

# Gene W Tyson

## List of Publications by Year in descending order

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Version: 2024-02-01

137  
papers

34,496  
citations

12303

69  
h-index

9553

142  
g-index

160  
all docs

160  
docs citations

160  
times ranked

29057  
citing authors

#	ARTICLE	IF	CITATIONS
1	Sulfate differentially stimulates but is not respired by diverse anaerobic methanotrophic archaea. <i>ISME Journal</i> , 2022, 16, 168-177.	4.4	21
2	Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. <i>PLoS Biology</i> , 2022, 20, e3001508.	2.6	62
3	Chemotaxis shapes the microscale organization of the ocean's microbiome. <i>Nature</i> , 2022, 605, 132-138.	13.7	51
4	Polyhydroxyalkanoate-driven current generation via acetate by an anaerobic methanotrophic consortium. <i>Water Research</i> , 2022, 221, 118743.	5.3	10
5	Expanding the phylogenetic distribution of cytochrome <i>b</i> -containing methanogenic archaea sheds light on the evolution of methanogenesis. <i>ISME Journal</i> , 2022, 16, 2373-2387.	4.4	12
6	Evidence for non-methanogenic metabolisms in globally distributed archaeal clades basal to the <i>Methanomassiliicoccales</i> . <i>Environmental Microbiology</i> , 2021, 23, 340-357.	1.8	19
7	Pregnant women who develop preeclampsia have lower abundance of the butyrate-producer <i>Coprococcus</i> in their gut microbiota. <i>Pregnancy Hypertension</i> , 2021, 23, 211-219.	0.6	42
8	Evaluation of the Microba Community Profiler for Taxonomic Profiling of Metagenomic Datasets From the Human Gut Microbiome. <i>Frontiers in Microbiology</i> , 2021, 12, 643682.	1.5	25
9	Critical evaluation of faecal microbiome preservation using metagenomic analysis. <i>ISME Communications</i> , 2021, 1, .	1.7	8
10	Methane-dependent selenate reduction by a bacterial consortium. <i>ISME Journal</i> , 2021, 15, 3683-3692.	4.4	17
11	Diverse sediment microbiota shape methane emission temperature sensitivity in Arctic lakes. <i>Nature Communications</i> , 2021, 12, 5815.	5.8	15
12	Successional dynamics and alternative stable states in a saline activated sludge microbial community over 9 years. <i>Microbiome</i> , 2021, 9, 199.	4.9	33
13	Autism-related dietary preferences mediate autism-gut microbiome associations. <i>Cell</i> , 2021, 184, 5916-5931.e17.	13.5	172
14	Microvolume DNA extraction methods for microscale amplicon and metagenomic studies. <i>ISME Communications</i> , 2021, 1, .	1.7	10
15	Accelerating microbial iron cycling promotes recementation of surface crusts in iron ore regions. <i>Microbial Biotechnology</i> , 2020, 13, 1960-1971.	2.0	10
16	Lateral Gene Transfer Drives Metabolic Flexibility in the Anaerobic Methane-Oxidizing Archaeal Family <i>Methanoperedenaceae</i> . <i>MBio</i> , 2020, 11, .	1.8	51
17	Anaerobic methane oxidation coupled to manganese reduction by members of the <i>Methanoperedenaceae</i> . <i>ISME Journal</i> , 2020, 14, 1030-1041.	4.4	203
18	The importance of designating type material for uncultured taxa. <i>Systematic and Applied Microbiology</i> , 2019, 42, 15-21.	1.2	149

