

Mircea Podar

List of Publications by Year in descending order

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130
papers

27,806
citations

38742
50
h-index

17105
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. Nature, 2012, 486, 207-214.	27.8	9,614
2	A framework for human microbiome research. Nature, 2012, 486, 215-221.	27.8	2,249
3	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. Nature Biotechnology, 2017, 35, 725-731.	17.5	1,512
4	Comparative Metagenomics of Microbial Communities. Science, 2005, 308, 554-557.	12.6	1,432
5	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. Nature, 2007, 450, 560-565.	27.8	1,181
6	Genome Streamlining in a Cosmopolitan Oceanic Bacterium. Science, 2005, 309, 1242-1245.	12.6	1,034
7	Distinct and complex bacterial profiles in human periodontitis and health revealed by 16S pyrosequencing. ISME Journal, 2012, 6, 1176-1185.	9.8	799
8	The Genetic Basis for Bacterial Mercury Methylation. Science, 2013, 339, 1332-1335.	12.6	778
9	Mercury Methylation by Novel Microorganisms from New Environments. Environmental Science & Technology, 2013, 47, 11810-11820.	10.0	575
10	Biogeography of the ecosystems of the healthy human body. Genome Biology, 2013, 14, R1.	9.6	540
11	Distinct Microbial Communities within the Endosphere and Rhizosphere of Populus deltoides Roots across Contrasting Soil Types. Applied and Environmental Microbiology, 2011, 77, 5934-5944.	3.1	524
12	The genome of Nanoarchaeum equitans: Insights into early archaeal evolution and derived parasitism. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12984-12988.	7.1	488
13	A comprehensive benchmarking study of protocols and sequencing platforms for 16S rRNA community profiling. BMC Genomics, 2016, 17, 55.	2.8	387
14	Global prevalence and distribution of genes and microorganisms involved in mercury methylation. Science Advances, 2015, 1, e1500675.	10.3	355
15	A Multifactor Analysis of Fungal and Bacterial Community Structure in the Root Microbiome of Mature Populus deltoides Trees. PLoS ONE, 2013, 8, e76382.	2.5	315
16	UGA is an additional glycine codon in uncultured SR1 bacteria from the human microbiota. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5540-5545.	7.1	290
17	A korarchaeal genome reveals insights into the evolution of the Archaea. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8102-8107.	7.1	253
18	Targeted isolation and cultivation of uncultivated bacteria by reverse genomics. Nature Biotechnology, 2019, 37, 1314-1321.	17.5	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.	3.1	225
20	Environmental Whole-Genome Amplification To Access Microbial Populations in Contaminated Sediments. Applied and Environmental Microbiology, 2006, 72, 3291-3301.	3.1	213
21	Exploring Nitrilase Sequence Space for Enantioselective Catalysis. Applied and Environmental Microbiology, 2004, 70, 2429-2436.	3.1	212
22	Host genetic and environmental effects on mouse intestinal microbiota. ISME Journal, 2012, 6, 2033-2044.	9.8	206
23	Comparative metagenomic and <scp>rRNA</scp> microbial diversity characterization using archaeal and bacterial synthetic communities. Environmental Microbiology, 2013, 15, 1882-1899.	3.8	202
24	Microbial community structure of hydrothermal deposits from geochemically different vent fields along the Mid-Atlantic Ridge. Environmental Microbiology, 2011, 13, 2158-2171.	3.8	174
25	Genomics-informed isolation and characterization of a symbiotic Nanoarchaeota system from a terrestrial geothermal environment. Nature Communications, 2016, 7, 12115.	12.8	154
26	A Molecular Phylogenetic Framework for the Phylum Ctenophora Using 18S rRNA Genes. Molecular Phylogenetics and Evolution, 2001, 21, 218-230.	2.7	146
27	Mercury and Other Heavy Metals Influence Bacterial Community Structure in Contaminated Tennessee Streams. Applied and Environmental Microbiology, 2011, 77, 302-311.	3.1	137
28	New opportunities revealed by biotechnological explorations of extremophiles. Current Opinion in Biotechnology, 2006, 17, 250-255.	6.6	126
29	Robust Mercury Methylation across Diverse Methanogenic Archaea. MBio, 2018, 9, .	4.1	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.	3.4	106
31	A genomic analysis of the archaeal system Ignicoccus hospitalis-Nanoarchaeum equitans. Genome Biology, 2008, 9, R158.	8.8	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.	4.6	102
33	The Stereochemical Course of Group II Intron Self-Splicing. Science, 1994, 266, 1685-1688.	12.6	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.	10.0	99
35	Group II intron splicing in vivo by first-step hydrolysis. Nature, 1998, 391, 915-918.	27.8	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.	3.1	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.	2.4	86
