

# Rolf Daniel

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6533413/publications.pdf>

Version: 2024-02-01

414  
papers

20,528  
citations

10389

72  
h-index

16650

123  
g-index

438  
all docs

438  
docs citations

438  
times ranked

22930  
citing authors

#	ARTICLE	IF	CITATIONS
1	Tax4Fun: predicting functional profiles from metagenomic 16S rRNA data. <i>Bioinformatics</i> , 2015, 31, 2882-2884.	4.1	1,283
2	Comparative genome and phenotypic analysis of three <i>Clostridioides difficile</i> strains isolated from a single patient provide insight into multiple infection of <i>C. difficile</i> . <i>BMC Genomics</i> , 2018, 19, 1.	2.8	725
3	The metagenomics of soil. <i>Nature Reviews Microbiology</i> , 2005, 3, 470-478.	28.6	699
4	Metagenomic Analyses: Past and Future Trends. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1153-1161.	3.1	597
5	Pyrosequencing-Based Assessment of Bacterial Community Structure Along Different Management Types in German Forest and Grassland Soils. <i>PLoS ONE</i> , 2011, 6, e17000.	2.5	480
6	The genome of the ammonia-oxidizing <i>Candidatus Nitrososphaera gargensis</i> : insights into metabolic versatility and environmental adaptations. <i>Environmental Microbiology</i> , 2012, 14, 3122-3145.	3.8	332
7	Tax4Fun2: prediction of habitat-specific functional profiles and functional redundancy based on 16S rRNA gene sequences. <i>Environmental Microbiomes</i> , 2020, 15, 11.	5.0	323
8	Horizon-Specific Bacterial Community Composition of German Grassland Soils, as Revealed by Pyrosequencing-Based Analysis of 16S rRNA Genes. <i>Applied and Environmental Microbiology</i> , 2010, 76, 6751-6759.	3.1	312
9	Driving forces of soil bacterial community structure, diversity, and function in temperate grasslands and forests. <i>Scientific Reports</i> , 2016, 6, 33696.	3.3	308
10	The soil metagenome – a rich resource for the discovery of novel natural products. <i>Current Opinion in Biotechnology</i> , 2004, 15, 199-204.	6.6	280
11	Screening of Environmental DNA Libraries for the Presence of Genes Conferring Lipolytic Activity on <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 2000, 66, 3113-3116.	3.1	272
12	An Ancient Pathway Combining Carbon Dioxide Fixation with the Generation and Utilization of a Sodium Ion Gradient for ATP Synthesis. <i>PLoS ONE</i> , 2012, 7, e33439.	2.5	246
13	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.	9.8	244
14	Interannual variation in land-use intensity enhances grassland multidiversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 308-313.	7.1	243
15	Genome sequence analyses of two isolates from the recent <i>Escherichia coli</i> outbreak in Germany reveal the emergence of a new pathotype: Entero-Aggregative-Haemorrhagic <i>Escherichia coli</i> (EAHEC). <i>Archives of Microbiology</i> , 2011, 193, 883-891.	2.2	238
16	New Mode of Energy Metabolism in the Seventh Order of Methanogens as Revealed by Comparative Genome Analysis of <i>Candidatus Methanoplasma termitum</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 1338-1352.	3.1	235
17	Is autoinducer-2 a universal signal for interspecies communication: a comparative genomic and phylogenetic analysis of the synthesis and signal transduction pathways. <i>BMC Evolutionary Biology</i> , 2004, 4, 36.	3.2	230
18	Phylogenetic Diversity and Metabolic Potential Revealed in a Glacier Ice Metagenome. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7519-7526.	3.1	213

#	ARTICLE	IF	CITATIONS
19	Reassessment of the <i>Listeria monocytogenes</i> pan-genome reveals dynamic integration hotspots and mobile genetic elements as major components of the accessory genome. <i>BMC Genomics</i> , 2013, 14, 47.	2.8	212
20	Advances in Recovery of Novel Biocatalysts from Metagenomes. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2009, 16, 25-37.	1.0	200
21	The impact of even-aged and uneven-aged forest management on regional biodiversity of multiple taxa in European beech forests. <i>Journal of Applied Ecology</i> , 2018, 55, 267-278.	4.0	188
22	Construction of Environmental DNA Libraries in <i>Escherichia coli</i> and Screening for the Presence of Genes Conferring Utilization of 4-Hydroxybutyrate. <i>Applied and Environmental Microbiology</i> , 1999, 65, 3901-3907.	3.1	187
23	Land-use choices follow profitability at the expense of ecological functions in Indonesian smallholder landscapes. <i>Nature Communications</i> , 2016, 7, 13137.	12.8	186
24	Achievements and new knowledge unraveled by metagenomic approaches. <i>Applied Microbiology and Biotechnology</i> , 2009, 85, 265-276.	3.6	176
25	Control of potassium homeostasis is an essential function of the second messenger cyclic di-AMP in <i>Bacillus subtilis</i> . <i>Science Signaling</i> , 2017, 10, .	3.6	162
26	Phylogenetic Analysis of a Microbialite-Forming Microbial Mat from a Hypersaline Lake of the Kiritimati Atoll, Central Pacific. <i>PLoS ONE</i> , 2013, 8, e66662.	2.5	160
27	Trade-offs between multifunctionality and profit in tropical smallholder landscapes. <i>Nature Communications</i> , 2020, 11, 1186.	12.8	156
28	Construction and Screening of Metagenomic Libraries Derived from Enrichment Cultures: Generation of a Gene Bank for Genes Conferring Alcohol Oxidoreductase Activity on <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 2003, 69, 1408-1416.	3.1	155
29	Deciphering associations between dissolved organic molecules and bacterial communities in a pelagic marine system. <i>ISME Journal</i> , 2016, 10, 1717-1730.	9.8	155
30	<i>Phaeobacter gallaeciensis</i> genomes from globally opposite locations reveal high similarity of adaptation to surface life. <i>ISME Journal</i> , 2012, 6, 2229-2244.	9.8	143
31	General Relationships between Abiotic Soil Properties and Soil Biota across Spatial Scales and Different Land-Use Types. <i>PLoS ONE</i> , 2012, 7, e43292.	2.5	142
32	Deep metagenome and metatranscriptome analyses of microbial communities affiliated with an industrial biogas fermenter, a cow rumen, and elephant feces reveal major differences in carbohydrate hydrolysis strategies. <i>Biotechnology for Biofuels</i> , 2016, 9, 121.	6.2	141
33	Large-scale reduction of the <i>Bacillus subtilis</i> genome: consequences for the transcriptional network, resource allocation, and metabolism. <i>Genome Research</i> , 2017, 27, 289-299.	5.5	137
34	Direct and cascading impacts of tropical land-use change on multi-trophic biodiversity. <i>Nature Ecology and Evolution</i> , 2017, 1, 1511-1519.	7.8	137
35	Identification and Characterization of Coenzyme B <sub>12</sub> -Dependent Glycerol Dehydratase- and Diol Dehydratase-Encoding Genes from Metagenomic DNA Libraries Derived from Enrichment Cultures. <i>Applied and Environmental Microbiology</i> , 2003, 69, 3048-3060.	3.1	132
36	Host Imprints on Bacterial Genomes—Rapid, Divergent Evolution in Individual Patients. <i>PLoS Pathogens</i> , 2010, 6, e1001078.	4.7	130

#	ARTICLE	IF	CITATIONS
37	Enrichment of chitinolytic microorganisms: isolation and characterization of a chitinase exhibiting antifungal activity against phytopathogenic fungi from a novel <i>Streptomyces</i> strain. <i>Applied Microbiology and Biotechnology</i> , 2005, 66, 434-442.	3.6	128
38	Fungal soil communities in a young transgenic poplar plantation form a rich reservoir for fungal root communities. <i>Ecology and Evolution</i> , 2012, 2, 1935-1948.	1.9	122
39	Biochemistry of coenzyme B12-dependent glycerol and diol dehydratases and organization of the encoding genes. <i>FEMS Microbiology Reviews</i> , 1998, 22, 553-566.	8.6	118
40	ICEPmu1, an integrative conjugative element (ICE) of <i>Pasteurella multocida</i> : analysis of the regions that comprise 12 antimicrobial resistance genes. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 84-90.	3.0	117
41	Impact of a phytoplankton bloom on the diversity of the active bacterial community in the southern North Sea as revealed by metatranscriptomic approaches. <i>FEMS Microbiology Ecology</i> , 2014, 87, 378-389.	2.7	113
42	A Novel Metagenomic Short-Chain Dehydrogenase/Reductase Attenuates <i>Pseudomonas aeruginosa</i> Biofilm Formation and Virulence on <i>Caenorhabditis elegans</i> . <i>PLoS ONE</i> , 2011, 6, e26278.	2.5	113
43	Biochemical and molecular characterization of the oxidative branch of glycerol utilization by <i>Citrobacter freundii</i> . <i>Journal of Bacteriology</i> , 1995, 177, 4392-4401.	2.2	112
44	Metagenome Survey of a Multispecies and Alga-Associated Biofilm Revealed Key Elements of Bacterial-Algal Interactions in Photobioreactors. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6196-6206.	3.1	111
45	Comparative Analysis of Plasmids in the Genus <i>Listeria</i> . <i>PLoS ONE</i> , 2010, 5, e12511.	2.5	110
46	ICEPmu1, an integrative conjugative element (ICE) of <i>Pasteurella multocida</i> : structure and transfer. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 91-100.	3.0	108
47	Comparative Genomics and Transcriptomics of <i>Propionibacterium acnes</i> . <i>PLoS ONE</i> , 2011, 6, e21581.	2.5	107
48	Purification of 1,3-propanediol dehydrogenase from <i>Citrobacter freundii</i> and cloning, sequencing, and overexpression of the corresponding gene in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 1995, 177, 2151-2156.	2.2	105
49	Bacterial community dynamics during polysaccharide degradation at contrasting sites in the Southern and Atlantic Oceans. <i>Environmental Microbiology</i> , 2015, 17, 3822-3831.	3.8	103
50	Screening of Environmental DNA Libraries for the Presence of Genes Conferring Na <sup>+</sup> (Li <sup>+</sup> )/H <sup>+</sup> Antiporter Activity on <i>Escherichia coli</i> : Characterization of the Recovered Genes and the Corresponding Gene Products. <i>Journal of Bacteriology</i> , 2001, 183, 6645-6653.	2.2	102
51	The Effects of Cropping Regimes on Fungal and Bacterial Communities of Wheat and Faba Bean in a Greenhouse Pot Experiment Differ between Plant Species and Compartment. <i>Frontiers in Microbiology</i> , 2017, 8, 902.	3.5	101
52	Poles Apart: Arctic and Antarctic Octadecabacter strains Share High Genome Plasticity and a New Type of Xanthorhodopsin. <i>PLoS ONE</i> , 2013, 8, e63422.	2.5	96
53	Adaptation of an abundant <i>Roseobacter</i> RCA organism to pelagic systems revealed by genomic and transcriptomic analyses. <i>ISME Journal</i> , 2015, 9, 371-384.	9.8	96
54	Impact of Lowland Rainforest Transformation on Diversity and Composition of Soil Prokaryotic Communities in Sumatra (Indonesia). <i>Frontiers in Microbiology</i> , 2015, 6, 1339.	3.5	92

