

Tanja Woyke

List of Publications by Year in descending order

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Version: 2024-02-01

215
papers

34,996
citations

5574

82
h-index

5394

164
g-index

248
all docs

248
docs citations

248
times ranked

27586
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Based Taxonomic Classification of the Phylum Actinobacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 2007.	3.5	2,599
2	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	27.8	2,239
3	Analysis of 1,000+ Type-Strain Genomes Substantially Improves Taxonomic Classification of Alphaproteobacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 468.	3.5	1,537
4	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.	17.5	1,512
5	Analysis of 1,000 Type-Strain Genomes Improves Taxonomic Classification of Bacteroidetes. <i>Frontiers in Microbiology</i> , 2019, 10, 2083.	3.5	1,281
6	Assembling Single-Cell Genomes and Mini-Metagenomes From Chimeric MDA Products. <i>Journal of Computational Biology</i> , 2013, 20, 714-737.	1.6	1,235
7	Metagenomic Discovery of Biomass-Degrading Genes and Genomes from Cow Rumen. <i>Science</i> , 2011, 331, 463-467.	12.6	1,135
8	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.	14.5	799
9	Improving the coverage of the cyanobacterial phylum using diversity-driven genome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1053-1058.	7.1	769
10	Plant compartment and biogeography affect microbiome composition in cultivated and native <i>Agave</i> species. <i>New Phytologist</i> , 2016, 209, 798-811.	7.3	663
11	Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	19.0	635
12	IMG 4 version of the integrated microbial genomes comparative analysis system. <i>Nucleic Acids Research</i> , 2014, 42, D560-D567.	14.5	555
13	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2012, 6, 1715-1727.	9.8	547
14	Potential for Chemolithoautotrophy Among Ubiquitous Bacteria Lineages in the Dark Ocean. <i>Science</i> , 2011, 333, 1296-1300.	12.6	510
15	Genome-Based Taxonomic Classification of Bacteroidetes. <i>Frontiers in Microbiology</i> , 2016, 7, 2003.	3.5	493
16	Genomic features of bacterial adaptation to plants. <i>Nature Genetics</i> , 2018, 50, 138-150.	21.4	480
17	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
18	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

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19	Primer and platform effects on 16S rRNA tag sequencing. <i>Frontiers in Microbiology</i> , 2015, 6, 771.	3.5	435
20	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018, 36, 359-367.	17.5	414
21	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
22	Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). <i>Frontiers in Microbiology</i> , 2017, 8, 682.	3.5	409
23	Viral dark matter and virus-host interactions resolved from publicly available microbial genomes. <i>ELife</i> , 2015, 4, .	6.0	400
24	Symbiosis insights through metagenomic analysis of a microbial consortium. <i>Nature</i> , 2006, 443, 950-955.	27.8	396
25	Microbial dark matter ecogenomics reveals complex synergistic networks in a methanogenic bioreactor. <i>ISME Journal</i> , 2015, 9, 1710-1722.	9.8	360
26	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.	14.5	332
27	Prevalent genome streamlining and latitudinal divergence of planktonic bacteria in the surface ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11463-11468.	7.1	328
28	The Genome of <i>Akkermansia muciniphila</i> , a Dedicated Intestinal Mucin Degradator, and Its Use in Exploring Intestinal Metagenomes. <i>PLoS ONE</i> , 2011, 6, e16876.	2.5	328
29	Assembling the Marine Metagenome, One Cell at a Time. <i>PLoS ONE</i> , 2009, 4, e5299.	2.5	320
30	UGA is an additional glycine codon in uncultured SR1 bacteria from the human microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5540-5545.	7.1	290
31	Gene Expression Profile of Glioblastoma Multiforme Invasive Phenotype Points to New Therapeutic Targets. <i>Neoplasia</i> , 2005, 7, 7-16.	5.3	289
32	Targeted metagenomics and ecology of globally important uncultured eukaryotic phytoplankton. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14679-14684.	7.1	257
33	Obtaining genomes from uncultivated environmental microorganisms using FACS-based single-cell genomics. <i>Nature Protocols</i> , 2014, 9, 1038-1048.	12.0	243
34	IMG/VR v3: an integrated ecological and evolutionary framework for interrogating genomes of uncultivated viruses. <i>Nucleic Acids Research</i> , 2021, 49, D764-D775.	14.5	240
35	Giant viruses with an expanded complement of translation system components. <i>Science</i> , 2017, 356, 82-85.	12.6	234
36	High-resolution phylogenetic microbial community profiling. <i>ISME Journal</i> , 2016, 10, 2020-2032.	9.8	232

