

Tanja Woyke

List of Publications by Year in descending order

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Version: 2024-02-01

215
papers

34,996
citations

6486

82
h-index

6177

164
g-index

248
all docs

248
docs citations

248
times ranked

30523
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. <i>PLoS Biology</i> , 2022, 20, e3001508.	2.6	62
2	DNA Methylation in <i>Ensifer</i> Species during Free-Living Growth and during Nitrogen-Fixing Symbiosis with <i>Medicago</i> spp.. <i>MSystems</i> , 2022, 7, e0109221.	1.7	7
3	Metagenomes and Metagenome-Assembled Genomes from Substrate-Amended Hot Spring Sediment Incubations from Yellowstone National Park. <i>Microbiology Resource Announcements</i> , 2022, 11, e0106521.	0.3	2
4	Impact of Harvest on Switchgrass Leaf Microbial Communities. <i>Genes</i> , 2022, 13, 22.	1.0	0
5	Dissecting the dominant hot spring microbial populations based on community-wide sampling at single-cell genomic resolution. <i>ISME Journal</i> , 2022, 16, 1337-1347.	4.4	15
6	The Genome of the Acid Soil-Adapted Strain <i>Rhizobium favelukesii</i> OR191 Encodes Determinants for Effective Symbiotic Interaction With Both an Inverted Repeat Lacking Clade and a Phaseoloid Legume Host. <i>Frontiers in Microbiology</i> , 2022, 13, 735911.	1.5	2
7	<i>Sodalis ligni</i> Strain 159R Isolated from an Anaerobic Lignin-Degrading Consortium. <i>Microbiology Spectrum</i> , 2022, 10, e0234621.	1.2	1
8	Community Structure and Microbial Associations in Sediment-Free Methanotrophic Enrichment Cultures from a Marine Methane Seep. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	8
9	A centimeter-long bacterium with DNA contained in metabolically active, membrane-bound organelles. <i>Science</i> , 2022, 376, 1453-1458.	6.0	45
10	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
11	The IMG/M data management and analysis system v.6.0: new tools and advanced capabilities. <i>Nucleic Acids Research</i> , 2021, 49, D751-D763.	6.5	332
12	IMG/VR v3: an integrated ecological and evolutionary framework for interrogating genomes of uncultivated viruses. <i>Nucleic Acids Research</i> , 2021, 49, D764-D775.	6.5	240
13	Description of <i>Candidatus Mesopelagibacter carboxydoxydans</i> and <i>Candidatus Anoxipelagibacter denitrificans</i> : Nitrate-reducing SAR11 genera that dominate mesopelagic and anoxic marine zones. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126185.	1.2	14
14	High Potential for Biomass-Degrading Enzymes Revealed by Hot Spring Metagenomics. <i>Frontiers in Microbiology</i> , 2021, 12, 668238.	1.5	16
15	A single-cell genomics pipeline for environmental microbial eukaryotes. <i>IScience</i> , 2021, 24, 102290.	1.9	7
16	Draft Genome Sequence of <i>Bordetella</i> sp. Strain FB-8, Isolated from a Former Uranium Mining Area in Germany. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
17	<i>Zymomonas</i> diversity and potential for biofuel production. <i>Biotechnology for Biofuels</i> , 2021, 14, 112.	6.2	10
18	Synthase-Selective Exploration of a Tunicate Microbiome by Activity-Guided Single-Cell Genomics. <i>ACS Chemical Biology</i> , 2021, 16, 813-819.	1.6	4

