

Nikos C Kyrpides

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5329977/publications.pdf>

Version: 2024-02-01

671
papers

83,868
citations

1792

103
h-index

677

254
g-index

716
all docs

716
docs citations

716
times ranked

57959
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012, 486, 207-214.	13.7	9,614
2	The Genomes On Line Database (GOLD) in 2009: status of genomic and metagenomic projects and their associated metadata. <i>Nucleic Acids Research</i> , 2010, 38, D346-D354.	6.5	6,188
3	The Genomes OnLine Database (GOLD) v.4: status of genomic and metagenomic projects and their associated metadata. <i>Nucleic Acids Research</i> , 2012, 40, D571-D579.	6.5	4,241
4	Genome-Based Taxonomic Classification of the Phylum Actinobacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 2007.	1.5	2,599
5	A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.	13.7	2,249
6	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	13.7	2,239
7	Analysis of 1,000+ Type-Strain Genomes Substantially Improves Taxonomic Classification of Alphaproteobacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 468.	1.5	1,537
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	The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon <i>Archaeoglobus fulgidus</i> . <i>Nature</i> , 1997, 390, 364-370.	13.7	1,460
10	Analysis of 1,000 Type-Strain Genomes Improves Taxonomic Classification of Bacteroidetes. <i>Frontiers in Microbiology</i> , 2019, 10, 2083.	1.5	1,281
11	IMG: the integrated microbial genomes database and comparative analysis system. <i>Nucleic Acids Research</i> , 2012, 40, D115-D122.	6.5	1,210
12	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007, 450, 560-565.	13.7	1,181
13	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008, 26, 541-547.	9.4	1,069
14	Protein interaction maps for complete genomes based on gene fusion events. <i>Nature</i> , 1999, 402, 86-90.	13.7	1,032
15	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009, 462, 1056-1060.	13.7	924
16	Uncovering Earth's virome. <i>Nature</i> , 2016, 536, 425-430.	13.7	880
17	IMG ER: a system for microbial genome annotation expert review and curation. <i>Bioinformatics</i> , 2009, 25, 2271-2278.	1.8	804
18	IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. <i>Nucleic Acids Research</i> , 2019, 47, D666-D677.	6.5	799

#	ARTICLE	IF	CITATIONS
19	Programmed DNA destruction by miniature CRISPR-Cas14 enzymes. <i>Science</i> , 2018, 362, 839-842.	6.0	757
20	CRISPR Recognition Tool (CRT): a tool for automatic detection of clustered regularly interspaced palindromic repeats. <i>BMC Bioinformatics</i> , 2007, 8, 209.	1.2	754
21	Genome sequence of <i>Bacillus cereus</i> and comparative analysis with <i>Bacillus anthracis</i> . <i>Nature</i> , 2003, 423, 87-91.	13.7	740
22	Minimum Information about a Biosynthetic Gene cluster. <i>Nature Chemical Biology</i> , 2015, 11, 625-631.	3.9	715
23	The genomic basis of trophic strategy in marine bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15527-15533.	3.3	685
24	Experimental Determination and System Level Analysis of Essential Genes in <i>Escherichia coli</i> MG1655. <i>Journal of Bacteriology</i> , 2003, 185, 5673-5684.	1.0	678
25	Critical Assessment of Metagenome Interpretation – a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	9.0	635
26	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. <i>Nature Biotechnology</i> , 2006, 24, 1263-1269.	9.4	634
27	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , 2021, 39, 105-114.	9.4	628
28	A Catalog of Reference Genomes from the Human Microbiome. <i>Science</i> , 2010, 328, 994-999.	6.0	621
29	Microbial species delineation using whole genome sequences. <i>Nucleic Acids Research</i> , 2015, 43, 6761-6771.	6.5	609
30	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	9.4	608
31	Toward an Online Repository of Standard Operating Procedures (SOPs) for (Meta)genomic Annotation. <i>OMICS A Journal of Integrative Biology</i> , 2008, 12, 137-141.	1.0	598
32	CheckV assesses the quality and completeness of metagenome-assembled viral genomes. <i>Nature Biotechnology</i> , 2021, 39, 578-585.	9.4	569
33	IMG 4 version of the integrated microbial genomes comparative analysis system. <i>Nucleic Acids Research</i> , 2014, 42, D560-D567.	6.5	555
34	The <i>Wolbachia</i> Genome of <i>Brugia malayi</i> : Endosymbiont Evolution within a Human Pathogenic Nematode. <i>PLoS Biology</i> , 2005, 3, e121.	2.6	529
35	The genome sequence of the facultative intracellular pathogen <i>Brucella melitensis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 443-448.	3.3	513
36	New insights from uncultivated genomes of the global human gut microbiome. <i>Nature</i> , 2019, 568, 505-510.	13.7	505

#	ARTICLE	IF	CITATIONS
37	Genome-Based Taxonomic Classification of Bacteroidetes. <i>Frontiers in Microbiology</i> , 2016, 7, 2003.	1.5	493
38	Complete sequence and comparative genome analysis of the dairy bacterium <i>Streptococcus thermophilus</i> . <i>Nature Biotechnology</i> , 2004, 22, 1554-1558.	9.4	485
39	GenePRIMP: a gene prediction improvement pipeline for prokaryotic genomes. <i>Nature Methods</i> , 2010, 7, 455-457.	9.0	468
40	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
41	Protein structure determination using metagenome sequence data. <i>Science</i> , 2017, 355, 294-298.	6.0	456
42	Complete genome sequence of DSM 30083T, the type strain (U5/41T) of <i>Escherichia coli</i> , and a proposal for delineating subspecies in microbial taxonomy. <i>Standards in Genomic Sciences</i> , 2014, 9, 2.	1.5	454
43	IMG/M: integrated genome and metagenome comparative data analysis system. <i>Nucleic Acids Research</i> , 2017, 45, D507-D516.	6.5	451
44	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018, 36, 359-367.	9.4	414
45	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
46	Comparison of the complete genome sequences of <i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a and pv. <i>tomato</i> DC3000. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11064-11069.	3.3	399
47	Symbiosis insights through metagenomic analysis of a microbial consortium. <i>Nature</i> , 2006, 443, 950-955.	13.7	396
48	Genome Project Standards in a New Era of Sequencing. <i>Science</i> , 2009, 326, 236-237.	6.0	382
49	Direct Comparisons of Illumina vs. Roche 454 Sequencing Technologies on the Same Microbial Community DNA Sample. <i>PLoS ONE</i> , 2012, 7, e30087.	1.1	360
50	The integrated microbial genomes (IMG) system. <i>Nucleic Acids Research</i> , 2006, 34, D344-D348.	6.5	355
51	The IMG/M data management and analysis system v.6.0: new tools and advanced capabilities. <i>Nucleic Acids Research</i> , 2021, 49, D751-D763.	6.5	332
52	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , 2007, 4, 495-500.	9.0	322
53	Genome Sequence and Analysis of the Oral Bacterium <i>Fusobacterium nucleatum</i> Strain ATCC 25586. <i>Journal of Bacteriology</i> , 2002, 184, 2005-2018.	1.0	311
54	IMG/M: a data management and analysis system for metagenomes. <i>Nucleic Acids Research</i> , 2007, 36, D534-D538.	6.5	309

#	ARTICLE	IF	CITATIONS
55	The Genomes OnLine Database (GOLD) v.5: a metadata management system based on a four level (meta)genome project classification. <i>Nucleic Acids Research</i> , 2015, 43, D1099-D1106.	6.5	309
56	The Genomes On Line Database (GOLD) in 2007: status of genomic and metagenomic projects and their associated metadata. <i>Nucleic Acids Research</i> , 2007, 36, D475-D479.	6.5	293
57	The M5nr: a novel non-redundant database containing protein sequences and annotations from multiple sources and associated tools. <i>BMC Bioinformatics</i> , 2012, 13, 141.	1.2	291
58	The standard operating procedure of the DOE-JGI Microbial Genome Annotation Pipeline (MGAP v.4). <i>Standards in Genomic Sciences</i> , 2015, 10, 86.	1.5	287
59	The Evolution of Host Specialization in the Vertebrate Gut Symbiont <i>Lactobacillus reuteri</i> . <i>PLoS Genetics</i> , 2011, 7, e1001314.	1.5	270
60	IMG/M 4 version of the integrated metagenome comparative analysis system. <i>Nucleic Acids Research</i> , 2014, 42, D568-D573.	6.5	270
61	A korarchaeal genome reveals insights into the evolution of the Archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8102-8107.	3.3	253
62	Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome. <i>Nature Microbiology</i> , 2021, 6, 960-970.	5.9	248
63	The complete genome sequence of the algal symbiont <i>Dinoroseobacter shibae</i> : a hitchhiker's guide to life in the sea. <i>ISME Journal</i> , 2010, 4, 61-77.	4.4	244
64	Prepublication data sharing. <i>Nature</i> , 2009, 461, 168-170.	13.7	243
65	IMG/M: the integrated metagenome data management and comparative analysis system. <i>Nucleic Acids Research</i> , 2012, 40, D123-D129.	6.5	242
66	IMG/VR v3: an integrated ecological and evolutionary framework for interrogating genomes of uncultivated viruses. <i>Nucleic Acids Research</i> , 2021, 49, D764-D775.	6.5	240
67	The integrated microbial genomes system: an expanding comparative analysis resource. <i>Nucleic Acids Research</i> , 2010, 38, D382-D390.	6.5	237
68	Giant viruses with an expanded complement of translation system components. <i>Science</i> , 2017, 356, 82-85.	6.0	234
69	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
70	The SPFH domain: implicated in regulating targeted protein turnover in stomatins and other membrane-associated proteins. <i>Trends in Biochemical Sciences</i> , 1999, 24, 425-427.	3.7	223
71	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
72	The Genomes On Line Database (GOLD) v.2: a monitor of genome projects worldwide. <i>Nucleic Acids Research</i> , 2006, 34, D332-D334.	6.5	220

#	ARTICLE	IF	CITATIONS
73	The DOE-JGI Standard Operating Procedure for the Annotations of Microbial Genomes. <i>Standards in Genomic Sciences</i> , 2009, 1, 63-67.	1.5	218
74	The ERGOTM genome analysis and discovery system. <i>Nucleic Acids Research</i> , 2003, 31, 164-171.	6.5	207
75	Metagenomics uncovers gaps in amplicon-based detection of microbial diversity. <i>Nature Microbiology</i> , 2016, 1, 15032.	5.9	207
76	Giant virus diversity and host interactions through global metagenomics. <i>Nature</i> , 2020, 578, 432-436.	13.7	207
77	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , 2019, 4, 1895-1906.	5.9	206
78	Genome Sequence and Analysis of the Soil Cellulolytic Actinomycete <i>Thermobifida fusca</i> YX. <i>Journal of Bacteriology</i> , 2007, 189, 2477-2486.	1.0	194
79	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	2.6	190
80	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016, 7, 10476.	5.8	189
81	The Genomic Standards Consortium. <i>PLoS Biology</i> , 2011, 9, e1001088.	2.6	180
82	The integrated microbial genomes (IMG) system in 2007: data content and analysis tool extensions. <i>Nucleic Acids Research</i> , 2007, 36, D528-D533.	6.5	179
83	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	6.5	177
84	The Earth Microbiome Project: Meeting report of the 1st EMP meeting on sample selection and acquisition at Argonne National Laboratory October 6th 2010. <i>Standards in Genomic Sciences</i> , 2010, 3, 249-253.	1.5	176
85	IMG/VR v.2.0: an integrated data management and analysis system for cultivated and environmental viral genomes. <i>Nucleic Acids Research</i> , 2019, 47, D678-D686.	6.5	174
86	Genome-based evolutionary history of <i>Pseudomonas</i> spp. <i>Environmental Microbiology</i> , 2018, 20, 2142-2159.	1.8	172
87	Genomes OnLine database (GOLD) v.7: updates and new features. <i>Nucleic Acids Research</i> , 2019, 47, D649-D659.	6.5	169
88	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	13.5	164
89	Large-Scale Analyses of Human Microbiomes Reveal Thousands of Small, Novel Genes. <i>Cell</i> , 2019, 178, 1245-1259.e14.	13.5	163
90	The standard operating procedure of the DOE-JGI Metagenome Annotation Pipeline (MAP v.4). <i>Standards in Genomic Sciences</i> , 2016, 11, 17.	1.5	161

#	ARTICLE	IF	CITATIONS
91	Genomes OnLine Database (GOLD) v.6: data updates and feature enhancements. <i>Nucleic Acids Research</i> , 2017, 45, D446-D456.	6.5	157
92	Comparative Metagenomic and Metatranscriptomic Analysis of Hindgut Paunch Microbiota in Wood- and Dung-Feeding Higher Termites. <i>PLoS ONE</i> , 2013, 8, e61126.	1.1	149
93	The Fast Changing Landscape of Sequencing Technologies and Their Impact on Microbial Genome Assemblies and Annotation. <i>PLoS ONE</i> , 2012, 7, e48837.	1.1	145
94	Genomes OnLine Database (GOLD) v.8: overview and updates. <i>Nucleic Acids Research</i> , 2021, 49, D723-D733.	6.5	143
95	A thermostable Cas9 with increased lifetime in human plasma. <i>Nature Communications</i> , 2017, 8, 1424.	5.8	142
96	Succession in the petroleum reservoir microbiome through an oil field production lifecycle. <i>ISME Journal</i> , 2017, 11, 2141-2154.	4.4	136
97	Murine colitis reveals a disease-associated bacteriophage community. <i>Nature Microbiology</i> , 2018, 3, 1023-1031.	5.9	132
98	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. <i>Nature Medicine</i> , 2020, 26, 941-951.	15.2	130
99	Large-scale contamination of microbial isolate genomes by Illumina PhiX control. <i>Standards in Genomic Sciences</i> , 2015, 10, 18.	1.5	127
100	Stop codon reassignments in the wild. <i>Science</i> , 2014, 344, 909-913.	6.0	124
101	Genome Data Provides High Support for Generic Boundaries in Burkholderia Sensu Lato. <i>Frontiers in Microbiology</i> , 2017, 8, 1154.	1.5	122
102	KOW: a novel motif linking a bacterial transcription factor with ribosomal proteins. <i>Trends in Biochemical Sciences</i> , 1996, 21, 425-426.	3.7	120
103	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
104	Nontargeted virus sequence discovery pipeline and virus clustering for metagenomic data. <i>Nature Protocols</i> , 2017, 12, 1673-1682.	5.5	115
105	Multiple syntrophic interactions in a terephthalate-degrading methanogenic consortium. <i>ISME Journal</i> , 2011, 5, 122-130.	4.4	114
106	The Complete Multipartite Genome Sequence of <i>Cupriavidus necator</i> JMP134, a Versatile Pollutant Degradier. <i>PLoS ONE</i> , 2010, 5, e9729.	1.1	112
107	Identification of a haloalkaliphilic and thermostable cellulase with improved ionic liquid tolerance. <i>Green Chemistry</i> , 2011, 13, 2083.	4.6	111
108	Engineering <i>Escherichia coli</i> for Biodiesel Production Utilizing a Bacterial Fatty Acid Methyltransferase. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8052-8061.	1.4	107