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37	Major role of nitrite-oxidizing bacteria in dark ocean carbon fixation. <i>Science</i> , 2017, 358, 1046-1051.	12.6	229
38	Differential depth distribution of microbial function and putative symbionts through sediment-hosted aquifers in the deep terrestrial subsurface. <i>Nature Microbiology</i> , 2018, 3, 328-336.	13.3	227
39	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , 2017, 35, 676-683.	17.5	222
40	One Bacterial Cell, One Complete Genome. <i>PLoS ONE</i> , 2010, 5, e10314.	2.5	215
41	Single-cell genomics-based analysis of virus-host interactions in marine surface bacterioplankton. <i>ISME Journal</i> , 2015, 9, 2386-2399.	9.8	207
42	Metagenomics uncovers gaps in amplicon-based detection of microbial diversity. <i>Nature Microbiology</i> , 2016, 1, 15032.	13.3	207
43	Giant virus diversity and host interactions through global metagenomics. <i>Nature</i> , 2020, 578, 432-436.	27.8	207
44	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , 2019, 4, 1895-1906.	13.3	206
45	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	5.6	190
46	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016, 7, 10476.	12.8	189
47	Comparative genomics of freshwater Fe-oxidizing bacteria: implications for physiology, ecology, and systematics. <i>Frontiers in Microbiology</i> , 2013, 4, 254.	3.5	188
48	Hydrogenotrophic methanogenesis in archaeal phylum Verstraetearchaeota reveals the shared ancestry of all methanogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5037-5044.	7.1	187
49	Ecology and evolution of viruses infecting uncultivated SUP05 bacteria as revealed by single-cell- and meta-genomics. <i>ELife</i> , 2014, 3, e03125.	6.0	186
50	Visualizing in situ translational activity for identifying and sorting slow-growing archaeal-bacterial consortia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4069-78.	7.1	180
51	Genome-based evolutionary history of <i>Pseudomonas</i> spp. <i>Environmental Microbiology</i> , 2018, 20, 2142-2159.	3.8	172
52	Phylogeny and physiology of candidate phylum Atribacteria (OP9/JS1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016, 10, 273-286.	9.8	166
53	Decontamination of MDA Reagents for Single Cell Whole Genome Amplification. <i>PLoS ONE</i> , 2011, 6, e26161.	2.5	163
54	SAR11 bacteria linked to ocean anoxia and nitrogen loss. <i>Nature</i> , 2016, 536, 179-183.	27.8	160