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19	Insights into the ecological roles and evolution of methyl-coenzyme M reductase-containing hot spring Archaea. <i>Nature Communications</i> , 2019, 10, 4574.	5.8	90
20	A genomic view of the reef-building coral <i>Porites lutea</i> and its microbial symbionts. <i>Nature Microbiology</i> , 2019, 4, 2090-2100.	5.9	160
21	An evolving view of methane metabolism in the Archaea. <i>Nature Reviews Microbiology</i> , 2019, 17, 219-232.	13.6	350
22	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	6.0	45
23	Acetate Production from Anaerobic Oxidation of Methane via Intracellular Storage Compounds. <i>Environmental Science &amp; Technology</i> , 2019, 53, 7371-7379.	4.6	48
24	Biochar-Mediated Anaerobic Oxidation of Methane. <i>Environmental Science &amp; Technology</i> , 2019, 53, 6660-6668.	4.6	92
25	Microbial Community Analyses Inform Geochemical Reaction Network Models for Predicting Pathways of Greenhouse Gas Production. <i>Frontiers in Earth Science</i> , 2019, 7, .	0.8	9
26	Consent insufficient for data release—Response. <i>Science</i> , 2019, 364, 446-446.	6.0	5
27	Discovery and ecogenomic context of a global <i>Caldiserica</i> -related phylum active in thawing permafrost, <i>Candidatus Cryoserica</i> phylum nov., <i>Ca. Cryoserica</i> class nov., <i>Ca. Cryosericales</i> ord. nov., <i>Ca. Cryoseriaceae</i> fam. nov., comprising the four species <i>Cryosericum septentrionale</i> gen. nov. sp. nov., <i>Ca. C. hinesii</i> sp. nov., <i>Ca. C. odellii</i> sp. nov., <i>Ca. C. terrychapinii</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2019, 42, 54-66.	1.2	42
28	Accelerating Bauxite Residue Remediation with Microbial Biotechnology. <i>Minerals, Metals and Materials Series</i> , 2019, , 69-77.	0.3	2
29	Goethite Reduction by a Neutrophilic Member of the Alphaproteobacterial Genus <i>Telmatospirillum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2938.	1.5	25
30	Divergent methyl-coenzyme M reductase genes in a deep-subseafloor Archaeoglobi. <i>ISME Journal</i> , 2019, 13, 1269-1279.	4.4	76
31	A phylogenomic and ecological analysis of the globally abundant Marine Group II archaea ( <i>Ca.</i> ) Tj ETQq1 1 0.784314 rgBT /Ove	4.4	158
32	Using Machine Learning To Predict Antimicrobial MICs and Associated Genomic Features for Nontyphoidal <i>Salmonella</i> . <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	181
33	The effect of methane and odd-chain fatty acids on 3-hydroxybutyrate (3HB) and 3-hydroxyvalerate (3HV) synthesis by a <i>Methylosinus</i> -dominated mixed culture. <i>Bioresources and Bioprocessing</i> , 2019, 6, .	2.0	18
34	Biogenic Methane Cycling in a Laboratory Model of an Abandoned Bituminous Coal Mine. <i>Geomicrobiology Journal</i> , 2018, 35, 491-502.	1.0	3
35	A methanotrophic archaeon couples anaerobic oxidation of methane to Fe(III) reduction. <i>ISME Journal</i> , 2018, 12, 1929-1939.	4.4	266
36	GraftM: a tool for scalable, phylogenetically informed classification of genes within metagenomes. <i>Nucleic Acids Research</i> , 2018, 46, e59-e59.	6.5	130