#	ARTICLE	IF	CITATIONS
109	Individual genome assembly from complex community short-read metagenomic datasets. <i>ISME Journal</i> , 2012, 6, 898-901.	4.4	106
110	High level of intergenera gene exchange shapes the evolution of haloarchaea in an isolated Antarctic lake. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16939-16944.	3.3	105
111	Genome-Scale Data Call for a Taxonomic Rearrangement of Geodermatophilaceae. <i>Frontiers in Microbiology</i> , 2017, 8, 2501.	1.5	105
112	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
113	HipMCL: a high-performance parallel implementation of the Markov clustering algorithm for large-scale networks. <i>Nucleic Acids Research</i> , 2018, 46, e33-e33.	6.5	104
114	Universal Protein Families and the Functional Content of the Last Universal Common Ancestor. <i>Journal of Molecular Evolution</i> , 1999, 49, 413-423.	0.8	103
115	Genomic Characterization of Methanomicrobiales Reveals Three Classes of Methanogens. <i>PLoS ONE</i> , 2009, 4, e5797.	1.1	103
116	Towards a balanced view of the bacterial tree of life. <i>Microbiome</i> , 2017, 5, 140.	4.9	102
117	Genome-based classification of micromonosporae with a focus on their biotechnological and ecological potential. <i>Scientific Reports</i> , 2018, 8, 525.	1.6	102
118	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541T). <i>Standards in Genomic Sciences</i> , 2009, 1, 12-20.	1.5	100
119	Complete genome sequence of the <i>Medicago</i> microsymbiont <i>Ensifer</i> (<i>Sinorhizobium</i>) <i>medicae</i> strain WSM419. <i>Standards in Genomic Sciences</i> , 2010, 2, 77-86.	1.5	100
120	Complete Genome Sequences of Six Strains of the Genus <i>Methylobacterium</i> . <i>Journal of Bacteriology</i> , 2012, 194, 4746-4748.	1.0	99
121	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
122	Whole-genome comparative analysis of three phytopathogenic <i>Xylella fastidiosa</i> strains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12403-12408.	3.3	94
123	Genomics of Aerobic Cellulose Utilization Systems in Actinobacteria. <i>PLoS ONE</i> , 2012, 7, e39331.	1.1	92
124	Metabolic dependencies govern microbial syntrophies during methanogenesis in an anaerobic digestion ecosystem. <i>Microbiome</i> , 2020, 8, 22.	4.9	91
125	The Genome of the Obligately Intracellular Bacterium <i>Ehrlichia canis</i> Reveals Themes of Complex Membrane Structure and Immune Evasion Strategies. <i>Journal of Bacteriology</i> , 2006, 188, 4015-4023.	1.0	90
126	Complete Genome of the Cellulolytic Ruminant Bacterium <i>Ruminococcus albus</i> 7. <i>Journal of Bacteriology</i> , 2011, 193, 5574-5575.	1.0	87

#	ARTICLE	IF	CITATIONS
127	IMG-ABC: A Knowledge Base To Fuel Discovery of Biosynthetic Gene Clusters and Novel Secondary Metabolites. <i>MBio</i> , 2015, 6, e00932.	1.8	87
128	Fifteen years of microbial genomics: meeting the challenges and fulfilling the dream. <i>Nature Biotechnology</i> , 2009, 27, 627-632.	9.4	83
129	The emergence of major cellular processes in evolution. <i>FEBS Letters</i> , 1996, 390, 119-123.	1.3	81
130	An experimental metagenome data management and analysis system. <i>Bioinformatics</i> , 2006, 22, e359-e367.	1.8	81
131	Sequencing of Multiple Clostridial Genomes Related to Biomass Conversion and Biofuel Production. <i>Journal of Bacteriology</i> , 2010, 192, 6494-6496.	1.0	81
132	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
133	IMG-ABC: new features for bacterial secondary metabolism analysis and targeted biosynthetic gene cluster discovery in thousands of microbial genomes. <i>Nucleic Acids Research</i> , 2017, 45, D560-D565.	6.5	78
134	Genomes OnLine Database (GOLD 1.0): a monitor of complete and ongoing genome projects world-wide. <i>Bioinformatics</i> , 1999, 15, 773-774.	1.8	77
135	Complete genome sequence of <i>Enterobacter lignolyticus</i> SCF1. <i>Standards in Genomic Sciences</i> , 2011, 5, 69-85.	1.5	76
136	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
137	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
138	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
139	Comparative genome analysis of <i>Bacillus cereus</i> group genomes with <i>Bacillus subtilis</i> . <i>FEMS Microbiology Letters</i> , 2005, 250, 175-184.	0.7	73
140	Complete Genome Sequences of <i>Desulfosporosinus orientis</i> DSM765, <i>Desulfosporosinus youngiae</i> DSM17734, <i>Desulfosporosinus meridiei</i> DSM13257, and <i>Desulfosporosinus acidiphilus</i> DSM22704. <i>Journal of Bacteriology</i> , 2012, 194, 6300-6301.	1.0	73
141	Genome Analysis of <i>F. nucleatum</i> sub spp <i>vincentii</i> and Its Comparison With the Genome of <i>F. nucleatum</i> ATCC 25586. <i>Genome Research</i> , 2003, 13, 1180-1189.	2.4	72
142	Novel Insights into the Diversity of Catabolic Metabolism from Ten Haloarchaeal Genomes. <i>PLoS ONE</i> , 2011, 6, e20237.	1.1	72
143	Complete genome sequence of <i>Thioalkalivibrio sulfidophilus</i> HL-EbGr7. <i>Standards in Genomic Sciences</i> , 2011, 4, 23-35.	1.5	72
144	Complete Genome Sequence of the Aerobic Marine Methanotroph <i>Methylomonas methanica</i> MC09. <i>Journal of Bacteriology</i> , 2011, 193, 7001-7002.	1.0	72

#	ARTICLE	IF	CITATIONS
145	Complete Genome sequence of Burkholderia phymatum STM815T, a broad host range and efficient nitrogen-fixing symbiont of Mimosa species. Standards in Genomic Sciences, 2014, 9, 763-774.	1.5	71
146	Functional and genomic diversity of methylophilic Rhodocyclaceae: description of Methyloversatilis discipulorum sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 2227-2233.	0.8	71
147	On the evolution of arginases and related enzymes. Journal of Molecular Evolution, 1994, 39, 101-4.	0.8	70
148	Draft Sequencing and Comparative Genomics of Xylella fastidiosa Strains Reveal Novel Biological Insights. Genome Research, 2002, 12, 1556-1563.	2.4	70
149	Complete genome sequence of Haliangium ochraceum type strain (SMP-2T). Standards in Genomic Sciences, 2010, 2, 96-106.	1.5	70
150	Feathermoss and epiphytic <i>Nostoc</i> cooperate differently: expanding the spectrum of plant-cyanobacteria symbiosis. ISME Journal, 2017, 11, 2821-2833.	4.4	69
151	Microbial co-habitation and lateral gene transfer: what transposases can tell us. Genome Biology, 2009, 10, R45.	13.9	68
152	Genome Sequence of the Fleming Strain of <i>Micrococcus luteus</i> , a Simple Free-Living Actinobacterium. Journal of Bacteriology, 2010, 192, 841-860.	1.0	68
153	Genomic Analysis of Caldithrix abyssi, the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum Calditrichaeota. Frontiers in Microbiology, 2017, 8, 195.	1.5	66
154	Focus: <i>Synergistetes</i> . Environmental Microbiology, 2009, 11, 1327-1329.	1.8	65
155	Draft genome sequence of Halomonas lutea strain YIM 91125T (DSM 23508T) isolated from the alkaline Lake Ebinur in Northwest China. Standards in Genomic Sciences, 2015, 10, 1.	1.5	65
156	ProDeGe: a computational protocol for fully automated decontamination of genomes. ISME Journal, 2016, 10, 269-272.	4.4	65
157	IMG-ABC v.5.0: an update to the IMG/Atlas of Biosynthetic Gene Clusters Knowledgebase. Nucleic Acids Research, 2020, 48, D422-D430.	6.5	64
158	Comparative Transcriptomics between Synechococcus PCC 7942 and Synechocystis PCC 6803 Provide Insights into Mechanisms of Stress Acclimation. PLoS ONE, 2014, 9, e109738.	1.1	63
159	Genome-informed Bradyrhizobium taxonomy: where to from here?. Systematic and Applied Microbiology, 2019, 42, 427-439.	1.2	62
160	Complete genome sequence of Rhizobium leguminosarum bv trifolii strain WSM2304, an effective microsymbiont of the South American clover Trifolium polymorphum.. Standards in Genomic Sciences, 2010, 2, 66-76.	1.5	60
161	A synthesis of bacterial and archaeal phenotypic trait data. Scientific Data, 2020, 7, 170.	2.4	59
162	Whole-genome sequence annotation: 'Going wrong with confidence'. Molecular Microbiology, 1999, 32, 886-887.	1.2	58

#	ARTICLE	IF	CITATIONS
163	Genome Analysis of the Anaerobic Thermohalophilic Bacterium <i>Halothermothrix orenii</i> . PLoS ONE, 2009, 4, e4192.	1.1	58
164	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> . Standards in Genomic Sciences, 2012, 6, 194-209.	1.5	58
165	Archaeal and bacterial hyperthermophiles: horizontal gene exchange or common ancestry?. Trends in Genetics, 1999, 15, 298-299.	2.9	57
166	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20T). Standards in Genomic Sciences, 2010, 2, 158-167.	1.5	56
167	Comparative Genomic Analysis of the Endosymbionts of Herbivorous Insects Reveals Eco-Environmental Adaptations: Biotechnology Applications. PLoS Genetics, 2013, 9, e1003131.	1.5	56
168	Functional Genomics of Novel Secondary Metabolites from Diverse Cyanobacteria Using Untargeted Metabolomics. Marine Drugs, 2013, 11, 3617-3631.	2.2	56
169	COVID-19 pandemic reveals the peril of ignoring metadata standards. Scientific Data, 2020, 7, 188.	2.4	56
170	DOE JGI Metagenome Workflow. MSystems, 2021, 6, .	1.7	56
171	A Genomic Encyclopedia of the Root Nodule Bacteria: assessing genetic diversity through a systematic biogeographic survey. Standards in Genomic Sciences, 2015, 10, 14.	1.5	55
172	Complete Genome Sequences for the Anaerobic, Extremely Thermophilic Plant Biomass-Degrading Bacteria <i>Caldicellulosiruptor hydrothermalis</i> , <i>Caldicellulosiruptor kristjanssonii</i> , <i>Caldicellulosiruptor kronotskyensis</i> , <i>Caldicellulosiruptor owensensis</i> , and <i>Caldicellulosiruptor lactoaceticus</i> . Journal of Bacteriology, 2011, 193, 1483-1484.	1.0	54
173	Improving Microbial Genome Annotations in an Integrated Database Context. PLoS ONE, 2013, 8, e54859.	1.1	54
174	Microbial ecology of an Antarctic hypersaline lake: genomic assessment of ecophysiology among dominant haloarchaea. ISME Journal, 2014, 8, 1645-1658.	4.4	54
175	Supporting community annotation and user collaboration in the integrated microbial genomes (IMG) system. BMC Genomics, 2016, 17, 307.	1.2	54
176	Facile Recoding of Selenocysteine in Nature. Angewandte Chemie - International Edition, 2016, 55, 5337-5341.	7.2	54
177	Sulfate-Reducing Bacteria That Produce Exopolymers Thrive in the Calcifying Zone of a Hypersaline Cyanobacterial Mat. Frontiers in Microbiology, 2019, 10, 862.	1.5	54
178	Gene Context Analysis in the Integrated Microbial Genomes (IMG) Data Management System. PLoS ONE, 2009, 4, e7979.	1.1	54
179	Genome Sequence of <i>Thermophilum pendens</i> Reveals an Exceptional Loss of Biosynthetic Pathways without Genome Reduction. Journal of Bacteriology, 2008, 190, 2957-2965.	1.0	53
180	Complete genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM1325, an effective microsymbiont of annual Mediterranean clovers.. Standards in Genomic Sciences, 2010, 2, 347-356.	1.5	53

#	ARTICLE	IF	CITATIONS
181	Complete genome sequence of <i>Thauera aminoaromatica</i> strain MZ1T. <i>Standards in Genomic Sciences</i> , 2012, 6, 325-335.	1.5	53
182	Genomic Methods and Microbiological Technologies for Profiling Novel and Extreme Environments for the Extreme Microbiome Project (XMP). <i>Journal of Biomolecular Techniques</i> , 2017, 28, 31-39.	0.8	53
183	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , 2019, 7, 157.	4.9	53
184	VPF-Class: taxonomic assignment and host prediction of uncultivated viruses based on viral protein families. <i>Bioinformatics</i> , 2021, 37, 1805-1813.	1.8	53
185	Prokaryotic community profiles at different operational stages of a Greek solar saltern. <i>Research in Microbiology</i> , 2008, 159, 609-627.	1.0	52
186	Comparative metagenomics of hydrocarbon and methane seeps of the Gulf of Mexico. <i>Scientific Reports</i> , 2017, 7, 16015.	1.6	52
187	On the Origin of Reverse Transcriptase-Using CRISPR-Cas Systems and Their Hyperdiverse, Enigmatic Spacer Repertoires. <i>MBio</i> , 2017, 8, .	1.8	52
188	The Complete Genome Sequence of <i>Thermoproteus tenax</i> : A Physiologically Versatile Member of the Crenarchaeota. <i>PLoS ONE</i> , 2011, 6, e24222.	1.1	51
189	Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3T). <i>Standards in Genomic Sciences</i> , 2011, 4, 100-110.	1.5	51
190	Complete genome sequence of <i>Dehalogenimonas lykanthroporepellens</i> type strain (BL-DC-9T) and comparison to "Dehalococcoides" strains. <i>Standards in Genomic Sciences</i> , 2012, 6, 251-264.	1.5	51
191	Draft Genome Sequence of <i>Frankia</i> sp. Strain CN3, an Atypical, Noninfective (Nod ⁺) Ineffective (Fix ⁻) Isolate from <i>Coriaria nepalensis</i> . <i>Genome Announcements</i> , 2013, 1, e0008513.	0.8	51
192	A scoutRNA Is Required for Some Type V CRISPR-Cas Systems. <i>Molecular Cell</i> , 2020, 79, 416-424.e5.	4.5	49
193	Complete genome sequence of the filamentous gliding predatory bacterium <i>Herpetosiphon aurantiacus</i> type strain (114-95T). <i>Standards in Genomic Sciences</i> , 2011, 5, 356-370.	1.5	47
194	Complete Genome Sequence of the Thermophilic Bacterium <i>Exiguobacterium</i> sp. AT1b. <i>Journal of Bacteriology</i> , 2011, 193, 2880-2881.	1.0	47
195	Microbiome Data Science: Understanding Our Microbial Planet. <i>Trends in Microbiology</i> , 2016, 24, 425-427.	3.5	47
196	How Much Do rRNA Gene Surveys Underestimate Extant Bacterial Diversity?. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	47
197	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
198	Complete genome sequence of <i>Isosphaera pallida</i> type strain (IS1BT). <i>Standards in Genomic Sciences</i> , 2011, 4, 63-71.	1.5	46