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19	Genomic Analysis of the Yet-Uncultured <i>Binatota</i> Reveals Broad Methylotrophic, Alkane-Degradation, and Pigment Production Capacities. <i>MBio</i> , 2021, 12, .	1.8	13
20	Genomics, Exometabolomics, and Metabolic Probing Reveal Conserved Proteolytic Metabolism of <i>Thermoflexus hugenholtzii</i> and Three Candidate Species From China and Japan. <i>Frontiers in Microbiology</i> , 2021, 12, 632731.	1.5	8
21	High-Quality Draft Genome Sequence of the Siderophilic and Thermophilic <i>Leptolyngbyaceae</i> Cyanobacterium JSC-12. <i>Microbiology Resource Announcements</i> , 2021, 10, e0049521.	0.3	2
22	<i>Hymenobacter caeli</i> sp. nov., an airborne bacterium isolated from King George Island, Antarctica. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
23	Recoding of stop codons expands the metabolic potential of two novel Asgardarchaeota lineages. <i>ISME Communications</i> , 2021, 1, .	1.7	23
24	A catalog of the diversity and ubiquity of bacterial microcompartments. <i>Nature Communications</i> , 2021, 12, 3809.	5.8	55
25	Lytic archaeal viruses infect abundant primary producers in Earth's crust. <i>Nature Communications</i> , 2021, 12, 4642.	5.8	28
26	Metapangenomics reveals depth-dependent shifts in metabolic potential for the ubiquitous marine bacterial SAR324 lineage. <i>Microbiome</i> , 2021, 9, 172.	4.9	25
27	The <i>Roseibium album</i> (<i>Labrenzia alba</i>) Genome Possesses Multiple Symbiosis Factors Possibly Underpinning Host-Microbe Relationships in the Marine Benthos. <i>Microbiology Resource Announcements</i> , 2021, 10, e0032021.	0.3	5
28	<i>Frigoriflavimonas asaccharolytica</i> gen. nov., sp. nov., a novel psychrophilic esterase and protease producing bacterium isolated from Antarctica. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1991-2002.	0.7	7
29	Morphological and Genomic Features of the New Klosneuvirinae Isolate Fadolivirus IHUMI-VV54. <i>Frontiers in Microbiology</i> , 2021, 12, 719703.	1.5	9
30	Epigenetic Regulation of <i>Nostoc punctiforme</i> ATCC 29133 in Response to Nitrogen Availability. <i>Journal of Student Research</i> , 2021, 10, .	0.0	0
31	A Genomic Perspective Across Earth's Microbiomes Reveals That Genome Size in Archaea and Bacteria Is Linked to Ecosystem Type and Trophic Strategy. <i>Frontiers in Microbiology</i> , 2021, 12, 761869.	1.5	29
32	GAL08, an Uncultivated Group of Acidobacteria, Is a Dominant Bacterial Clade in a Neutral Hot Spring. <i>Frontiers in Microbiology</i> , 2021, 12, 787651.	1.5	1
33	Genome analysis of the marine bacterium <i>Kiloniella laminariae</i> and first insights into comparative genomics with related <i>Kiloniella</i> species. <i>Archives of Microbiology</i> , 2020, 202, 815-824.	1.0	9
34	Novel copper-containing membrane monooxygenases (CuMMOs) encoded by alkane-utilizing <i>Betaproteobacteria</i> . <i>ISME Journal</i> , 2020, 14, 714-726.	4.4	16
35	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. <i>ISME Journal</i> , 2020, 14, 659-675.	4.4	69
36	Mixotrophic Iron-Oxidizing <i>Thiomonas</i> Isolates from an Acid Mine Drainage-Affected Creek. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	9