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55	Comparison of 26 Sphingomonad Genomes Reveals Diverse Environmental Adaptations and Biodegradative Capabilities. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3724-3733.	3.1	151
56	The Fast Changing Landscape of Sequencing Technologies and Their Impact on Microbial Genome Assemblies and Annotation. <i>PLoS ONE</i> , 2012, 7, e48837.	2.5	145
57	Rokubacteria: Genomic Giants among the Uncultured Bacterial Phyla. <i>Frontiers in Microbiology</i> , 2017, 8, 2264.	3.5	142
58	Comparative single-cell genomics reveals potential ecological niches for the freshwater actinobacteria lineage. <i>ISME Journal</i> , 2014, 8, 2503-2516.	9.8	137
59	Comparative Genomics Suggests an Independent Origin of Cytoplasmic Incompatibility in <i>Cardinium hertigii</i> . <i>PLoS Genetics</i> , 2012, 8, e1003012.	3.5	135
60	Niche differentiation is spatially and temporally regulated in the rhizosphere. <i>ISME Journal</i> , 2020, 14, 999-1014.	9.8	135
61	Impact of single-cell genomics and metagenomics on the emerging view of extremophile "microbial dark matter". <i>Extremophiles</i> , 2014, 18, 865-875.	2.3	133
62	Genomic sequencing of single microbial cells from environmental samples. <i>Current Opinion in Microbiology</i> , 2008, 11, 198-204.	5.1	130
63	Elucidating Bacterial Gene Functions in the Plant Microbiome. <i>Cell Host and Microbe</i> , 2018, 24, 475-485.	11.0	129
64	Stop codon reassignments in the wild. <i>Science</i> , 2014, 344, 909-913.	12.6	124
65	Genome Data Provides High Support for Generic Boundaries in <i>Burkholderia</i> Ssensu Lato. <i>Frontiers in Microbiology</i> , 2017, 8, 1154.	3.5	122
66	The trajectory of microbial single-cell sequencing. <i>Nature Methods</i> , 2017, 14, 1045-1054.	19.0	120
67	Single-cell enabled comparative genomics of a deep ocean SAR11 bathytype. <i>ISME Journal</i> , 2014, 8, 1440-1451.	9.8	119
68	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
69	Single-cell genomics reveals complex carbohydrate degradation patterns in poribacterial symbionts of marine sponges. <i>ISME Journal</i> , 2013, 7, 2287-2300.	9.8	113
70	Hidden diversity of soil giant viruses. <i>Nature Communications</i> , 2018, 9, 4881.	12.8	112
71	Phylogenomics suggests oxygen availability as a driving force in Thaumarchaeota evolution. <i>ISME Journal</i> , 2019, 13, 2150-2161.	9.8	108
72	Single-cell genomics reveals features of a <i>Colwellia</i> species that was dominant during the Deepwater Horizon oil spill. <i>Frontiers in Microbiology</i> , 2014, 5, 332.	3.5	106

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73	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.	7.1	105
74	Genome-Scale Data Call for a Taxonomic Rearrangement of Geodermatophilaceae. <i>Frontiers in Microbiology</i> , 2017, 8, 2501.	3.5	105
75	In Silico Analysis of the Metabolic Potential and Niche Specialization of Candidate Phylum "Latescibacteria" (WS3). <i>PLoS ONE</i> , 2015, 10, e0127499.	2.5	102
76	Towards a balanced view of the bacterial tree of life. <i>Microbiome</i> , 2017, 5, 140.	11.1	102
77	Genome-based classification of micromonosporae with a focus on their biotechnological and ecological potential. <i>Scientific Reports</i> , 2018, 8, 525.	3.3	102
78	Leveraging single-cell genomics to expand the fungal tree of life. <i>Nature Microbiology</i> , 2018, 3, 1417-1428.	13.3	101
79	Genome Sequence of <i>Candidatus Frankia datiscaae</i> Dg1, the Uncultured Microsymbiont from Nitrogen-Fixing Root Nodules of the Dicot <i>Datisca glomerata</i> . <i>Journal of Bacteriology</i> , 2011, 193, 7017-7018.	2.2	99
80	Complete Genome Sequences of Six Strains of the Genus <i>Methylobacterium</i> . <i>Journal of Bacteriology</i> , 2012, 194, 4746-4748.	2.2	99
81	Diverse Marinimicrobia bacteria may mediate coupled biogeochemical cycles along eco-thermodynamic gradients. <i>Nature Communications</i> , 2017, 8, 1507.	12.8	99
82	Genome Sequence of the Obligate Methanotroph <i>Methylosinus trichosporium</i> Strain OB3b. <i>Journal of Bacteriology</i> , 2010, 192, 6497-6498.	2.2	98
83	Gill bacteria enable a novel digestive strategy in a wood-feeding mollusk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5096-104.	7.1	98
84	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
85	Genomic differentiation among wild cyanophages despite widespread horizontal gene transfer. <i>BMC Genomics</i> , 2016, 17, 930.	2.8	96
86	Genomic and Metabolic Diversity of Marine Group I Thaumarchaeota in the Mesopelagic of Two Subtropical Gyres. <i>PLoS ONE</i> , 2014, 9, e95380.	2.5	95
87	Metabolic potential of a single cell belonging to one of the most abundant lineages in freshwater bacterioplankton. <i>ISME Journal</i> , 2013, 7, 137-147.	9.8	94
88	Metabolic versatility of small archaea Micrarchaeota and Parvarchaeota. <i>ISME Journal</i> , 2018, 12, 756-775.	9.8	91
89	Next generation sequencing data of a defined microbial mock community. <i>Scientific Data</i> , 2016, 3, 160081.	5.3	90
90	Insights into the metabolism, lifestyle and putative evolutionary history of the novel archaeal phylum <i>Diapherotrites</i> ™. <i>ISME Journal</i> , 2015, 9, 447-460.	9.8	89