#	ARTICLE	IF	CITATIONS
199	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
200	Complete genome sequence of <i>Thioalkalivibrio</i> sp. K90mix. <i>Standards in Genomic Sciences</i> , 2011, 5, 341-355.	1.5	45
201	<i>Trichodesmium</i> genome maintains abundant, widespread noncoding DNA in situ, despite oligotrophic lifestyle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4251-4256.	3.3	45
202	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	6.0	45
203	Complete genome sequence of <i>Veillonella parvula</i> type strain (Te3T). <i>Standards in Genomic Sciences</i> , 2010, 2, 57-65.	1.5	44
204	Complete genome sequence of <i>Rhodospirillum rubrum</i> type strain (S1T). <i>Standards in Genomic Sciences</i> , 2011, 4, 293-302.	1.5	44
205	Genome Sequence of the <i>Verrucomicrobium Opitutus terrae</i> PB90-1, an Abundant Inhabitant of Rice Paddy Soil Ecosystems. <i>Journal of Bacteriology</i> , 2011, 193, 2367-2368.	1.0	44
206	Complete genome sequence of <i>Dehalobacter restrictus</i> PER-K23T. <i>Standards in Genomic Sciences</i> , 2013, 8, 375-388.	1.5	44
207	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
208	Antarctic archaea-virus interactions: metaproteome-led analysis of invasion, evasion and adaptation. <i>ISME Journal</i> , 2015, 9, 2094-2107.	4.4	44
209	Empirical Comparison of Visualization Tools for Larger-Scale Network Analysis. <i>Advances in Bioinformatics</i> , 2017, 2017, 1-8.	5.7	44
210	Single-cell genomics of co-sorted Nanoarchaeota suggests novel putative host associations and diversification of proteins involved in symbiosis. <i>Microbiome</i> , 2018, 6, 161.	4.9	44
211	The eubacterial transcriptional activator Lrp is present in the Archaeon <i>Pyrococcus furiosus</i> . <i>Trends in Biochemical Sciences</i> , 1995, 20, 140-141.	3.7	43
212	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
213	IMG/M-HMP: A Metagenome Comparative Analysis System for the Human Microbiome Project. <i>PLoS ONE</i> , 2012, 7, e40151.	1.1	43
214	Complete genome sequence of <i>Anabaena variabilis</i> ATCC 29413. <i>Standards in Genomic Sciences</i> , 2014, 9, 562-573.	1.5	43
215	Genome sequence and description of the anaerobic lignin-degrading bacterium <i>Tolumonas lignolytica</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2015, 10, 106.	1.5	43
216	Complete genome sequence of the phenanthrene-degrading soil bacterium <i>Delftia acidovorans</i> Cs1-4. <i>Standards in Genomic Sciences</i> , 2015, 10, 55.	1.5	43

#	ARTICLE	IF	CITATIONS
217	Complete genome sequence of <i>Nitrosomonas</i> sp. Is79, an ammonia oxidizing bacterium adapted to low ammonium concentrations. <i>Standards in Genomic Sciences</i> , 2013, 7, 469-482.	1.5	43
218	Genome analysis of <i>Desulfotomaculum kuznetsovii</i> strain 17T reveals a physiological similarity with <i>Pelotomaculum thermopropionicum</i> strain SIT.. <i>Standards in Genomic Sciences</i> , 2013, 8, 69-87.	1.5	42
219	Insights into the dynamics between viruses and their hosts in a hot spring microbial mat. <i>ISME Journal</i> , 2020, 14, 2527-2541.	4.4	42
220	Complete genome sequence of <i>Treponema succinifaciens</i> type strain (6091T). <i>Standards in Genomic Sciences</i> , 2011, 4, 361-370.	1.5	41
221	Novel protein families in archaean genomes. <i>Nucleic Acids Research</i> , 1995, 23, 565-570.	6.5	40
222	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1T). <i>Standards in Genomic Sciences</i> , 2010, 2, 176-184.	1.5	40
223	Complete genome sequence of <i>Arcobacter nitrofigilis</i> type strain (CIT). <i>Standards in Genomic Sciences</i> , 2010, 2, 300-308.	1.5	40
224	Draft Genome Sequence of <i>Frankia</i> sp. Strain BCU110501, a Nitrogen-Fixing Actinobacterium Isolated from Nodules of <i>Discaria trinevis</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	40
225	Complete genome sequence of the lignin-degrading bacterium <i>Klebsiella</i> sp. strain BRL6-2. <i>Standards in Genomic Sciences</i> , 2014, 9, 19.	1.5	40
226	Draft genome sequence of marine alphaproteobacterial strain HIMB11, the first cultivated representative of a unique lineage within the <i>Roseobacter</i> clade possessing an unusually small genome. <i>Standards in Genomic Sciences</i> , 2014, 9, 632-645.	1.5	40
227	Habitat-Lite: A GSC Case Study Based on Free Text Terms for Environmental Metadata. <i>OMICS A Journal of Integrative Biology</i> , 2008, 12, 129-136.	1.0	39
228	Draft Genome Sequence of <i>Frankia</i> sp. Strain QA3, a Nitrogen-Fixing Actinobacterium Isolated from the Root Nodule of <i>Alnus nitida</i> . <i>Genome Announcements</i> , 2013, 1, e0010313.	0.8	39
229	Draft Genome Sequence of <i>Frankia</i> sp. Strain BMG5.12, a Nitrogen-Fixing Actinobacterium Isolated from Tunisian Soils. <i>Genome Announcements</i> , 2013, 1, .	0.8	39
230	Complete genome sequence of <i>Actinosynnema mirum</i> type strain (101T). <i>Standards in Genomic Sciences</i> , 2009, 1, 46-53.	1.5	38
231	Complete genome sequence of <i>Cellulomonas flavigena</i> type strain (134T). <i>Standards in Genomic Sciences</i> , 2010, 3, 15-25.	1.5	38
232	ClAMS: A Classifier for Metagenomic Sequences. <i>Standards in Genomic Sciences</i> , 2011, 5, 248-253.	1.5	38
233	Annotation of metagenome short reads using proxygenes. <i>Bioinformatics</i> , 2008, 24, i7-i13.	1.8	37
234	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

#	ARTICLE	IF	CITATIONS
235	Complete genome sequence of <i>Desulfarculus baarsii</i> type strain (2st14T). <i>Standards in Genomic Sciences</i> , 2010, 3, 276-284.	1.5	37
236	Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph <i>Sulfuricurvum kujjense</i> type strain (YK-1T). <i>Standards in Genomic Sciences</i> , 2012, 6, 94-103.	1.5	37
237	Metagenomic investigation of the geologically unique <i>Hellenic Volcanic Arc</i> reveals a distinctive ecosystem with unexpected physiology. <i>Environmental Microbiology</i> , 2016, 18, 1122-1136.	1.8	37
238	Complete genome sequence of <i>Sulfurimonas autotrophica</i> type strain (OK10T). <i>Standards in Genomic Sciences</i> , 2010, 3, 194-202.	1.5	37
239	Complete genome sequence of <i>Desulfomicrobium baculatum</i> type strain (XT). <i>Standards in Genomic Sciences</i> , 2009, 1, 29-37.	1.5	36
240	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
241	Complete Genome Sequence of the Ethanol-Producing <i>Zymomonas mobilis</i> subsp. <i>mobilis</i> Centrotype ATCC 29191. <i>Journal of Bacteriology</i> , 2012, 194, 5966-5967.	1.0	36
242	A comparative genomics perspective on the genetic content of the alkaliphilic haloarchaeon <i>Natrialba magadii</i> ATCC 43099T. <i>BMC Genomics</i> , 2012, 13, 165.	1.2	36
243	Microbial metagenomes and metatranscriptomes during a coastal phytoplankton bloom. <i>Scientific Data</i> , 2019, 6, 129.	2.4	36
244	The <i>Rhodobacter capsulatus</i> genome. <i>Photosynthesis Research</i> , 2001, 70, 43-52.	1.6	35
245	Complete genome sequence of <i>Desulfotomaculum acetoxidans</i> type strain (5575T). <i>Standards in Genomic Sciences</i> , 2009, 1, 242-253.	1.5	35
246	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
247	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
248	Complete genome sequence of the halophilic and highly halotolerant <i>Chromohalobacter salexigens</i> type strain (1H11T). <i>Standards in Genomic Sciences</i> , 2011, 5, 379-388.	1.5	35
249	Complete genome sequence of <i>Thermomonospora curvata</i> type strain (B9T). <i>Standards in Genomic Sciences</i> , 2011, 4, 13-22.	1.5	35
250	Complete genome sequence of <i>Methanoculleus marisnigri</i> Romesser et al. 1981 type strain JR1. <i>Standards in Genomic Sciences</i> , 2009, 1, 189-196.	1.5	34
251	Complete genome sequence of <i>Pirellula staleyi</i> type strain (ATCC 27377T). <i>Standards in Genomic Sciences</i> , 2009, 1, 308-316.	1.5	34
252	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

#	ARTICLE	IF	CITATIONS
253	Permanent draft genome of <i>Thiobacillus thioparus</i> DSM 505T, an obligately chemolithoautotrophic member of the Betaproteobacteria. <i>Standards in Genomic Sciences</i> , 2017, 12, 10.	1.5	34
254	Toward a Standards-Compliant Genomic and Metagenomic Publication Record. <i>OMICS A Journal of Integrative Biology</i> , 2008, 12, 157-160.	1.0	33
255	Complete genome sequence of <i>Meiothermus ruber</i> type strain (21T). <i>Standards in Genomic Sciences</i> , 2010, 3, 26-36.	1.5	33
256	A call for standardized classification of metagenome projects. <i>Environmental Microbiology</i> , 2010, 12, 1803-1805.	1.8	33
257	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
258	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
259	Complete genome sequence of <i>Polynucleobacter necessarius</i> subsp. <i>asymbioticus</i> type strain (QLW-P1DMWA-1T). <i>Standards in Genomic Sciences</i> , 2012, 6, 74-83.	1.5	33
260	Discovery of Novel Plant Interaction Determinants from the Genomes of 163 Root Nodule Bacteria. <i>Scientific Reports</i> , 2015, 5, 16825.	1.6	33
261	Complete genome sequence of <i>Methanospirillum hungatei</i> type strain JF1. <i>Standards in Genomic Sciences</i> , 2016, 11, 2.	1.5	33
262	Complete genome sequence of <i>Acidimicrobium ferrooxidans</i> type strain (ICPT). <i>Standards in Genomic Sciences</i> , 2009, 1, 38-45.	1.5	32
263	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
264	Complete genome sequence of <i>Haloterrigena turkmenica</i> type strain (4kT). <i>Standards in Genomic Sciences</i> , 2010, 2, 107-116.	1.5	32
265	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
266	Complete genome sequence of <i>Ferroglobus placidus</i> AEDII12DO. <i>Standards in Genomic Sciences</i> , 2011, 5, 50-60.	1.5	32
267	Complete Genome Sequence of <i>Paenibacillus</i> strain Y4.12MC10, a Novel <i>Paenibacillus lautus</i> strain Isolated from Obsidian Hot Spring in Yellowstone National Park. <i>Standards in Genomic Sciences</i> , 2012, 6, 381-400.	1.5	32
268	Genomes of ubiquitous marine and hypersaline <i>Hydrogenovibrio</i> , <i>Thiomicrobacter</i> and <i>Thiomicrospira</i> spp. encode a diversity of mechanisms to sustain chemolithoautotrophy in heterogeneous environments. <i>Environmental Microbiology</i> , 2018, 20, 2686-2708.	1.8	32
269	<i>Arboriscoccus pini</i> gen. nov., sp. nov., an endophyte from a pine tree of the class Alphaproteobacteria, emended description of <i>Geminicoccus roseus</i> , and proposal of <i>Geminicoccaceae</i> fam. nov.. <i>Systematic and Applied Microbiology</i> , 2018, 41, 94-100.	1.2	32
270	Influence of the polar light cycle on seasonal dynamics of an Antarctic lake microbial community. <i>Microbiome</i> , 2020, 8, 116.	4.9	32