38	Contrasting taxonomic stratification of microbial communities in two hypersaline meromictic lakes. <i>ISME Journal</i> , 2015, 9, 2642-2656.	9.8	82
39	Cellulases: ambiguous nonhomologous enzymes in a genomic perspective. <i>Trends in Biotechnology</i> , 2011, 29, 473-479.	9.3	78
40	Complete and Draft Genome Sequences of Six Members of the <i>Aquificales</i> . <i>Journal of Bacteriology</i> , 2009, 191, 1992-1993.	2.2	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.	2.8	76
42	Stereochemical Selectivity of Group II Intron Splicing, Reverse Splicing, and Hydrolysis Reactions. <i>Molecular and Cellular Biology</i> , 1995, 15, 4466-4478.	2.3	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.	3.1	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.	3.1	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.	7.1	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.	2.5	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.	3.5	58
49	Regulatory Elements Involved in Tax-Mediated Transactivation of the HTLV-I LTR. <i>Virology</i> , 1993, 196, 442-450.	2.4	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.	3.8	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.	3.1	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.	3.5	52
53	Characterization of Archaeal Community in Contaminated and Uncontaminated Surface Stream Sediments. <i>Microbial Ecology</i> , 2010, 60, 784-795.	2.8	51
54	Comparative Genomics Guides Elucidation of Vitamin B ₁₂ Biosynthesis in Novel Human-Associated <i>Akkermansia</i> Strains. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	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.	3.5	48
56	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	12.6	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.	9.8	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.	11.1	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.	2.5	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.	3.1	42
61	Genome Sequence of the Mercury-Methylating Strain <i>Desulfovibrio desulfuricans</i> ND132. <i>Journal of Bacteriology</i> , 2011, 193, 2078-2079.	2.2	41
62	Complete Genome Sequence of the Cellulolytic Thermophile <i>Caldicellulosiruptor obsidiansis</i> OB47 ^T . <i>Journal of Bacteriology</i> , 2010, 192, 6099-6100.	2.2	39
63	Carbon Amendments Alter Microbial Community Structure and Net Mercury Methylation Potential in Sediments. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	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.	3.3	36
66	Hexavalent Chromium Reduction under Fermentative Conditions with Lactate Stimulated Native Microbial Communities. <i>PLoS ONE</i> , 2013, 8, e83909.	2.5	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.	3.1	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.	3.5	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.	7.1	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.	3.5	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, .	3.1	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.	3.5	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, .	4.1	32
74	Structure determination of the HgcAB complex using metagenome sequence data: insights into microbial mercury methylation. Communications Biology, 2020, 3, 320.	4.4	30
75	Machine learning-based prediction of enzyme substrate scope: Application to bacterial nitrilases. Proteins: Structure, Function and Bioinformatics, 2021, 89, 336-347.	2.6	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.	2.5	29
77	The two steps of group II intron self-splicing are mechanistically distinguishable. Rna, 1998, 4, 890-900.	3.5	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.	3.0	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.	1.8	26
80	Culture Independent Genomic Comparisons Reveal Environmental Adaptations for Altiarchaeales. Frontiers in Microbiology, 2016, 7, 1221.	3.5	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.	3.5	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.	4.6	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.	2.2	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.	3.5	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.	3.5	21
87	[8] Reactions catalyzed by group II introns in Vitro. Methods in Enzymology, 1996, 264, 66-86.	1.0	20
88	Community Analysis of Plant Biomass-Degrading Microorganisms from Obsidian Pool, Yellowstone National Park. Microbial Ecology, 2015, 69, 333-345.	2.8	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.	2.9	20
90	Single-Cell Genomics and the Oral Microbiome. Journal of Dental Research, 2020, 99, 613-620.	5.2	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.	8.2	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.	3.5	17
