

# Mircea Podar

## List of Publications by Year in descending order

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130  
papers

27,806  
citations

38720

50  
h-index

17090

122  
g-index

147  
all docs

147  
docs citations

147  
times ranked

32300  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012, 486, 207-214.	13.7	9,614
2	A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.	13.7	2,249
3	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
4	Comparative Metagenomics of Microbial Communities. <i>Science</i> , 2005, 308, 554-557.	6.0	1,432
5	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007, 450, 560-565.	13.7	1,181
6	Genome Streamlining in a Cosmopolitan Oceanic Bacterium. <i>Science</i> , 2005, 309, 1242-1245.	6.0	1,034
7	Distinct and complex bacterial profiles in human periodontitis and health revealed by 16S pyrosequencing. <i>ISME Journal</i> , 2012, 6, 1176-1185.	4.4	799
8	The Genetic Basis for Bacterial Mercury Methylation. <i>Science</i> , 2013, 339, 1332-1335.	6.0	778
9	Mercury Methylation by Novel Microorganisms from New Environments. <i>Environmental Science &amp; Technology</i> , 2013, 47, 11810-11820.	4.6	575
10	Biogeography of the ecosystems of the healthy human body. <i>Genome Biology</i> , 2013, 14, R1.	13.9	540
11	Distinct Microbial Communities within the Endosphere and Rhizosphere of <i>Populus deltoides</i> Roots across Contrasting Soil Types. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5934-5944.	1.4	524
12	The genome of <i>Nanoarchaeum equitans</i> : Insights into early archaeal evolution and derived parasitism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12984-12988.	3.3	488
13	A comprehensive benchmarking study of protocols and sequencing platforms for 16S rRNA community profiling. <i>BMC Genomics</i> , 2016, 17, 55.	1.2	387
14	Global prevalence and distribution of genes and microorganisms involved in mercury methylation. <i>Science Advances</i> , 2015, 1, e1500675.	4.7	355
15	A Multifactor Analysis of Fungal and Bacterial Community Structure in the Root Microbiome of Mature <i>Populus deltoides</i> Trees. <i>PLoS ONE</i> , 2013, 8, e76382.	1.1	315
16	UGA is an additional glycine codon in uncultured SR1 bacteria from the human microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5540-5545.	3.3	290
17	A korarchaeal genome reveals insights into the evolution of the Archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8102-8107.	3.3	253
18	Targeted isolation and cultivation of uncultivated bacteria by reverse genomics. <i>Nature Biotechnology</i> , 2019, 37, 1314-1321.	9.4	231