#	ARTICLE	IF	CITATIONS
271	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
272	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
273	Complete genome sequence of <i>Acidaminococcus fermentans</i> type strain (VR4T). <i>Standards in Genomic Sciences</i> , 2010, 3, 1-14.	1.5	31
274	Estimating DNA coverage and abundance in metagenomes using a gamma approximation. <i>Bioinformatics</i> , 2010, 26, 295-301.	1.8	31
275	Complete genome sequence of <i>Arthrobacter phenanthrenivorans</i> type strain (Sphe3). <i>Standards in Genomic Sciences</i> , 2011, 4, 123-130.	1.5	31
276	<i>Thermus oshimai</i> JL-2 and <i>T. thermophilus</i> JL-18 genome analysis illuminates pathways for carbon, nitrogen, and sulfur cycling. <i>Standards in Genomic Sciences</i> , 2013, 7, 449-468.	1.5	31
277	Draft Genome Sequences of 10 Strains of the Genus <i>Exiguobacterium</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	31
278	NAP: The Network Analysis Profiler, a web tool for easier topological analysis and comparison of medium-scale biological networks. <i>BMC Research Notes</i> , 2017, 10, 278.	0.6	31
279	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
280	Complete genome sequence of <i>Paludibacter propionigenes</i> type strain (WB4T). <i>Standards in Genomic Sciences</i> , 2011, 4, 36-44.	1.5	30
281	Genome Sequence of the Ethanol-Producing <i>Zymomonas mobilis</i> subsp. <i>mobilis</i> Lectotype Strain ATCC 10988. <i>Journal of Bacteriology</i> , 2011, 193, 5051-5052.	1.0	30
282	Complete genome sequence of <i>Polynucleobacter necessarius</i> subsp. <i>asymbioticus</i> type strain (QLW-P1DMWA-1T). <i>Standards in Genomic Sciences</i> , 2012, 6, 1-14.	1.5	30
283	High quality draft genome sequences of <i>Pseudomonas fulva</i> DSM 17717T, <i>Pseudomonas parafulva</i> DSM 17004T and <i>Pseudomonas cremoricolorata</i> DSM 17059T type strains. <i>Standards in Genomic Sciences</i> , 2016, 11, 55.	1.5	30
284	Structure determination of the HgcAB complex using metagenome sequence data: insights into microbial mercury methylation. <i>Communications Biology</i> , 2020, 3, 320.	2.0	30
285	Absence of genome reduction in diverse, facultative endohyphal bacteria. <i>Microbial Genomics</i> , 2017, 3, e000101.	1.0	30
286	Complete genome sequence of <i>Methanocorpusculum labreanum</i> type strain Z. <i>Standards in Genomic Sciences</i> , 2009, 1, 197-203.	1.5	29
287	Complete genome sequence of <i>Sulfurospirillum deleyianum</i> type strain (5175T). <i>Standards in Genomic Sciences</i> , 2010, 2, 149-157.	1.5	29
288	Genomic composition and dynamics among <i>Methanomicrobiales</i> predict adaptation to contrasting environments. <i>ISME Journal</i> , 2017, 11, 87-99.	4.4	29

#	ARTICLE	IF	CITATIONS
289	Draft genome sequences of <i>Bradyrhizobium shewense</i> sp. nov. ERR11T and <i>Bradyrhizobium yuanmingense</i> CCBAU 10071T. <i>Standards in Genomic Sciences</i> , 2017, 12, 74.	1.5	29
290	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. <i>Nature Communications</i> , 2021, 12, 5483.	5.8	29
291	Reclassification of a <i>Polynucleobacter cosmopolitanus</i> strain isolated from tropical Lake Victoria as <i>Polynucleobacter victoriensis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 5087-5093.	0.8	29
292	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , 2014, 9, 599-601.	1.5	29
293	Complete genome sequence of <i>Kangiella koreensis</i> type strain (SW-125T). <i>Standards in Genomic Sciences</i> , 2009, 1, 226-233.	1.5	28
294	Complete genome sequence of <i>Coraliomargarita akajimensis</i> type strain (04OKA010-24T). <i>Standards in Genomic Sciences</i> , 2010, 2, 290-299.	1.5	28
295	Complete genome sequence of <i>Cellulophaga algicola</i> type strain (IC166T). <i>Standards in Genomic Sciences</i> , 2011, 4, 72-80.	1.5	28
296	Complete Genome Sequence of the Anaerobic, Halophilic Alkalithermophile <i>Natranaerobius thermophilus</i> JW/NM-WN-LF. <i>Journal of Bacteriology</i> , 2011, 193, 4023-4024.	1.0	28
297	Genome and Transcriptome of <i>Clostridium phytofermentans</i> , Catalyst for the Direct Conversion of Plant Feedstocks to Fuels. <i>PLoS ONE</i> , 2015, 10, e0118285.	1.1	28
298	Draft Genome Sequence of <i>Methyloferula stellata</i> AR4, an Obligate Methanotroph Possessing Only a Soluble Methane Monooxygenase. <i>Genome Announcements</i> , 2015, 3, .	0.8	28
299	Atypical Divergence of SARS-CoV-2 Orf8 from Orf7a within the Coronavirus Lineage Suggests Potential Stealthy Viral Strategies in Immune Evasion. <i>MBio</i> , 2021, 12, .	1.8	28
300	Comparative Genome Analysis in the Integrated Microbial Genomes (IMG) System. <i>Methods in Molecular Biology</i> , 2007, 395, 35-56.	0.4	28
301	A changing of the guard. <i>Environmental Microbiology</i> , 2009, 11, 551-553.	1.8	27
302	Complete genome sequence of <i>Sphaerobacter thermophilus</i> type strain (S 6022T). <i>Standards in Genomic Sciences</i> , 2010, 2, 49-56.	1.5	27
303	Complete genome sequence of <i>Streptosporangium roseum</i> type strain (NI 9100T). <i>Standards in Genomic Sciences</i> , 2010, 2, 29-37.	1.5	27
304	Draft genome sequence of strain HIMB100, a cultured representative of the SAR116 clade of marine Alphaproteobacteria. <i>Standards in Genomic Sciences</i> , 2011, 5, 269-278.	1.5	27
305	Complete genome sequence of the rapeseed plant-growth promoting <i>Serratia plymuthica</i> strain AS9. <i>Standards in Genomic Sciences</i> , 2012, 6, 54-62.	1.5	27
306	Genome sequence of <i>Rhizobium leguminosarum</i> bv <i>trifolii</i> strain WSM1689, the microsymbiont of the one flowered clover <i>Trifolium uniflorum</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 527-539.	1.5	27

#	ARTICLE	IF	CITATIONS
307	Genome analysis of <i>Desulfotomaculum gibsoniae</i> strain GrollT a highly versatile Gram-positive sulfate-reducing bacterium. <i>Standards in Genomic Sciences</i> , 2014, 9, 821-839.	1.5	27
308	Comparing polysaccharide decomposition between the type strains <i>Gramella echinicola</i> KMM 6050T (DSM 19838T) and <i>Gramella portivictoriae</i> UST040801-001T (DSM 23547T), and emended description of <i>Gramella echinicola</i> Nedashkovskaya et al. 2005 emend. Shahina et al. 2014 and <i>Gramella portivictoriae</i> Lau et al. 2005. <i>Standards in Genomic Sciences</i> , 2016, 11, 37.	1.5	27
309	Contrasting Pathways for Anaerobic Methane Oxidation in Gulf of Mexico Cold Seep Sediments. <i>MSystems</i> , 2019, 4, .	1.7	27
310	Description of <i>Trichococcus ilysis</i> sp. nov. by combined physiological and in silico genome hybridization analyses. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 3957-3963.	0.8	27
311	The complete genome sequence of <i>Staphylothermus marinus</i> reveals differences in sulfur metabolism among heterotrophic Crenarchaeota. <i>BMC Genomics</i> , 2009, 10, 145.	1.2	26
312	Complete genome sequence of <i>Archaeoglobus profundus</i> type strain (AV18T). <i>Standards in Genomic Sciences</i> , 2010, 2, 327-346.	1.5	26
313	Complete genome sequence of <i>Gordonia bronchialis</i> type strain (3410T). <i>Standards in Genomic Sciences</i> , 2010, 2, 19-28.	1.5	26
314	Complete genome sequence of <i>Haliscomenobacter hydrossis</i> type strain (OT). <i>Standards in Genomic Sciences</i> , 2011, 4, 352-360.	1.5	26
315	Genome sequence of the moderately thermophilic, amino-acid-degrading and sulfur-reducing bacterium <i>Thermovirga lienii</i> type strain (Cas60314T). <i>Standards in Genomic Sciences</i> , 2012, 6, 230-239.	1.5	26
316	Genome sequence of the homoacetogenic bacterium <i>Holophaga foetida</i> type strain (TMBS4T). <i>Standards in Genomic Sciences</i> , 2012, 6, 174-184.	1.5	26
317	Non-contiguous finished genome sequence of plant-growth promoting <i>Serratia proteamaculans</i> S4. <i>Standards in Genomic Sciences</i> , 2013, 8, 441-449.	1.5	26
318	Genome sequence of <i>Phaeobacter inhibens</i> type strain (T5T), a secondary metabolite producing representative of the marine <i>Roseobacter</i> clade, and emendation of the species description of <i>Phaeobacter inhibens</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 334-350.	1.5	26
319	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , 2014, 9, 599-601.	1.5	26
320	Transfer RNAs with novel cloverleaf structures. <i>Nucleic Acids Research</i> , 2017, 45, gkw898.	6.5	26
321	Complete genome sequence of <i>Desulfurivibrio alkaliphilus</i> strain AHT2T, a haloalkaliphilic sulfidogen from Egyptian hypersaline alkaline lakes. <i>Standards in Genomic Sciences</i> , 2016, 11, 67.	1.5	26
322	Draft genome sequence of type strain HBR26T and description of <i>Rhizobium aethiopicum</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2017, 12, 14.	1.5	26
323	Evolutionary implications of duplications and Balbiani rings in <i>Drosophila</i> . A study of <i>Drosophila serrata</i> . <i>Genome</i> , 1990, 33, 478-485.	0.9	25
324	Parallel origins of the nucleosome core and eukaryotic transcription from Archaea. <i>Journal of Molecular Evolution</i> , 1996, 42, 234-239.	0.8	25

#	ARTICLE	IF	CITATIONS
325	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
326	Complete genome sequence of <i>Anaerococcus prevotii</i> type strain (PC1T). <i>Standards in Genomic Sciences</i> , 2009, 1, 159-165.	1.5	25
327	Complete genome sequence of <i>Brachybacterium faecium</i> type strain (Schefferle 6-10T). <i>Standards in Genomic Sciences</i> , 2009, 1, 3-11.	1.5	25
328	Complete genome sequence of <i>Dyadobacter fermentans</i> type strain (NS114T). <i>Standards in Genomic Sciences</i> , 2009, 1, 133-140.	1.5	25
329	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
330	Complete Genome Sequence of the Thermophilic, Piezophilic, Heterotrophic Bacterium <i>Marinitoga piezophila</i> KA3. <i>Journal of Bacteriology</i> , 2012, 194, 5974-5975.	1.0	25
331	Genome analyses of the carboxydrotrophic sulfate-reducers <i>Desulfotomaculum nigrificans</i> and <i>Desulfotomaculum carboxydivorans</i> and reclassification of <i>Desulfotomaculum caboxydivorans</i> as a later synonym of <i>Desulfotomaculum nigrificans</i> . <i>Standards in Genomic Sciences</i> , 2014, 9, 655-675.	1.5	25
332	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
333	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
334	Complete genome sequence of <i>Saccharomonospora viridis</i> type strain (P101T). <i>Standards in Genomic Sciences</i> , 2009, 1, 141-149.	1.5	24
335	Complete genome sequence of <i>Conexibacter woesei</i> type strain (ID131577T). <i>Standards in Genomic Sciences</i> , 2010, 2, 212-219.	1.5	24
336	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
337	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
338	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
339	Complete genome sequence of <i>Halogeometricum borinquense</i> type strain (PR3T). <i>Standards in Genomic Sciences</i> , 2009, 1, 150-158.	1.5	23
340	Complete genome sequence of <i>Thermanaerovibrio acidaminovorans</i> type strain (Su883T). <i>Standards in Genomic Sciences</i> , 2009, 1, 254-261.	1.5	23
341	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
342	Complete genome sequence of <i>Thermobispora bispora</i> type strain (R51T). <i>Standards in Genomic Sciences</i> , 2010, 2, 318-326.	1.5	23

#	ARTICLE	IF	CITATIONS
343	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
344	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
345	The complete genome sequence of <i>Clostridium indolis</i> DSM 755T. <i>Standards in Genomic Sciences</i> , 2014, 9, 1089-1104.	1.5	23
346	Draft Genome Sequence of <i>Frankia</i> sp. Strain DC12, an Atypical, Noninfective, Ineffective Isolate from <i>Datisca cannabina</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	23
347	Draft Genome Sequences of Gammaproteobacterial Methanotrophs Isolated from Marine Ecosystems. <i>Genome Announcements</i> , 2016, 4, .	0.8	23
348	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
349	Complete genome sequence of <i>Desulfohalobium retbaense</i> type strain (HR100T). <i>Standards in Genomic Sciences</i> , 2010, 2, 38-48.	1.5	22
350	Complete genome sequence of <i>Leadbetterella byssophila</i> type strain (4M15T). <i>Standards in Genomic Sciences</i> , 2011, 4, 2-12.	1.5	22
351	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
352	Complete genome sequence of <i>Mycobacterium</i> sp. strain (Spyr1) and reclassification to <i>Mycobacterium gilvum</i> Spyr1. <i>Standards in Genomic Sciences</i> , 2011, 5, 144-153.	1.5	22
353	Genome Sequence of the Ethanol-Producing <i>Zymomonas mobilis</i> subsp. <i>pomaceae</i> Lectotype Strain ATCC 29192. <i>Journal of Bacteriology</i> , 2011, 193, 5049-5050.	1.0	22
354	Complete genome sequence of the plant-associated <i>Serratia plymuthica</i> strain AS13. <i>Standards in Genomic Sciences</i> , 2012, 7, 22-30.	1.5	22
355	Complete genome sequence of the sulfate-reducing firmicute <i>Desulfotomaculum ruminis</i> type strain (DLT). <i>Standards in Genomic Sciences</i> , 2012, 7, 304-319.	1.5	22
356	Genome sequence of the <i>Lotus</i> spp. microsymbiont <i>Mesorhizobium loti</i> strain R7A. <i>Standards in Genomic Sciences</i> , 2014, 9, 6.	1.5	22
357	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
358	Complete genome of <i>Nitrosospira briensis</i> C-128, an ammonia-oxidizing bacterium from agricultural soil. <i>Standards in Genomic Sciences</i> , 2016, 11, 46.	1.5	22
359	A Functional Mini-Integrase in a Two-Protein Type V-C CRISPR System. <i>Molecular Cell</i> , 2019, 73, 727-737.e3.	4.5	22
360	A Comparison of Microbial Genome Web Portals. <i>Frontiers in Microbiology</i> , 2019, 10, 208.	1.5	22