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37	Insights into the dynamics between viruses and their hosts in a hot spring microbial mat. ISME Journal, 2020, 14, 2527-2541.	4.4	42
38	Influence of the polar light cycle on seasonal dynamics of an Antarctic lake microbial community. Microbiome, 2020, 8, 116.	4.9	32
39	High-Quality Draft Genome Sequences of the Uncultured Delta3 Endosymbiont (Deltaproteobacteria) Assembled from Metagenomes of the Gutless Marine Worm <i>Olavius algarvensis</i> . Microbiology Resource Announcements, 2020, 9, .	0.3	3
40	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. Frontiers in Microbiology, 2020, 11, 1848.	1.5	62
41	Molecular Dialogues between Early Divergent Fungi and Bacteria in an Antagonism versus a Mutualism. MBio, 2020, 11, .	1.8	19
42	Ecological and genomic analyses of candidate phylum WPS bacteria in an unvegetated soil. Environmental Microbiology, 2020, 22, 3143-3157.	1.8	42
43	Novel heavy metal resistance gene clusters are present in the genome of <i>Cupriavidus neocaledonicus</i> STM 6070, a new species of <i>Mimosa pudica</i> microsymbiont isolated from heavy-metal-rich mining site soil. BMC Genomics, 2020, 21, 214.	1.2	18
44	Lipid analysis of CO ₂ -rich subsurface aquifers suggests an autotrophy-based deep biosphere with lysolipids enriched in CPR bacteria. ISME Journal, 2020, 14, 1547-1560.	4.4	29
45	Advantages and Limits of Metagenomic Assembly and Binning of a Giant Virus. MSystems, 2020, 5, .	1.7	14
46	A pipeline for targeted metagenomics of environmental bacteria. Microbiome, 2020, 8, 21.	4.9	39
47	Giant virus diversity and host interactions through global metagenomics. Nature, 2020, 578, 432-436.	13.7	207
48	Niche differentiation is spatially and temporally regulated in the rhizosphere. ISME Journal, 2020, 14, 999-1014.	4.4	135
49	Hiding in Plain Sight: The Globally Distributed Bacterial Candidate Phylum PAUC34f. Frontiers in Microbiology, 2020, 11, 376.	1.5	5
50	Draft Genome Sequence of <i>Yokenella regensburgei</i> Strain WCD67, Isolated from the Boxelder Bug. Microbiology Resource Announcements, 2020, 9, .	0.3	1
51	One Complete and Seven Draft Genome Sequences of Subdivision 1 and 3 <i>Acidobacteria</i> Isolated from Soil. Microbiology Resource Announcements, 2020, 9, .	0.3	5
52	Analysis of 1,000+ Type-Strain Genomes Substantially Improves Taxonomic Classification of Alphaproteobacteria. Frontiers in Microbiology, 2020, 11, 468.	1.5	1,537
53	Complementary Metagenomic Approaches Improve Reconstruction of Microbial Diversity in a Forest Soil. MSystems, 2020, 5, .	1.7	45
54	<i>Hymenobacter artigasi</i> sp. nov., isolated from air sampling in maritime Antarctica. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4935-4941.	0.8	14