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91	Complete Genome of the Cellulolytic Ruminal Bacterium <i>Ruminococcus albus</i> 7. <i>Journal of Bacteriology</i> , 2011, 193, 5574-5575.	2.2	87
92	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. <i>Nature Communications</i> , 2019, 10, 463.	12.8	87
93	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
94	Impact of library preparation protocols and template quantity on the metagenomic reconstruction of a mock microbial community. <i>BMC Genomics</i> , 2015, 16, 856.	2.8	79
95	The Candidate Phylum Poribacteria by Single-Cell Genomics: New Insights into Phylogeny, Cell-Compartmentation, Eukaryote-Like Repeat Proteins, and Other Genomic Features. <i>PLoS ONE</i> , 2014, 9, e87353.	2.5	79
96	Comparative Genomic Insights into Ecophysiology of Neutrophilic, Microaerophilic Iron Oxidizing Bacteria. <i>Frontiers in Microbiology</i> , 2015, 6, 1265.	3.5	78
97	Complete genome sequence of <i>Enterobacter lignolyticus</i> -SCF1. <i>Standards in Genomic Sciences</i> , 2011, 5, 69-85.	1.5	76
98	Complete genome sequence of <i>Planctomyces brasiliensis</i> type strain (DSM 5305T), phylogenomic analysis and reclassification of Planctomycetes 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 Planctomycetales and the family Planctomycetaceae. <i>Standards in Genomic Sciences</i> , 2014, 9, 10.	1.5	76
99	Shotgun metagenome data of a defined mock community using Oxford Nanopore, PacBio and Illumina technologies. <i>Scientific Data</i> , 2019, 6, 285.	5.3	75
100	Single-cell genomics reveal low recombination frequencies in freshwater bacteria of the SAR11 clade. <i>Genome Biology</i> , 2013, 14, R130.	9.6	74
101	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
102	Uncultivated thermophiles: current status and spotlight on <i>Aigarchaeota</i> TM . <i>Current Opinion in Microbiology</i> , 2015, 25, 136-145.	5.1	70
103	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. <i>ISME Journal</i> , 2020, 14, 659-675.	9.8	69
104	Microfluidic-based mini-metagenomics enables discovery of novel microbial lineages from complex environmental samples. <i>ELife</i> , 2017, 6, .	6.0	69
105	Complete Genome Sequence of the Cellulolytic Thermophile <i>Clostridium thermocellum</i> DSM1313. <i>Journal of Bacteriology</i> , 2011, 193, 2906-2907.	2.2	66
106	Tuning fresh: radiation through rewiring of central metabolism in streamlined bacteria. <i>ISME Journal</i> , 2016, 10, 1902-1914.	9.8	66
107	ProDeGe: a computational protocol for fully automated decontamination of genomes. <i>ISME Journal</i> , 2016, 10, 269-272.	9.8	65
108	Plant compartment and genetic variation drive microbiome composition in switchgrass roots. <i>Environmental Microbiology Reports</i> , 2019, 11, 185-195.	2.4	65