#	ARTICLE	IF	CITATIONS
361	Complete genome sequence of <i>Streptobacillus moniliformis</i> type strain (9901T). <i>Standards in Genomic Sciences</i> , 2009, 1, 300-307.	1.5	21
362	Complete genome sequence of the melanogenic marine bacterium <i>Marinomonas mediterranea</i> type strain (MMB-1T).. <i>Standards in Genomic Sciences</i> , 2012, 6, 63-73.	1.5	21
363	Complete genome sequence of the Antarctic <i>Halorubrum lacusprofundi</i> type strain ACAM 34. <i>Standards in Genomic Sciences</i> , 2016, 11, 70.	1.5	21
364	Genome-guided analysis allows the identification of novel physiological traits in <i>Trichococcus</i> species. <i>BMC Genomics</i> , 2020, 21, 24.	1.2	21
365	Thousands of small, novel genes predicted in global phage genomes. <i>Cell Reports</i> , 2022, 39, 110984.	2.9	21
366	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
367	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
368	Genome Sequence of <i>Streptomyces viridosporus</i> Strain T7A ATCC 39115, a Lignin-Degrading Actinomycete. <i>Genome Announcements</i> , 2013, 1, .	0.8	20
369	Ten Years of Maintaining and Expanding a Microbial Genome and Metagenome Analysis System. <i>Trends in Microbiology</i> , 2015, 23, 730-741.	3.5	20
370	RNA-Dependent Cysteine Biosynthesis in Bacteria and Archaea. <i>MBio</i> , 2017, 8, .	1.8	20
371	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
372	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
373	Complete genome sequence of <i>Serratia plymuthica</i> strain AS12. <i>Standards in Genomic Sciences</i> , 2012, 6, 165-173.	1.5	19
374	Whole Genome Sequencing of <i>Thermus oshimai</i> JL-2 and <i>Thermus thermophilus</i> JL-18, Incomplete Denitrifiers from the United States Great Basin. <i>Genome Announcements</i> , 2013, 1, .	0.8	19
375	Molecular Dialogues between Early Divergent Fungi and Bacteria in an Antagonism versus a Mutualism. <i>MBio</i> , 2020, 11, .	1.8	19
376	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium <i>Starkeya novella</i> type strain (ATCC 8093T). <i>Standards in Genomic Sciences</i> , 2012, 7, 44-58.	1.5	19
377	Genome of <i>Methanocaldococcus (methanococcus) jannaschii</i> . <i>Methods in Enzymology</i> , 2001, 330, 40-123.	0.4	18
378	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

#	ARTICLE	IF	CITATIONS
379	Complete genome sequence of Spirochaeta smaragdinae type strain (SEBR 4228T). Standards in Genomic Sciences, 2010, 3, 1-9.	1.5	18
380	Complete genome sequence of Marivirga tractuosa type strain (H-43T). Standards in Genomic Sciences, 2011, 4, 154-162.	1.5	18
381	The Earth Microbiome Project: The Meeting Report for the 1st International Earth Microbiome Project Conference, Shenzhen, China, June 13th-15th 2011. Standards in Genomic Sciences, 2011, 5, 243-247.	1.5	18
382	High quality draft genome sequence of Olivibacter sitiensis type strain (AW-6T), a diphenol degrader with genes involved in the catechol pathway. Standards in Genomic Sciences, 2014, 9, 783-793.	1.5	18
383	Novel heavy metal resistance gene clusters are present in the genome of Cupriavidus neocaledonicus STM 6070, a new species of Mimosa pudica microsymbiont isolated from heavy-metal-rich mining site soil. BMC Genomics, 2020, 21, 214.	1.2	18
384	Errors in Genome Reviews. , 1998, 281, 1453c-1453.		18
385	Methanococcus jannaschii Genome: Revisited. Genome Science & Technology, 1996, 1, 329-338.	1.2	17
386	Complete genome sequence of Cryptobacterium curtum type strain (12-3T). Standards in Genomic Sciences, 2009, 1, 93-100.	1.5	17
387	Complete genome sequence of Methanothermus fervidus type strain (V24ST). Standards in Genomic Sciences, 2010, 3, 315-324.	1.5	17
388	Genome Sequence of the Ethene- and Vinyl Chloride-Oxidizing Actinomycete Nocardioides sp. Strain JS614. Journal of Bacteriology, 2011, 193, 3399-3400.	1.0	17
389	Heterologous Expression and Characterization of Two 1-Hydroxy-2-Naphthoic Acid Dioxygenases from Arthrobacter phenanthrenivorans. Applied and Environmental Microbiology, 2012, 78, 621-627.	1.4	17
390	Genome sequence of the Leisingera aquimarina type strain (DSM 24565T), a member of the marine Roseobacter clade rich in extrachromosomal elements. Standards in Genomic Sciences, 2013, 8, 389-402.	1.5	17
391	Complete genome sequence of Mesorhizobium ciceri bv. biserrulae type strain (WSM1271T). Standards in Genomic Sciences, 2013, 9, 462-472.	1.5	17
392	Genome of Methanoregula boonei 6A8 reveals adaptations to oligotrophic peatland environments. Microbiology (United Kingdom), 2015, 161, 1572-1581.	0.7	17
393	Complete Genome Sequence of Anaeromyxobacter sp. Fw109-5, an Anaerobic, Metal-Reducing Bacterium Isolated from a Contaminated Subsurface Environment. Genome Announcements, 2015, 3, .	0.8	17
394	Illuminating the Virosphere Through Global Metagenomics. Annual Review of Biomedical Data Science, 2021, 4, 369-391.	2.8	17
395	Nucleic acid-binding metabolic enzymes: Living fossils of stereochemical interactions?. Journal of Molecular Evolution, 1995, 40, 564-569.	0.8	16
396	Complete genome sequence of Sanguibacter keddieii type strain (ST-74T). Standards in Genomic Sciences, 2009, 1, 110-118.	1.5	16

#	ARTICLE	IF	CITATIONS
397	Complete genome sequence of <i>Denitrovibrio acetiphilus</i> type strain (N2460T). <i>Standards in Genomic Sciences</i> , 2010, 2, 270-279.	1.5	16
398	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
399	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
400	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium <i>Starkeya novella</i> type strain (ATCC 8093T). <i>Standards in Genomic Sciences</i> , 2012, 7, 44-58.	1.5	16
401	Complete genome sequence of <i>Enterobacter</i> sp. IIT-BT 08: A potential microbial strain for high rate hydrogen production. <i>Standards in Genomic Sciences</i> , 2013, 9, 359-369.	1.5	16
402	High quality draft genome sequence of <i>Flavobacterium rivuli</i> type strain WB 3.3-2T (DSM 21788T), a valuable source of polysaccharide decomposing enzymes. <i>Standards in Genomic Sciences</i> , 2015, 10, 46.	1.5	16
403	Draft genome sequence of <i>Dethiobacter alkaliphilus</i> strain AHT1T, a gram-positive sulfidogenic polyextremophile. <i>Standards in Genomic Sciences</i> , 2017, 12, 57.	1.5	16
404	Structural and functional features of the intracellular amino terminus of DEG/ENaC ion channels. <i>Current Biology</i> , 2001, 11, R205-R208.	1.8	15
405	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
406	Complete genome sequence of <i>Weeksella virosa</i> type strain (9751T). <i>Standards in Genomic Sciences</i> , 2011, 4, 81-90.	1.5	15
407	Complete Genome Sequence of <i>Desulfurococcus fermentans</i> , a Hyperthermophilic Cellulolytic Crenarchaeon Isolated from a Freshwater Hot Spring in Kamchatka, Russia. <i>Journal of Bacteriology</i> , 2012, 194, 5703-5704.	1.0	15
408	Complete Genome of <i>Serratia</i> sp. Strain FGI 94, a Strain Associated with Leaf-Cutter Ant Fungus Gardens. <i>Genome Announcements</i> , 2013, 1, e0023912.	0.8	15
409	Complete genome sequence of the marine methyl-halide oxidizing <i>Leisingera methylohalidivorans</i> type strain (DSM 14336T), a representative of the Roseobacter clade. <i>Standards in Genomic Sciences</i> , 2013, 9, 128-141.	1.5	15
410	Complete Genome Sequences of <i>Caldicellulosiruptor</i> sp. Strain Rt8.B8, <i>Caldicellulosiruptor</i> sp. Strain Wai35.B1, and <i>Thermoanaerobacter cellulolyticus</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	15
411	High quality draft genome sequence of <i>Meganema perideroedes</i> str. Gr1T and a proposal for its reclassification to the family Meganemaceae fam. nov.. <i>Standards in Genomic Sciences</i> , 2015, 10, 23.	1.5	15
412	Permanent draft genome of <i>Thermithiobacillus tepidarius</i> DSM 3134T, a moderately thermophilic, obligately chemolithoautotrophic member of the Acidithiobacillia. <i>Standards in Genomic Sciences</i> , 2016, 11, 74.	1.5	15
413	Metagenome Sequencing to Explore Phylogenomics of Terrestrial Cyanobacteria. <i>Microbiology Resource Announcements</i> , 2021, 10, e0025821.	0.3	15
414	Dissecting the dominant hot spring microbial populations based on community-wide sampling at single-cell genomic resolution. <i>ISME Journal</i> , 2022, 16, 1337-1347.	4.4	15

#	ARTICLE	IF	CITATIONS
415	Mechanisms of Specificity in mRNA Degradation: Autoregulation and Cognate Interactions. <i>Journal of Theoretical Biology</i> , 1993, 163, 373-392.	0.8	14
416	Tetratricopeptide-repeat proteins in the archaeon <i>Methanococcus jannaschii</i> . <i>Trends in Biochemical Sciences</i> , 1998, 23, 245-247.	3.7	14
417	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
418	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
419	Complete genome sequence of <i>Ferrimonas balearica</i> type strain (PATT). <i>Standards in Genomic Sciences</i> , 2010, 3, 174-182.	1.5	14
420	Complete genome sequence of <i>Thermosphaera aggregans</i> type strain (M11TLT). <i>Standards in Genomic Sciences</i> , 2010, 2, 245-259.	1.5	14
421	Complete genome sequence of <i>Bacteroides helcogenes</i> type strain (P 36-108T). <i>Standards in Genomic Sciences</i> , 2011, 4, 45-53.	1.5	14
422	Complete genome sequence of <i>Deinococcus maricopensis</i> type strain (LB-34T). <i>Standards in Genomic Sciences</i> , 2011, 4, 163-172.	1.5	14
423	Genome Sequence of <i>Victivallis vadensis</i> ATCC BAA-548, an Anaerobic Bacterium from the Phylum Lentisphaerae, Isolated from the Human Gastrointestinal Tract. <i>Journal of Bacteriology</i> , 2011, 193, 2373-2374.	1.0	14
424	Complete genome sequence of the thermophilic sulfate-reducing ocean bacterium <i>Thermodesulfator indicus</i> type strain (CIR29812T). <i>Standards in Genomic Sciences</i> , 2012, 6, 155-164.	1.5	14
425	Complete genome sequence of the orange-red pigmented, radioresistant <i>Deinococcus proteolyticus</i> type strain (MRPT). <i>Standards in Genomic Sciences</i> , 2012, 6, 240-250.	1.5	14
426	Toward a standard in structural genome annotation for prokaryotes. <i>Standards in Genomic Sciences</i> , 2015, 10, 45.	1.5	14
427	Draft Genome Sequence of the Moderately Halophilic Methanotroph <i>Methylohalobius crimeensis</i> Strain 10Ki. <i>Genome Announcements</i> , 2015, 3, .	0.8	14
428	High quality draft genome of <i>Nakamurella lactea</i> type strain, a rock actinobacterium, and emended description of <i>Nakamurella lactea</i> . <i>Standards in Genomic Sciences</i> , 2017, 12, 4.	1.5	14
429	Impact of Soil Salinity on the Cowpea Nodule-Microbiome and the Isolation of Halotolerant PGPR Strains to Promote Plant Growth under Salinity Stress. <i>Phytobiomes Journal</i> , 2020, 4, 364-374.	1.4	14
430	<i>Hymenobacter artigasi</i> sp. nov., isolated from air sampling in maritime Antarctica. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4935-4941.	0.8	14
431	Complete genome sequence of <i>Methanoplanus petrolearius</i> type strain (SEBR 4847T). <i>Standards in Genomic Sciences</i> , 2010, 3, 203-211.	1.5	14
432	Meeting Report from the Genomic Standards Consortium (GSC) Workshops 6 and 7. <i>Standards in Genomic Sciences</i> , 2009, 1, 68-71.	1.5	13

#	ARTICLE	IF	CITATIONS
433	Complete genome sequence of Syntrophothermus lipocalidus type strain (TGB-C1T). Standards in Genomic Sciences, 2010, 3, 268-275.	1.5	13
434	Complete genome sequence of Nitratifactor salsuginis type strain (E9137-1T). Standards in Genomic Sciences, 2011, 4, 322-330.	1.5	13
435	Complete genome sequence of the hyperthermophilic chemolithoautotroph Pyrolobus fumarii type strain (1AT). Standards in Genomic Sciences, 2011, 4, 381-392.	1.5	13
436	Genome sequence of the soil bacterium Saccharomonospora azurea type strain (NA-128T). Standards in Genomic Sciences, 2012, 6, 220-229.	1.5	13
437	Genome sequence of Ensifer meliloti strain WSM1022; a highly effective microsymbiont of the model legume Medicago truncatula A17. Standards in Genomic Sciences, 2013, 9, 315-324.	1.5	13
438	Finished Genome of Zymomonas mobilis subsp. <i>mobilis</i> Strain CP4, an Applied Ethanol Producer. Genome Announcements, 2014, 2, .	0.8	13
439	Partial genome sequence of the haloalkaliphilic soda lake bacterium Thioalkalivibrio thiocyanoxidans ARh 2T. Standards in Genomic Sciences, 2015, 10, 85.	1.5	13
440	Draft Genome Sequence of <i>Frankia</i> Strain G2, a Nitrogen-Fixing Actinobacterium Isolated from <i>Casuarina equisetifolia</i> and Able To Nodulate Actinorhizal Plants of the Order <i>Rhamales</i> . Genome Announcements, 2016, 4, .	0.8	13
441	<i>Paenibacillus aquistagni</i> sp. nov., isolated from an artificial lake accumulating industrial wastewater. Antonie Van Leeuwenhoek, 2017, 110, 1189-1197.	0.7	13
442	Draft genome sequence of the cellulolytic endophyte Chitinophaga costaii A37T2T. Standards in Genomic Sciences, 2017, 12, 53.	1.5	13
443	Draft Genome Sequence of Methylocapsa palarum NE2 T , an Obligate Methanotroph from Subarctic Soil. Genome Announcements, 2017, 5, .	0.8	13
444	Laying the Foundation for a Genomic Rosetta Stone: Creating Information Hubs through the Use of Consensus Identifiers. OMICS A Journal of Integrative Biology, 2008, 12, 123-127.	1.0	12
445	Complete genome sequence of Beutenbergia cavernae type strain (HK1 0122T). Standards in Genomic Sciences, 2009, 1, 21-28.	1.5	12
446	Complete genome sequence of Thermosediminibacter oceani type strain (JW/IW-1228PT). Standards in Genomic Sciences, 2010, 3, 108-116.	1.5	12
447	Complete genome sequence of Hydrogenobacter thermophilus type strain (TK-6T). Standards in Genomic Sciences, 2011, 4, 131-143.	1.5	12
448	Complete genome sequence of Hirschia baltica type strain (IFAM 1418T). Standards in Genomic Sciences, 2011, 5, 287-297.	1.5	12
449	Genome sequence of the moderately thermophilic halophile Flexistipes sinusarabici strain (MAS10T). Standards in Genomic Sciences, 2011, 5, 86-96.	1.5	12
450	Complete genome sequence of the bile-resistant pigment-producing anaerobe Alistipes finegoldii type strain (AHN2437T). Standards in Genomic Sciences, 2013, 8, 26-36.	1.5	12

