

# Anja Poehlein

## List of Publications by Year in descending order

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232  
papers

6,674  
citations

81900

39  
h-index

91884

69  
g-index

240  
all docs

240  
docs citations

240  
times ranked

8222  
citing authors

#	ARTICLE	IF	CITATIONS
1	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> . BMC Genomics, 2018, 19, 1.	2.8	725
2	The genome of <i>Clostridium kluyveri</i> , a strict anaerobe with unique metabolic features. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2128-2133.	7.1	409
3	The genome of the ammonia-oxidizing <i>Candidatus Nitrososphaera gargensis</i> : insights into metabolic versatility and environmental adaptations. Environmental Microbiology, 2012, 14, 3122-3145.	3.8	332
4	The genome sequence of <i>Clostridium tetani</i> , the causative agent of tetanus disease. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1316-1321.	7.1	324
5	An Ancient Pathway Combining Carbon Dioxide Fixation with the Generation and Utilization of a Sodium Ion Gradient for ATP Synthesis. PLoS ONE, 2012, 7, e33439.	2.5	246
6	New Mode of Energy Metabolism in the Seventh Order of Methanogens as Revealed by Comparative Genome Analysis of <i>Candidatus Methanoplasma termitum</i> . Applied and Environmental Microbiology, 2015, 81, 1338-1352.	3.1	235
7	Proteomic identification of secreted proteins of <i>Propionibacterium acnes</i> . BMC Microbiology, 2010, 10, 230.	3.3	142
8	Prevalence of <i>Propionibacterium acnes</i> in diseased prostates and its inflammatory and transforming activity on prostate epithelial cells. International Journal of Medical Microbiology, 2011, 301, 69-78.	3.6	126
9	Bacterial Anaerobic Synthesis Gas (Syngas) and CO <sub>2</sub> + H <sub>2</sub> Fermentation. Advances in Applied Microbiology, 2018, 103, 143-221.	2.4	118
10	Metagenome Survey of a Multispecies and Alga-Associated Biofilm Revealed Key Elements of Bacterial-Algal Interactions in Photobioreactors. Applied and Environmental Microbiology, 2013, 79, 6196-6206.	3.1	111
11	A Novel High-Resolution Single Locus Sequence Typing Scheme for Mixed Populations of <i>Propionibacterium acnes</i> In Vivo. PLoS ONE, 2014, 9, e104199.	2.5	111
12	Industrial Acetogenic Biocatalysts: A Comparative Metabolic and Genomic Analysis. Frontiers in Microbiology, 2016, 7, 1036.	3.5	85
13	No evidence for a bovine mastitis <i>Escherichia coli</i> pathotype. BMC Genomics, 2017, 18, 359.	2.8	85
14	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. PLoS ONE, 2014, 9, e106707.	2.5	80
15	The Complete Genome Sequence of <i>Clostridium acetium</i> : a Missing Link between Rnf- and Cytochrome-Containing Autotrophic Acetogens. MBio, 2015, 6, e01168-15.	4.1	75
16	<i>Bacillus thuringiensis</i> and <i>Bacillus weihenstephanensis</i> Inhibit the Growth of Phytopathogenic <i>Verticillium</i> Species. Frontiers in Microbiology, 2016, 7, 2171.	3.5	74
17	Methanol metabolism in the acetogenic bacterium <i>Acetobacterium woodii</i> . Environmental Microbiology, 2018, 20, 4369-4384.	3.8	73
18	The Pathogenicity Island-Associated K15 Capsule Determinant Exhibits a Novel Genetic Structure and Correlates with Virulence in Uropathogenic <i>Escherichia coli</i> Strain 536. Infection and Immunity, 2004, 72, 5993-6001.	2.2	67