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55	Draft genome of <i>Rosenbergiella nectarea</i> strain 8N4 ^T provides insights into the potential role of this species in its plant host. PeerJ, 2020, 8, e8822.	0.9	7
56	Genomes From Uncultivated Microorganisms. , 2019, , .		4
57	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. Nature Microbiology, 2019, 4, 1895-1906.	5.9	206
58	Analysis of 1,000 Type-Strain Genomes Improves Taxonomic Classification of Bacteroidetes. Frontiers in Microbiology, 2019, 10, 2083.	1.5	1,281
59	A single-cell genome perspective on studying intracellular associations in unicellular eukaryotes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20190082.	1.8	1
60	Conservation of Endophyte Bacterial Community Structure Across Two Panicum Grass Species. Frontiers in Microbiology, 2019, 10, 2181.	1.5	19
61	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. Nature Communications, 2019, 10, 463.	5.8	87
62	Beyond the census of human gut dwellers. Nature Reviews Microbiology, 2019, 17, 401-401.	13.6	3
63	Improved Draft Genome Sequence of <i>Pseudomonas poae</i> A2-S9, a Strain with Plant Growth-Promoting Activity. Microbiology Resource Announcements, 2019, 8, .	0.3	5
64	Improved Draft Genome Sequence of <i>Bacillus</i> sp. Strain YF23, Which Has Plant Growth-Promoting Activity. Microbiology Resource Announcements, 2019, 8, .	0.3	1
65	Complete Genome Sequence of <i>Serratia quinivorans</i> Strain 124R, a Facultative Anaerobe Isolated on Organosolv Lignin as a Sole Carbon Source. Microbiology Resource Announcements, 2019, 8, .	0.3	1
66	Sulfate-Reducing Bacteria That Produce Exopolymers Thrive in the Calcifying Zone of a Hypersaline Cyanobacterial Mat. Frontiers in Microbiology, 2019, 10, 862.	1.5	54
67	Phylogenomics suggests oxygen availability as a driving force in Thaumarchaeota evolution. ISME Journal, 2019, 13, 2150-2161.	4.4	108
68	Genome-informed Bradyrhizobium taxonomy: where to from here?. Systematic and Applied Microbiology, 2019, 42, 427-439.	1.2	62
69	Genomic Characterization of Candidate Division LCP-89 Reveals an Atypical Cell Wall Structure, Microcompartment Production, and Dual Respiratory and Fermentative Capacities. Applied and Environmental Microbiology, 2019, 85, .	1.4	14
70	Four Draft Single-Cell Genome Sequences of Novel, Nearly Identical <i>Kiritimatiella</i> Strains Isolated from the Continental Deep Subsurface. Microbiology Resource Announcements, 2019, 8, .	0.3	23
71	Draft Genome of <i>Burkholderia cenocepacia</i> TAtI-371, a Strain from the <i>Burkholderia cepacia</i> Complex Retains Antagonism in Different Carbon and Nitrogen Sources. Current Microbiology, 2019, 76, 566-574.	1.0	3
72	High-quality draft genome sequence of <i>Pseudomonas aeruginosa</i> strain ai, an environmental isolate resistant to heavy metals. Extremophiles, 2019, 23, 399-405.	0.9	9

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73	Carboxydrotrophy potential of uncultivated Hydrothermarchaeota from the seafloor crustal biosphere. <i>ISME Journal</i> , 2019, 13, 1457-1468.	4.4	31
74	Direct pathway cloning of the sodorifen biosynthetic gene cluster and recombinant generation of its product in <i>E. coli</i> . <i>Microbial Cell Factories</i> , 2019, 18, 32.	1.9	27
75	Hydrogenotrophic methanogenesis in archaeal phylum Verstraetearchaeota reveals the shared ancestry of all methanogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5037-5044.	3.3	187
76	Community ecology across bacteria, archaea and microbial eukaryotes in the sediment and seawater of coastal Puerto Nuevo, Baja California. <i>PLoS ONE</i> , 2019, 14, e0212355.	1.1	44
77	Complete Genome Sequence for <i>Asinibacterium</i> sp. Strain OR53 and Draft Genome Sequence for <i>Asinibacterium</i> sp. Strain OR43, Two Bacteria Tolerant to Uranium. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	6
78	Improved Draft Genome Sequence of <i>Microbacterium</i> sp. Strain LKL04, a Bacterial Endophyte Associated with Switchgrass Plants. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	8
79	Shotgun metagenome data of a defined mock community using Oxford Nanopore, PacBio and Illumina technologies. <i>Scientific Data</i> , 2019, 6, 285.	2.4	75
80	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , 2019, 7, 157.	4.9	53
81	Entities inside one another – a matryoshka doll in biology?. <i>Environmental Microbiology Reports</i> , 2019, 11, 26-28.	1.0	6
82	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
83	Plant compartment and genetic variation drive microbiome composition in switchgrass roots. <i>Environmental Microbiology Reports</i> , 2019, 11, 185-195.	1.0	65
84	IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. <i>Nucleic Acids Research</i> , 2019, 47, D666-D677.	6.5	799
85	Functional Signatures of the Epiphytic Prokaryotic Microbiome of Agaves and Cacti. <i>Frontiers in Microbiology</i> , 2019, 10, 3044.	1.5	41
86	High-quality draft genome sequences of <i>Pseudomonas monteilii</i> DSM 14164T, <i>Pseudomonas mosselii</i> DSM 17497T, <i>Pseudomonas plecoglossicida</i> DSM 15088T, <i>Pseudomonas taiwanensis</i> DSM 21245T and <i>Pseudomonas vranovensis</i> DSM 16006T: taxonomic considerations. <i>Access Microbiology</i> , 2019, 1, e000067.	0.2	10
87	Draft Genome Sequence of Mn(II)-Oxidizing Bacterium <i>Oxalobacteraceae</i> sp. Strain AB_14. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
88	Genomes of ubiquitous marine and hypersaline <i>Hydrogenovibrio</i> , <i>Thiomicrobacter</i> and <i>Thiomicrospira</i> spp. encode a diversity of mechanisms to sustain chemolithoautotrophy in heterogeneous environments. <i>Environmental Microbiology</i> , 2018, 20, 2686-2708.	1.8	32
89	Genome-based evolutionary history of <i>Pseudomonas</i> spp. <i>Environmental Microbiology</i> , 2018, 20, 2142-2159.	1.8	172
90	Differential depth distribution of microbial function and putative symbionts through sediment-hosted aquifers in the deep terrestrial subsurface. <i>Nature Microbiology</i> , 2018, 3, 328-336.	5.9	227