#	ARTICLE	IF	CITATIONS
55	Prospecting for biocatalysts and drugs in the genomes of non-cultured microorganisms. <i>Current Opinion in Biotechnology</i> , 2004, 15, 285-290.	6.6	91
56	The lung microbiome regulates brain autoimmunity. <i>Nature</i> , 2022, 603, 138-144.	27.8	91
57	Rapid Identification of Genes Encoding DNA Polymerases by Function-Based Screening of Metagenomic Libraries Derived from Glacial Ice. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2964-2968.	3.1	87
58	Intensive tropical land use massively shifts soil fungal communities. <i>Scientific Reports</i> , 2019, 9, 3403.	3.3	86
59	Industrial Acetogenic Biocatalysts: A Comparative Metabolic and Genomic Analysis. <i>Frontiers in Microbiology</i> , 2016, 7, 1036.	3.5	85
60	No evidence for a bovine mastitis <i>Escherichia coli</i> pathotype. <i>BMC Genomics</i> , 2017, 18, 359.	2.8	85
61	How to Kill the Honey Bee Larva: Genomic Potential and Virulence Mechanisms of <i>Paenibacillus</i> larvae. <i>PLoS ONE</i> , 2014, 9, e90914.	2.5	84
62	Metagenomes of Complex Microbial Consortia Derived from Different Soils as Sources for Novel Genes Conferring Formation of Carbonyls from Short-Chain Polyols on <i>Escherichia coli</i> . <i>Journal of Molecular Microbiology and Biotechnology</i> , 2003, 5, 46-56.	1.0	83
63	Bacterial endophyte communities of three agricultural important grass species differ in their response towards management regimes. <i>Scientific Reports</i> , 2017, 7, 40914.	3.3	83
64	Rhodobacteraceae on the marine brown alga <i>Fucus spiralis</i> are abundant and show physiological adaptation to an epiphytic lifestyle. <i>Systematic and Applied Microbiology</i> , 2017, 40, 370-382.	2.8	83
65	The green impact: bacterioplankton response toward a phytoplankton spring bloom in the southern North Sea assessed by comparative metagenomic and metatranscriptomic approaches. <i>Frontiers in Microbiology</i> , 2015, 6, 805.	3.5	82
66	Physiological homogeneity among the endosymbionts of <i>Riftia pachyptila</i> and <i>Tevnia jerichonana</i> revealed by proteogenomics. <i>ISME Journal</i> , 2012, 6, 766-776.	9.8	80
67	Wastewater Irrigation Increases the Abundance of Potentially Harmful Gammaproteobacteria in Soils in Mezquital Valley, Mexico. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5282-5291.	3.1	80
68	A Comparative Metagenome Survey of the Fecal Microbiota of a Breast- and a Plant-Fed Asian Elephant Reveals an Unexpectedly High Diversity of Glycoside Hydrolase Family Enzymes. <i>PLoS ONE</i> , 2014, 9, e106707.	2.5	80
69	Microbial Diversity and Biochemical Potential Encoded by Thermal Spring Metagenomes Derived from the Kamchatka Peninsula. <i>Archaea</i> , 2013, 2013, 1-13.	2.3	79
70	Gene prediction in metagenomic fragments: A large scale machine learning approach. <i>BMC Bioinformatics</i> , 2008, 9, 217.	2.6	78
71	Involvement of Two Latex-Clearing Proteins during Rubber Degradation and Insights into the Subsequent Degradation Pathway Revealed by the Genome Sequence of <i>Gordonia polyisoprenivorans</i> Strain VH2. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2874-2887.	3.1	78
72	Isolation and Characterization of Metalloproteases with a Novel Domain Structure by Construction and Screening of Metagenomic Libraries. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2506-2516.	3.1	77

#	ARTICLE	IF	CITATIONS
73	Cloning, sequencing, and overexpression of the genes encoding coenzyme B <sub>12</sub> -dependent glycerol dehydratase of <i>Citrobacter freundii</i> . <i>Journal of Bacteriology</i> , 1996, 178, 5793-5796.	2.2	75
74	The Complete Genome Sequence of <i>Clostridium aceticum</i> : a Missing Link between Rnf- and Cytochrome-Containing Autotrophic Acetogens. <i>MBio</i> , 2015, 6, e01168-15.	4.1	75
75	Identification and expression of the genes and purification and characterization of the gene products involved in reactivation of coenzyme B <sub>12</sub> -dependent glycerol dehydratase of <i>Citrobacter freundii</i> . <i>FEBS Journal</i> , 2001, 268, 2369-2378.	0.2	74
76	Fine Spatial Scale Variation of Soil Microbial Communities under European Beech and Norway Spruce. <i>Frontiers in Microbiology</i> , 2016, 7, 2067.	3.5	74
77	Metagenomic discovery of novel enzymes and biosurfactants in a slaughterhouse biofilm microbial community. <i>Scientific Reports</i> , 2016, 6, 27035.	3.3	74
78	<i>Bacillus thuringiensis</i> and <i>Bacillus weihenstephanensis</i> Inhibit the Growth of Phytopathogenic <i>Verticillium</i> Species. <i>Frontiers in Microbiology</i> , 2016, 7, 2171.	3.5	74
79	Prokaryotic Diversity and Community Patterns in Antarctic Continental Shelf Sponges. <i>Frontiers in Marine Science</i> , 2019, 6, .	2.5	74
80	Methanol metabolism in the acetogenic bacterium <i>Acetobacterium woodii</i> . <i>Environmental Microbiology</i> , 2018, 20, 4369-4384.	3.8	73
81	Complete genome sequence and metabolic potential of the quinaldine-degrading bacterium <i>Arthrobacter</i> sp. Rue61a. <i>BMC Genomics</i> , 2012, 13, 534.	2.8	72
82	Tree Species Shape Soil Bacterial Community Structure and Function in Temperate Deciduous Forests. <i>Frontiers in Microbiology</i> , 2019, 10, 1519.	3.5	71
83	Host-Pathogen Coevolution: The Selective Advantage of <i>Bacillus thuringiensis</i> Virulence and Its Cry Toxin Genes. <i>PLoS Biology</i> , 2015, 13, e1002169.	5.6	69
84	Biogeography and phylogenetic diversity of a cluster of exclusively marine myxobacteria. <i>ISME Journal</i> , 2012, 6, 1260-1272.	9.8	67
85	Identification and characterization of novel cellulolytic and hemicellulolytic genes and enzymes derived from German grassland soil metagenomes. <i>Biotechnology Letters</i> , 2012, 34, 663-675.	2.2	67
86	Identification of novel lipolytic genes and gene families by screening of metagenomic libraries derived from soil samples of the German Biodiversity Exploratories. <i>FEMS Microbiology Ecology</i> , 2011, 78, 188-201.	2.7	66
87	Molecular Keys to the <i>Janthinobacterium</i> and <i>Duganella</i> spp. Interaction with the Plant Pathogen <i>Fusarium graminearum</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1668.	3.5	66
88	Sustained sensing in potassium homeostasis: Cyclic di-AMP controls potassium uptake by KimA at the levels of expression and activity. <i>Journal of Biological Chemistry</i> , 2019, 294, 9605-9614.	3.4	66
89	Complete Genome Sequence of the Type Strain <i>Cupriavidus necator</i> N-1. <i>Journal of Bacteriology</i> , 2011, 193, 5017-5017.	2.2	64
90	Genome-guided analysis of physiological and morphological traits of the fermentative acetate oxidizer <i>Thermacetogenium phaeum</i> . <i>BMC Genomics</i> , 2012, 13, 723.	2.8	64

#	ARTICLE	IF	CITATIONS
91	Glycerol conversion to 1,3-propanediol by <i>Clostridium pasteurianum</i> : cloning and expression of the gene encoding 1,3-propanediol dehydrogenase. <i>FEMS Microbiology Letters</i> , 2006, 154, 337-345.	1.8	63
92	A genome-guided analysis of energy conservation in the thermophilic, cytochrome-free acetogenic bacterium <i>Thermoanaerobacter</i> <i>Äkivui</i> . <i>BMC Genomics</i> , 2014, 15, 1139.	2.8	63
93	Microbial solvent formation revisited by comparative genome analysis. <i>Biotechnology for Biofuels</i> , 2017, 10, 58.	6.2	60
94	Analysis and comparative genomics of ICEMh1, a novel integrative and conjugative element (ICE) of <i>Mannheimia haemolytica</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 93-97.	3.0	59
95	Properties and sequence of the coenzyme B12-dependent glycerol dehydratase of <i>Clostridium pasteurianum</i> . <i>FEMS Microbiology Letters</i> , 1998, 164, 21-28.	1.8	58
96	Drylands soil bacterial community is affected by land use change and different irrigation practices in the Mezquital Valley, Mexico. <i>Scientific Reports</i> , 2018, 8, 1413.	3.3	58
97	Sequencing, annotation, and comparative genome analysis of the gerbil-adapted <i>Helicobacter pylori</i> strain B8. <i>BMC Genomics</i> , 2010, 11, 335.	2.8	57
98	Molecular Basis of Macrolide, Triamidine, and Lincosamide Resistance in <i>Pasteurella multocida</i> from Bovine Respiratory Disease. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 2475-2477.	3.2	57
99	Aquatic adaptation of a laterally acquired pectin degradation pathway in marine gammaproteobacteria. <i>Environmental Microbiology</i> , 2017, 19, 2320-2333.	3.8	57
100	Nitrogen fixation in a chemoautotrophic lucinid symbiosis. <i>Nature Microbiology</i> , 2017, 2, 16193.	13.3	56
101	Roots from beech ( <i>Fagus sylvatica</i> L.) and ash ( <i>Fraxinus excelsior</i> L.) differentially affect soil microorganisms and carbon dynamics. <i>Soil Biology and Biochemistry</i> , 2013, 61, 23-32.	8.8	55
102	<i>Planktomarina temperata</i> gen. nov., sp. nov., belonging to the globally distributed RCA cluster of the marine <i>Roseobacter</i> clade, isolated from the German Wadden Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 4207-4217.	1.7	55
103	Comparative genome analysis and genome-guided physiological analysis of <i>Roseobacter litoralis</i> . <i>BMC Genomics</i> , 2011, 12, 324.	2.8	54
104	High abundance of heterotrophic prokaryotes in hydrothermal springs of the Azores as revealed by a network of 16S rRNA gene-based methods. <i>Extremophiles</i> , 2013, 17, 649-662.	2.3	54
105	Effects of Fertilization and Sampling Time on Composition and Diversity of Entire and Active Bacterial Communities in German Grassland Soils. <i>PLoS ONE</i> , 2015, 10, e0145575.	2.5	54
106	Full-Genome Sequence of the Plant Growth-Promoting Bacterium <i>Pseudomonas protegens</i> CHA0. <i>Genome Announcements</i> , 2014, 2, .	0.8	53
107	Insights into the Microbial Degradation of Rubber and Gutta-Percha by Analysis of the Complete Genome of <i>Nocardia nova</i> SH22a. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3895-3907.	3.1	53
108	The <i>Janthinobacterium</i> sp. HH01 Genome Encodes a Homologue of the <i>V. cholerae</i> CqsA and <i>L. pneumophila</i> LqsA Autoinducer Synthases. <i>PLoS ONE</i> , 2013, 8, e55045.	2.5	52