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19	Molecular Keys to the Janthinobacterium and Duganella spp. Interaction with the Plant Pathogen Fusarium graminearum. <i>Frontiers in Microbiology</i> , 2016, 7, 1668.	3.5	66
20	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
21	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
22	CRISPR/cas Loci of Type II <i>Propionibacterium acnes</i> Confer Immunity against Acquisition of Mobile Elements Present in Type I <i>P. acnes</i> . <i>PLoS ONE</i> , 2012, 7, e34171.	2.5	64
23	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
24	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
25	Microbial solvent formation revisited by comparative genome analysis. <i>Biotechnology for Biofuels</i> , 2017, 10, 58.	6.2	60
26	Analysis and comparative genomics of ICE <sub>Mh1</sub> , 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
27	Nitrogen fixation in a chemoautotrophic lucinid symbiosis. <i>Nature Microbiology</i> , 2017, 2, 16193.	13.3	56
28	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
29	The Janthinobacterium 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
30	Multilocus sequence typing (MLST) analysis of <i>Propionibacterium acnes</i> isolates from radical prostatectomy specimens. <i>Prostate</i> , 2013, 73, 770-777.	2.3	51
31	Proteome Analysis of Human Sebaceous Follicle Infundibula Extracted from Healthy and Acne-Affected Skin. <i>PLoS ONE</i> , 2014, 9, e107908.	2.5	50
32	Genome stability of <i>Propionibacterium acnes</i> : a comprehensive study of indels and homopolymeric tracts. <i>Scientific Reports</i> , 2016, 6, 20662.	3.3	49
33	<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
34	Genome Analysis of the Biotechnologically Relevant Acidophilic Iron Oxidising Strain JA12 Indicates Phylogenetic and Metabolic Diversity within the Novel Genus <i>Ferroplasma</i> . <i>PLoS ONE</i> , 2016, 11, e0146832.	2.5	48
35	The Purine-Utilizing Bacterium <i>Clostridium acidurici</i> 9a: A Genome-Guided Metabolic Reconsideration. <i>PLoS ONE</i> , 2012, 7, e51662.	2.5	46
36	Common skin bacteria protect their host from oxidative stress through secreted antioxidant RoxP. <i>Scientific Reports</i> , 2019, 9, 3596.	3.3	46

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37	<i>Propionibacterium acnes</i> host cell tropism contributes to vimentin-mediated invasion and induction of inflammation. Cellular Microbiology, 2012, 14, 1720-1733.	2.1	43
38	First Insights into the Genome of the Gram-Negative, Endospore-Forming Organism <i>Sporomusa ovata</i> Strain H1 DSM 2662. Genome Announcements, 2013, 1, .	0.8	42
39	Gene Loss and Horizontal Gene Transfer Contributed to the Genome Evolution of the Extreme Acidophile <i>Ferroplasma acidiphilum</i> . Frontiers in Microbiology, 2016, 7, 797.	3.5	42
40	<i>Propionibacterium acnes</i> phylogenetic type III is associated with progressive macular hypomelanosis. European Journal of Microbiology and Immunology, 2017, 7, 37-45.	2.8	42
41	Mutagenesis of <i>Propionibacterium acnes</i> and analysis of two CAMP factor knock-out mutants. Journal of Microbiological Methods, 2010, 83, 211-216.	1.6	40
42	Complete Genome Sequence of <i>Bacillus thuringiensis</i> Strain 407 Cry-. Genome Announcements, 2013, 1, .	0.8	40
43	Analysis of the Genome and Metabolome of Marine Myxobacteria Reveals High Potential for Biosynthesis of Novel Specialized Metabolites. Scientific Reports, 2018, 8, 16600.	3.3	40
44	Formate metabolism in the acetogenic bacterium <i>Acetobacterium woodii</i> . Environmental Microbiology, 2021, 23, 4214-4227.	3.8	39
45	A Janus-Faced Bacterium: Host-Beneficial and -Detrimental Roles of <i>Cutibacterium acnes</i> . Frontiers in Microbiology, 2021, 12, 673845.	3.5	37
46	Biogeography and environmental genomics of the Roseobacter-affiliated pelagic CHAB-I-5 lineage. Nature Microbiology, 2016, 1, 16063.	13.3	36
47	Identification of the first glyphosate transporter by genomic adaptation. Environmental Microbiology, 2019, 21, 1287-1305.	3.8	36
48	Proposal for the reclassification of obligately purine-fermenting bacteria <i>Clostridium acidurici</i> (Barker 1938) and <i>Clostridium purinilyticum</i> (D'Amore 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 Tjallingii 1977) as <i>Gottschalkia angustum</i> gen. nov. comb. nov. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2711-2719.	3.7	36
49	Genome Sequence of <i>Brevibacillus laterosporus</i> LMG 15441, a Pathogen of Invertebrates. Journal of Bacteriology, 2011, 193, 5535-5536.	2.2	35
50	Life based on phosphite: a genome-guided analysis of <i>Desulfotignum phosphitoxidans</i> . BMC Genomics, 2013, 14, 753.	2.8	35
51	Plant resistome profiling in evolutionary old bog vegetation provides new clues to understand emergence of multi-resistance. ISME Journal, 2021, 15, 921-937.	9.8	33
52	Globally Abundant <i>Candidatus</i> <i>Udaeobacter</i> Benefits from Release of Antibiotics in Soil and Potentially Performs Trace Gas Scavenging. MSphere, 2020, 5, .	2.9	32
53	Active metabolic pathways of anaerobic methane oxidation in paddy soils. Soil Biology and Biochemistry, 2021, 156, 108215.	8.8	32
54	Whole-Genome Draft Sequences of Six Commensal Fecal and Six Mastitis-Associated <i>Escherichia coli</i> Strains of Bovine Origin. Genome Announcements, 2016, 4, .	0.8	31