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91	Arboriscoccus pini gen. nov., sp. nov., an endophyte from a pine tree of the class Alphaproteobacteria, emended description of Geminicoccus roseus, and proposal of Geminicoccaceae fam. nov.. Systematic and Applied Microbiology, 2018, 41, 94-100.	1.2	32
92	Genomic features of bacterial adaptation to plants. Nature Genetics, 2018, 50, 138-150.	9.4	480
93	Genome-based classification of micromonosporae with a focus on their biotechnological and ecological potential. Scientific Reports, 2018, 8, 525.	1.6	102
94	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. Nature Biotechnology, 2018, 36, 359-367.	9.4	414
95	Genomic Changes Associated with the Evolutionary Transitions of Nostoc to a Plant Symbiont. Molecular Biology and Evolution, 2018, 35, 1160-1175.	3.5	54
96	Metabolic versatility of small archaea Micrarchaeota and Parvarchaeota. ISME Journal, 2018, 12, 756-775.	4.4	91
97	Sequencing of Genomes from Environmental Single Cells. Methods in Molecular Biology, 2018, 1712, 97-111.	0.4	1
98	Hidden diversity of soil giant viruses. Nature Communications, 2018, 9, 4881.	5.8	112
99	Single cell genomic and transcriptomic evidence for the use of alternative nitrogen substrates by anammox bacteria. ISME Journal, 2018, 12, 2706-2722.	4.4	45
100	Genome Sequences of Actinobacteria from Extreme Environments in Colombia. Microbiology Resource Announcements, 2018, 7, .	0.3	3
101	Leveraging single-cell genomics to expand the fungal tree of life. Nature Microbiology, 2018, 3, 1417-1428.	5.9	101
102	Elucidating Bacterial Gene Functions in the Plant Microbiome. Cell Host and Microbe, 2018, 24, 475-485.	5.1	129
103	Draft Genome Sequences of New Isolates and the Known Species of the Family Microbacteriaceae Associated with Plants. Microbiology Resource Announcements, 2018, 7, .	0.3	3
104	Thermus sediminis sp. nov., a thiosulfate-oxidizing and arsenate-reducing organism isolated from Little Hot Creek in the Long Valley Caldera, California. Extremophiles, 2018, 22, 983-991.	0.9	20
105	Genome-Based Taxonomic Classification of the Phylum Actinobacteria. Frontiers in Microbiology, 2018, 9, 2007.	1.5	2,599
106	Single-cell genomics of co-sorted Nanoarchaeota suggests novel putative host associations and diversification of proteins involved in symbiosis. Microbiome, 2018, 6, 161.	4.9	44
107	High-Quality Draft Genome Sequences of Eight Bacteria Isolated from Fungus Gardens Grown by Trachymyrmex septentrionalis Ants. Microbiology Resource Announcements, 2018, 7, .	0.3	3
108	Polynucleobacter meluiroseus sp. nov., a bacterium isolated from a lake located in the mountains of the Mediterranean island of Corsica. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1975-1985.	0.8	18

