

# Rolf Daniel

## List of Publications by Year in descending order

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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	Enhancing rhizoremediation of petroleum hydrocarbons through bioaugmentation with a plant growth-promoting bacterial consortium. <i>Chemosphere</i> , 2022, 289, 133143.	8.2	18
2	Characterization of glyphosate-resistant <i>Burkholderia anthina</i> and <i>Burkholderia cenocepacia</i> isolates from a commercial Roundup® solution. <i>Environmental Microbiology Reports</i> , 2022, 14, 70-84.	2.4	11
3	Transcriptional Landscape of Ectomycorrhizal Fungi and Their Host Provides Insight into N Uptake from Forest Soil. <i>MSystems</i> , 2022, 7, e0095721.	3.8	11
4	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
5	Dietary shifts and social interactions drive temporal fluctuations of the gut microbiome from wild redfronted lemurs. <i>ISME Communications</i> , 2022, 2, .	4.2	16
6	Early Effects of Fertilizer and Herbicide Reduction on Root-Associated Biota in Oil Palm Plantations. <i>Agronomy</i> , 2022, 12, 199.	3.0	4
7	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
8	Drivers of gut microbiome variation within and between groups of a wild Malagasy primate. <i>Microbiome</i> , 2022, 10, 28.	11.1	19
9	The lung microbiome regulates brain autoimmunity. <i>Nature</i> , 2022, 603, 138-144.	27.8	91
10	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
11	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
12	Increased Butyrate Production in <i>Clostridium saccharoperbutylacetonicum</i> from Lignocellulose-Derived Sugars. <i>Applied and Environmental Microbiology</i> , 2022, , e0241921.	3.1	3
13	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
14	Energy-conserving dimethyl sulfoxide reduction in the acetogenic bacterium <i>Moorella thermoacetica</i> . <i>Environmental Microbiology</i> , 2022, 24, 2000-2012.	3.8	7
15	<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
16	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
17	Seasonal and Zonal Succession of Bacterial Communities in North Sea Salt Marsh Sediments. <i>Microorganisms</i> , 2022, 10, 859.	3.6	7
18	Native Cultivable Bacteria from the Blueberry Microbiome as Novel Potential Biocontrol Agents. <i>Microorganisms</i> , 2022, 10, 969.	3.6	10

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19	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
20	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
21	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
22	<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
23	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
24	Complete Genome Sequence of <i>Stenotrophomonas indicatrix</i> DAIF1. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	2
25	Screening Methods for Isolation of Biocontrol Epiphytic Yeasts against <i>Penicillium digitatum</i> in Lemons. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 166.	3.5	13
26	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
27	Discovery of novel community-relevant small proteins in a simplified human intestinal microbiome. <i>Microbiome</i> , 2021, 9, 55.	11.1	24
28	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
29	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
30	CAZymes in <i>Maribacter dokdonensis</i> 62-1 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
31	Growth of the acetogenic bacterium <i>Acetobacterium woodii</i> on glycerol and dihydroxyacetone. <i>Environmental Microbiology</i> , 2021, 23, 2648-2658.	3.8	3
32	A 20 kb lineage-specific genomic region tames virulence in pathogenic amphidiploid <i>Verticillium longisporum</i> . <i>Molecular Plant Pathology</i> , 2021, 22, 939-953.	4.2	6
33	Formate metabolism in the acetogenic bacterium <i>Acetobacterium woodii</i> . <i>Environmental Microbiology</i> , 2021, 23, 4214-4227.	3.8	39
34	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
35	Morphological and Metabolite Responses of Potatoes under Various Phosphorus Levels and Their Amelioration by Plant Growth-Promoting Rhizobacteria. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5162.	4.1	17
36	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

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37	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
38	Metagenome-Assembled Genome Sequences from Different Wastewater Treatment Stages in Germany. <i>Microbiology Resource Announcements</i> , 2021, 10, e0050421.	0.6	6
39	Functional Redundancy and Specialization of the Conserved Cold Shock Proteins in <i>Bacillus subtilis</i> . <i>Microorganisms</i> , 2021, 9, 1434.	3.6	7
40	Lactate metabolism in strictly anaerobic microorganisms with a soluble $\text{NAD}^+$ -dependent lactate dehydrogenase. <i>Environmental Microbiology</i> , 2021, 23, 4661-4672.	3.8	8
41	<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
42	The <i>Bacillus subtilis</i> Minimal Genome Compendium. <i>ACS Synthetic Biology</i> , 2021, 10, 2767-2771.	3.8	23
43	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
44	Cysteine: an overlooked energy and carbon source. <i>Scientific Reports</i> , 2021, 11, 2139.	3.3	22
45	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
46	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
47	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
48	Assessment of the plasmidome of an extremophilic microbial community from the Diamante Lake, Argentina. <i>Scientific Reports</i> , 2021, 11, 21459.	3.3	2
49	Metagenome Sequences of a Wastewater Treatment Plant Digester Sludge-Derived Enrichment Culture. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
50	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
51	Complete Genome of <i>Roseobacter ponti</i> DSM 106830T. <i>Genome Biology and Evolution</i> , 2020, 12, 1013-1018.	2.5	3
52	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
53	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
54	Resistance to serine in <i>Bacillus subtilis</i> : identification of the serine transporter YbeC and of a metabolic network that links serine and threonine metabolism. <i>Environmental Microbiology</i> , 2020, 22, 3937-3949.	3.8	16