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109	Genome-informed Bradyrhizobium taxonomy: where to from here?. Systematic and Applied Microbiology, 2019, 42, 427-439.	2.8	62
110	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. Frontiers in Microbiology, 2020, 11, 1848.	3.5	62
111	Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. PLoS Biology, 2022, 20, e3001508.	5.6	62
112	Complete genome sequence of the termite hindgut bacterium Spirochaeta coccoides type strain (SPN1T), reclassification in the genus Sphaerochaeta as Sphaerochaeta coccoides comb. nov. and emendations of the family Spirochaetaceae and the genus Sphaerochaeta. Standards in Genomic Sciences, 2012, 6, 194-209.	1.5	58
113	Reconstructing each cell's genome within complex microbial communities—A dream or reality?. Frontiers in Microbiology, 2014, 5, 771.	3.5	58
114	A catalog of the diversity and ubiquity of bacterial microcompartments. Nature Communications, 2021, 12, 3809.	12.8	55
115	Genomic Changes Associated with the Evolutionary Transitions of Nostoc to a Plant Symbiont. Molecular Biology and Evolution, 2018, 35, 1160-1175.	8.9	54
116	Sulfate-Reducing Bacteria That Produce Exopolymers Thrive in the Calcifying Zone of a Hypersaline Cyanobacterial Mat. Frontiers in Microbiology, 2019, 10, 862.	3.5	54
117	Diversity, evolution, and classification of virophages uncovered through global metagenomics. Microbiome, 2019, 7, 157.	11.1	53
118	Single cell genomic and transcriptomic evidence for the use of alternative nitrogen substrates by anammox bacteria. ISME Journal, 2018, 12, 2706-2722.	9.8	45
119	Complementary Metagenomic Approaches Improve Reconstruction of Microbial Diversity in a Forest Soil. MSystems, 2020, 5, .	3.8	45
120	A centimeter-long bacterium with DNA contained in metabolically active, membrane-bound organelles. Science, 2022, 376, 1453-1458.	12.6	45
121	Genome sequence of the thermophilic fresh-water bacterium Spirochaeta caldaria type strain (H11), reclassification of Spirochaeta caldaria, Spirochaeta stenostrepta, and Spirochaeta zuelzeriae in the genus Treponema as Treponema caldaria comb. nov., Treponema stenostrepta comb. nov., and Treponema zuelzeriae comb. nov., and emendation of the genus Treponema. Standards in Genomic Sciences, 2013, 8, 88-105.	1.5	44
122	Single-cell genomics of co-sorted Nanoarchaeota suggests novel putative host associations and diversification of proteins involved in symbiosis. Microbiome, 2018, 6, 161.	11.1	44
123	Community ecology across bacteria, archaea and microbial eukaryotes in the sediment and seawater of coastal Puerto Nuevo, Baja California. PLoS ONE, 2019, 14, e0212355.	2.5	44
124	Insights into the dynamics between viruses and their hosts in a hot spring microbial mat. ISME Journal, 2020, 14, 2527-2541.	9.8	42
125	Ecological and genomic analyses of candidate phylum <sc>WPS</sc> bacteria in an unvegetated soil. Environmental Microbiology, 2020, 22, 3143-3157.	3.8	42
126	Functional Signatures of the Epiphytic Prokaryotic Microbiome of Agaves and Cacti. Frontiers in Microbiology, 2019, 10, 3044.	3.5	41