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55	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
56	Cutibacterium acnes is an intracellular and intra-articular commensal of the human shoulder joint. <i>Journal of Shoulder and Elbow Surgery</i> , 2021, 30, 16-26.	2.6	29
57	Pan-genome analysis of the genus <i>Fingoldia</i> identifies two distinct clades, strain-specific heterogeneity, and putative virulence factors. <i>Scientific Reports</i> , 2018, 8, 266.	3.3	28
58	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
59	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
60	Permanent draft genome sequence of <i>Acidiphilium</i> sp. JA12-A1. <i>Standards in Genomic Sciences</i> , 2015, 10, 56.	1.5	26
61	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
62	The Curious Case of <i>Achromobacter eurydice</i> , a Gram-Variable Pleomorphic Bacterium Associated with European Foulbrood Disease in Honeybees. <i>Microbial Ecology</i> , 2018, 75, 1-6.	2.8	26
63	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
64	Bacterial signatures and their inflammatory potentials associated with prostate cancer. <i>Apmis</i> , 2020, 128, 80-91.	2.0	26
65	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
66	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
67	Discovery of novel community-relevant small proteins in a simplified human intestinal microbiome. <i>Microbiome</i> , 2021, 9, 55.	11.1	24
68	The <i>Bacillus subtilis</i> Minimal Genome Compendium. <i>ACS Synthetic Biology</i> , 2021, 10, 2767-2771.	3.8	23
69	Production of the Fragrance Geraniol in Peroxisomes of a Product-Tolerant Baker's Yeast. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 582052.	4.1	22
70	Cysteine: an overlooked energy and carbon source. <i>Scientific Reports</i> , 2021, 11, 2139.	3.3	22
71	Complete Genome Sequence of the Solvent Producer <i>Clostridium saccharobutylicum</i> NCP262 (DSM) Tj ETQq1 1 0.784314 r gBT /Overlo	0.8	21
72	Complete Genome Sequence of the Solvent Producer <i>Clostridium saccharoperbutylacetonicum</i> Strain DSM 14923. <i>Genome Announcements</i> , 2014, 2, .	0.8	21