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37	Soil Viruses Are Underexplored Players in Ecosystem Carbon Processing. <i>MSystems</i> , 2018, 3, .	1.7	189
38	Methanotrophy across a natural permafrost thaw environment. <i>ISME Journal</i> , 2018, 12, 2544-2558.	4.4	102
39	Culture- and metagenomics-enabled analyses of the <i>Methanosphaera</i> genus reveals their monophyletic origin and differentiation according to genome size. <i>ISME Journal</i> , 2018, 12, 2942-2953.	4.4	24
40	Genome-centric view of carbon processing in thawing permafrost. <i>Nature</i> , 2018, 560, 49-54.	13.7	337
41	Host-linked soil viral ecology along a permafrost thaw gradient. <i>Nature Microbiology</i> , 2018, 3, 870-880.	5.9	372
42	The effect of bituminous coal on methanogenic mixed cultures and pure cultures of <i>Methanococcus</i> and <i>Methanosarcina</i> . <i>Fuel</i> , 2017, 205, 60-70.	3.4	9
43	Comparison of microbial communities across sections of a corroding sewer pipe and the effects of wastewater flooding. <i>Biofouling</i> , 2017, 33, 780-792.	0.8	24
44	Redefining the sponge-symbiont acquisition paradigm: sponge microbes exhibit chemotaxis towards host-derived compounds. <i>Environmental Microbiology Reports</i> , 2017, 9, 750-755.	1.0	20
45	Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. <i>Nature Microbiology</i> , 2017, 2, 1533-1542.	5.9	1,465
46	Characterization of a highly efficient antibiotic-degrading metallo- $\beta$ -lactamase obtained from an uncultured member of a permafrost community. <i>Metallomics</i> , 2017, 9, 1157-1168.	1.0	17
47	Methane-Fueled Syntrophy through Extracellular Electron Transfer: Uncovering the Genomic Traits Conserved within Diverse Bacterial Partners of Anaerobic Methanotrophic Archaea. <i>MBio</i> , 2017, 8, .	1.8	62
48	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
49	Adding stable carbon isotopes improves model representation of the role of microbial communities in peatland methane cycling. <i>Journal of Advances in Modeling Earth Systems</i> , 2017, 9, 1412-1430.	1.3	18
50	A microfluidics-based in situ chemotaxis assay to study the behaviour of aquatic microbial communities. <i>Nature Microbiology</i> , 2017, 2, 1344-1349.	5.9	60
51	Gene and genome-centric analyses of koala and wombat fecal microbiomes point to metabolic specialization for digestion. <i>PeerJ</i> , 2017, 5, e4075.	0.9	24
52	Genome-Centric Analysis of Microbial Populations Enriched by Hydraulic Fracture Fluid Additives in a Coal Bed Methane Production Well. <i>Frontiers in Microbiology</i> , 2016, 7, 731.	1.5	67
53	The Opportunity for High-Performance Biomaterials from Methane. <i>Microorganisms</i> , 2016, 4, 11.	1.6	97
54	Genome-centric resolution of microbial diversity, metabolism and interactions in anaerobic digestion. <i>Environmental Microbiology</i> , 2016, 18, 3144-3158.	1.8	123

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55	Anode potential influences the structure and function of anodic electrode and electrolyte-associated microbiomes. <i>Scientific Reports</i> , 2016, 6, 39114.	1.6	57
56	Metagenomic and metaproteomic analyses of <i>Accumulibacter phosphatis</i> -enriched floccular and granular biofilm. <i>Environmental Microbiology</i> , 2016, 18, 273-287.	1.8	51
57	Phylogenomic analysis of <i>Candidatus</i> <i>Thiomargarita</i> species: free-living representatives from a <i>Tenericutes</i> clade found in methane seeps. <i>ISME Journal</i> , 2016, 10, 2679-2692.	4.4	88
58	OrfM: a fast open reading frame predictor for metagenomic data. <i>Bioinformatics</i> , 2016, 32, 2702-2703.	1.8	33
59	pH and Organic Carbon Dose Rates Control Microbially Driven Bioremediation Efficacy in Alkaline Bauxite Residue. <i>Environmental Science &amp; Technology</i> , 2016, 50, 11164-11173.	4.6	51
60	Methylotrophic methanogenesis discovered in the archaeal phylum Verstraetearchaeota. <i>Nature Microbiology</i> , 2016, 1, 16170.	5.9	459
61	The influence of hydrogeological disturbance and mining on coal seam microbial communities. <i>Geobiology</i> , 2016, 14, 163-175.	1.1	21
62	The effect of coal rank on biogenic methane potential and microbial composition. <i>International Journal of Coal Geology</i> , 2016, 154-155, 205-212.	1.9	66
63	Marine microbial communities of the Great Barrier Reef lagoon are influenced by riverine floodwaters and seasonal weather events. <i>PeerJ</i> , 2016, 4, e1511.	0.9	53
64	Diuron tolerance and potential degradation by pelagic microbiomes in the Great Barrier Reef lagoon. <i>PeerJ</i> , 2016, 4, e1758.	0.9	7
65	Validation of picogram- and femtogram-input DNA libraries for microscale metagenomics. <i>PeerJ</i> , 2016, 4, e2486.	0.9	64
66	Do You Kiss Your Mother with That Mouth? An Authentic Large-Scale Undergraduate Research Experience in Mapping the Human Oral Microbiome. <i>Journal of Microbiology and Biology Education</i> , 2015, 16, 50-60.	0.5	31
67	Archaeal and bacterial communities across a chronosequence of drained lake basins in arctic alaska. <i>Scientific Reports</i> , 2015, 5, 18165.	1.6	15
68	The ReFuGe 2020 Consortium using "omics" approaches to explore the adaptability and resilience of coral holobionts to environmental change. <i>Frontiers in Marine Science</i> , 2015, 2, .	1.2	24
69	Habitat-specific environmental conditions primarily control the microbiomes of the coral <i>Seriatopora hystrix</i> . <i>ISME Journal</i> , 2015, 9, 1916-1927.	4.4	172
70	Chemotaxis by natural populations of coral reef bacteria. <i>ISME Journal</i> , 2015, 9, 1764-1777.	4.4	60
71	A laboratory investigation of interactions between denitrifying anaerobic methane oxidation (DAMO) and anammox processes in anoxic environments. <i>Scientific Reports</i> , 2015, 5, 8706.	1.6	71
72	CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. <i>Genome Research</i> , 2015, 25, 1043-1055.	2.4	7,539