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127	A pipeline for targeted metagenomics of environmental bacteria. <i>Microbiome</i> , 2020, 8, 21.	11.1	39
128	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.	2.2	36
129	Discovery of Novel Plant Interaction Determinants from the Genomes of 163 Root Nodule Bacteria. <i>Scientific Reports</i> , 2015, 5, 16825.	3.3	33
130	Genomes of ubiquitous marine and hypersaline <i>Hydrogenovibrio</i> and <i>Thiomicrothrix</i> spp. encode a diversity of mechanisms to sustain chemolithoautotrophy in heterogeneous environments. <i>Environmental Microbiology</i> , 2018, 20, 2686-2708.	3.8	32
131	<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.	2.8	32
132	Influence of the polar light cycle on seasonal dynamics of an Antarctic lake microbial community. <i>Microbiome</i> , 2020, 8, 116.	11.1	32
133	Carboxydrotrophy potential of uncultivated Hydrothermarchaeota from the subseafloor crustal biosphere. <i>ISME Journal</i> , 2019, 13, 1457-1468.	9.8	31
134	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
135	Effects of sample treatments on genome recovery via single-cell genomics. <i>ISME Journal</i> , 2014, 8, 2546-2549.	9.8	29
136	Genomic composition and dynamics among <i>Methanomicrobiales</i> predict adaptation to contrasting environments. <i>ISME Journal</i> , 2017, 11, 87-99.	9.8	29
137	Lipid analysis of CO ₂ -rich subsurface aquifers suggests an autotrophy-based deep biosphere with lysolipids enriched in CPR bacteria. <i>ISME Journal</i> , 2020, 14, 1547-1560.	9.8	29
138	A Genomic Perspective Across Earth's Microbiomes Reveals That Genome Size in Archaea and Bacteria Is Linked to Ecosystem Type and Trophic Strategy. <i>Frontiers in Microbiology</i> , 2021, 12, 761869.	3.5	29
139	Lytic archaeal viruses infect abundant primary producers in Earth's crust. <i>Nature Communications</i> , 2021, 12, 4642.	12.8	28
140	Direct pathway cloning of the sodorifen biosynthetic gene cluster and recombinant generation of its product in <i>E. coli</i> . <i>Microbial Cell Factories</i> , 2019, 18, 32.	4.0	27
141	Searching for new branches on the tree of life. <i>Science</i> , 2014, 346, 698-699.	12.6	25
142	Metapangenomics reveals depth-dependent shifts in metabolic potential for the ubiquitous marine bacterial SAR324 lineage. <i>Microbiome</i> , 2021, 9, 172.	11.1	25
143	Novel approaches in function-driven single-cell genomics. <i>FEMS Microbiology Reviews</i> , 2017, 41, 538-548.	8.6	24
144	Four Draft Single-Cell Genome Sequences of Novel, Nearly Identical <i>Kiritimatiella</i> Strains Isolated from the Continental Deep Subsurface. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	23

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145	Recoding of stop codons expands the metabolic potential of two novel Asgardarchaeota lineages. ISME Communications, 2021, 1, .	4.2	23
146	Yellowstone Lake Nanoarchaeota. <i>Frontiers in Microbiology</i> , 2013, 4, 274.	3.5	22
147	acdc “ Automated Contamination Detection and Confidence estimation for single-cell genome data. <i>BMC Bioinformatics</i> , 2016, 17, 543.	2.6	22
148	Genomic analysis of three <i>Bifidobacterium</i> species isolated from the calf gastrointestinal tract. <i>Scientific Reports</i> , 2016, 6, 30768.	3.3	20
149	<i>Thermus sediminis</i> sp. nov., a thiosulfate-oxidizing and arsenate-reducing organism isolated from Little Hot Creek in the Long Valley Caldera, California. <i>Extremophiles</i> , 2018, 22, 983-991.	2.3	20
150	Complete Genome Sequence of <i>Micromonospora</i> Strain L5, a Potential Plant-Growth-Regulating Actinomycete, Originally Isolated from <i>Casuarina equisetifolia</i> Root Nodules. <i>Genome Announcements</i> , 2013, 1, .	0.8	19
151	Genomics of Methylophony in Gram-Positive Methylamine-Utilizing Bacteria. <i>Microorganisms</i> , 2015, 3, 94-112.	3.6	19
152	Conservation of Endophyte Bacterial Community Structure Across Two <i>Panicum</i> Grass Species. <i>Frontiers in Microbiology</i> , 2019, 10, 2181.	3.5	19
153	Molecular Dialogues between Early Divergent Fungi and Bacteria in an Antagonism versus a Mutualism. <i>MBio</i> , 2020, 11, .	4.1	19
154	Novel heavy metal resistance gene clusters are present in the genome of <i>Cupriavidus neocaledonicus</i> STM 6070, a new species of <i>Mimosa pudica</i> microsymbiont isolated from heavy-metal-rich mining site soil. <i>BMC Genomics</i> , 2020, 21, 214.	2.8	18
155	<i>Polynucleobacter meluiroseus</i> sp. nov., a bacterium isolated from a lake located in the mountains of the Mediterranean island of Corsica. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1975-1985.	1.7	18
156	Function-driven single-cell genomics. <i>Microbial Biotechnology</i> , 2015, 8, 38-39.	4.2	17
157	Genome of <i>Methanoregula boonei</i> 6A8 reveals adaptations to oligotrophic peatland environments. <i>Microbiology (United Kingdom)</i> , 2015, 161, 1572-1581.	1.8	17
158	Genome analysis of <i>Candidatus</i> <i>Ancillula trichonymphae</i> ™, first representative of a deep-branching clade of <i>Bifidobacteriales</i> , strengthens evidence for convergent evolution in flagellate endosymbionts. <i>Environmental Microbiology Reports</i> , 2016, 8, 865-873.	2.4	16
159	Novel copper-containing membrane monooxygenases (CuMMOs) encoded by alkane-utilizing <i>Betaproteobacteria</i> . <i>ISME Journal</i> , 2020, 14, 714-726.	9.8	16
160	High Potential for Biomass-Degrading Enzymes Revealed by Hot Spring Metagenomics. <i>Frontiers in Microbiology</i> , 2021, 12, 668238.	3.5	16
161	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.	9.8	15
162	Genomic Characterization of Candidate Division LCP-89 Reveals an Atypical Cell Wall Structure, Microcompartment Production, and Dual Respiratory and Fermentative Capacities. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	14