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73	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
74	Prevalence of Flp Pili-Encoding Plasmids in <i>Cutibacterium acnes</i> Isolates Obtained from Prostatic Tissue. <i>Frontiers in Microbiology</i> , 2017, 8, 2241.	3.5	21
75	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
76	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
77	When the going gets tough: Emergence of a complex methane-driven interaction network during recovery from desiccation-rewetting. <i>Soil Biology and Biochemistry</i> , 2021, 153, 108109.	8.8	20
78	Response of a methane-driven interaction network to stressor intensification. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	19
79	<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
80	The <i>Bacillus</i> phage <scp>SP1 <sup>2</sup> </scp> and its relatives: a temperate phage model system reveals new strains, species, prophage integration loci, conserved proteins and lysogeny management components. <i>Environmental Microbiology</i> , 2022, 24, 2098-2118.	3.8	19
81	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
82	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
83	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
84	Genome Sequence of the Acetogenic Bacterium <i>Oxobacter pfennigii</i> DSM 3222 <sup>T</sup>. <i>Genome Announcements</i> , 2015, 3, .	0.8	17
85	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
86	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
87	Role of Wax Ester Synthase/Acyl Coenzyme A:Diacylglycerol Acyltransferase in Oleaginous <i>Streptomyces</i> sp. Strain G25. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5969-5981.	3.1	16
88	Resistance to serine in <i>Bacillus subtilis</i>: identification of the serine transporter <scp>YbeC</scp> and of a metabolic network that links serine and threonine metabolism. <i>Environmental Microbiology</i> , 2020, 22, 3937-3949.	3.8	16
89	Microbial Gutta-Percha Degradation Shares Common Steps with Rubber Degradation by <i>Nocardia nova</i> SH22a. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1140-1149.	3.1	15
90	Closed Genome Sequence of <i>Clostridium pasteurianum</i> ATCC 6013. <i>Genome Announcements</i> , 2015, 3, .	0.8	15

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91	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
92	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
93	<i>Staphylococcus saccharolyticus</i> : An Overlooked Human Skin Colonizer. <i>Microorganisms</i> , 2020, 8, 1105.	3.6	14
94	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
95	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
96	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
97	Genome Sequence of the Acetogenic Bacterium <i>Butyrivibrio methylotrophicus</i> DSM 3468 <sup>T</sup> . <i>Genome Announcements</i> , 2016, 4, .	0.8	13
98	Mutagenesis Induced by Sub-Lethal Doses of Ciprofloxacin: Genotypic and Phenotypic Differences Between the <i>Pseudomonas aeruginosa</i> Strain PA14 and Clinical Isolates. <i>Frontiers in Microbiology</i> , 2019, 10, 1553.	3.5	13
99	The third pillar of metal homeostasis in <i>Cupriavidus metallidurans</i> CH34: preferences are controlled by extracytoplasmic function sigma factors. <i>Metallomics</i> , 2019, 11, 291-316.	2.4	13
100	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
101	Genome and Proteome Analysis of <i>Rhodococcus erythropolis</i> MI2: Elucidation of the 4,4'-Dithiodibutyric Acid Catabolism. <i>PLoS ONE</i> , 2016, 11, e0167539.	2.5	12
102	Genome Sequence of the Acetogenic Bacterium <i>Acetobacterium wieringae</i> DSM 1911 <sup>T</sup> . <i>Genome Announcements</i> , 2016, 4, .	0.8	12
103	Genome Sequence of the Acetogenic Bacterium <i>Moorella mulderi</i> DSM 14980 T. <i>Genome Announcements</i> , 2016, 4, .	0.8	12
104	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
105	Comparative Genomics of Nonoutbreak <i>Pseudomonas aeruginosa</i> Strains Underlines Genome Plasticity and Geographic Relatedness of the Global Clone ST235. <i>Genome Biology and Evolution</i> , 2018, 10, 1852-1857.	2.5	12
106	<i>Staphylococcus saccharolyticus</i> Isolated From Blood Cultures and Prosthetic Joint Infections Exhibits Excessive Genome Decay. <i>Frontiers in Microbiology</i> , 2019, 10, 478.	3.5	12
107	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
108	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