93	High Throughput Cultivation for Isolation of Novel Marine Microorganisms. <i>Oceanography</i> , 2006, 19, 120-125.	1.0	17
94	Cultivating the Bacterial Microbiota of <i>Populus</i> Roots. <i>MSystems</i> , 2021, 6, e0130620.	3.8	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.	6.5	15
96	Temporal Dynamics of In-Field Bioreactor Populations Reflect the Groundwater System and Respond Predictably to Perturbation. <i>Environmental Science & Technology</i> , 2017, 51, 2879-2889.	10.0	15
97	Hypersaline sapropels act as hotspots for microbial dark matter. <i>Scientific Reports</i> , 2017, 7, 6150.	3.3	15
98	Microbial Diversity and Sulfur Cycling in an Early Earth Analogue: From Ancient Novelty to Modern Commonality. <i>MBio</i> , 2022, 13, e0001622.	4.1	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.	2.2	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, .	1.7	13
101	Sequencing Intractable DNA to Close Microbial Genomes. <i>PLoS ONE</i> , 2012, 7, e41295.	2.5	11
102	A biodiversity-based approach to development of performance enzymes: Applied metagenomics and directed evolution. <i>Industrial Biotechnology</i> , 2005, 1, 283-287.	0.8	10
103	Genomics of the Uncultivated, Periodontitis-Associated Bacterium <i>Tannerella</i> sp. BU045 (Oral) Tj ETQq1 1 0.784314 rgBT /Over	3.8	10
104	Bacterial Group II Introns in a Deep-Sea Hydrothermal Vent Environment. <i>Applied and Environmental Microbiology</i> , 2002, 68, 6392-6398.	3.1	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.	2.6	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.	2.4	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.	12.6	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. Microbiology Resource Announcements, 2019, 8, .	0.6	5
110	In-field bioreactors demonstrate dynamic shifts in microbial communities in response to geochemical perturbations. PLoS ONE, 2020, 15, e0232437.	2.5	5
111	Two-Component Systems in Microbial Communities: Approaches and Resources for Generating and Analyzing Metagenomic Data Sets. Methods in Enzymology, 2007, 422, 32-46.	1.0	2
112	Single Cell Whole Genome Amplification of Uncultivated Organisms. Microbiology Monographs, 2009, , 241-256.	0.6	2
113	Draft Genome Sequence of <i>Pyrodictium occultum</i> PL19 T , a Marine Hyperthermophilic Species of Archaea That Grows Optimally at 105°C. Genome Announcements, 2016, 4, .	0.8	2
114	Draft Genome Sequence of <i>Larkinella</i> sp. Strain BK230, Isolated from <i>Populus deltoides</i> Roots. Microbiology Resource Announcements, 2020, 9, .	0.6	2
115	Metagenome-Assembled Genome Sequences of Novel Prokaryotic Species from the Mercury-Contaminated East Fork Poplar Creek, Oak Ridge, Tennessee, USA. Microbiology Resource Announcements, 2021, 10, .	0.6	2
116	Single Cell Whole Genome Amplification of Uncultivated Organisms. Microbiology Monographs, 2009, , 83-99.	0.6	2
117	Draft Genome Sequence of <i>Schaalia odontolytica</i> Strain ORNL0103, a Basibiont of <i>Candidatus</i> <i>Saccharibacteria</i> HMT352. Microbiology Resource Announcements, 2021, 10, e0079321.	0.6	2
118	Draft Genome Sequence of a Novel <i>Thermofilum</i> sp. Strain from a New Zealand Hot Spring Enrichment Culture. Genome Announcements, 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. Microbiology Resource Announcements, 2020, 9, .	0.6	1
120	Complete Genome Sequence of <i>Starkeya</i> sp. Strain ORNL1, a Soil Alphaproteobacterium Isolated from the Rhizosphere of <i>Populus deltoides</i> . Microbiology Resource Announcements, 2020, 9, .	0.6	1
121	Complete Genome Sequence of Human Oral <i>Actinomyces</i> sp. HMT897 Strain ORNL0104, a Host of the <i>Saccharibacterium</i> (TM7) HMT351. Microbiology Resource Announcements, 2021, 10, .	0.6	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. Environmental Sciences: Processes and Impacts, 2022, 24, 1392-1405.	3.5	1
124	Complete Genome Sequence of Human Oral <i>Saccharibacterium</i> <i>Candidatus</i> <i>Nanosynbacter</i> sp. HMT352 Strain KC1. Microbiology Resource Announcements, 2022, , e0120521.	0.6	1
125	Draft Genome Sequence of a <i>Dictyoglomus</i> sp. from an Enrichment Culture of a New Zealand Geothermal Spring. Genome Announcements, 2018, 6, .	0.8	0
126	Complete Genome Sequence of <i>Desulfobulbus oligotrophicus</i> Prop6, an Anaerobic Deltabacterota Strain That Lacks Mercury Methylation Capability. Microbiology Resource Announcements, 2021, 10, .	0.6	0

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127	Complete Genome Sequence of Human Oral <i>Actinomyces</i> sp. HMT175 Strain ORNL0102, a Host of the <i>Saccharibacterium</i> (TM7) HMT957. Microbiology Resource Announcements, 2021, 10, e0041221.	0.6	0
128	Targeted Genomic Characterization, Uncultured Bacteria from Human Microbiota, Project. , 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