#	ARTICLE	IF	CITATIONS
163	Advantages and Limits of Metagenomic Assembly and Binning of a Giant Virus. <i>MSystems</i> , 2020, 5, .	3.8	14
164	Description of <i>Candidatus Mesopelagibacter carboxydoxydans</i> and <i>Candidatus Anoxipelagibacter denitrificans</i> : Nitrate-reducing SAR11 genera that dominate mesopelagic and anoxic marine zones. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126185.	2.8	14
165	<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.	1.7	14
166	Finished Genome of <i>Zymomonas mobilis</i> subsp. <i>mobilis</i> Strain CP4, an Applied Ethanol Producer. <i>Genome Announcements</i> , 2014, 2, .	0.8	13
167	Genomic Analysis of the Yet-Uncultured <i>Binatota</i> Reveals Broad Methylotrophic, Alkane-Degradation, and Pigment Production Capacities. <i>MBio</i> , 2021, 12, .	4.1	13
168	Resequencing and annotation of the <i>Nostoc punctiforme</i> ATCC 29133 genome: facilitating biofuel and high-value chemical production. <i>AMB Express</i> , 2017, 7, 42.	3.0	12
169	Analysis of single-cell genome sequences of bacteria and archaea. <i>Emerging Topics in Life Sciences</i> , 2017, 1, 249-255.	2.6	10
170	<i>Zymomonas</i> diversity and potential for biofuel production. <i>Biotechnology for Biofuels</i> , 2021, 14, 112.	6.2	10
171	<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, .	1.7	10
172	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.	0.5	10
173	Complete Genome Sequence of <i>Methanosphaerula palustris</i> E1-9C, a Hydrogenotrophic Methanogen Isolated from a Minerotrophic Fen Peatland. <i>Genome Announcements</i> , 2015, 3, .	0.8	9
174	High-quality draft genome sequence of <i>Pseudomonas aeruginosa</i> strain ai, an environmental isolate resistant to heavy metals. <i>Extremophiles</i> , 2019, 23, 399-405.	2.3	9
175	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.	2.2	9
176	Mixotrophic Iron-Oxidizing <i>Thiomonas</i> Isolates from an Acid Mine Drainage-Affected Creek. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	9
177	Morphological and Genomic Features of the New Klosneuvirinae Isolate Fadolivirus IHUMI-VV54. <i>Frontiers in Microbiology</i> , 2021, 12, 719703.	3.5	9
178	Improved Draft Genome Sequence of <i>Microbacterium</i> sp. Strain LKL04, a Bacterial Endophyte Associated with Switchgrass Plants. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	8
179	Genomics, Exometabolomics, and Metabolic Probing Reveal Conserved Proteolytic Metabolism of <i>Thermoflexus hugenholtzii</i> and Three Candidate Species From China and Japan. <i>Frontiers in Microbiology</i> , 2021, 12, 632731.	3.5	8
180	Community Structure and Microbial Associations in Sediment-Free Methanotrophic Enrichment Cultures from a Marine Methane Seep. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	3.1	8