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109	Metagenomes of Wastewater at Different Treatment Stages in Central Germany. Microbiology Resource Announcements, 2020, 9, .	0.6	12
110	Quasi-essentiality of RNase Y in <i>Bacillus subtilis</i> is caused by its critical role in the control of mRNA homeostasis. Nucleic Acids Research, 2021, 49, 7088-7102.	14.5	12
111	<i>Sphingomonas jeddahensis</i> sp. nov., isolated from Saudi Arabian desert soil. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4057-4063.	1.7	12
112	Complete Genome Sequence of Amino Acid-Utilizing Eubacterium acidaminophilum al-2 (DSM 3953). Genome Announcements, 2014, 2, .	0.8	11
113	Genome sequence of <i>Pedobacter glucosidilyticus</i> DD6b, isolated from zooplankton <i>Daphnia magna</i> . Standards in Genomic Sciences, 2015, 10, 100.	1.5	11
114	Complete Genome Sequence of Rnf- and Cytochrome-Containing Autotrophic Acetogen <i>Clostridium acetatum</i> DSM 1496. Genome Announcements, 2015, 3, .	0.8	11
115	Draft genome sequence of the marine Rhodobacteraceae strain O3.65, cultivated from oil-polluted seawater of the Deepwater Horizon oil spill. Standards in Genomic Sciences, 2016, 11, 81.	1.5	11
116	Genetic and physiological analysis of biofilm formation on different plastic surfaces by <i>Sphingomonas</i> sp. strain S2M10 reveals an essential function of sphingane biosynthesis. Microbiology (United Kingdom), 2020, 166, 918-935.	1.8	11
117	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
118	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
119	Complete Genome sequence of the nematocidal <i>Bacillus thuringiensis</i> MYBT18246. Standards in Genomic Sciences, 2017, 12, 48.	1.5	10
120	Prevalence of blaKPC-2, blaKPC-3 and blaKPC-30-carrying Plasmids in <i>Klebsiella pneumoniae</i> Isolated in a Brazilian Hospital. Pathogens, 2021, 10, 332.	2.8	10
121	Native Cultivable Bacteria from the Blueberry Microbiome as Novel Potential Biocontrol Agents. Microorganisms, 2022, 10, 969.	3.6	10
122	The genome of <i>Variovorax paradoxus</i> 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
123	Draft Genome Sequence of the Butanoic Acid-Producing Bacterium <i>Clostridium luticellarii</i> DSM 29923, Used for Strong Aromatic Chinese Liquor Production. Genome Announcements, 2018, 6, .	0.8	9
124	Iron targeted transcriptome study draws attention to novel redox protein candidates involved in ferrous iron oxidation in <i>Ferroplasma</i> sp. JA12. Research in Microbiology, 2018, 169, 618-627.	2.1	9
125	Microbial epibiotic community of the deep-sea galatheid squat lobster <i>Munidopsis alvisca</i> . Scientific Reports, 2022, 12, 2675.	3.3	9
126	Predicting the Metabolic Potential of the Novel Iron Oxidising Bacterium " <i>Ferroplasma</i> " sp. JA12 Using Comparative Genomics. Advanced Materials Research, 0, 825, 153-156.	0.3	8



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127	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
128	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
129	Complete genome sequence of the nematocidal <i>Bacillus thuringiensis</i> MYBT18247. <i>Journal of Biotechnology</i> , 2017, 260, 48-52.	3.8	8
130	Draft Genome Sequence of the Thermophilic Acetogen <i>Moorella humiferrea</i> DSM 23265. <i>Genome Announcements</i> , 2018, 6, .	0.8	8
131	Draft Genome Sequence of the Hydrogenogenic Carboxydotroph <i>Moorella stamsii</i> DSM 26271. <i>Genome Announcements</i> , 2018, 6, .	0.8	8
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180	First Insights into the Draft Genome Sequence of the Endophyte <i>Paenibacillus amylolyticus</i> Strain GM1FR, Isolated from <i>Festuca rubra</i> L. <i>Genome Announcements</i> , 2018, 6, .	0.8	3

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