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19	Targeted Access to the Genomes of Low-Abundance Organisms in Complex Microbial Communities. Applied and Environmental Microbiology, 2007, 73, 3205-3214.	1.4	225
20	Environmental Whole-Genome Amplification To Access Microbial Populations in Contaminated Sediments. Applied and Environmental Microbiology, 2006, 72, 3291-3301.	1.4	213
21	Exploring Nitrilase Sequence Space for Enantioselective Catalysis. Applied and Environmental Microbiology, 2004, 70, 2429-2436.	1.4	212
22	Host genetic and environmental effects on mouse intestinal microbiota. ISME Journal, 2012, 6, 2033-2044.	4.4	206
23	Comparative metagenomic and <scp>rRNA</scp> microbial diversity characterization using archaeal and bacterial synthetic communities. Environmental Microbiology, 2013, 15, 1882-1899.	1.8	202
24	Microbial community structure of hydrothermal deposits from geochemically different vent fields along the Mid-Atlantic Ridge. Environmental Microbiology, 2011, 13, 2158-2171.	1.8	174
25	Genomics-informed isolation and characterization of a symbiotic Nanoarchaeota system from a terrestrial geothermal environment. Nature Communications, 2016, 7, 12115.	5.8	154
26	A Molecular Phylogenetic Framework for the Phylum Ctenophora Using 18S rRNA Genes. Molecular Phylogenetics and Evolution, 2001, 21, 218-230.	1.2	146
27	Mercury and Other Heavy Metals Influence Bacterial Community Structure in Contaminated Tennessee Streams. Applied and Environmental Microbiology, 2011, 77, 302-311.	1.4	137
28	New opportunities revealed by biotechnological explorations of extremophiles. Current Opinion in Biotechnology, 2006, 17, 250-255.	3.3	126
29	Robust Mercury Methylation across Diverse Methanogenic Archaea. MBio, 2018, 9, .	1.8	112
30	Discovery of Pectin-degrading Enzymes and Directed Evolution of a Novel Pectate Lyase for Processing Cotton Fabric. Journal of Biological Chemistry, 2005, 280, 9431-9438.	1.6	106
31	A genomic analysis of the archaeal system Ignicoccus hospitalis-Nanoarchaeum equitans. Genome Biology, 2008, 9, R158.	3.8	104
32	Insights into archaeal evolution and symbiosis from the genomes of a nanoarchaeon and its inferred crenarchaeal host from Obsidian Pool, Yellowstone National Park. Biology Direct, 2013, 8, 9.	1.9	102
33	The stereochemical course of group II intron self-splicing. Science, 1994, 266, 1685-1688.	6.0	101
34	Determining the Reliability of Measuring Mercury Cycling Gene Abundance with Correlations with Mercury and Methylmercury Concentrations. Environmental Science & Technology, 2019, 53, 8649-8663.	4.6	99
35	Group II intron splicing in vivo by first-step hydrolysis. Nature, 1998, 391, 915-918.	13.7	94
36	<i>Caldicellulosiruptor obsidiansis</i> sp. nov., an Anaerobic, Extremely Thermophilic, Cellulolytic Bacterium Isolated from Obsidian Pool, Yellowstone National Park. Applied and Environmental Microbiology, 2010, 76, 1014-1020.	1.4	91

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37	Inter-field variability in the microbial communities of hydrothermal vent deposits from a back-arc basin. <i>Geobiology</i> , 2012, 10, 333-346.	1.1	86
38	Contrasting taxonomic stratification of microbial communities in two hypersaline meromictic lakes. <i>ISME Journal</i> , 2015, 9, 2642-2656.	4.4	82
39	Cellulases: ambiguous nonhomologous enzymes in a genomic perspective. <i>Trends in Biotechnology</i> , 2011, 29, 473-479.	4.9	78
40	Complete and Draft Genome Sequences of Six Members of the <i>Aquificales</i> . <i>Journal of Bacteriology</i> , 2009, 191, 1992-1993.	1.0	76
41	A new symbiotic nanoarchaeote ( <i>Candidatus Nanoclepta minutus</i> ) and its host ( <i>Zestosphaera</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 2019, 42, 94-106.	1.2	76
42	Stereochemical Selectivity of Group II Intron Splicing, Reverse Splicing, and Hydrolysis Reactions. <i>Molecular and Cellular Biology</i> , 1995, 15, 4466-4478.	1.1	73
43	Site-Directed Mutagenesis of HgcA and HgcB Reveals Amino Acid Residues Important for Mercury Methylation. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3205-3217.	1.4	73
44	Development and Validation of Broad-Range Qualitative and Clade-Specific Quantitative Molecular Probes for Assessing Mercury Methylation in the Environment. <i>Applied and Environmental Microbiology</i> , 2016, 82, 6068-6078.	1.4	73
45	The heteromeric Nanoarchaeum equitans splicing endonuclease cleaves noncanonical bulge-helix-bulge motifs of joined tRNA halves. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 17934-17939.	3.3	71
46	Evolution of a microbial nitrilase gene family: a comparative and environmental genomics study. <i>BMC Evolutionary Biology</i> , 2005, 5, 42.	3.2	66
47	Proteomic Characterization of Cellular and Molecular Processes that Enable the Nanoarchaeum equitans-Ignicoccus hospitalis Relationship. <i>PLoS ONE</i> , 2011, 6, e22942.	1.1	65
48	More than one way to splice an RNA: Branching without a bulge and splicing without branching in group II introns. <i>Rna</i> , 1998, 4, 1186-1202.	1.6	58
49	Regulatory Elements Involved in Tax-Mediated Transactivation of the HTLV-I LTR. <i>Virology</i> , 1993, 196, 442-450.	1.1	56
50	Diversity and genomic insights into the uncultured <i>Candidatus Chloroflexi</i> from the human microbiota. <i>Environmental Microbiology</i> , 2014, 16, 2635-2643.	1.8	55
51	Enrichment of Root Endophytic Bacteria from <i>Populus deltoides</i> and Single-Cell-Genomics Analysis. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5698-5708.	1.4	53
52	A Complex Endomembrane System in the Archaeon <i>Ignicoccus hospitalis</i> Tapped by Nanoarchaeum equitans. <i>Frontiers in Microbiology</i> , 2017, 8, 1072.	1.5	52
53	Characterization of Archaeal Community in Contaminated and Uncontaminated Surface Stream Sediments. <i>Microbial Ecology</i> , 2010, 60, 784-795.	1.4	51
54	Comparative Genomics Guides Elucidation of Vitamin B <sub>12</sub> Biosynthesis in Novel Human-Associated <i>Akkermansia</i> Strains. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	48