#	ARTICLE	IF	CITATIONS
109	Paenilarvins: Iturin Family Lipopeptides from the Honey Bee Pathogen <i>Paenibacillus larvae</i> . ChemBioChem, 2014, 15, 1947-1955.	2.6	51
110	Growth temperature-dependent activity of glycerol dehydratase in <i>Escherichia coli</i> expressing the <i>Citrobacter freundii</i> dharegulon. FEMS Microbiology Letters, 1992, 100, 281-285.	1.8	50
111	Sequence of the hyperplastic genome of the naturally competent <i>Thermus scotoductus</i> SA-01. BMC Genomics, 2011, 12, 577.	2.8	49
112	RNA-Based Assessment of Diversity and Composition of Active Archaeal Communities in the German Bight. Archaea, 2012, 2012, 1-8.	2.3	49
113	Adaptation of <i>Bacillus subtilis</i> to Life at Extreme Potassium Limitation. MBio, 2017, 8, .	4.1	49
114	<i>Caproicibacter fermentans</i> gen. nov., sp. nov., a new caproate-producing bacterium and emended description of the genus <i>Caproiciproducens</i> . International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4269-4279.	1.7	49
115	Land Use Type Significantly Affects Microbial Gene Transcription in Soil. Microbial Ecology, 2014, 67, 919-930.	2.8	48
116	Genome Analysis of the Biotechnologically Relevant Acidophilic Iron Oxidising Strain JA12 Indicates Phylogenetic and Metabolic Diversity within the Novel Genus <i>Ferrovum</i> . PLoS ONE, 2016, 11, e0146832.	2.5	48
117	Changes in Trophic Groups of Protists With Conversion of Rainforest Into Rubber and Oil Palm Plantations. Frontiers in Microbiology, 2019, 10, 240.	3.5	48
118	Characterization and optimization of <i>Bacillus subtilis</i> ATCC 6051 as an expression host. Journal of Biotechnology, 2013, 163, 97-104.	3.8	47
119	Complete Genome Sequence of the Broad-Host-Range Strain <i>Sinorhizobium fredii</i> USDA257. Journal of Bacteriology, 2012, 194, 4483-4483.	2.2	46
120	The Purine-Utilizing Bacterium <i>Clostridium acidurici</i> 9a: A Genome-Guided Metabolic Reconsideration. PLoS ONE, 2012, 7, e51662.	2.5	46
121	VOC emission of various <i>Serratia</i> species and isolates and genome analysis of <i>Serratia plymuthica</i> 4Rx13. FEMS Microbiology Letters, 2014, 352, 45-53.	1.8	46
122	Assembly processes of trophic guilds in the root mycobiome of temperate forests. Molecular Ecology, 2019, 28, 348-364.	3.9	46
123	Leaf litter is the main driver for changes in bacterial community structures in the rhizosphere of ash and beech. Applied Soil Ecology, 2013, 72, 150-160.	4.3	45
124	How Rainforest Conversion to Agricultural Systems in Sumatra (Indonesia) Affects Active Soil Bacterial Communities. Frontiers in Microbiology, 2018, 9, 2381.	3.5	44
125	Treephyler: fast taxonomic profiling of metagenomes. Bioinformatics, 2010, 26, 960-961.	4.1	43
126	Genome-Wide RNA Sequencing Analysis of Quorum Sensing-Controlled Regulons in the Plant-Associated <i>Burkholderia glumae</i> PG1 Strain. Applied and Environmental Microbiology, 2015, 81, 7993-8007.	3.1	43



#	ARTICLE	IF	CITATIONS
127	First Insights into the Genome of the Gram-Negative, Endospore-Forming Organism <i>Sporomusa ovata</i> Strain HI DSM 2662. <i>Genome Announcements</i> , 2013, 1, .	0.8	42
128	Gene Loss and Horizontal Gene Transfer Contributed to the Genome Evolution of the Extreme Acidophile <i>Ferroplasma acidiphilum</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 797.	3.5	42
129	RNA-Seq of <i>Bacillus licheniformis</i> : active regulatory RNA features expressed within a productive fermentation. <i>BMC Genomics</i> , 2013, 14, 667.	2.8	40
130	Engineering <i>Bacillus subtilis</i> for the conversion of the antimetabolite 4-hydroxy-l-threonine to pyridoxine. <i>Metabolic Engineering</i> , 2015, 29, 196-207.	7.0	40
131	Formate metabolism in the acetogenic bacterium <i>Acetobacterium woodii</i> . <i>Environmental Microbiology</i> , 2021, 23, 4214-4227.	3.8	39
132	Unravelling the effects of tropical land use conversion on the soil microbiome. <i>Environmental Microbiomes</i> , 2020, 15, 5.	5.0	37
133	Genome Resequencing of the Virulent and Multidrug-Resistant Reference Strain <i>Clostridium difficile</i> 630. <i>Genome Announcements</i> , 2015, 3, .	0.8	36
134	Biogeography and environmental genomics of the <i>Roseobacter</i> -affiliated pelagic CHAB-I-5 lineage. <i>Nature Microbiology</i> , 2016, 1, 16063.	13.3	36
135	Linking Compositional and Functional Predictions to Decipher the Biogeochemical Significance in DFAA Turnover of Abundant Bacterioplankton Lineages in the North Sea. <i>Microorganisms</i> , 2017, 5, 68.	3.6	36
136	Identification of the first glyphosate transporter by genomic adaptation. <i>Environmental Microbiology</i> , 2019, 21, 1287-1305.	3.8	36
137	Proposal for the reclassification of obligately purine-fermenting bacteria <i>Clostridium acidurici</i> (Barker 1938) and <i>Clostridium purinilyticum</i> (D'Arre et al. 1981) as <i>Gottschalkia acidurici</i> gen. nov. comb. nov. and <i>Gottschalkia purinilytica</i> comb. nov. and of <i>Eubacterium angustum</i> (Beuscher and Tj ETQq1 1 0.784314 rgB4/Overlook International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2711-2719.	1.7	36
138	Genome Sequence of <i>Brevibacillus laterosporus</i> LMG 15441, a Pathogen of Invertebrates. <i>Journal of Bacteriology</i> , 2011, 193, 5535-5536.	2.2	35
139	Life based on phosphite: a genome-guided analysis of <i>Desulfotignum phosphitoxidans</i> . <i>BMC Genomics</i> , 2013, 14, 753.	2.8	35
140	Effects of Halide Ions on the Carbamidocyclophane Biosynthesis in <i>Nostoc</i> sp. CAVN2. <i>Marine Drugs</i> , 2016, 14, 21.	4.6	35
141	Status quo in physiological proteomics of the uncultured <i>Riftia pachyptila</i> endosymbiont. <i>Proteomics</i> , 2011, 11, 3106-3117.	2.2	34
142	Aerobic and anaerobic methane oxidation in terrestrial mud volcanoes in the Northern Apennines. <i>Sedimentary Geology</i> , 2012, 263-264, 210-219.	2.1	34
143	Comprehensive molecular, genomic and phenotypic analysis of a major clone of <i>Enterococcus faecalis</i> MLST ST40. <i>BMC Genomics</i> , 2015, 16, 175.	2.8	33
144	Nitrile-Degrading Bacteria Isolated from Compost. <i>Frontiers in Environmental Science</i> , 2017, 5, .	3.3	33