#	ARTICLE	IF	CITATIONS
451	Genome sequence of <i>Phaeobacter caeruleus</i> type strain (DSM 24564T), a surface-associated member of the marine <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , 2013, 8, 403-419.	1.5	12
452	Complete genome sequence of <i>Mesorhizobium opportunistum</i> type strain WSM2075T. <i>Standards in Genomic Sciences</i> , 2013, 9, 294-303.	1.5	12
453	Genome sequence of <i>Ensifer</i> sp. TW10; a <i>Tephrosia wallichii</i> (Biyani) microsymbiont native to the Indian Thar Desert. <i>Standards in Genomic Sciences</i> , 2013, 9, 304-314.	1.5	12
454	Genome sequence of <i>Phaeobacter daeponensis</i> type strain (DSM 23529T), a facultatively anaerobic bacterium isolated from marine sediment, and emendation of <i>Phaeobacter daeponensis</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 142-159.	1.5	12
455	Genome sequence of the <i>Lotus corniculatus</i> microsymbiont <i>Mesorhizobium loti</i> strain R88B. <i>Standards in Genomic Sciences</i> , 2014, 9, 3.	1.5	12
456	Recombination should not be an afterthought. <i>Nature Reviews Microbiology</i> , 2020, 18, 606-606.	13.6	12
457	Genome sequence of <i>Phaeobacter caeruleus</i> type strain (DSM 24564(T)), a surface-associated member of the marine <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , 2013, 8, 403-19.	1.5	12
458	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
459	Complete genome sequence of <i>Thermobaculum terrenum</i> ™ type strain (YNP1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 153-162.	1.5	11
460	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FIGlyRT). <i>Standards in Genomic Sciences</i> , 2011, 4, 371-380.	1.5	11
461	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
462	Complete genome sequence of <i>Bacteroides salanitronis</i> type strain (BL78T). <i>Standards in Genomic Sciences</i> , 2011, 4, 191-199.	1.5	11
463	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
464	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
465	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
466	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
467	Complete genome sequence of <i>Mesorhizobium australicum</i> type strain (WSM2073T). <i>Standards in Genomic Sciences</i> , 2013, 9, 410-419.	1.5	11
468	Genome sequence of the exopolysaccharide-producing <i>Salipiger mucosus</i> type strain (DSM 16094T), a moderately halophilic member of the <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , 2014, 9, 1333-1345.	1.5	11

#	ARTICLE	IF	CITATIONS
469	Genome sequence of <i>Shimia</i> str. SK013, a representative of the <i>Roseobacter</i> group isolated from marine sediment. <i>Standards in Genomic Sciences</i> , 2016, 11, 25.	1.5	11
470	High-quality permanent draft genome sequence of the <i>Bradyrhizobium elkanii</i> type strain USDA 76T, isolated from <i>Glycine max</i> (L.) Merr. <i>Standards in Genomic Sciences</i> , 2017, 12, 26.	1.5	11
471	Complete genome sequence of <i>Ilyobacter polytropus</i> type strain (CuHbu1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 304-314.	1.5	10
472	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
473	Complete genome sequence of <i>Thermaerobacter marianensis</i> type strain (7p75aT). <i>Standards in Genomic Sciences</i> , 2010, 3, 337-345.	1.5	10
474	Complete genome sequence of <i>Xylanimonas cellulositytica</i> type strain (XIL07T). <i>Standards in Genomic Sciences</i> , 2010, 2, 1-8.	1.5	10
475	Complete genome sequence of <i>Segniliparus rotundus</i> type strain (CDC 1076T). <i>Standards in Genomic Sciences</i> , 2010, 2, 203-211.	1.5	10
476	Complete genome sequence of <i>Desulfurococcus mucosus</i> type strain (O7/1T). <i>Standards in Genomic Sciences</i> , 2011, 4, 173-182.	1.5	10
477	Complete genome sequence of <i>Calditerrivibrio nitroreducens</i> type strain (Yu37-1T). <i>Standards in Genomic Sciences</i> , 2011, 4, 54-62.	1.5	10
478	Complete genome sequence of <i>Tsukamurella paurometabola</i> type strain (no. 33T). <i>Standards in Genomic Sciences</i> , 2011, 4, 342-351.	1.5	10
479	Complete genome sequence of the facultatively anaerobic, appendaged bacterium <i>Muricauda ruestringensis</i> type strain (B1T). <i>Standards in Genomic Sciences</i> , 2012, 6, 185-193.	1.5	10
480	Complete genome sequence of <i>Marinomonas posidonica</i> type strain (IVIA-Po-181T). <i>Standards in Genomic Sciences</i> , 2012, 7, 31-43.	1.5	10
481	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain TA1. <i>Standards in Genomic Sciences</i> , 2013, 9, 243-253.	1.5	10
482	Crowdsourcing and curation: perspectives from biology and natural language processing. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw115.	1.4	10
483	Complete Genome Sequence of <i>Alkaliphilus metalliredigens</i> Strain QYMF, an Alkaliphilic and Metal-Reducing Bacterium Isolated from Borax-Contaminated Leachate Ponds. <i>Genome Announcements</i> , 2016, 4, .	0.8	10
484	High-quality genome sequence of the radioresistant bacterium <i>Deinococcus ficus</i> KS 0460. <i>Standards in Genomic Sciences</i> , 2017, 12, 46.	1.5	10
485	Microbiomes of Velloziaceae from phosphorus-impooverished soils of the campos rupestres, a biodiversity hotspot. <i>Scientific Data</i> , 2019, 6, 140.	2.4	10
486	<i>Hymenobacter caeli</i> sp. nov., an airborne bacterium isolated from King George Island, Antarctica. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10

#	ARTICLE	IF	CITATIONS
487	High-quality draft genome sequences of <i>Pseudomonas monteilii</i> DSM 14164T, <i>Pseudomonas mosselii</i> DSM 17497T, <i>Pseudomonas plecoglossicida</i> DSM 15088T, <i>Pseudomonas taiwanensis</i> DSM 21245T and <i>Pseudomonas vranovensis</i> DSM 16006T: taxonomic considerations. <i>Access Microbiology</i> , 2019, 1, e000067.	0.2	10
488	Draft genome and description of <i>Consotaella salsifontis</i> gen. nov. sp. nov., a halophilic, free-living, nitrogen-fixing alphaproteobacterium isolated from an ancient terrestrial saline spring. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3744-3751.	0.8	10
489	Permanent draft genome sequence of <i>Dethiosulfovibrio peptidovorans</i> type strain (SEBR 4207T). <i>Standards in Genomic Sciences</i> , 2010, 3, 85-92.	1.5	9
490	Non-contiguous finished genome sequence of <i>Aminomonas paucivorans</i> type strain (GLU-3T). <i>Standards in Genomic Sciences</i> , 2010, 3, 285-293.	1.5	9
491	Non-contiguous finished genome sequence of <i>Bacteroides coprosuis</i> type strain (PC139T). <i>Standards in Genomic Sciences</i> , 2011, 4, 233-243.	1.5	9
492	Complete genome sequence of <i>Halopiger xanaduensis</i> type strain (SH-6T). <i>Standards in Genomic Sciences</i> , 2012, 6, 31-42.	1.5	9
493	Genome sequence of the phage-gene rich marine <i>Phaeobacter arcticus</i> type strain DSM 23566T. <i>Standards in Genomic Sciences</i> , 2013, 8, 450-464.	1.5	9
494	Genome sequence of the <i>Lebeckia ambigua</i> -nodulating <i>Burkholderia sprentiae</i> strain WSM5005T. <i>Standards in Genomic Sciences</i> , 2013, 9, 385-394.	1.5	9
495	High quality draft genome sequence of the slightly halophilic bacterium <i>Halomonas zhanjiangensis</i> type strain JSM 078169T (DSM 21076T) from a sea urchin in southern China. <i>Standards in Genomic Sciences</i> , 2014, 9, 1020-1030.	1.5	9
496	High-quality permanent draft genome sequence of <i>Rhizobium sullae</i> strain WSM1592; a <i>Hedysarum coronarium</i> microsymbiont from Sassari, Italy. <i>Standards in Genomic Sciences</i> , 2015, 10, 44.	1.5	9
497	Genome Sequence of <i>Porticoccus hydrocarbonoclasticus</i> Strain MCTG13d, an Obligate Polycyclic Aromatic Hydrocarbon-Degrading Bacterium Associated with Marine Eukaryotic Phytoplankton. <i>Genome Announcements</i> , 2015, 3, .	0.8	9
498	Complete Genome Sequence of <i>Methanosphaerula palustris</i> E1-9C ^T , a Hydrogenotrophic Methanogen Isolated from a Minerotrophic Fen Peatland. <i>Genome Announcements</i> , 2015, 3, .	0.8	9
499	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. <i>Standards in Genomic Sciences</i> , 2017, 12, 21.	1.5	9
500	Genome analysis of the marine bacterium <i>Kiloniella laminariae</i> and first insights into comparative genomics with related <i>Kiloniella</i> species. <i>Archives of Microbiology</i> , 2020, 202, 815-824.	1.0	9
501	ThiD-TenA: A Gene Pair Fusion in Eukaryotes. <i>Journal of Molecular Evolution</i> , 1997, 45, 708-711.	0.8	8
502	A ferredoxin-like domain in RNA polymerase 30/40-kDa subunits. <i>Trends in Biochemical Sciences</i> , 1998, 23, 169-170.	3.7	8
503	Complete genome sequence of <i>Staphylothermus marinus</i> Stetter and Fiala 1986 type strain F1. <i>Standards in Genomic Sciences</i> , 2009, 1, 183-188.	1.5	8
504	Complete genome sequence of <i>Arcanobacterium haemolyticum</i> type strain (11018T). <i>Standards in Genomic Sciences</i> , 2010, 3, 126-135.	1.5	8

#	ARTICLE	IF	CITATIONS
505	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 10. Standards in Genomic Sciences, 2010, 3, 225-231.	1.5	8
506	A data analysis and coordination center for the human microbiome project. Genome Biology, 2010, 11, O13.	13.9	8
507	Complete genome sequence of the thermophilic sulfur-reducer <i>Hippea maritima</i> type strain (MH2T). Standards in Genomic Sciences, 2011, 4, 303-311.	1.5	8
508	The Metadata Coverage Index (MCI): A standardized metric for quantifying database metadata richness. Standards in Genomic Sciences, 2012, 6, 444-453.	1.5	8
509	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
510	Complete genome sequence of <i>Coriobacterium glomerans</i> type strain (PW2T) from the midgut of <i>Pyrhocoris apterus</i> L. (red soldier bug). Standards in Genomic Sciences, 2013, 8, 15-25.	1.5	8
511	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
512	Genome sequence of the <i>Litoreaibacter arenae</i> type strain (DSM 19593T), a member of the Roseobacter clade isolated from sea sand. Standards in Genomic Sciences, 2013, 9, 117-127.	1.5	8
513	Genome sequence and emended description of <i>Leisingera nanhaiensis</i> strain DSM 24252T isolated from marine sediment. Standards in Genomic Sciences, 2014, 9, 585-601.	1.5	8
514	High quality draft genome sequence of <i>Leucobacter chironomi</i> strain MM2LBT (DSM 19883T) isolated from a <i>Chironomus</i> sp. egg mass. Standards in Genomic Sciences, 2015, 10, 21.	1.5	8
515	Genome Sequence of <i>Arenibacter algicola</i> Strain TG409, a Hydrocarbon-Degrading Bacterium Associated with Marine Eukaryotic Phytoplankton. Genome Announcements, 2016, 4, .	0.8	8
516	Draft Genome Sequence of Heavy Metal-Resistant <i>Cupriavidus alkaliphilus</i> ASC-732 T , Isolated from Agave Rhizosphere in the Northeast of Mexico. Genome Announcements, 2016, 4, .	0.8	8
517	Improved Draft Genome Sequence of <i>Microbacterium</i> sp. Strain LKL04, a Bacterial Endophyte Associated with Switchgrass Plants. Microbiology Resource Announcements, 2019, 8, .	0.3	8
518	Genomics, Exometabolomics, and Metabolic Probing Reveal Conserved Proteolytic Metabolism of <i>Thermoflexus hugenholtzii</i> and Three Candidate Species From China and Japan. Frontiers in Microbiology, 2021, 12, 632731.	1.5	8
519	The Role of IL-4 in Human Myeloid Leukemia: Stimulation of RNA Synthesis and Transduction of Differentiation Signals through an IL-4 Receptor Leads to Functional and HLA Positive HL-60 Cells. Leukemia and Lymphoma, 1992, 7, 235-242.	0.6	7
520	Standards in Genomic Sciences. Standards in Genomic Sciences, 2009, 1, 1-2.	1.5	7
521	Complete genome sequence of <i>Intrasporangium calvum</i> type strain (7 KIPT). Standards in Genomic Sciences, 2010, 3, 294-303.	1.5	7
522	Meeting report: GSC M5 roundtable at the 13th International Society for Microbial Ecology meeting in Seattle, WA, USA August 22-27, 2010. Standards in Genomic Sciences, 2010, 3, 235-239.	1.5	7