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55	Comparative Analysis of Microbial Diversity Across Temperature Gradients in Hot Springs From Yellowstone and Iceland. <i>Frontiers in Microbiology</i> , 2020, 11, 1625.	1.5	48
56	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	6.0	45
57	Life on the edge: functional genomic response of <i>Ignicoccus hospitalis</i> to the presence of <i>Nanoarchaeum equitans</i> . <i>ISME Journal</i> , 2015, 9, 101-114.	4.4	44
58	Single-cell genomics of co-sorted Nanoarchaeota suggests novel putative host associations and diversification of proteins involved in symbiosis. <i>Microbiome</i> , 2018, 6, 161.	4.9	44
59	Multiple Single-Cell Genomes Provide Insight into Functions of Uncultured Deltaproteobacteria in the Human Oral Cavity. <i>PLoS ONE</i> , 2013, 8, e59361.	1.1	44
60	Microbial Community Succession during Lactate Amendment and Electron Acceptor Limitation Reveals a Predominance of Metal-Reducing <i>Pelosinus</i> spp. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2082-2091.	1.4	42
61	Genome Sequence of the Mercury-Methylating Strain <i>Desulfovibrio desulfuricans</i> ND132. <i>Journal of Bacteriology</i> , 2011, 193, 2078-2079.	1.0	41
62	Complete Genome Sequence of the Cellulolytic Thermophile <i>Caldicellulosiruptor obsidiansis</i> OB47. <i>Journal of Bacteriology</i> , 2010, 192, 6099-6100.	1.0	39
63	Carbon Amendments Alter Microbial Community Structure and Net Mercury Methylation Potential in Sediments. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	38
64	Development and characterization of stable anaerobic thermophilic methanogenic microbiomes fermenting switchgrass at decreasing residence times. <i>Biotechnology for Biofuels</i> , 2018, 11, 243.	6.2	37
65	Establishment and metabolic analysis of a model microbial community for understanding trophic and electron accepting interactions of subsurface anaerobic environments. <i>BMC Microbiology</i> , 2010, 10, 149.	1.3	36
66	Hexavalent Chromium Reduction under Fermentative Conditions with Lactate Stimulated Native Microbial Communities. <i>PLoS ONE</i> , 2013, 8, e83909.	1.1	36
67	Ultrastructural and Single-Cell-Level Characterization Reveals Metabolic Versatility in a Microbial Eukaryote Community from an Ice-Covered Antarctic Lake. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3659-3670.	1.4	36
68	Microbial community structure with trends in methylation gene diversity and abundance in mercury-contaminated rice paddy soils in Guizhou, China. <i>Environmental Sciences: Processes and Impacts</i> , 2018, 20, 673-685.	1.7	36
69	Complex subsurface hydrothermal fluid mixing at a submarine arc volcano supports distinct and highly diverse microbial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 32627-32638.	3.3	36
70	Mutations of the two-nucleotide bulge of D5 of a group II intron block splicing in vitro and in vivo: phenotypes and suppressor mutations. <i>Rna</i> , 1996, 2, 1161-72.	1.6	35
71	Genus-Wide Assessment of Lignocellulose Utilization in the Extremely Thermophilic Genus <i>Caldicellulosiruptor</i> by Genomic, Pangenomic, and Metagenomic Analyses. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	33
72	An Improved hgcAB Primer Set and Direct High-Throughput Sequencing Expand Hg-Methylator Diversity in Nature. <i>Frontiers in Microbiology</i> , 2020, 11, 541554.	1.5	33