#	ARTICLE	IF	CITATIONS
145	Genome sequence of the sulfur-oxidizing <i>Bathymodiolus thermophilus</i> gill endosymbiont. <i>Standards in Genomic Sciences</i> , 2017, 12, 50.	1.5	32
146	Microbial community composition and dynamics in high-temperature biogas reactors using industrial bioethanol waste as substrate. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 9095-9106.	3.6	31
147	Whole-Genome Draft Sequences of Six Commensal Fecal and Six Mastitis-Associated <i>Escherichia coli</i> Strains of Bovine Origin. <i>Genome Announcements</i> , 2016, 4, .	0.8	31
148	Calcium dynamics in microbialite-forming exopolymer-rich mats on the atoll of <i>Kiritimati</i> , Republic of Kiribati, Central Pacific. <i>Geobiology</i> , 2015, 13, 170-180.	2.4	30
149	Isolation of a new Thermoanaerobacterium thermosaccharolyticum strain (FH1) producing a thermostable dextranase.. <i>Journal of General and Applied Microbiology</i> , 2001, 47, 187-192.	0.7	29
150	The inhibiting effect of nitrate fertilisation on methane uptake of a temperate forest soil is influenced by labile carbon. <i>Biology and Fertility of Soils</i> , 2012, 48, 621-631.	4.3	29
151	A Terpene Synthase Is Involved in the Synthesis of the Volatile Organic Compound Sodorifen of <i>Serratia plymuthica</i> 4Rx13. <i>Frontiers in Microbiology</i> , 2016, 7, 737.	3.5	29
152	Reconstruction of the Metabolic Potential of Acidophilic Sideroxydans Strains from the Metagenome of an Microaerophilic Enrichment Culture of Acidophilic Iron-Oxidizing Bacteria from a Pilot Plant for the Treatment of Acid Mine Drainage Reveals Metabolic Versatility and Adaptation to Life at Low pH. <i>Frontiers in Microbiology</i> , 2016, 7, 2082.	3.5	29
153	Topoisomerase IV can functionally replace all type 1A topoisomerases in <i>Bacillus subtilis</i> . <i>Nucleic Acids Research</i> , 2019, 47, 5231-5242.	14.5	29
154	Genomic features and insights into the biology of <i>Mycoplasma fermentans</i> . <i>Microbiology (United Kingdom)</i> , 2018, 158, 1075-1084.	1.8	28
155	Estimates of Soil Bacterial Ribosome Content and Diversity Are Significantly Affected by the Nucleic Acid Extraction Method Employed. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2595-2607.	3.1	28
156	Potentially Active Iron, Sulfur, and Sulfate Reducing Bacteria in Skagerrak and Bothnian Bay Sediments. <i>Geomicrobiology Journal</i> , 2017, 34, 840-850.	2.0	28
157	Comparative Genomics and Description of Putative Virulence Factors of <i>Melissococcus plutonius</i> , the Causative Agent of European Foulbrood Disease in Honey Bees. <i>Genes</i> , 2018, 9, 419.	2.4	28
158	Essentiality of c-di-AMP in <i>Bacillus subtilis</i> : Bypassing mutations converge in potassium and glutamate homeostasis. <i>PLoS Genetics</i> , 2021, 17, e1009092.	3.5	28
159	Impact of grassland management regimes on bacterial endophyte diversity differs with grass species. <i>Letters in Applied Microbiology</i> , 2016, 62, 323-329.	2.2	27
160	Permanent draft genome sequence of <i>Acidiphilium</i> sp. JA12-A1. <i>Standards in Genomic Sciences</i> , 2015, 10, 56.	1.5	26
161	Functional Screening of Hydrolytic Activities Reveals an Extremely Thermostable Cellulase from a Deep-Sea Archaeon. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 95.	4.1	26
162	Complete Genome Sequences of <i>Escherichia coli</i> Strains 1303 and ECC-1470 Isolated from Bovine Mastitis. <i>Genome Announcements</i> , 2015, 3, .	0.8	26

#	ARTICLE	IF	CITATIONS
163	Contrasting effects of grassland management modes on species-abundance distributions of multiple groups. <i>Agriculture, Ecosystems and Environment</i> , 2017, 237, 143-153.	5.3	26
164	Prevalence and Strain Characterization of Clostridioides ( <i>Clostridium</i> ) <i>difficile</i> in Representative Regions of Germany, Ghana, Tanzania and Indonesia – A Comparative Multi-Center Cross-Sectional Study. <i>Frontiers in Microbiology</i> , 2018, 9, 1843.	3.5	26
165	Cobaviruses – a new globally distributed phage group infecting <i>Rhodobacteraceae</i> in marine ecosystems. <i>ISME Journal</i> , 2019, 13, 1404-1421.	9.8	26
166	Enhancement of gene detection frequencies by combining DNA-based stable-isotope probing with the construction of metagenomic DNA libraries. <i>World Journal of Microbiology and Biotechnology</i> , 2006, 22, 363-368.	3.6	25
167	Complete Genome Sequence of the Type Strain of the Acetogenic Bacterium <i>Moorella thermoacetica</i> DSM 521 <sup>T</sup> . <i>Genome Announcements</i> , 2015, 3, .	0.8	25
168	Deciphering bacterial and fungal endophyte communities in leaves of two maple trees with green islands. <i>Scientific Reports</i> , 2019, 9, 14183.	3.3	25
169	Signal peptide peptidase activity connects the unfolded protein response to plant defense suppression by <i>Ustilago maydis</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007734.	4.7	25
170	Discovery of novel community-relevant small proteins in a simplified human intestinal microbiome. <i>Microbiome</i> , 2021, 9, 55.	11.1	24
171	Complete Genome Sequences of the Chemolithoautotrophic Oligotropha carboxidovorans Strains OM4 and OM5. <i>Journal of Bacteriology</i> , 2011, 193, 5043-5043.	2.2	23
172	Size unlimited markerless deletions by a transconjugative plasmid-system in <i>Bacillus licheniformis</i> . <i>Journal of Biotechnology</i> , 2013, 167, 365-369.	3.8	23
173	Bacterial succession along a sediment porewater gradient at Lake Neusiedl in Austria. <i>Scientific Data</i> , 2019, 6, 163.	5.3	23
174	The <i>Bacillus subtilis</i> Minimal Genome Compendium. <i>ACS Synthetic Biology</i> , 2021, 10, 2767-2771.	3.8	23
175	Hierarchical mutational events compensate for glutamate auxotrophy of a <i>Bacillus subtilis</i> <i>gltC</i> mutant. <i>Environmental Microbiology Reports</i> , 2017, 9, 279-289.	2.4	22
176	Functional Metagenomics Reveals an Overlooked Diversity and Novel Features of Soil-Derived Bacterial Phosphatases and Phytases. <i>MBio</i> , 2019, 10, .	4.1	22
177	Shifts in root and soil chemistry drive the assembly of belowground fungal communities in tropical land-use systems. <i>Soil Biology and Biochemistry</i> , 2021, 154, 108140.	8.8	22
178	Diversity and metagenome analysis of a hydrocarbon-degrading bacterial consortium from asphalt lakes located in Wietze, Germany. <i>AMB Express</i> , 2021, 11, 89.	3.0	22
179	Cysteine: an overlooked energy and carbon source. <i>Scientific Reports</i> , 2021, 11, 2139.	3.3	22
180	Insights into the Genome of the Enteric Bacterium <i>Escherichia blattae</i> : Cobalamin (B <sub>12</sub> ) Biosynthesis, B <sub>12</sub> -Dependent Reactions, and Inactivation of the Gene Region Encoding B <sub>12</sub> -Dependent Glycerol Dehydratase by a New Mu-Like Prophage. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2004, 8, 150-168.	1.0	21

#	ARTICLE	IF	CITATIONS
181	Complete Genome Sequence of the Solvent Producer <i>Clostridium saccharobutylicum</i> NCP262 (DSM) Tj ETQq1 1 0.784314 rgBT /Overlo	0.8	21
182	Complete Genome Sequence of the Solvent Producer <i>Clostridium saccharoperbutylacetonicum</i> Strain DSM 14923. <i>Genome Announcements</i> , 2014, 2, .	0.8	21
183	Complete Genome Sequence of the Acetogenic Bacterium <i>Moorella thermoacetica</i> DSM 2955 <sup>T</sup>. <i>Genome Announcements</i> , 2015, 3, .	0.8	21
184	The consequence of an additional NADH dehydrogenase paralog on the growth of <i>Gluconobacter oxydans</i> DSM3504. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 375-386.	3.6	21
185	Trophic and Non-Trophic Interactions in a Biodiversity Experiment Assessed by Next-Generation Sequencing. <i>PLoS ONE</i> , 2016, 11, e0148781.	2.5	21
186	A novel, versatile family IV carboxylesterase exhibits high stability and activity in a broad pH spectrum. <i>Biotechnology Letters</i> , 2017, 39, 577-587.	2.2	21
187	Soil and root nutrient chemistry structure root-associated fungal assemblages in temperate forests. <i>Environmental Microbiology</i> , 2020, 22, 3081-3095.	3.8	21
188	Authigenic formation of Ca-Mg carbonates in the shallow alkaline Lake Neusiedl, Austria. <i>Biogeosciences</i> , 2020, 17, 2085-2106.	3.3	21
189	Complete Genome Sequence of <i>Staphylococcus aureus</i> 6850, a Highly Cytotoxic and Clinically Virulent Methicillin-Sensitive Strain with Distant Relatedness to Prototype Strains. <i>Genome Announcements</i> , 2013, 1, .	0.8	20
190	Complete Genome Sequence of <i>Geobacillus</i> sp. Strain GHH01, a Thermophilic Lipase-Secreting Bacterium. <i>Genome Announcements</i> , 2013, 1, e0009213.	0.8	20
191	Complete Genome Sequence of <i>Mannheimia haemolytica</i> Strain 42548 from a Case of Bovine Respiratory Disease. <i>Genome Announcements</i> , 2013, 1, .	0.8	20
192	Screening of Metagenomic and Genomic Libraries Reveals Three Classes of Bacterial Enzymes That Overcome the Toxicity of Acrylate. <i>PLoS ONE</i> , 2014, 9, e97660.	2.5	20
193	Complete Genome Sequence of the Nitrogen-Fixing and Solvent-Producing <i>Clostridium pasteurianum</i> DSM 525. <i>Genome Announcements</i> , 2015, 3, .	0.8	20
194	Agroforestry Management Systems Drive the Composition, Diversity, and Function of Fungal and Bacterial Endophyte Communities in <i>Theobroma Cacao</i> Leaves. <i>Microorganisms</i> , 2020, 8, 405.	3.6	20
195	Two Ways To Convert a Low-Affinity Potassium Channel to High Affinity: Control of <i>Bacillus subtilis</i> KtrCD by Glutamate. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	20
196	Living in a Puddle of Mud: Isolation and Characterization of Two Novel Caulobacteraceae Strains <i>Brevundimonas pondensis</i> sp. nov. and <i>Brevundimonas goettingensis</i> sp. nov.. <i>Applied Microbiology</i> , 2021, 1, 38-59.	1.6	20
197	Identification of the syntrophic partners in a coculture coupling anaerobic methanol oxidation to Fe(III) reduction. <i>FEMS Microbiology Letters</i> , 1999, 180, 197-203.	1.8	19
198	Genome Sequence of the Polysaccharide-Degrading, Thermophilic Anaerobe <i>Spirochaeta thermophila</i> DSM 6192. <i>Journal of Bacteriology</i> , 2010, 192, 6492-6493.	2.2	19