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181	Draft genome sequence of <i>Pseudomonas extremaustralis</i> strain USBA-GBX 515 isolated from Superparamo soil samples in Colombian Andes. <i>Standards in Genomic Sciences</i> , 2017, 12, 78.	1.5	7
182	A single-cell genomics pipeline for environmental microbial eukaryotes. <i>IScience</i> , 2021, 24, 102290.	4.1	7
183	<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.	1.7	7
184	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.	2.0	7
185	DNA Methylation in <i>Ensifer</i> Species during Free-Living Growth and during Nitrogen-Fixing Symbiosis with <i>Medicago</i> spp.. <i>MSystems</i> , 2022, 7, e0109221.	3.8	7
186	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, .	0.6	6
187	Entities inside one another – a matryoshka doll in biology?. <i>Environmental Microbiology Reports</i> , 2019, 11, 26-28.	2.4	6
188	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, .	0.6	5
189	Hiding in Plain Sight: The Globally Distributed Bacterial Candidate Phylum PAUC34f. <i>Frontiers in Microbiology</i> , 2020, 11, 376.	3.5	5
190	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, .	0.6	5
191	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.	0.6	5
192	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
193	Genomes From Uncultivated Microorganisms. , 2019, , .		4
194	Synthase-Selective Exploration of a Tunicate Microbiome by Activity-Guided Single-Cell Genomics. <i>ACS Chemical Biology</i> , 2021, 16, 813-819.	3.4	4
195	Draft Genome Sequence of Mn(II)-Oxidizing Bacterium <i>Oxalobacteraceae</i> sp. Strain AB_14. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
196	Genome Sequences of Actinobacteria from Extreme Environments in Colombia. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	3
197	Draft Genome Sequences of New Isolates and the Known Species of the Family Microbacteriaceae Associated with Plants. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	3
198	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, .	0.6	3

#	ARTICLE	IF	CITATIONS
199	Beyond the census of human gut dwellers. <i>Nature Reviews Microbiology</i> , 2019, 17, 401-401.	28.6	3
200	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.	2.2	3
201	High-Quality Draft Genome Sequences of the Uncultured Delta3 Endosymbiont (Deltaproteobacteria) Assembled from Metagenomes of the Gutless Marine Worm <i>Olavius algarvensis</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	3
202	High-Quality Draft Genome Sequence of the Siderophilic and Thermophilic <i>Leptolyngbyaceae</i> Cyanobacterium JSC-12. <i>Microbiology Resource Announcements</i> , 2021, 10, e0049521.	0.6	2
203	Metagenomes and Metagenome-Assembled Genomes from Substrate-Amended Hot Spring Sediment Incubations from Yellowstone National Park. <i>Microbiology Resource Announcements</i> , 2022, 11, e0106521.	0.6	2
204	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.	3.5	2
205	Sequencing of Genomes from Environmental Single Cells. <i>Methods in Molecular Biology</i> , 2018, 1712, 97-111.	0.9	1
206	A single-cell genome perspective on studying intracellular associations in unicellular eukaryotes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190082.	4.0	1
207	Improved Draft Genome Sequence of <i>Bacillus</i> sp. Strain YF23, Which Has Plant Growth-Promoting Activity. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
208	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, .	0.6	1
209	Draft Genome Sequence of <i>Yokenella regensburgei</i> Strain WCD67, Isolated from the Boxelder Bug. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
210	GAL08, an Uncultivated Group of Acidobacteria, Is a Dominant Bacterial Clade in a Neutral Hot Spring. <i>Frontiers in Microbiology</i> , 2021, 12, 787651.	3.5	1
211	<i>Sodalis ligni</i> Strain 159R Isolated from an Anaerobic Lignin-Degrading Consortium. <i>Microbiology Spectrum</i> , 2022, 10, e0234621.	3.0	1
212	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
213	Draft Genome Sequence of <i>Bordetella</i> sp. Strain FB-8, Isolated from a Former Uranium Mining Area in Germany. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	0
214	Epigenetic Regulation of <i>Nostoc punctiforme</i> ATCC 29133 in Response to Nitrogen Availability. <i>Journal of Student Research</i> , 2021, 10, .	0.1	0
215	Impact of Harvest on Switchgrass Leaf Microbial Communities. <i>Genes</i> , 2022, 13, 22.	2.4	0