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73	Selective Enrichment Establishes a Stable Performing Community for Microbial Electrosynthesis of Acetate from CO <sub>2</sub> . Environmental Science & Technology, 2015, 49, 8833-8843.	4.6	243
74	Expanding our view of genomic diversity in <i>Candidatus</i> <i>Acumulibacter</i> clades. Environmental Microbiology, 2015, 17, 1574-1585.	1.8	98
75	Temperature and solids retention time control microbial population dynamics and volatile fatty acid production in replicated anaerobic digesters. Scientific Reports, 2015, 5, 8496.	1.6	104
76	Effects of nitrate dosing on sulfidogenic and methanogenic activities in sewer sediment. Water Research, 2015, 74, 155-165.	5.3	59
77	Where Next for Microbiome Research?. PLoS Biology, 2015, 13, e1002050.	2.6	115
78	Methane metabolism in the archaeal phylum Bathyarchaeota revealed by genome-centric metagenomics. Science, 2015, 350, 434-438.	6.0	677
79	Temporal changes in microbial community composition during culture enrichment experiments with Indonesian coals. International Journal of Coal Geology, 2015, 137, 66-76.	1.9	47
80	A Phylogenomic Analysis of the Bacterial Phylum Fibrobacteres. Frontiers in Microbiology, 2015, 6, 1469.	1.5	125
81	First genomic insights into members of a candidate bacterial phylum responsible for wastewater bulking. PeerJ, 2015, 3, e740.	0.9	157
82	Back from the dead; the curious tale of the predatory cyanobacterium <i>Vampirovibrio chlorellavorus</i> . PeerJ, 2015, 3, e968.	0.9	104
83	GroopM: an automated tool for the recovery of population genomes from related metagenomes. PeerJ, 2014, 2, e603.	0.9	254
84	An Expanded Genomic Representation of the Phylum Cyanobacteria. Genome Biology and Evolution, 2014, 6, 1031-1045.	1.1	326
85	The Bio-Community Perl toolkit for microbial ecology. Bioinformatics, 2014, 30, 1926-1927.	1.8	16
86	Deterministic processes guide long-term synchronised population dynamics in replicate anaerobic digesters. ISME Journal, 2014, 8, 2015-2028.	4.4	328
87	Metagenomics Using Next-Generation Sequencing. Methods in Molecular Biology, 2014, 1096, 183-201.	0.4	77
88	Linking microbial community structure, interactions and function in anaerobic digesters using new molecular techniques. Current Opinion in Biotechnology, 2014, 27, 55-64.	3.3	314
89	STAMP: statistical analysis of taxonomic and functional profiles. Bioinformatics, 2014, 30, 3123-3124.	1.8	3,456
90	Methane dynamics regulated by microbial community response to permafrost thaw. Nature, 2014, 514, 478-481.	13.7	321