#	ARTICLE	IF	CITATIONS
199	Construction of Small-Insert and Large-Insert Metagenomic Libraries. <i>Methods in Molecular Biology</i> , 2010, 668, 39-50.	0.9	19
200	Fermentation stage-dependent adaptations of <i>Bacillus licheniformis</i> during enzyme production. <i>Microbial Cell Factories</i> , 2013, 12, 120.	4.0	19
201	<i>Legionella oakridgensis</i> ATCC 33761 genome sequence and phenotypic characterization reveals its replication capacity in amoebae. <i>International Journal of Medical Microbiology</i> , 2013, 303, 514-528.	3.6	19
202	Metagenomic and Metatranscriptomic Analyses of Bacterial Communities Derived From a Calcifying Karst Water Creek Biofilm and Tufa. <i>Geomicrobiology Journal</i> , 2015, 32, 316-331.	2.0	19
203	<i>Entomobacter blattae</i> gen. nov., sp. nov., a new member of the Acetobacteraceae isolated from the gut of the cockroach <i>Gromphadorhina portentosa</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	1.7	19
204	Drivers of gut microbiome variation within and between groups of a wild Malagasy primate. <i>Microbiome</i> , 2022, 10, 28.	11.1	19
205	Complete Genome Sequence of <i>Clostridium stercorarium</i> subsp. <i>stercorarium</i> Strain DSM 8532, a Thermophilic Degrader of Plant Cell Wall Fibers. <i>Genome Announcements</i> , 2013, 1, e0007313.	0.8	18
206	First Insights into the Completely Annotated Genome Sequence of <i>Bacillus licheniformis</i> Strain 9945A. <i>Genome Announcements</i> , 2013, 1, .	0.8	18
207	Distinct compositions of free-living, particle-associated and benthic communities of the <i>Roseobacter</i> group in the North Sea. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv145.	2.7	18
208	FnrL and Three Dnr Regulators Are Used for the Metabolic Adaptation to Low Oxygen Tension in <i>Dinoroseobacter shibae</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 642.	3.5	18
209	Changes of DNA topology affect the global transcription landscape and allow rapid growth of a <i>Bacillus subtilis</i> mutant lacking carbon catabolite repression. <i>Metabolic Engineering</i> , 2018, 45, 171-179.	7.0	18
210	Impact of Nitriles on Bacterial Communities. <i>Frontiers in Environmental Science</i> , 2019, 7, .	3.3	18
211	Genome Sequence of the Caproic Acid-Producing Bacterium <i>Caproiciproducens galactitolivorans</i> BS-1 (JCM 30532). <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	18
212	One size fits all? Relationships among group size, health, and ecology indicate a lack of an optimal group size in a wild lemur population. <i>Behavioral Ecology and Sociobiology</i> , 2019, 73, 1.	1.4	18
213	<i>Pseudoceanicola algae</i> sp. nov., isolated from the marine macroalga <i>Fucus spiralis</i> , shows genomic and physiological adaptations for an algae-associated lifestyle. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126166.	2.8	18
214	Enhancing rhizoremediation of petroleum hydrocarbons through bioaugmentation with a plant growth-promoting bacterial consortium. <i>Chemosphere</i> , 2022, 289, 133143.	8.2	18
215	Significance of gene variants for the functional biogeography of the near-surface Atlantic Ocean microbiome. <i>Nature Communications</i> , 2022, 13, 456.	12.8	18
216	Deconstructing <i>Methanosarcina acetivorans</i> into an acetogenic archaeon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	18

#	ARTICLE	IF	CITATIONS
217	The Anaerobic Way of Life. , 2006, , 86-101.		17
218	Complete Genome Sequence of Carnobacterium sp. 17-4. Journal of Bacteriology, 2011, 193, 3403-3404.	2.2	17
219	Unravelling the complete genome sequence of Advenella mimigardefordensis strain DPN7T and novel insights in the catabolism of the xenobiotic polythioester precursor 3,3-dithiodipropionate. Microbiology (United Kingdom), 2014, 160, 1401-1416.	1.8	17
220	Genome Sequence of the Acetogenic Bacterium Oxobacter pfennigii DSM 3222 <sup>T</sup>. Genome Announcements, 2015, 3, .	0.8	17
221	Complete Genome Sequence of Bacillus subtilis subsp. subtilis Strain 3NA. Genome Announcements, 2015, 3, .	0.8	17
222	Expression of membrane-bound dehydrogenases from a mother of vinegar metagenome in Gluconobacter oxydans. Applied Microbiology and Biotechnology, 2017, 101, 7901-7912.	3.6	17
223	Comparative Genomic Analysis of Members of the Genera <i>Methanosphaera</i> and <i>Methanobrevibacter</i> Reveals Distinct Clades with Specific Potential Metabolic Functions. Archaea, 2018, 2018, 1-9.	2.3	17
224	First Report on the Plasmidome From a High-Altitude Lake of the Andean Puna. Frontiers in Microbiology, 2020, 11, 1343.	3.5	17
225	Morphological and Metabolite Responses of Potatoes under Various Phosphorus Levels and Their Amelioration by Plant Growth-Promoting Rhizobacteria. International Journal of Molecular Sciences, 2021, 22, 5162.	4.1	17
226	Role of Wax Ester Synthase/Acyl Coenzyme A:Diacylglycerol Acyltransferase in Oleaginous Streptomyces sp. Strain G25. Applied and Environmental Microbiology, 2016, 82, 5969-5981.	3.1	16
227	Biochemical profiles of two thermostable and organic solvent-tolerant esterases derived from a compost metagenome. Applied Microbiology and Biotechnology, 2019, 103, 3421-3437.	3.6	16
228	Resistance to serine in <i>Bacillus subtilis</i>: identification of the serine transporter <sc>YbeC</sc> and of a metabolic network that links serine and threonine metabolism. Environmental Microbiology, 2020, 22, 3937-3949.	3.8	16
229	Growth temperature-dependent activity of glycerol dehydratase in Escherichia coli expressing the Citrobacter freundii dha regulon. FEMS Microbiology Letters, 1992, 100, 281-285.	1.8	16
230	Dietary shifts and social interactions drive temporal fluctuations of the gut microbiome from wild redfronted lemurs. ISME Communications, 2022, 2, .	4.2	16
231	Novel organic solvent-tolerant esterase isolated by metagenomics: insights into the lipase/esterase classification. Revista Argentina De Microbiologia, 2013, 45, 3-12.	0.7	16
232	The Na <sup>+</sup> -translocating ATPase of Acetobacterium woodii is a F1F0-type enzyme as deduced from the primary structure of its Î², Î³ and Î¼ subunits. Biochimica Et Biophysica Acta - Bioenergetics, 1995, 1229, 393-397.	1.0	15
233	Complete Genome Sequence of the B 12 -Producing Shimwellia blattae Strain DSM 4481, Isolated from a Cockroach. Journal of Bacteriology, 2012, 194, 4436-4436.	2.2	15
234	Diversity Measures in Environmental Sequences Are Highly Dependent on Alignment Quality Data from ITS and New LSU Primers Targeting Basidiomycetes. PLoS ONE, 2012, 7, e32139.	2.5	15



#	ARTICLE	IF	CITATIONS
235	Closed Genome Sequence of <i>Clostridium pasteurianum</i> ATCC 6013. <i>Genome Announcements</i> , 2015, 3, .	0.8	15
236	Gut bacterial communities of diarrheic patients with indications of <i>Clostridioides difficile</i> infection. <i>Scientific Data</i> , 2017, 4, 170152.	5.3	15
237	Impact of sea level change on coastal soil organic matter, priming effects and prokaryotic community assembly. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	15
238	Land Use Change and Water Quality Use for Irrigation Alters Drylands Soil Fungal Community in the Mezquital Valley, Mexico. <i>Frontiers in Microbiology</i> , 2019, 10, 1220.	3.5	15
239	Seasonal variation in the diet of the serotine bat ( <i>Eptesicus serotinus</i> ): A high-resolution analysis using DNA metabarcoding. <i>Basic and Applied Ecology</i> , 2020, 49, 1-12.	2.7	15
240	First Complete Genome Sequences of <i>Janthinobacterium lividum</i> EIF1 and EIF2 and Their Comparative Genome Analysis. <i>Genome Biology and Evolution</i> , 2020, 12, 1782-1788.	2.5	15
241	Molecular Identification and In Vitro Plant Growth-Promoting Activities of Culturable Potato ( <i>Solanum tuberosum</i> L.) Rhizobacteria in Tanzania. <i>Potato Research</i> , 2021, 64, 67-95.	2.7	15
242	Tree species composition and soil properties in pure and mixed beech-conifer stands drive soil fungal communities. <i>Forest Ecology and Management</i> , 2021, 502, 119709.	3.2	15
243	Structural peculiarities of linear megaplasmid, pLMA1, from <i>Micrococcus luteus</i> interfere with pyrosequencing reads assembly. <i>Biotechnology Letters</i> , 2010, 32, 1853-1862.	2.2	14
244	Genome Sequence of <i>Paenibacillus alvei</i> DSM 29, a Secondary Invader during European Foulbrood Outbreaks. <i>Journal of Bacteriology</i> , 2012, 194, 6365-6365.	2.2	14
245	<i>N</i> -Acylated Alanine Methyl Esters (NAMEs) from <i>Roseovarius tolerans</i> , Structural Analogs of Quorum Sensing Autoinducers, <i>N</i> -Acylhomoserine Lactones. <i>Chemistry and Biodiversity</i> , 2013, 10, 1559-1573.	2.1	14
246	Bacteriohopanepolyols in a stratified cyanobacterial mat from Kiritimati (Christmas Island, Kiribati). <i>Organic Geochemistry</i> , 2013, 55, 55-62.	1.8	14
247	Complete Genome Sequence of pAP13, a Large Linear Plasmid of a <i>Brevibacterium</i> Strain Isolated from a Saline Lake at 4,200 Meters above Sea Level in Argentina. <i>Genome Announcements</i> , 2013, 1, .	0.8	14
248	First Complete Sequence of a Giant Linear Plasmid from a <i>Micrococcus</i> Strain Isolated from an Extremely High-Altitude Lake. <i>Genome Announcements</i> , 2013, 1, .	0.8	13
249	Genome-guided insights into the versatile metabolic capabilities of the mercaptosuccinate-utilizing <i>proteobacterium</i> <i>V</i> <i>ariovorax paradoxus</i> strain <i>B</i> . <i>Environmental Microbiology</i> , 2014, 16, 3370-3386.	3.8	13
250	Cell physiology of the biotechnological relevant bacterium <i>Bacillus pumilus</i> —An omics-based approach. <i>Journal of Biotechnology</i> , 2014, 192, 204-214.	3.8	13
251	Genome sequence of <i>Clostridium sporogenes</i> DSM 795T, an amino acid-degrading, nontoxic surrogate of neurotoxin-producing <i>Clostridium botulinum</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 40.	1.5	13
252	High quality draft genome of <i>Lactobacillus kunkeei</i> EFB6, isolated from a German European foulbrood outbreak of honeybees. <i>Standards in Genomic Sciences</i> , 2015, 10, 16.	1.5	13