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55	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
56	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
57	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
58	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
59	Soil bacterial community structures in relation to different oil palm management practices. <i>Scientific Data</i> , 2020, 7, 421.	5.3	11
60	Legacy Effects Overshadow Tree Diversity Effects on Soil Fungal Communities in Oil Palm-Enrichment Plantations. <i>Microorganisms</i> , 2020, 8, 1577.	3.6	9
61	Soil and root nutrient chemistry structure root-associated fungal assemblages in temperate forests. <i>Environmental Microbiology</i> , 2020, 22, 3081-3095.	3.8	21
62	Genome Sequence of <i>Komagataeibacter saccharivorans</i> Strain JH1, Isolated from Fruit Flies. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	5
63	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
64	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
65	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
66	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
67	Saprotrophic and Ectomycorrhizal Fungi Contribute Differentially to Organic P Mobilization in Beech-Dominated Forest Ecosystems. <i>Frontiers in Forests and Global Change</i> , 2020, 3, .	2.3	11
68	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
69	Trade-offs between multifunctionality and profit in tropical smallholder landscapes. <i>Nature Communications</i> , 2020, 11, 1186.	12.8	156
70	First Report on the Plasmidome From a High-Altitude Lake of the Andean Puna. <i>Frontiers in Microbiology</i> , 2020, 11, 1343.	3.5	17
71	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
72	Unravelling the effects of tropical land use conversion on the soil microbiome. <i>Environmental Microbiomes</i> , 2020, 15, 5.	5.0	37

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73	Metagenomes of Wastewater at Different Treatment Stages in Central Germany. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	12
74	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
75	Authigenic formation of Ca-Mg carbonates in the shallow alkaline Lake Neusiedl, Austria. <i>Biogeosciences</i> , 2020, 17, 2085-2106.	3.3	21
76	From sequence to function: a new workflow for nitrilase identification. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 4957-4970.	3.6	9
77	<i>Caproicibacter fermentans</i> gen. nov., sp. nov., a new caproate-producing bacterium and emended description of the genus <i>Caproiciproducens</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4269-4279.	1.7	49
78	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
79	Complete Genome Sequence of <i>Sporomusa termitida</i> DSM 4440 T. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
80	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
81	Impact of Nitriles on Bacterial Communities. <i>Frontiers in Environmental Science</i> , 2019, 7, .	3.3	18
82	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
83	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
84	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
85	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
86	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
87	Effects of a high-cultivation temperature on the physiology of three different <i>Yarrowia lipolytica</i> strains. <i>FEMS Yeast Research</i> , 2019, 19, .	2.3	9
88	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
89	Genome Sequence of the Caproic Acid-Producing Bacterium <i>Caproiciproducens galactitolivorans</i> BS-1 <sup>T</sup> (JCM 30532). <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	18
90	Prokaryotic Diversity and Community Patterns in Antarctic Continental Shelf Sponges. <i>Frontiers in Marine Science</i> , 2019, 6, .	2.5	74

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91	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
92	Bacterial succession along a sediment porewater gradient at Lake Neusiedl in Austria. <i>Scientific Data</i> , 2019, 6, 163.	5.3	23
93	Identification of the first glyphosate transporter by genomic adaptation. <i>Environmental Microbiology</i> , 2019, 21, 1287-1305.	3.8	36
94	Tree Species Shape Soil Bacterial Community Structure and Function in Temperate Deciduous Forests. <i>Frontiers in Microbiology</i> , 2019, 10, 1519.	3.5	71
95	Functional Metagenomics Reveals a New Catalytic Domain, the Metallo- $\beta$ -Lactamase Superfamily Domain, Associated with Phytase Activity. <i>MSphere</i> , 2019, 4, .	2.9	6
96	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
97	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
98	Intensive tropical land use massively shifts soil fungal communities. <i>Scientific Reports</i> , 2019, 9, 3403.	3.3	86
99	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
100	Biochemical profiles of two thermostable and organic solvent-tolerant esterases derived from a compost metagenome. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 3421-3437.	3.6	16
101	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
102	Functional Metagenomics Reveals an Overlooked Diversity and Novel Features of Soil-Derived Bacterial Phosphatases and Phytases. <i>MBio</i> , 2019, 10, .	4.1	22
103	Characteristics of the First Protein Tyrosine Phosphatase with Phytase Activity from a Soil Metagenome. <i>Genes</i> , 2019, 10, 101.	2.4	8
104	Changes in Trophic Groups of Protists With Conversion of Rainforest Into Rubber and Oil Palm Plantations. <i>Frontiers in Microbiology</i> , 2019, 10, 240.	3.5	48
105	Assembly processes of trophic guilds in the root mycobiome of temperate forests. <i>Molecular Ecology</i> , 2019, 28, 348-364.	3.9	46
106	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
107	<i>Entomobacter blattae</i> gen. nov., sp. nov., a new member of the <i>Acetobacteraceae</i> 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
108	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