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73	Insights into the Evolution of Host Association through the Isolation and Characterization of a Novel Human Periodontal Pathobiont, <i>Desulfobulbus oralis</i> . MBio, 2018, 9, .	1.8	32
74	Structure determination of the HgcAB complex using metagenome sequence data: insights into microbial mercury methylation. Communications Biology, 2020, 3, 320.	2.0	30
75	Machine learning-based prediction of enzyme substrate scope: Application to bacterial nitrilases. Proteins: Structure, Function and Bioinformatics, 2021, 89, 336-347.	1.5	30
76	Single Cell Genomics of Uncultured, Health-Associated <i>Tannerella</i> BU063 (Oral Taxon 286) and Comparison to the Closely Related Pathogen <i>Tannerella forsythia</i> . PLoS ONE, 2014, 9, e89398.	1.1	29
77	The two steps of group II intron self-splicing are mechanistically distinguishable. Rna, 1998, 4, 890-900.	1.6	28
78	Untargeted metabolomics studies employing NMR and LC-MS reveal metabolic coupling between <i>Nanoarchaeum equitans</i> and its archaeal host <i>Ignicoccus hospitalis</i> . Metabolomics, 2015, 11, 895-907.	1.4	27
79	Characterization of the Deltaproteobacteria in contaminated and uncontaminated stream sediments and identification of potential mercury methylators. Aquatic Microbial Ecology, 2012, 66, 271-282.	0.9	26
80	Culture Independent Genomic Comparisons Reveal Environmental Adaptations for Altiarchaeales. Frontiers in Microbiology, 2016, 7, 1221.	1.5	25
81	A UV-induced, Mg(2+)-dependent crosslink traps an active form of domain 3 of a self-splicing group II intron. Rna, 1995, 1, 828-40.	1.6	25
82	The prokaryotic V4R domain is the likely ancestor of a key component of the eukaryotic vesicle transport system. Biology Direct, 2008, 3, 2.	1.9	24
83	Draft Genome Sequences for Two Metal-Reducing <i>Pelosinus fermentans</i> Strains Isolated from a Cr(VI)-Contaminated Site and for Type Strain R7. Journal of Bacteriology, 2012, 194, 5147-5148.	1.0	24
84	Structure, mineralogy, and microbial diversity of geothermal spring microbialites associated with a deep oil drilling in Romania. Frontiers in Microbiology, 2015, 6, 253.	1.5	24
85	Characterization of Fatty Acids in Crenarchaeota by GC-MS and NMR. Archaea, 2015, 2015, 1-9.	2.3	23
86	Domain 5 binds near a highly conserved dinucleotide in the joiner linking domains 2 and 3 of a group II intron. Rna, 1998, 4, 151-66.	1.6	21
87	[8] Reactions catalyzed by group II introns in Vitro. Methods in Enzymology, 1996, 264, 66-86.	0.4	20
88	Community Analysis of Plant Biomass-Degrading Microorganisms from Obsidian Pool, Yellowstone National Park. Microbial Ecology, 2015, 69, 333-345.	1.4	20
89	A Microbe Associated with Sleep Revealed by a Novel Systems Genetic Analysis of the Microbiome in Collaborative Cross Mice. Genetics, 2020, 214, 719-733.	1.2	20
90	Single-Cell Genomics and the Oral Microbiome. Journal of Dental Research, 2020, 99, 613-620.	2.5	18