#	ARTICLE	IF	CITATIONS
253	Complete genome sequence of the lipase producing strain <i>Burkholderia glumae</i> PG1. <i>Journal of Biotechnology</i> , 2015, 204, 3-4.	3.8	13
254	Genome Sequence of the Acetogenic Bacterium <i>Butyribacterium methylotrophicum</i> DSM 3468 <sup>T</sup>. <i>Genome Announcements</i> , 2016, 4, .	0.8	13
255	Mutations improving production and secretion of extracellular lipase by <i>Burkholderia glumae</i> PG1. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 1265-1273.	3.6	13
256	Complementary Metaproteomic Approaches to Assess the Bacterioplankton Response toward a Phytoplankton Spring Bloom in the Southern North Sea. <i>Frontiers in Microbiology</i> , 2017, 8, 442.	3.5	13
257	Metagenome Assembly and Metagenome-Assembled Genome Sequences from a Historical Oil Field Located in Wietze, Germany. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	13
258	Screening Methods for Isolation of Biocontrol Epiphytic Yeasts against <i>Penicillium digitatum</i> in Lemons. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 166.	3.5	13
259	CAZymes in <i>Maribacter dokdonensis</i> 62â€“1 From the Patagonian Shelf: Genomics and Physiology Compared to Related Flavobacteria and a Co-occurring <i>Alteromonas</i> Strain. <i>Frontiers in Microbiology</i> , 2021, 12, 628055.	3.5	13
260	Genome and Proteome Analysis of <i>Rhodococcus erythropolis</i> MI2: Elucidation of the 4,4-Å-Dithiodibutyric Acid Catabolism. <i>PLoS ONE</i> , 2016, 11, e0167539.	2.5	12
261	Genome Sequence of the Acetogenic Bacterium <i>Acetobacterium wieringae</i> DSM 1911 <sup>T</sup>. <i>Genome Announcements</i> , 2016, 4, .	0.8	12
262	Draft Genome Sequence of <i>Cutaneotrichosporon curvatus</i> DSM 101032 (Formerly <i>Cryptococcus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4, .	0.8	12
263	Complete Genome Sequence of the Autotrophic Acetogen <i>Clostridium formicaceticum</i> DSM 92 <sup>T</sup> Using Nanopore and Illumina Sequencing Data. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
264	Phenotypic and Transcriptomic Analyses of Seven Clinical <i>Stenotrophomonas maltophilia</i> Isolates Identify a Small Set of Shared and Commonly Regulated Genes Involved in the Biofilm Lifestyle. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	12
265	Genome-Based Comparison of All Species of the Genus <i>Moorella</i> , and Status of the Species <i>Moorella thermoacetica</i> and <i>Moorella thermoautotrophica</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 3070.	3.5	12
266	Metagenomes of Wastewater at Different Treatment Stages in Central Germany. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	12
267	A Novel Carboxylesterase Derived from a Compost Metagenome Exhibiting High Stability and Activity towards High Salinity. <i>Genes</i> , 2021, 12, 122.	2.4	12
268	Quasi-essentiality of RNase Y in <i>Bacillus subtilis</i> is caused by its critical role in the control of mRNA homeostasis. <i>Nucleic Acids Research</i> , 2021, 49, 7088-7102.	14.5	12
269	<i>Sphingomonas jeddahensis</i> sp. nov., isolated from Saudi Arabian desert soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 4057-4063.	1.7	12
270	Construction of Environmental Libraries for Functional Screening of Enzyme Activity. , 0, , 63-78.		11

#	ARTICLE	IF	CITATIONS
271	Complete Genome Sequence of Amino Acid-Utilizing Eubacterium acidaminophilum al-2 (DSM 3953). Genome Announcements, 2014, 2, .	0.8	11
272	Genome sequence of Pedobacter glucosidilyticus DD6b, isolated from zooplankton Daphnia magna. Standards in Genomic Sciences, 2015, 10, 100.	1.5	11
273	Complete Genome Sequence of Rnf- and Cytochrome-Containing Autotrophic Acetogen Clostridium aceticum DSM 1496. Genome Announcements, 2015, 3, .	0.8	11
274	Complete Genome Sequence of the Clostridium difficile Type Strain DSM 1296 T. Genome Announcements, 2015, 3, .	0.8	11
275	Complete Genome Sequence of the Linear Plasmid pJD12 Hosted by <i>Micrococcus</i> sp. D12, Isolated from a High-Altitude Volcanic Lake in Argentina. Genome Announcements, 2015, 3, .	0.8	11
276	Soil bacterial community structures in relation to different oil palm management practices. Scientific Data, 2020, 7, 421.	5.3	11
277	Saprotrophic and Ectomycorrhizal Fungi Contribute Differentially to Organic P Mobilization in Beech-Dominated Forest Ecosystems. Frontiers in Forests and Global Change, 2020, 3, .	2.3	11
278	Characterization of glyphosate-resistant <i>Burkholderia anthina</i> and <i>Burkholderia cenocepacia</i> isolates from a commercial Roundup® solution. Environmental Microbiology Reports, 2022, 14, 70-84.	2.4	11
279	Transcriptional Landscape of Ectomycorrhizal Fungi and Their Host Provides Insight into N Uptake from Forest Soil. MSystems, 2022, 7, e0095721.	3.8	11
280	Complete Genome Sequence of the Urethral Catheter Isolate Myroides sp. A21. Genome Announcements, 2015, 3, .	0.8	10
281	Complete Genome Sequence of the Amino Acid-Fermenting <i>Clostridium propionicum</i> X2 (DSM) Tj ETQq1 1 0.784314 18 BT /Over	0.8	10
282	Function-Based Metagenomic Library Screening and Heterologous Expression Strategy for Genes Encoding Phosphatase Activity. Methods in Molecular Biology, 2017, 1539, 249-260.	0.9	10
283	Native Cultivable Bacteria from the Blueberry Microbiome as Novel Potential Biocontrol Agents. Microorganisms, 2022, 10, 969.	3.6	10
284	The genome of Variovorax paradoxus strain TBEA6 provides new understandings for the catabolism of 3,3-thiodipropionic acid and hence the production of polythioesters. Journal of Biotechnology, 2015, 209, 85-95.	3.8	9
285	Construction of Small-Insert and Large-Insert Metagenomic Libraries. Methods in Molecular Biology, 2017, 1539, 1-12.	0.9	9
286	Draft Genome Sequence of the Butanoic Acid-Producing Bacterium Clostridium luticellarii DSM 29923, Used for Strong Aromatic Chinese Liquor Production. Genome Announcements, 2018, 6, .	0.8	9
287	Editorial: Molecular Ecology and Genetic Diversity of the Roseobacter Clade. Frontiers in Microbiology, 2018, 9, 1185.	3.5	9
288	Effects of a high-cultivation temperature on the physiology of three different Yarrowia lipolytica strains. FEMS Yeast Research, 2019, 19, .	2.3	9

#	ARTICLE	IF	CITATIONS
289	Primary Production in the Water Column as Major Structuring Element of the Biogeographical Distribution and Function of Archaea in Deep-Sea Sediments of the Central Pacific Ocean. <i>Archaea</i> , 2019, 2019, 1-12.	2.3	9
290	Legacy Effects Overshadow Tree Diversity Effects on Soil Fungal Communities in Oil Palm-Enrichment Plantations. <i>Microorganisms</i> , 2020, 8, 1577.	3.6	9
291	From sequence to function: a new workflow for nitrilase identification. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 4957-4970.	3.6	9
292	Predicting the Metabolic Potential of the Novel Iron Oxidising Bacterium " <i>Ferroplasma</i> " sp. JA12 Using Comparative Genomics. <i>Advanced Materials Research</i> , 0, 825, 153-156.	0.3	8
293	First Insights into the Genome of the Amino Acid-Metabolizing Bacterium <i>Clostridium litorale</i> DSM 5388. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
294	Genome Sequence of the Moderately Acidophilic Sulfate-Reducing Firmicute <i>Desulfosporosinus acididurans</i> (Strain M1 T). <i>Genome Announcements</i> , 2015, 3, .	0.8	8
295	Complete Genome Sequence of <i>Bacillus subtilis</i> subsp. <i>subtilis</i> Strain 6. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
296	Links between seawater flooding, soil ammonia oxidiser communities and their response to changes in salinity. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	8
297	Draft Genome Sequence of the Thermophilic Acetogen <i>Moorella humiferrea</i> DSM 23265. <i>Genome Announcements</i> , 2018, 6, .	0.8	8
298	Draft Genome Sequence of the Hydrogenogenic Carboxydrotroph <i>Moorella stamsii</i> DSM 26271. <i>Genome Announcements</i> , 2018, 6, .	0.8	8
299	Characteristics of the First Protein Tyrosine Phosphatase with Phytase Activity from a Soil Metagenome. <i>Genes</i> , 2019, 10, 101.	2.4	8
300	Lactate metabolism in strictly anaerobic microorganisms with a soluble NAD <sup>+</sup> -dependent lactate dehydrogenase. <i>Environmental Microbiology</i> , 2021, 23, 4661-4672.	3.8	8
301	Thermostable Xylanase and ̢-Glucanase Derived from the Metagenome of the Avachinsky Crater in Kamchatka (Russia). <i>Current Biotechnology</i> , 2013, 2, 284-293.	0.4	8
302	Down in the pond: Isolation and characterization of a new <i>Serratia marcescens</i> strain (LVF3) from the surface water near frog's lettuce ( <i>Groenlandia densa</i> ). <i>PLoS ONE</i> , 2021, 16, e0259673.	2.5	8
303	Thermophilic Composting of Human Feces: Development of Bacterial Community Composition and Antimicrobial Resistance Gene Pool. <i>Frontiers in Microbiology</i> , 2022, 13, 824834.	3.5	8
304	Purification and characterization of an extracellular lipase from <i>Clostridium tetanomorphum</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2006, 22, 431-435.	3.6	7
305	First Insights into the Genome Sequence of the Strictly Anaerobic Homoacetogenic <i>Sporomusa sphaeroides</i> Strain E (DSM 2875). <i>Genome Announcements</i> , 2017, 5, .	0.8	7
306	The Draft Genome of the Non-Host-Associated <i>Methanobrevibacter arboriphilus</i> Strain DH1 Encodes a Large Repertoire of Adhesin-Like Proteins. <i>Archaea</i> , 2017, 2017, 1-9.	2.3	7