#	ARTICLE	IF	CITATIONS
523	Complete genome sequence of <i>Mahella australiensis</i> type strain (50-1 BONT). Standards in Genomic Sciences, 2011, 4, 331-341.	1.5	7
524	Complete genome sequence of <i>Staphylothermus hellenicus</i> P8T. Standards in Genomic Sciences, 2011, 5, 12-20.	1.5	7
525	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
526	Genome sequence of the <i>Listia angolensis</i> microsymbiont <i>Microvirga lotononidis</i> strain WSM3557T. Standards in Genomic Sciences, 2013, 9, 540-550.	1.5	7
527	Permanent draft genome sequences of the symbiotic nitrogen fixing <i>Ensifer meliloti</i> strains BO21CC and AK58. Standards in Genomic Sciences, 2013, 9, 352-333.	1.5	7
528	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
529	High-quality permanent draft genome sequence of <i>Ensifer</i> sp. PC2, isolated from a nitrogen-fixing root nodule of the legume tree (Khejri) native to the Thar Desert of India. Standards in Genomic Sciences, 2016, 11, 43.	1.5	7
530	High-quality draft genome sequence of the <i>Thermus amyloliquefaciens</i> type strain YIM 77409T with an incomplete denitrification pathway. Standards in Genomic Sciences, 2016, 11, 20.	1.5	7
531	Draft genome sequence of <i>Pseudomonas extremaustralis</i> strain USBA-GBX 515 isolated from Superparamo soil samples in Colombian Andes. Standards in Genomic Sciences, 2017, 12, 78.	1.5	7
532	Draft genome of <i>Paraburkholderia caballeronis</i> TNe-841T, a free-living, nitrogen-fixing, tomato plant-associated bacterium. Standards in Genomic Sciences, 2017, 12, 80.	1.5	7
533	<i>Frigoriflavimonas asaccharolytica</i> gen. nov., sp. nov., a novel psychrophilic esterase and protease producing bacterium isolated from Antarctica. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1991-2002.	0.7	7
534	Draft genome of <i>Rosenbergiella nectarea</i> strain 8N4 ^T provides insights into the potential role of this species in its plant host. <i>PeerJ</i> , 2020, 8, e8822.	0.9	7
535	Reverse Interpretation: A Hypothetical Selection Mechanism for Adaptive Mutagenesis Based on Autoregulated mRNA Stability. <i>Journal of Theoretical Biology</i> , 1994, 167, 373-380.	0.8	6
536	Integration of phenotypic metadata and protein similarity in Archaea using a spectral bipartitioning approach. <i>Nucleic Acids Research</i> , 2009, 37, 2096-2104.	6.5	6
537	Complete genome sequence of <i>Tolomonas auensis</i> type strain (TA 4T). Standards in Genomic Sciences, 2011, 5, 112-120.	1.5	6
538	Genome sequence of <i>Burkholderia mimosarum</i> strain LMG 23256T, a <i>Mimosa pigra</i> microsymbiont from Anso, Taiwan. Standards in Genomic Sciences, 2013, 9, 484-494.	1.5	6
539	Genome sequence of <i>Ensifer arboris</i> strain LMG 14919T; a microsymbiont of the legume <i>Prosopis chilensis</i> growing in Kosti, Sudan. Standards in Genomic Sciences, 2013, 9, 473-483.	1.5	6
540	Complete Genome Sequence of <i>Methanoregula formicica</i> SMSP ^T , a Mesophilic Hydrogenotrophic Methanogen Isolated from a Methanogenic Upflow Anaerobic Sludge Blanket Reactor. <i>Genome Announcements</i> , 2014, 2, .	0.8	6

#	ARTICLE	IF	CITATIONS
541	Genome sequence of <i>Microvirga lupini</i> strain LUT6T, a novel <i>Lupinus</i> alphaproteobacterial microsymbiont from Texas. <i>Standards in Genomic Sciences</i> , 2014, 9, 1159-1167.	1.5	6
542	High-quality permanent draft genome sequence of the <i>Parapiptadenia rigida</i> -nodulating <i>Cupriavidus</i> sp. strain UYPR2.512. <i>Standards in Genomic Sciences</i> , 2015, 10, 13.	1.5	6
543	High quality draft genome sequence and analysis of <i>Pontibacter roseus</i> type strain SRC-1T (DSM 17521T) isolated from muddy waters of a drainage system in Chandigarh, India. <i>Standards in Genomic Sciences</i> , 2015, 10, 8.	1.5	6
544	Genome Sequence of <i>Halomonas</i> sp. Strain MCTG39a, a Hydrocarbon-Degrading and Exopolymeric Substance-Producing Bacterium. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
545	Complete genome sequence of the haloalkaliphilic, obligately chemolithoautotrophic thiosulfate and sulfide-oxidizing β -proteobacterium <i>Thioalkalimicrobium cyclicum</i> type strain ALM 1 (DSM 14477T). <i>Standards in Genomic Sciences</i> , 2016, 11, 38.	1.5	6
546	High-quality-draft genome sequence of the fermenting bacterium <i>Anaerobium acetethylicum</i> type strain GluBS11T (DSM 29698). <i>Standards in Genomic Sciences</i> , 2017, 12, 24.	1.5	6
547	Genome Sequence of <i>Verrucomicrobium</i> sp. Strain GAS474, a Novel Bacterium Isolated from Soil. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
548	Metagenomes and metatranscriptomes from boreal potential and actual acid sulfate soil materials. <i>Scientific Data</i> , 2019, 6, 207.	2.4	6
549	Complete Genome Sequence for <i>Asinibacterium</i> sp. Strain OR53 and Draft Genome Sequence for <i>Asinibacterium</i> sp. Strain OR43, Two Bacteria Tolerant to Uranium. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	6
550	Identification of Protein-Tyrosine Phosphatases in Archaea. <i>Journal of Molecular Evolution</i> , 1999, 48, 625-627.	0.8	5
551	The Positive Role of the Ecological Community in the Genomic Revolution. <i>Microbial Ecology</i> , 2007, 53, 507-511.	1.4	5
552	Genome sequence of the ocean sediment bacterium <i>Saccharomonospora marina</i> type strain (XMU15T). <i>Standards in Genomic Sciences</i> , 2012, 6, 265-275.	1.5	5
553	Draft Genome Sequence of an Oscillatorian Cyanobacterium, Strain ESFC-1. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
554	Genome sequence of the phylogenetically isolated spirochete <i>Leptonema illini</i> type strain (3055T). <i>Standards in Genomic Sciences</i> , 2013, 8, 177-187.	1.5	5
555	Genome sequence of the <i>Lotus</i> spp. microsymbiont <i>Mesorhizobium loti</i> strain NZP2037. <i>Standards in Genomic Sciences</i> , 2014, 9, 7.	1.5	5
556	High-quality permanent draft genome sequence of the <i>Lebeckia ambigua</i> -nodulating <i>Burkholderia</i> sp. strain WSM4176. <i>Standards in Genomic Sciences</i> , 2015, 10, 79.	1.5	5
557	High-quality permanent draft genome sequence of the extremely osmotolerant diphenol degrading bacterium <i>Halotalea alkalilenta</i> AW-7T, and emended description of the genus <i>Halotalea</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 52.	1.5	5
558	Complete genome sequence of <i>Thioalkalivibrio paradoxus</i> type strain ARh 1T, an obligately chemolithoautotrophic haloalkaliphilic sulfur-oxidizing bacterium isolated from a Kenyan soda lake. <i>Standards in Genomic Sciences</i> , 2015, 10, 105.	1.5	5

#	ARTICLE	IF	CITATIONS
559	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. Tv2a.2, a microsymbiont of <i>Tachigali versicolor</i> discovered in Barro Colorado Island of Panama. <i>Standards in Genomic Sciences</i> , 2015, 10, 27.	1.5	5
560	Permanent Improved High-Quality Draft Genome Sequence of <i>Nocardia casuarinae</i> Strain BMG51109, an Endophyte of Actinorhizal Root Nodules of <i>Casuarina glauca</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	5
561	High-Quality Draft Genomes from <i>Thermus caliditerrae</i> YIM 77777 and <i>T. Âtengchongensis</i> YIM 77401, Isolates from Tengchong, China. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
562	High-quality draft genome sequence of <i>Sedimenticola selenatireducens</i> strain AK4OH1T, a gammaproteobacterium isolated from estuarine sediment. <i>Standards in Genomic Sciences</i> , 2016, 11, 66.	1.5	5
563	Draft genome sequence of <i>Actinotignum schaalii</i> DSM 15541T: Genetic insights into the lifestyle, cell fitness and virulence. <i>PLoS ONE</i> , 2017, 12, e0188914.	1.1	5
564	Improved Draft Genome Sequence of <i>Pseudomonas poae</i> A2-S9, a Strain with Plant Growth-Promoting Activity. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
565	Consent insufficient for data release”Response. <i>Science</i> , 2019, 364, 446-446.	6.0	5
566	One Complete and Seven Draft Genome Sequences of Subdivision 1 and 3 <i>Acidobacteria</i> Isolated from Soil. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	5
567	The <i>Roseibium album</i> (<i>Labrenzia alba</i>) Genome Possesses Multiple Symbiosis Factors Possibly Underpinning Host-Microbe Relationships in the Marine Benthos. <i>Microbiology Resource Announcements</i> , 2021, 10, e0032021.	0.3	5
568	A Transient GCN4 mRNA Destabilization Follows GCN4 Translational Derepression. <i>Journal of Biological Chemistry</i> , 1995, 270, 17317-17320.	1.6	4
569	Meeting Report: Towards a Critical Assessment of Functional Annotation Experiment (CAFAE) for bacterial genome annotation. <i>Standards in Genomic Sciences</i> , 2010, 3, 240-242.	1.5	4
570	Complete genome sequence of <i>Oceanithermus profundus</i> type strain (506T). <i>Standards in Genomic Sciences</i> , 2011, 4, 210-220.	1.5	4
571	Data shopping in an open marketplace: Introducing the Ontogrator web application for marking up data using ontologies and browsing using facets. <i>Standards in Genomic Sciences</i> , 2011, 4, 286-292.	1.5	4
572	Draft Genome Sequence of <i>Pseudomonas azotifigens</i> Strain DSM 17556 T (6H33b T), a Nitrogen Fixer Strain Isolated from a Compost Pile. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
573	Complete Genome Sequence of the Hyperthermophilic Sulfate-Reducing Bacterium <i>Thermodesulfobacterium geofontis</i> OPF15 ^T . <i>Genome Announcements</i> , 2013, 1, e0016213.	0.8	4
574	Genome sequence of the chemoheterotrophic soil bacterium <i>Saccharomonospora cyanea</i> type strain (NA-134T). <i>Standards in Genomic Sciences</i> , 2013, 9, 28-41.	1.5	4
575	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain SRDI565.. <i>Standards in Genomic Sciences</i> , 2013, 9, 220-231.	1.5	4
576	Genome sequence of the South American clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM597. <i>Standards in Genomic Sciences</i> , 2013, 9, 264-272.	1.5	4

#	ARTICLE	IF	CITATIONS
577	Complete Genome of <i>Enterobacteriaceae</i> Bacterium Strain FGI 57, a Strain Associated with Leaf-Cutter Ant Fungus Gardens. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
578	High quality draft genome sequence of <i>Bacteroides barnesiae</i> type strain BL2T (DSM 18169T) from chicken caecum. <i>Standards in Genomic Sciences</i> , 2015, 10, 48.	1.5	4
579	Draft Genome Sequence of the Cellulolytic and Xylanolytic Thermophile <i>Clostridium clariflavum</i> Strain 4-2a. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
580	Genome Sequence of the Alkaline-Tolerant <i>Cellulomonas</i> sp. Strain FA1. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
581	High-Quality Draft Genome Sequence of <i>Kallotenue papyrolyticum</i> JKG1 T Reveals Broad Heterotrophic Capacity Focused on Carbohydrate and Amino Acid Metabolism. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
582	Genome Sequence of <i>Polycyclovorans algicola</i> Strain TG408, an Obligate Polycyclic Aromatic Hydrocarbon-Degrading Bacterium Associated with Marine Eukaryotic Phytoplankton. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
583	High-quality permanent draft genome sequence of <i>Ensifer meliloti</i> strain 4H41, an effective salt- and drought-tolerant microsymbiont of <i>Phaseolus vulgaris</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 34.	1.5	4
584	Microbial Benthic Communities in the Aegean Sea. <i>Handbook of Environmental Chemistry</i> , 2020, , 1.	0.2	4
585	The "Minimum Information about an ENvironmental Sequence" (MIENS) specification. <i>Nature Precedings</i> , 0, , .	0.1	4
586	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FIGlyR). <i>Standards in Genomic Sciences</i> , 2011, 4, 371-80.	1.5	4
587	Medicago root nodule microbiomes: insights into a complex ecosystem with potential candidates for plant growth promotion. <i>Plant and Soil</i> , 0, , 1.	1.8	4
588	Investigation of intracellular signals generated by γ -interferon and IL-4 leading to the induction of class II antigen expression. <i>Mediators of Inflammation</i> , 1993, 2, 343-348.	1.4	3
589	The core histone fold: Limits to functional versatility. <i>Journal of Molecular Evolution</i> , 1996, 43, 541-542.	0.8	3
590	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 9. <i>Standards in Genomic Sciences</i> , 2010, 3, 216-224.	1.5	3
591	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
592	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain SRDI943.. <i>Standards in Genomic Sciences</i> , 2013, 9, 232-242.	1.5	3
593	Genome sequence of the <i>Trifolium rueppellianum</i> -nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM2012.. <i>Standards in Genomic Sciences</i> , 2013, 9, 283-293.	1.5	3
594	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