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91	Discovery of a novel methanogen prevalent in thawing permafrost. <i>Nature Communications</i> , 2014, 5, 3212.	5.8	170
92	CopyRighter: a rapid tool for improving the accuracy of microbial community profiles through lineage-specific gene copy number correction. <i>Microbiome</i> , 2014, 2, 11.	4.9	225
93	Biomass retention on electrodes rather than electrical current enhances stability in anaerobic digestion. <i>Water Research</i> , 2014, 54, 211-221.	5.3	133
94	Anaerobic oxidation of methane coupled to nitrate reduction in a novel archaeal lineage. <i>Nature</i> , 2013, 500, 567-570.	13.7	1,029
95	Sequencing platform and library preparation choices impact viral metagenomes. <i>BMC Genomics</i> , 2013, 14, 320.	1.2	90
96	Drivers of microbial community composition in mesophilic and thermophilic temperature-phased anaerobic digestion pre-treatment reactors. <i>Water Research</i> , 2013, 47, 7098-7108.	5.3	111
97	Diverse populations of lake water bacteria exhibit chemotaxis towards inorganic nutrients. <i>ISME Journal</i> , 2013, 7, 1661-1664.	4.4	44
98	In-Solution Fluorescence In Situ Hybridization and Fluorescence-Activated Cell Sorting for Single Cell and Population Genome Recovery. <i>Methods in Enzymology</i> , 2013, 531, 3-19.	0.4	18
99	Dynamics of Cathode-Associated Microbial Communities and Metabolite Profiles in a Glycerol-Fed Bioelectrochemical System. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4008-4014.	1.4	64
100	Spatial uniformity of microbial diversity in a continuous bioelectrochemical system. <i>Bioresource Technology</i> , 2013, 129, 599-605.	4.8	35
101	Coral reef invertebrate microbiomes correlate with the presence of photosymbionts. <i>ISME Journal</i> , 2013, 7, 1452-1458.	4.4	146
102	Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. <i>Nature Biotechnology</i> , 2013, 31, 533-538.	9.4	1,176
103	Shining a Light on Dark Sequencing: Characterising Errors in Ion Torrent PGM Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003031.	1.5	265
104	Crass: identification and reconstruction of CRISPR from unassembled metagenomic data. <i>Nucleic Acids Research</i> , 2013, 41, e105-e105.	6.5	146
105	Future reef decalcification under a business-as-usual CO <sub>2</sub> emission scenario. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15342-15347.	3.3	152
106	Activation of the Jasmonic Acid Plant Defence Pathway Alters the Composition of Rhizosphere Bacterial Communities. <i>PLoS ONE</i> , 2013, 8, e56457.	1.1	163
107	Grinder: a versatile amplicon and shotgun sequence simulator. <i>Nucleic Acids Research</i> , 2012, 40, e94-e94.	6.5	180
108	High-Throughput Amplicon Sequencing Reveals Distinct Communities within a Corroding Concrete Sewer System. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7160-7162.	1.4	64