#	ARTICLE	IF	CITATIONS
307	Draft Genome Sequence of the Endophyte <i>Bacillus mycoides</i> Strain GM6LP Isolated from <i>Lolium perenne</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	7
308	Draft Genome Sequences of the Obligatory Marine Myxobacterial Strains <i>Enhygromyxa salina</i> SWB005 and SWB007. <i>Genome Announcements</i> , 2018, 6, .	0.8	7
309	Complete Genome Sequence of the <i>Methanococcus maripaludis</i> Type Strain JJ (DSM 2067), a Model for Selenoprotein Synthesis in Archaea. <i>Genome Announcements</i> , 2018, 6, .	0.8	7
310	Genome sequence analysis of the temperate bacteriophage TBP2 of the solvent producer <i>Clostridium saccharoperbutylacetonicum</i> N1-4 (HMT, ATCC 27021). <i>FEMS Microbiology Letters</i> , 2020, 367, .	1.8	7
311	Functional Redundancy and Specialization of the Conserved Cold Shock Proteins in <i>Bacillus subtilis</i> . <i>Microorganisms</i> , 2021, 9, 1434.	3.6	7
312	Energy-conserving dimethyl sulfoxide reduction in the acetogenic bacterium <i>Moorella thermoacetica</i> . <i>Environmental Microbiology</i> , 2022, 24, 2000-2012.	3.8	7
313	<i>Agromyces archimandritae</i> sp. nov., isolated from the cockroach <i>Archimandrita tessellata</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	7
314	Seasonal and Zonal Succession of Bacterial Communities in North Sea Salt Marsh Sediments. <i>Microorganisms</i> , 2022, 10, 859.	3.6	7
315	Draft Genome Sequence of the Methanotrophic Gammaproteobacterium <i>Methyloglobulus morosus</i> DSM 22980 Strain KoM1. <i>Genome Announcements</i> , 2013, 1, .	0.8	6
316	Genome Sequence of the Acidophilic Iron Oxidizer <i>Ferrimicrobium acidiphilum</i> Strain T23. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
317	Draft Genome Sequence of Purine-Degrading <i>Clostridium cylindrosporium</i> HC-1 (DSM 605). <i>Genome Announcements</i> , 2015, 3, .	0.8	6
318	Genome Sequence of the Acidophilic Ferrous Iron-Oxidizing Isolate <i>Acidithrix ferrooxidans</i> Strain Py-F3, the Proposed Type Strain of the Novel Actinobacterial Genus <i>Acidithrix</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	6
319	Draft Genome Sequence of <i>Komagataeibacter europaeus</i> CECT 8546, a Cellulose-Producing Strain of Vinegar Elaborated by the Traditional Method. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
320	Genome Sequence of the Autotrophic Acetogen <i>Clostridium magnum</i> DSM 2767. <i>Genome Announcements</i> , 2016, 4, .	0.8	6
321	Draft Genome Sequence of the Strict Anaerobe <i>Clostridium neopropionicum</i> X4 (DSM 3847 T). <i>Genome Announcements</i> , 2016, 4, .	0.8	6
322	Draft Genome Sequence of <i>Pseudomonas putida</i> Strain GM4FR, an Endophytic Bacterium Isolated from <i>Festuca rubra</i> L. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
323	Draft Genome Sequence of <i>Komagataeibacter maltaceti</i> LMG 1529, a Vinegar-Producing Acetic Acid Bacterium Isolated from Malt Vinegar Brewery Acetifiers. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
324	Functional Metagenomics Reveals a New Catalytic Domain, the Metallo-β-Lactamase Superfamily Domain, Associated with Phytase Activity. <i>MSphere</i> , 2019, 4, .	2.9	6

#	ARTICLE	IF	CITATIONS
325	A 20â€b lineageâ€specific genomic region tames virulence in pathogenic amphidiploid <i>Verticillium longisporum</i> . <i>Molecular Plant Pathology</i> , 2021, 22, 939-953.	4.2	6
326	Metagenome-Assembled Genome Sequences from Different Wastewater Treatment Stages in Germany. <i>Microbiology Resource Announcements</i> , 2021, 10, e0050421.	0.6	6
327	Biochemistry of coenzyme B12-dependent glycerol and diol dehydratases and organization of the encoding genes. <i>FEMS Microbiology Reviews</i> , 1998, 22, 553-566.	8.6	6
328	Soil Layers Matter: Vertical Stratification of Root-Associated Fungal Assemblages in Temperate Forests Reveals Differences in Habitat Colonization. <i>Microorganisms</i> , 2021, 9, 2131.	3.6	6
329	Metagenomic Insights Into the Changes of Antibiotic Resistance and Pathogenicity Factor Pools Upon Thermophilic Composting of Human Excreta. <i>Frontiers in Microbiology</i> , 2022, 13, 826071.	3.5	6
330	Draft Genome Sequence of the Phenazine-Producing <i>Pseudomonas fluorescens</i> Strain 2-79. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
331	Draft Genome Sequence of <i>Bacillus pumilus</i> Strain GM3FR, an Endophyte Isolated from Aerial Plant Tissues of <i>Festuca rubra</i> L. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
332	Complete Genome Sequence of vB_BveP-Goe6, a Virus Infecting <i>Bacillus velezensis</i> FZB42. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
333	A metagenomic collection of novel and highly efficient biocatalysts for industrial biotechnology. <i>Impact</i> , 2018, 2018, 82-84.	0.1	5
334	Genome sequence of <i>Planktotalea frisia</i> type strain (SH6-1T), a representative of the <i>Roseobacter</i> group isolated from the North Sea during a phytoplankton bloom. <i>Standards in Genomic Sciences</i> , 2018, 13, 7.	1.5	5
335	Genome Sequence of <i>Komagataeibacter saccharivorans</i> Strain JH1, Isolated from Fruit Flies. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	5
336	Complete Genome Sequence of <i>Pseudomonas balearica</i> Strain EC28, an Iron-Oxidizing Bacterium Isolated from Corroded Steel. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	5
337	A <i>Bacillus subtilis</i> mutant suppresses vitamin B6 limitation by acquiring mutations enhancing <i>pdxS</i> gene dosage and ammonium assimilation. <i>Environmental Microbiology Reports</i> , 2021, 13, 218-233.	2.4	5
338	The carnitine degradation pathway of <i>Acinetobacter baumannii</i> and its role in virulence. <i>Environmental Microbiology</i> , 2022, 24, 4437-4448.	3.8	5
339	Draft Genome Sequence of <i>Serratia</i> sp. Strain DD3, Isolated from the Guts of <i>Daphnia magna</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	4
340	Draft Genome Sequence of Purine-Degrading <i>Gottschalkia purinilyticum</i> (Formerly <i>Clostridium</i> ) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 14	0.8	4
341	Draft Genome Sequence of the Strict Anaerobe <i>Clostridium homopropionicum</i> LuHBu1 (DSM 5847). <i>Genome Announcements</i> , 2015, 3, .	0.8	4
342	Complete Genome Sequence of the Nonpathogenic Soil-Dwelling Bacterium <i>Clostridium sporogenes</i> Strain NCIMB 10696. <i>Genome Announcements</i> , 2015, 3, .	0.8	4

#	ARTICLE	IF	CITATIONS
343	First Insights into the Draft Genome of <i>Clostridium colicanis</i> DSM 13634, Isolated from Canine Feces. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
344	Genetic Variability of Myxoma Virus Genomes. <i>Journal of Virology</i> , 2017, 91, .	3.4	4
345	Preliminary Investigation of Species Diversity of Rice Hopper Parasitoids in Southeast Asia. <i>Insects</i> , 2018, 9, 19.	2.2	4
346	First Insights Into Bacterial Gastrointestinal Tract Communities of the Eurasian Beaver ( <i>Castor fiber</i> ). <i>Frontiers in Microbiology</i> , 2019, 10, 1646.	3.5	4
347	Complete Genome Sequence of the Prototrophic <i>Bacillus subtilis</i> subsp. <i>subtilis</i> Strain SP1. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	4
348	Complete Genome Sequence of <i>Shewanella chilikensis</i> Strain DC57, Isolated from Corroded Seal Rings at a Floating Oil Production System in Australia. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	4
349	Early Effects of Fertilizer and Herbicide Reduction on Root-Associated Biota in Oil Palm Plantations. <i>Agronomy</i> , 2022, 12, 199.	3.0	4
350	DNA- and RNA-based bacterial communities and geochemical zonation under changing sediment porewater dynamics on the Aldabra Atoll. <i>Scientific Reports</i> , 2022, 12, 4257.	3.3	4
351	Comparative Genomics Underlines the Functional and Taxonomic Diversity of Novel <i>Ferroplasma</i> Related Iron Oxidizing Bacteria. <i>Advanced Materials Research</i> , 2015, 1130, 15-18.	0.3	3
352	Genome Sequence of the Acidophilic Sulfate-Reducing Peptococcaceae Strain CEB3. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
353	Genome sequence of <i>Shinella</i> sp. strain DD12, isolated from homogenized guts of starved <i>Daphnia magna</i> . <i>Standards in Genomic Sciences</i> , 2016, 11, 14.	1.5	3
354	Genome Sequence of Creatinine-Fermenting <i>Tissierella creatinophila</i> Strain KRE 4 (DSM) Tj ETQq0 0 0 rgBT / Overlock 10	0.8	3
355	Genome Sequence of the Homoacetogenic, Gram-Negative, Endospore-Forming Bacterium <i>Sporomusa acidovorans</i> DSM 3132. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
356	First Insights into the Genome Sequence of <i>Pseudomonas oleovorans</i> DSM 1045. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
357	Draft Genome Sequence of the Endophyte <i>Bacillus mycoides</i> Strain GM5LP Isolated from <i>Lolium perenne</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	3
358	Complete Genome Sequences of pLMA1 and pLMA7, Two Large Linear Plasmids of <i>Micrococcus</i> Strains Isolated from a High-Altitude Lake in Argentina. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
359	Distinct relationships between fluorescence in situ hybridization and 16S rRNA gene- and amplicon-based sequencing data of bacterioplankton lineages. <i>Systematic and Applied Microbiology</i> , 2019, 42, 126000.	2.8	3
360	Complete Genome of <i>Roseobacter ponti</i> DSM 106830T. <i>Genome Biology and Evolution</i> , 2020, 12, 1013-1018.	2.5	3