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91	Characterization of subsurface media from locations up- and down-gradient of a uranium-contaminated aquifer. <i>Chemosphere</i> , 2020, 255, 126951.	4.2	18
92	Photocrosslinking of 4-thio uracil-containing RNAs supports a side-by-side arrangement of domains 5 and 6 of a group II intron. <i>Rna</i> , 1999, 5, 318-329.	1.6	17
93	High Throughput Cultivation for Isolation of Novel Marine Microorganisms. <i>Oceanography</i> , 2006, 19, 120-125.	0.5	17
94	Cultivating the Bacterial Microbiota of <i>Populus</i> Roots. <i>MSystems</i> , 2021, 6, e0130620.	1.7	17
95	Rescuing Those Left Behind: Recovering and Characterizing Underdigested Membrane and Hydrophobic Proteins To Enhance Proteome Measurement Depth. <i>Analytical Chemistry</i> , 2015, 87, 7720-7728.	3.2	15
96	Temporal Dynamics of In-Field Bioreactor Populations Reflect the Groundwater System and Respond Predictably to Perturbation. <i>Environmental Science &amp; Technology</i> , 2017, 51, 2879-2889.	4.6	15
97	Hypersaline sapropels act as hotspots for microbial dark matter. <i>Scientific Reports</i> , 2017, 7, 6150.	1.6	15
98	Microbial Diversity and Sulfur Cycling in an Early Earth Analogue: From Ancient Novelty to Modern Commonality. <i>MBio</i> , 2022, 13, e0001622.	1.8	15
99	Genome Sequence of the Mercury-Methylating and Pleomorphic <i>Desulfovibrio africanus</i> Strain Walvis Bay. <i>Journal of Bacteriology</i> , 2011, 193, 4037-4038.	1.0	14
100	<i>Pseudodesulfovibrio mercurii</i> sp. nov., a mercury-methylating bacterium isolated from sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	13
101	Sequencing Intractable DNA to Close Microbial Genomes. <i>PLoS ONE</i> , 2012, 7, e41295.	1.1	11
102	A biodiversity-based approach to development of performance enzymes: Applied metagenomics and directed evolution. <i>Industrial Biotechnology</i> , 2005, 1, 283-287.	0.5	10
103	Genomics of the Uncultivated, Periodontitis-Associated Bacterium <i>Tannerella</i> sp. BU045 (Oral) Tj ETQq1 1 0,784314 rgBT /Ove FO	1.7	10
104	Bacterial Group II Introns in a Deep-Sea Hydrothermal Vent Environment. <i>Applied and Environmental Microbiology</i> , 2002, 68, 6392-6398.	1.4	8
105	An intersubunit disulfide bridge stabilizes the tetrameric nucleoside diphosphate kinase of <i>Aquifex aeolicus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1658-1668.	1.5	8
106	Multi-omics analysis provides insight to the <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> association. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 2218-2227.	1.1	6
107	Microbial diversity analysis of two full-scale seawater desalination treatment trains provides insights into detrimental biofilm formation. , 2021, 1, 100001.		6
108	Consent insufficient for data release”Response. <i>Science</i> , 2019, 364, 446-446.	6.0	5