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109	Resequencing and annotation of the <i>Nostoc punctiforme</i> ATCC 29133 genome: facilitating biofuel and high-value chemical production. <i>AMB Express</i> , 2017, 7, 42.	1.4	12
110	Novel approaches in function-driven single-cell genomics. <i>FEMS Microbiology Reviews</i> , 2017, 41, 538-548.	3.9	24
111	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , 2017, 35, 676-683.	9.4	222
112	Giant viruses with an expanded complement of translation system components. <i>Science</i> , 2017, 356, 82-85.	6.0	234
113	The trajectory of microbial single-cell sequencing. <i>Nature Methods</i> , 2017, 14, 1045-1054.	9.0	120
114	Critical Assessment of Metagenome Interpretation – a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	9.0	635
115	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	9.4	1,512
116	Major role of nitrite-oxidizing bacteria in dark ocean carbon fixation. <i>Science</i> , 2017, 358, 1046-1051.	6.0	229
117	Diverse Marine microbes may mediate coupled biogeochemical cycles along eco-thermodynamic gradients. <i>Nature Communications</i> , 2017, 8, 1507.	5.8	99
118	Genomic composition and dynamics among <i>Methanomicrobiales</i> predict adaptation to contrasting environments. <i>ISME Journal</i> , 2017, 11, 87-99.	4.4	29
119	Towards a balanced view of the bacterial tree of life. <i>Microbiome</i> , 2017, 5, 140.	4.9	102
120	Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). <i>Frontiers in Microbiology</i> , 2017, 8, 682.	1.5	409
121	Genome Data Provides High Support for Generic Boundaries in Burkholderia Sensu Lato. <i>Frontiers in Microbiology</i> , 2017, 8, 1154.	1.5	122
122	Rokubacteria: Genomic Giants among the Uncultured Bacterial Phyla. <i>Frontiers in Microbiology</i> , 2017, 8, 2264.	1.5	142
123	Genome-Scale Data Call for a Taxonomic Rearrangement of Geodermatophilaceae. <i>Frontiers in Microbiology</i> , 2017, 8, 2501.	1.5	105
124	Draft genome sequence of <i>Pseudomonas extremaustralis</i> strain USBA-GBX 515 isolated from Superparamo soil samples in Colombian Andes. <i>Standards in Genomic Sciences</i> , 2017, 12, 78.	1.5	7
125	Draft genome sequence of <i>Dethiosulfovibrio salsuginis</i> DSM 21565T an anaerobic, slightly halophilic bacterium isolated from a Colombian saline spring. <i>Standards in Genomic Sciences</i> , 2017, 12, 86.	1.5	0
126	Analysis of single-cell genome sequences of bacteria and archaea. <i>Emerging Topics in Life Sciences</i> , 2017, 1, 249-255.	1.1	10