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109	Application of metatranscriptomics to soil environments. <i>Journal of Microbiological Methods</i> , 2012, 91, 246-251.	0.7	142
110	Fast, accurate error-correction of amplicon pyrosequences using Acacia. <i>Nature Methods</i> , 2012, 9, 425-426.	9.0	322
111	Integrated metatranscriptomic and metagenomic analyses of stratified microbial assemblages in the open ocean. <i>ISME Journal</i> , 2011, 5, 999-1013.	4.4	230
112	Phage Encoded H-NS: A Potential Achilles Heel in the Bacterial Defence System. <i>PLoS ONE</i> , 2011, 6, e20095.	1.1	59
113	Fixation-free fluorescence <i>in situ</i> hybridization for targeted enrichment of microbial populations. <i>ISME Journal</i> , 2010, 4, 1352-1356.	4.4	69
114	Widespread known and novel phosphonate utilization pathways in marine bacteria revealed by functional screening and metagenomic analyses. <i>Environmental Microbiology</i> , 2010, 12, 222-238.	1.8	166
115	Insights into the Diversity of Eukaryotes in Acid Mine Drainage Biofilm Communities. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2192-2199.	1.4	103
116	Metatranscriptomics reveals unique microbial small RNAs in the ocean's water column. <i>Nature</i> , 2009, 459, 266-269.	13.7	249
117	Rapidly evolving CRISPRs implicated in acquired resistance of microorganisms to viruses. <i>Environmental Microbiology</i> , 2008, 10, 200-207.	1.8	289
118	Metagenomics. <i>Nature</i> , 2008, 455, 481-483.	13.7	352
119	Bridges and Chasms: Summary of the IMAGE 2 Meeting in Montreal, Canada, 30 April to 3 May 2007. <i>Journal of Bacteriology</i> , 2008, 190, 792-797.	1.0	1
120	Microbial community gene expression in ocean surface waters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3805-3810.	3.3	699
121	Genome dynamics in a natural archaeal population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1883-1888.	3.3	123
122	Genetic Exchange Across a Species Boundary in the Archaeal Genus <i>Ferroplasma</i> . <i>Genetics</i> , 2007, 177, 407-416.	1.2	67
123	Strain-resolved community proteomics reveals recombining genomes of acidophilic bacteria. <i>Nature</i> , 2007, 446, 537-541.	13.7	205
124	Strainer: software for analysis of population variation in community genomic datasets. <i>BMC Bioinformatics</i> , 2007, 8, 398.	1.2	30
125	A Synthetic Maternal-Effect Selfish Genetic Element Drives Population Replacement in <i>Drosophila</i> . <i>Science</i> , 2007, 316, 597-600.	6.0	188
126	Lineages of Acidophilic Archaea Revealed by Community Genomic Analysis. <i>Science</i> , 2006, 314, 1933-1935.	6.0	217



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127	Environmental shotgun sequencing. , 2005, , .		0
128	The Search for a Molecular-Level Understanding of the Processes that Underpin the Earth's Biogeochemical Cycles. Reviews in Mineralogy and Geochemistry, 2005, 59, 1-7.	2.2	12
129	Genome-Directed Isolation of the Key Nitrogen Fixer <i>Leptospirillum ferrodiazotrophum</i> sp. nov. from an Acidophilic Microbial Community. Applied and Environmental Microbiology, 2005, 71, 6319-6324.	1.4	225
130	Cultivating the uncultivated: a community genomics perspective. Trends in Microbiology, 2005, 13, 411-415.	3.5	89
131	Community proteomics of a natural microbial biofilm. Science, 2005, 308, 1915-20.	6.0	509
132	Community Proteomics of a Natural Microbial Biofilm. Science, 2005, 308, 1915-1920.	6.0	134
133	Community structure and metabolism through reconstruction of microbial genomes from the environment. Nature, 2004, 428, 37-43.	13.7	2,045
134	Design and Evaluation of 16S rRNA-Targeted Oligonucleotide Probes for Fluorescence In Situ Hybridization. , 2002, 179, 029-042.		116
135	Filamentous Chloroflexi (green non-sulfur bacteria) are abundant in wastewater treatment processes with biological nutrient removal c cThe EMBL accession numbers for the sequences reported in this paper are X84472 (strain SBR1029 16S rDNA), X84474 (strain SBR1031 16S rDNA), X84498 (strain SBR1064) Tj E00q1 1 0.764314		764
136	Investigation of Candidate Division TM7, a Recently Recognized Major Lineage of the Domain Bacteria with No Known Pure-Culture Representatives. Applied and Environmental Microbiology, 2001, 67, 411-419.	1.4	311
137	The IsoGenie database: an interdisciplinary data management solution for ecosystems biology and environmental research. PeerJ, 0, 8, e9467.	0.9	5