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109	Complete Genome Sequence of <i>Terriglobus albidus</i> Strain ORNL, an Acidobacterium Isolated from the <i>Populus deltoides</i> Rhizosphere. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
110	In-field bioreactors demonstrate dynamic shifts in microbial communities in response to geochemical perturbations. <i>PLoS ONE</i> , 2020, 15, e0232437.	1.1	5
111	Two-Component Systems in Microbial Communities: Approaches and Resources for Generating and Analyzing Metagenomic Data Sets. <i>Methods in Enzymology</i> , 2007, 422, 32-46.	0.4	2
112	Single Cell Whole Genome Amplification of Uncultivated Organisms. <i>Microbiology Monographs</i> , 2009, , 241-256.	0.3	2
113	Draft Genome Sequence of <i>Pyrodictium occultum</i> PL19 T , a Marine Hyperthermophilic Species of Archaea That Grows Optimally at 105°C. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
114	Draft Genome Sequence of <i>Larkinella</i> sp. Strain BK230, Isolated from <i>Populus deltoides</i> Roots. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
115	Metagenome-Assembled Genome Sequences of Novel Prokaryotic Species from the Mercury-Contaminated East Fork Poplar Creek, Oak Ridge, Tennessee, USA. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
116	Single Cell Whole Genome Amplification of Uncultivated Organisms. <i>Microbiology Monographs</i> , 2009, , 83-99.	0.3	2
117	Draft Genome Sequence of <i>Schaalia odontolytica</i> Strain ORNL0103, a Basibiont of <i>Candidatus</i> <i>Saccharibacteria</i> HMT352. <i>Microbiology Resource Announcements</i> , 2021, 10, e0079321.	0.3	2
118	Draft Genome Sequence of a Novel <i>Thermofilum</i> sp. Strain from a New Zealand Hot Spring Enrichment Culture. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
119	Complete Genome Sequence of the Novel <i>Roseimicrobium</i> sp. Strain ORNL1, a <i>Verrucomicrobium</i> Isolated from the <i>Populus deltoides</i> Rhizosphere. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
120	Complete Genome Sequence of <i>Starkeya</i> sp. Strain ORNL1, a Soil Alphaproteobacterium Isolated from the Rhizosphere of <i>Populus deltoides</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
121	Complete Genome Sequence of Human Oral <i>Actinomyces</i> sp. HMT897 Strain ORNL0104, a Host of the <i>Saccharibacterium</i> (TM7) HMT351. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
122	Targeted Genomic Characterization, Uncultured Bacteria from Human Microbiota, Project. , 2013, , 1-2.		1
123	Incorporating concentration-dependent sediment microbial activity into methylmercury production kinetics modeling. <i>Environmental Sciences: Processes and Impacts</i> , 2022, 24, 1392-1405.	1.7	1
124	Complete Genome Sequence of Human Oral <i>Saccharibacterium</i> <i>Candidatus</i> <i>Nanosynbacter</i> sp. HMT352 Strain KC1. <i>Microbiology Resource Announcements</i> , 2022, , e0120521.	0.3	1
125	Draft Genome Sequence of a <i>Dictyoglomus</i> sp. from an Enrichment Culture of a New Zealand Geothermal Spring. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
126	Complete Genome Sequence of <i>Desulfobulbus oligotrophicus</i> Prop6, an Anaerobic Deltabacterota Strain That Lacks Mercury Methylation Capability. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0



#	ARTICLE	IF	CITATIONS
127	Complete Genome Sequence of Human Oral <i>Actinomyces</i> sp. HMT175 Strain ORNL0102, a Host of the <i>Saccharibacterium</i> (TM7) HMT957. <i>Microbiology Resource Announcements</i> , 2021, 10, e0041221.	0.3	0
128	Targeted Genomic Characterization, Uncultured Bacteria from Human Microbiota, <i>Project.</i> , 2015, , 621-622.		0
129	Effects of syntrophic interactions on methyl-mercury generation., 2021, , .		0
130	A System Biology Approach to Discern the Native Biochemical Function of Hg Methylation Proteins in <i>Desulfovibrio desulfuricans</i> ND132., 2020, , .		0