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109	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
110	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
111	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
112	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
113	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
114	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
115	Complete Genome Sequence of vB_BveP-Goe6, a Virus Infecting <i>Bacillus velezensis</i> FZB42. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
116	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
117	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
118	Draft Genome Sequence of the Thermophilic Acetogen <i>Moorella humiferrea</i> DSM 23265. <i>Genome Announcements</i> , 2018, 6, .	0.8	8
119	Comparative Genomic Analysis of Members of the Genera <i>Methanosphaera</i> and <i>Methanobrevibacter</i> Reveals Distinct Clades with Specific Potential Metabolic Functions. <i>Archaea</i> , 2018, 2018, 1-9.	2.3	17
120	Draft Genome Sequence of <i>Komagataeibacter maltaceti</i> LMG 1529 <sup>T</sup> , a Vinegar-Producing Acetic Acid Bacterium Isolated from Malt Vinegar Brewery Acetifiers. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
121	Prevalence and Strain Characterization of <i>Clostridioides</i> ( <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
122	How Rainforest Conversion to Agricultural Systems in Sumatra (Indonesia) Affects Active Soil Bacterial Communities. <i>Frontiers in Microbiology</i> , 2018, 9, 2381.	3.5	44
123	Draft Genome Sequence of the Butanoic Acid-Producing Bacterium <i>Clostridium luticellarii</i> DSM 29923, Used for Strong Aromatic Chinese Liquor Production. <i>Genome Announcements</i> , 2018, 6, .	0.8	9
124	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
125	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
126	A metagenomic collection of novel and highly efficient biocatalysts for industrial biotechnology. <i>Impact</i> , 2018, 2018, 82-84.	0.1	5



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127	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
128	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
129	Draft Genome Sequence of the Hydrogenogenic Carboxydrotroph <i>Moorella stamsii</i> DSM 26271. <i>Genome Announcements</i> , 2018, 6, .	0.8	8
130	Editorial: Molecular Ecology and Genetic Diversity of the Roseobacter Clade. <i>Frontiers in Microbiology</i> , 2018, 9, 1185.	3.5	9
131	Methanol metabolism in the acetogenic bacterium <i>Acetobacterium woodii</i> . <i>Environmental Microbiology</i> , 2018, 20, 4369-4384.	3.8	73
132	Preliminary Investigation of Species Diversity of Rice Hopper Parasitoids in Southeast Asia. <i>Insects</i> , 2018, 9, 19.	2.2	4
133	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
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157	Insights into the Genome of the Anaerobic Acetogen <i>Sporomusa silvacetica</i> DSM 10669. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
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164	No evidence for a bovine mastitis <i>Escherichia coli</i> pathotype. <i>BMC Genomics</i> , 2017, 18, 359.	2.8	85
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180	Genome Sequence of <i>Lactobacillus sunkii</i> Strain CG_D. <i>Genome Announcements</i> , 2017, 5, .	0.8	0

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182	Proposal for the reclassification of obligately purine-fermenting bacteria <i>Clostridium acidurict</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 ETQq0 0 0 rgBT <sub>1</sub> /Overlock 10 Tf 50 International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2711-2719.	0.8	1
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198	Complete Genome Sequence of <i>Bacillus subtilis</i> subsp. <i>subtilis</i> Strain $\hat{t}6$ . <i>Genome Announcements</i> , 2016, 4, .	0.8	8

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200	Complete Genome Sequence of the Amino Acid-Fermenting <i>Clostridium propionicum</i> X2 (DSM) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	10
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260	Genome Sequence of the Moderately Acidophilic Sulfate-Reducing Firmicute <i>Desulfosporosinus acidurans</i> (Strain M1 T). <i>Genome Announcements</i> , 2015, 3, .	0.8	8
261	Genome Sequence of the Acidophilic Sulfate-Reducing Peptococcaceae Strain CEB3. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
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