#	ARTICLE	IF	CITATIONS
361	Novel Antimicrobial Cellulose Fleece Inhibits Growth of Human-Derived Biofilm-Forming Staphylococci During the SIRIUS19 Simulated Space Mission. <i>Frontiers in Microbiology</i> , 2020, 11, 1626.	3.5	3
362	Growth of the acetogenic bacterium <i>Acetobacterium woodii</i> on glycerol and dihydroxyacetone. <i>Environmental Microbiology</i> , 2021, 23, 2648-2658.	3.8	3
363	Increased Butyrate Production in <i>Clostridium saccharoperbutylacetonicum</i> from Lignocellulose-Derived Sugars. <i>Applied and Environmental Microbiology</i> , 2022, , e0241921.	3.1	3
364	The Anaerobic Way of Life. , 2013, , 259-273.		2
365	Draft Genome Sequence of <i>Desulfotignum phosphitoxidans</i> DSM 13687 Strain FiPS-3. <i>Genome Announcements</i> , 2013, 1, .	0.8	2
366	Approaches in Metagenome Research: Progress and Challenges. , 2014, , 1-7.		2
367	Closed Genome Sequence of <i>Octadecabacter temperatus</i> SB1, the First Mesophilic Species of the Genus <i>Octadecabacter</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	2
368	Draft Genome Sequence of <i>Roseovarius tolerans</i> EL-164, a Producer of N -Acylated Alanine Methyl Esters and N -Acylhomoserine Lactones. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
369	Draft Genome Sequence of the Beneficial Rhizobacterium <i>Pseudomonas fluorescens</i> DSM 8569, a Natural Isolate of Oilseed Rape ( <i>Brassica napus</i> ). <i>Genome Announcements</i> , 2015, 3, .	0.8	2
370	First Insights into the Genome Sequence of the Halophilic Archaeon <i>Halalkalicoccus paucihalophilus</i> (DSM 24557). <i>Genome Announcements</i> , 2016, 4, .	0.8	2
371	Genome Sequence of the Poly-3-Hydroxybutyrate Producer <i>Clostridium acetireducens</i> DSM 10703. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
372	Insights into the Genome of the Anaerobic Acetogen <i>Sporomusa silvacetica</i> DSM 10669. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
373	Genome sequencing and description of <i>Oerskovia enterophila</i> VJag, an agar- and cellulose-degrading bacterium. <i>Standards in Genomic Sciences</i> , 2017, 12, 30.	1.5	2
374	Draft Genome Sequences of <i>Sphingomonas mucosissima</i> DSM 17494 and <i>Sphingomonas dokdonensis</i> DSM 21029. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
375	The unexpected function of a Flavin-dependent oxidoreductase (Fox) from <i>Variovorax paradoxus</i> TBEA6.. <i>FEMS Microbiology Letters</i> , 2018, 365, .	1.8	2
376	Draft Genome Sequence of <i>Bacillus</i> sp. Strain M21, Isolated from the Arid Area of Matmata, Tunisia. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
377	Draft Genome Sequence of the Endophyte <i>Paenibacillus</i> sp. Strain GM2FR Isolated from <i>Festuca rubra</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	2
378	Complete Genome Sequence of <i>Marinobacter</i> sp. Strain JH2, Isolated from Seawater of the Kiel Fjord. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2



#	ARTICLE	IF	CITATIONS
379	Metagenome Sequences of a Wastewater Treatment Plant Digester Sludge-Derived Enrichment Culture. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
380	Whole-Genome Sequences of Three Plant Growth-Promoting Rhizobacteria Isolated from <i>Solanum tuberosum</i> L. Rhizosphere in Tanzania. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
381	Complete Genome Sequence of <i>Stenotrophomonas indicatrix</i> DAIF1. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	2
382	Complete Genome Sequence of <i>Kinneretia</i> sp. Strain DAIF2, Isolated from a Freshwater Pond. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	2
383	<i>Pontibacillus</i> sp. ALD_SL1 and <i>Psychroflexus</i> sp. ALD_RP9, two novel moderately halophilic bacteria isolated from sediment and water from the Aldabra Atoll, Seychelles. <i>PLoS ONE</i> , 2021, 16, e0256639.	2.5	2
384	Growth temperature-dependent activity of glycerol dehydratase in <i>Escherichia coli</i> expressing the <i>Citrobacter freundii</i> <i>dha regulon</i> . <i>FEMS Microbiology Letters</i> , 1992, 100, 281-285.	1.8	2
385	Glycerol conversion to 1,3-propanediol by <i>Clostridium pasteurianum</i> : cloning and expression of the gene encoding 1,3-propanediol dehydrogenase. <i>FEMS Microbiology Letters</i> , 1997, 154, 337-345.	1.8	2
386	Properties and sequence of the coenzyme B12-dependent glycerol dehydratase of <i>Clostridium pasteurianum</i> . <i>FEMS Microbiology Letters</i> , 1998, 164, 21-28.	1.8	2
387	Assessment of the plasmidome of an extremophilic microbial community from the Diamante Lake, Argentina. <i>Scientific Reports</i> , 2021, 11, 21459.	3.3	2
388	Molecular Insight into Gene Response of Diorcinol- and Rubrolide-Treated Biofilms of the Emerging Pathogen <i>Stenotrophomonas maltophilia</i> . <i>Microbiology Spectrum</i> , 2022, , e0258221.	3.0	2
389	Glacier Metagenomics. , 2013, , 1-9.		1
390	First Insights into the Genome of <i>Fructobacillus</i> sp. EFB-N1, Isolated from Honey Bee Larva Infected with European Foulbrood. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
391	Genome Sequence of <i>Jannaschia aquimarina</i> GSW-M26, a Member of the <i>Roseobacter</i> Clade. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
392	Genome Sequence of the Facultative Anaerobe <i>Oerskovia enterophila</i> DFA-19 (DSM 43852 <sup>T</sup> ) Tj ETQq0.0 0 rgBT <sub>1</sub> /Overlock	0.8	1
393	First Insights into the Genome of the Moderately Thermophilic Bacterium <i>Clostridium tepidiprofundii</i> SG 508 T. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
394	Genome Sequence of Uric Acid-Fermenting <i>Eubacterium angustum</i> DSM 1989 T (MK-1). <i>Genome Announcements</i> , 2017, 5, .	0.8	1
395	First Insight into the Genome Sequence of <i>Clostridium thermobutyricum</i> DSM 4928, a Butyrate-Producing Moderate Thermophile. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
396	First Insights into the Genome Sequence of <i>Clostridium oryzae</i> DSM 28571, Isolated from the Soil of a Japanese Rice Field. <i>Genome Announcements</i> , 2017, 5, .	0.8	1

#	ARTICLE	IF	CITATIONS
397	First Insights into the Genome Sequence of the Cellulolytic Bacterium <i>Clostridium hungatei</i> DSM 14427. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
398	First Insights into the Genome Sequence of <i>Clostridium thermopalmarium</i> DSM 5974, a Butyrate-Producing Bacterium Isolated from Palm Wine. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
399	Metagenomic Screening for Lipolytic Genes Reveals an Ecology-Clustered Distribution Pattern. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
400	Complete Genome Sequence of <i>Alkalihalobacillus</i> sp. Strain LMS39, a Haloalkaliphilic Bacterium Isolated from a Hypersaline Lake. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.6	1
401	Physiological, Genomic, and Proteomic Characterization of New <i>Ferroplasma</i> Strains Obtained from a Pilot Plant for Mine-Water Treatment. <i>Advanced Materials Research</i> , 0, 825, 149-152.	0.3	0
402	First Insights into the Genome of the N-Methylhydantoin-Degrading <i>Clostridium</i> sp. Strain FS41 (DSM) Tj ETQq0 0 0 rgBT /Overlock 10	0.8	0
403	Genome Sequence of <i>Enterococcus faecalis</i> Strain CG_E. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
404	First Insights into the Genome of the Cr(VI)-Reducing Bacterium <i>Clostridium chromiireducens</i> DSM 23318. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
405	First Insights into the Genome Sequence of the Alkaliphilic Thermotolerant Bacterium <i>Clostridium thermoalkaliphilum</i> JW/YL23-2 T. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
406	Genome Sequence of <i>Lactobacillus sunkii</i> Strain CG_D. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
407	First Insight into the Genome Sequence of <i>Clostridium vincentii</i> DSM 10228, Isolated from Sediment of the McMurdo Ice Shelf, Antarctica. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
408	First Insight into the Genome Sequence of <i>Clostridium liquoris</i> DSM 100320, a Butyrate- and Ethanol-Producing Bacterium. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
409	Draft Genome Sequence of <i>Enterobacter roggenkampii</i> Strain OS53, Isolated from Corroded Pipework at an Offshore Oil Production Facility. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
410	Complete Genome Sequence of <i>Escherichia coli</i> GW-AmxH19, Isolated from Hospital Wastewater in Greifswald, Germany. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
411	Complete Genome Sequence of <i>Sporomusa termitida</i> DSM 4440 T. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
412	Optimising High-Throughput Sequencing Data Analysis, from Gene Database Selection to the Analysis of Compositional Data: A Case Study on Tropical Soil Nematodes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
413	Decoupling of Pore Water Chemistry, Bacterial Community Profiles, and Carbonate Mud Diagenesis in a Land-Locked Pool on Aldabra (Seychelles, Indian Ocean). <i>Geomicrobiology Journal</i> , 0, , 1-19.	2.0	0
414	Identification of the syntrophic partners in a coculture coupling anaerobic methanol oxidation to Fe(III) reduction. <i>FEMS Microbiology Letters</i> , 1999, 180, 197-203.	1.8	0