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127	Microfluidic-based mini-metagenomics enables discovery of novel microbial lineages from complex environmental samples. <i>ELife</i> , 2017, 6, .	2.8	69
128	Genome-Based Taxonomic Classification of Bacteroidetes. <i>Frontiers in Microbiology</i> , 2016, 7, 2003.	1.5	493
129	Visualizing in situ translational activity for identifying and sorting slow-growing archaeal~bacterial consortia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4069-78.	3.3	180
130	acdc â€“ Automated Contamination Detection and Confidence estimation for single-cell genome data. <i>BMC Bioinformatics</i> , 2016, 17, 543.	1.2	22
131	SAR11 bacteria linked to ocean anoxia and nitrogen loss. <i>Nature</i> , 2016, 536, 179-183.	13.7	160
132	Genome analysis of â€“ <i>Candidatus</i> Ancillula trichonymphaeâ€™™, first representative of a deepâ€“branching clade of <i>Bifidobacteriales</i> , strengthens evidence for convergent evolution in flagellate endosymbionts. <i>Environmental Microbiology Reports</i> , 2016, 8, 865-873.	1.0	16
133	Genomic differentiation among wild cyanophages despite widespread horizontal gene transfer. <i>BMC Genomics</i> , 2016, 17, 930.	1.2	96
134	Genomic analysis of three <i>Bifidobacterium</i> species isolated from the calf gastrointestinal tract. <i>Scientific Reports</i> , 2016, 6, 30768.	1.6	20
135	Metagenomics uncovers gaps in amplicon-based detection of microbial diversity. <i>Nature Microbiology</i> , 2016, 1, 15032.	5.9	207
136	Next generation sequencing data of a defined microbial mock community. <i>Scientific Data</i> , 2016, 3, 160081.	2.4	90
137	High quality draft genome sequences of <i>Pseudomonas fulva</i> DSM 17717T, <i>Pseudomonas parafulva</i> DSM 17004T and <i>Pseudomonas cremoricolorata</i> DSM 17059T type strains. <i>Standards in Genomic Sciences</i> , 2016, 11, 55.	1.5	30
138	Tuning fresh: radiation through rewiring of central metabolism in streamlined bacteria. <i>ISME Journal</i> , 2016, 10, 1902-1914.	4.4	66
139	High-resolution phylogenetic microbial community profiling. <i>ISME Journal</i> , 2016, 10, 2020-2032.	4.4	232
140	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016, 7, 10476.	5.8	189
141	Plant compartment and biogeography affect microbiome composition in cultivated and native <i>Agave</i> species. <i>New Phytologist</i> , 2016, 209, 798-811.	3.5	663
142	ProDeGe: a computational protocol for fully automated decontamination of genomes. <i>ISME Journal</i> , 2016, 10, 269-272.	4.4	65
143	Phylogeny and physiology of candidate phylum â€“Atribacteriaâ€™™ (OP9/JS1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016, 10, 273-286.	4.4	166
144	Functionâ€“driven singleâ€“cell genomics. <i>Microbial Biotechnology</i> , 2015, 8, 38-39.	2.0	17

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145	Discovery of Novel Plant Interaction Determinants from the Genomes of 163 Root Nodule Bacteria. <i>Scientific Reports</i> , 2015, 5, 16825.	1.6	33
146	Impact of library preparation protocols and template quantity on the metagenomic reconstruction of a mock microbial community. <i>BMC Genomics</i> , 2015, 16, 856.	1.2	79
147	Genomics of Methylotrophy in Gram-Positive Methylamine-Utilizing Bacteria. <i>Microorganisms</i> , 2015, 3, 94-112.	1.6	19
148	Primer and platform effects on 16S rRNA tag sequencing. <i>Frontiers in Microbiology</i> , 2015, 6, 771.	1.5	435
149	Comparative Genomic Insights into Ecophysiology of Neutrophilic, Microaerophilic Iron Oxidizing Bacteria. <i>Frontiers in Microbiology</i> , 2015, 6, 1265.	1.5	78
150	In Silico Analysis of the Metabolic Potential and Niche Specialization of Candidate Phylum "Latescibacteria" (WS3). <i>PLoS ONE</i> , 2015, 10, e0127499.	1.1	102
151	Viral dark matter and virus-host interactions resolved from publicly available microbial genomes. <i>ELife</i> , 2015, 4, .	2.8	400
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