#	ARTICLE	IF	CITATIONS
595	Genome sequence of the lupin-nodulating <i>Bradyrhizobium</i> sp. strain WSM1417. <i>Standards in Genomic Sciences</i> , 2013, 9, 273-282.	1.5	3
596	Genome sequence of the acid-tolerant <i>Burkholderia</i> sp. strain WSM2230 from Karijini National Park, Australia. <i>Standards in Genomic Sciences</i> , 2013, 9, 551-561.	1.5	3
597	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
598	Genome sequence of the dark pink pigmented <i>Listia bainesii</i> microsymbiont <i>Methylobacterium</i> sp. WSM2598. <i>Standards in Genomic Sciences</i> , 2014, 9, 5.	1.5	3
599	Genome sequence of the <i>Medicago</i> -nodulating <i>Ensifer meliloti</i> commercial inoculant strain RRI128. <i>Standards in Genomic Sciences</i> , 2014, 9, 602-613.	1.5	3
600	Genome sequence of the <i>Wenxinia marina</i> type strain (DSM 24838T), a representative of the <i>Roseobacter</i> group isolated from oilfield sediments. <i>Standards in Genomic Sciences</i> , 2014, 9, 855-865.	1.5	3
601	High-quality draft genome sequence of <i>Gracilimonas tropica</i> CL-CB462T (DSM 19535T), isolated from a <i>Synechococcus</i> culture. <i>Standards in Genomic Sciences</i> , 2015, 10, 98.	1.5	3
602	High-quality permanent draft genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> strain GB30; an effective microsymbiont of <i>Pisum sativum</i> growing in Poland. <i>Standards in Genomic Sciences</i> , 2015, 10, 36.	1.5	3
603	High-Quality Draft Genome Sequence of <i>Desulfovibrio carbinolophilus</i> FW-101-2B, an Organic Acid-Oxidizing Sulfate-Reducing Bacterium Isolated from Uranium(VI)-Contaminated Groundwater. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
604	Genome sequence of <i>Bradyrhizobium</i> sp. WSM1253; a microsymbiont of <i>Ornithopus compressus</i> from the Greek Island of Sifnos. <i>Standards in Genomic Sciences</i> , 2015, 10, 113.	1.5	3
605	Permanent Draft Genome Sequence of <i>Nocardia</i> sp. BMG111209, an Actinobacterium Isolated from Nodules of <i>Casuarina glauca</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	3
606	High-quality draft genome sequence of <i>Flavobacterium suncheonense</i> GH29-5T (DSM 17707T) isolated from greenhouse soil in South Korea, and emended description of <i>Flavobacterium suncheonense</i> GH29-5T. <i>Standards in Genomic Sciences</i> , 2016, 11, 42.	1.5	3
607	Complete Genome Sequence of <i>Nitrosomonas cryotolerans</i> ATCC 49181, a Phylogenetically Distinct Ammonia-Oxidizing Bacterium Isolated from Arctic Waters. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
608	Genome Sequence of <i>Oceanicola</i> sp. Strain MCTG156(1a), Isolated from a Scottish Coastal Phytoplankton Net Sample. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
609	Genome Sequences of Actinobacteria from Extreme Environments in Colombia. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	3
610	Draft Genome Sequences of New Isolates and the Known Species of the Family Microbacteriaceae Associated with Plants. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	3
611	High-Quality Draft Genome Sequences of Eight Bacteria Isolated from Fungus Gardens Grown by <i>Trachymyrmex septentrionalis</i> Ants. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	3
612	Draft Genome of <i>Burkholderia cenocepacia</i> TAtI-371, a Strain from the <i>Burkholderia cepacia</i> Complex Retains Antagonism in Different Carbon and Nitrogen Sources. <i>Current Microbiology</i> , 2019, 76, 566-574.	1.0	3

#	ARTICLE	IF	CITATIONS
613	Establishment of computational biology in Greece and Cyprus: Past, present, and future. <i>PLoS Computational Biology</i> , 2019, 15, e1007532.	1.5	3
614	The Santorini Volcanic Complex as a Valuable Source of Enzymes for Bioenergy. <i>Energies</i> , 2021, 14, 1414.	1.6	3
615	Different Molecular Mechanisms Lead to Same Endpoints with Different Function: TNF- α Induces Non Functional CSF-1 Receptors on HL-60 Cells in Contrast to Interferon- β . <i>Journal of Receptors and Signal Transduction</i> , 1992, 12, 59-70.	1.2	2
616	Meeting Report: "Metagenomics, Metadata and Meta-analysis" (M3) Workshop at the Pacific Symposium on Biocomputing 2010. <i>Standards in Genomic Sciences</i> , 2010, 2, 357-360.	1.5	2
617	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
618	Genome sequence of <i>Ensifer medicae</i> strain WSM1115; an acid-tolerant <i>Medicago</i> -nodulating microsymbiont from Samothraki, Greece. <i>Standards in Genomic Sciences</i> , 2013, 9, 514-526.	1.5	2
619	Genome sequence of the acid-tolerant <i>Burkholderia</i> sp. strain WSM2232 from Karijini National Park, Australia. <i>Standards in Genomic Sciences</i> , 2013, 9, 1168-1180.	1.5	2
620	Complete Genome Sequence of <i>Methanolinea tarda</i> NOBI-1, a Hydrogenotrophic Methanogen Isolated from Methanogenic Digester Sludge. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
621	High quality draft genome sequence of <i>Brachymonas chironomi</i> AIMA4T (DSM 19884T) isolated from a <i>Chironomus</i> sp. egg mass. <i>Standards in Genomic Sciences</i> , 2015, 10, 29.	1.5	2
622	High-quality permanent draft genome sequence of the <i>Parapiptadenia rigida</i> -nodulating <i>Burkholderia</i> sp. strain UYPR1.413. <i>Standards in Genomic Sciences</i> , 2015, 10, 31.	1.5	2
623	Partial genome sequence of <i>Thioalkalivibrio thiocyanodenitrificans</i> ARhD 1T, a chemolithoautotrophic haloalkaliphilic sulfur-oxidizing bacterium capable of complete denitrification. <i>Standards in Genomic Sciences</i> , 2015, 10, 84.	1.5	2
624	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. Ai1a-2; a microsymbiont of <i>Andira inermis</i> discovered in Costa Rica. <i>Standards in Genomic Sciences</i> , 2015, 10, 33.	1.5	2
625	High-quality permanent draft genome sequence of the <i>Mimosa asperata</i> - nodulating <i>Cupriavidus</i> sp. strain AMP6. <i>Standards in Genomic Sciences</i> , 2015, 10, 80.	1.5	2
626	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. Th.b2, a microsymbiont of <i>Amphicarpaea bracteata</i> collected in Johnson City, New York. <i>Standards in Genomic Sciences</i> , 2015, 10, 24.	1.5	2
627	High-Quality draft genome sequence of the <i>Lotus</i> spp. microsymbiont <i>Mesorhizobium loti</i> strain CJ3Sym. <i>Standards in Genomic Sciences</i> , 2015, 10, 54.	1.5	2
628	Application of Long Sequence Reads To Improve Genomes for <i>Clostridium thermocellum</i> AD2, <i>Clostridium thermocellum</i> LQRI, and <i>Pelosinus fermentans</i> R7. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
629	An improved high-quality draft genome sequence of <i>Carnobacterium inihbens</i> subsp. <i>inhibens</i> strain KIT. <i>Standards in Genomic Sciences</i> , 2016, 11, 65.	1.5	2
630	MlxS-HCR: a MlxS extension defining a minimal information standard for sequence data from environments pertaining to hydrocarbon resources. <i>Standards in Genomic Sciences</i> , 2016, 11, 78.	1.5	2

#	ARTICLE	IF	CITATIONS
631	Permanent draft genome sequence of <i>Desulfurococcus mobilis</i> type strain DSM 2161, a thermoacidophilic sulfur-reducing crenarchaeon isolated from acidic hot springs of Hveravellir, Iceland. <i>Standards in Genomic Sciences</i> , 2016, 11, 3.	1.5	2
632	High quality permanent draft genome sequence of <i>Chryseobacterium bovis</i> DSM 19482T, isolated from raw cow milk. <i>Standards in Genomic Sciences</i> , 2017, 12, 31.	1.5	2
633	Permanent Draft Genome Sequence of <i>Desulfurococcus amylolyticus</i> Strain Z-533 ^T , a Peptide and Starch Degradar Isolated from Thermal Springs in the Kamchatka Peninsula and Kunashir Island, Russia. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
634	High-quality draft genome sequence of <i>Rhizobium mesoamericanum</i> strain STM6155, a <i>Mimosa pudica</i> microsymbiont from New Caledonia. <i>Standards in Genomic Sciences</i> , 2017, 12, 7.	1.5	2
635	Draft Genome Sequences of Three Strains of a Novel Rhizobiales Species Isolated from Forest Soil. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
636	Metagenomes and Metatranscriptomes of a Glucose-Amended Agricultural Soil. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
637	The Genome of the Acid Soil-Adapted Strain <i>Rhizobium favelukesii</i> OR191 Encodes Determinants for Effective Symbiotic Interaction With Both an Inverted Repeat Lacking Clade and a Phaseoloid Legume Host. <i>Frontiers in Microbiology</i> , 2022, 13, 735911.	1.5	2
638	SOP for pathway inference in Integrated Microbial Genomes (IMG). <i>Standards in Genomic Sciences</i> , 2010, 5, 420-423.	1.5	1
639	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 8. <i>Standards in Genomic Sciences</i> , 2010, 3, 93-96.	1.5	1
640	Meeting report of the RNA Ontology Consortium January 8-9, 2011. <i>Standards in Genomic Sciences</i> , 2011, 4, 252-256.	1.5	1
641	Conceptualizing a Genomics Software Institute (GSI). <i>Standards in Genomic Sciences</i> , 2012, 6, 136-144.	1.5	1
642	Genome sequence of <i>Ensifer medicae</i> strain WSM1369; an effective microsymbiont of the annual legume <i>Medicago sphaerocarpos</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 420-430.	1.5	1
643	High-quality permanent draft genome sequence of the <i>Lebeckia</i> - nodulating <i>Burkholderia dilworthii</i> strain WSM3556T. <i>Standards in Genomic Sciences</i> , 2015, 10, 64.	1.5	1
644	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. strain WSM1743 - an effective microsymbiont of an <i>Indigofera</i> sp. growing in Australia. <i>Standards in Genomic Sciences</i> , 2015, 10, 87.	1.5	1
645	Genome sequence of the pink-pigmented marine bacterium <i>Loktanella hongkongensis</i> type strain (UST950701-009PT), a representative of the <i>Roseobacter</i> group. <i>Standards in Genomic Sciences</i> , 2015, 10, 51.	1.5	1
646	High quality draft genome sequence of <i>Corynebacterium ulceribovis</i> type strain IMMIB-L1395T (DSM) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.5	1
647	High-quality permanent draft genome sequence of <i>Ensifer medicae</i> strain WSM244, a microsymbiont isolated from <i>Medicago polymorpha</i> growing in alkaline soil. <i>Standards in Genomic Sciences</i> , 2015, 10, 126.	1.5	1
648	Genome Sequence of <i>Marinobacter</i> sp. Strain MCTG268 Isolated from the Cosmopolitan Marine Diatom <i>Skeletonema costatum</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	1

#	ARTICLE	IF	CITATIONS
649	Near-Complete Genome Sequence of <i>Thalassospira</i> sp. Strain KO164 Isolated from a Lignin-Enriched Marine Sediment Microcosm. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
650	High quality permanent draft genome sequence of <i>Phaseolibacter flectens</i> ATCC 12775T, a plant pathogen of French bean pods. <i>Standards in Genomic Sciences</i> , 2016, 11, 4.	1.5	1
651	Evolution of a multi-step phosphorelay signal transduction system in <i>Ensifer</i> : recruitment of the sigma factor RpoN and a novel enhancer-binding protein triggers acid-activated gene expression. <i>Molecular Microbiology</i> , 2017, 103, 829-844.	1.2	1
652	Genome Sequence of <i>Roseovarius</i> sp. Strain MCTG156(2b) Isolated from a Phytoplankton Net Trawl on the Scottish West Coast. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
653	Draft genome sequence of <i>Marinobacterium rhizophilum</i> CL-YJ9T (DSM 18822T), isolated from the rhizosphere of the coastal tidal-flat plant <i>Suaeda japonica</i> . <i>Standards in Genomic Sciences</i> , 2017, 12, 65.	1.5	1
654	Draft Genome Sequence of <i>Monaibacterium marinum</i> C7 ^T , Isolated from Seawater from the Menai Straits, Wales, United Kingdom. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
655	Complete Genome Sequence of <i>Thermoanaerobacterium</i> sp. Strain RBIITD, a Butyrate- and Butanol-Producing Thermophile. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
656	Improved Draft Genome Sequence of <i>Bacillus</i> sp. Strain YF23, Which Has Plant Growth-Promoting Activity. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
657	Complete Genome Sequence of <i>Serratia quinivorans</i> Strain 124R, a Facultative Anaerobe Isolated on Organosolv Lignin as a Sole Carbon Source. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
658	Metagenomes from Experimental Hydrologic Manipulation of Restored Coastal Plain Wetland Soils (Tyrell County, North Carolina). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
659	Draft Genome Sequence of <i>Yokenella regensburgei</i> Strain WCD67, Isolated from the Boxelder Bug. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
660	Metatranscriptomic Sequencing of a Cyanobacterial Soil-Surface Consortium with and without a Diverse Underlying Soil Microbiome. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
661	Complete genome sequence of <i>Mesorhizobium australicum</i> type strain (WSM2073T). <i>Standards in Genomic Sciences</i> , 2013, 9, 1-15.	1.5	1
662	Comparative Genome Analysis in the Integrated Microbial Genomes (IMG) System. , 0, , 35-56.		1
663	Identifying candidate structured RNAs in CRISPR operons. <i>RNA Biology</i> , 2022, 19, 678-685.	1.5	1
664	<i>Sodalis ligni</i> Strain 159R Isolated from an Anaerobic Lignin-Degrading Consortium. <i>Microbiology Spectrum</i> , 2022, 10, e0234621.	1.2	1
665	Alive and well at 100. <i>Standards in Genomic Sciences</i> , 2011, 4, 1-1.	1.5	0
666	Genome sequence of the <i>Ornithopus/Lupinus</i> -nodulating <i>Bradyrhizobium</i> sp. strain WSM471. <i>Standards in Genomic Sciences</i> , 2013, 9, 254-263.	1.5	0

#	ARTICLE	IF	CITATIONS
667	Genome sequence of <i>Ensifer medicae</i> Di28; an effective N ₂ -fixing microsymbiont of <i>Medicago murex</i> and <i>M. polymorpha</i> . <i>Standards in Genomic Sciences</i> , 2014, 9, 4.	1.5	0
668	High-Quality Draft Genome Sequence of <i>Thermocrinis jamiesonii</i> GBS1 ^T Isolated from Great Boiling Spring, Nevada. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
669	High-quality draft genome sequence of <i>Ensifer meliloti</i> Mlalz-1, a microsymbiont of <i>Medicago laciniata</i> (L.) miller collected in Lanzarote, Canary Islands, Spain. <i>Standards in Genomic Sciences</i> , 2017, 12, 58.	1.5	0
670	Draft genome sequence of <i>Dethiosulfovibrio salsuginis</i> DSM 21565T an anaerobic, slightly halophilic bacterium isolated from a Colombian saline spring. <i>Standards in Genomic Sciences</i> , 2017, 12, 86.	1.5	0
671	Draft genome sequence of <i>Chryseobacterium limigenitum</i> SUR2 T (LMG 28734 T) isolated from dehydrated sludge. <i>Brazilian Journal of Microbiology</i> , 2018, 49, 5-6.	0.8	0