sequence of <i>Carboxydotherrmus hydrogenoformans</i> Z-2901. <i>PLoS Genetics</i> , 2005, preprint, e65.	1.5	1
409	<i>Evolution</i> . <i>By</i> Nicholas H. Barton, Derek E. G. Briggs, Jonathan A. Eisen, David Goldstein, Nipam H. Patel. Cold Spring Harbor (New York): Cold Spring Harbor Laboratory Press. \$100.00. xiv + 833 p.; ill.; index. 9780879696849. 2007.. <i>Quarterly Review of Biology</i> , 2008, 83, 204-205.	0.0	0
410	Draft Genome Sequences of Extended-Spectrum β -Lactamase-Producing <i>Escherichia coli</i> Strains Isolated from Patients in Lebanon. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
411	Draft Genome Sequence of the Endosymbiont <i>Candidatus</i> <i>Ruthia magnifica</i> UCD-CM (Phylum) Tj ETQq1 1 0.784314 rgBT	0.8	0
412	Draft Genome Sequence of <i>Enterococcus faecalis</i> Strain UCD-PD3. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
413	Additional Draft Genome Sequences of <i>Escherichia coli</i> Strains Isolated from Septic Patients. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
414	Draft Genome Sequence of <i>Klebsiella pneumoniae</i> UCD-JA29 Isolated from a Patient with Sepsis. <i>Genome Announcements</i> , 2016, 4, .	0.8	0

#	ARTICLE	IF	CITATIONS
415	Reply to McDonald, "Protections against the Risk of Airborne SARS-CoV-2 Infection"; MSystems, 2020, 5, .	1.7	0
416	Bacterial Community Sequences of Submerged Aquatic Vegetation in the Potomac River. Microbiology Resource Announcements, 2020, 9, .	0.3	0
417	Genetic and physical mapping of DNA replication origins in <i>Haloferax volcanii</i> . PLoS Genetics, 2005, preprint, e77.	1.5	0
418	Methylisothiazolinone in household items - a growing (or well, killing) problem #germophobia. The Winnower, 2015, , .	0.0	0
419	11+ things everyone needs to know about microbes. The Winnower, 2015, , .	0.0	0
420	PHYLOGENETIC DIVERSITY OF THE MICROBIAL MATS IN LAKE FRYXELL, ANTARCTICA. , 2016, , .		0
421	Even Superheroes Need Help Sometimes: Three Incredible Tales of Microbial Symbiosis. Frontiers for Young Minds, 0, 6, .	0.8	0
422	An Incredible Invisible World: How Microorganisms Could Take Care of Corals in Difficult Times. Frontiers for Young Minds, 0, 8, .	0.8	0
423	Title is missing!. , 2020, 15, e0223033.		0
424	Title is missing!. , 2020, 15, e0223033.		0
425	Title is missing!. , 2020, 15, e0223033.		0
426	Title is missing!. , 2020, 15, e0223033.		0
427	Fungi, bacteria and oomycota opportunistically isolated from the seagrass, <i>Zostera marina</i> . , 2020, 15, e0236135.		0
428	Fungi, bacteria and oomycota opportunistically isolated from the seagrass, <i>Zostera marina</i> . , 2020, 15, e0236135.		0
429	Fungi, bacteria and oomycota opportunistically isolated from the seagrass, <i>Zostera marina</i> . , 2020, 15, e0236135.		0
430	Fungi, bacteria and oomycota opportunistically isolated from the seagrass, <i>Zostera marina</i> . , 2020, 15, e0236135.		0