Gw Tyson

List of Articles by Year
in descending order

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136 peer-reviewed articles	31,590 peer-reviewed citations	18234 62 peer-reviewed h-index	43527 6.98 score
155 documents	39561 doc citations	17325 68 h-index	54542 citing authors

#	ARTICLE	IF	CITATIONS
1	CoverM: read alignment statistics for metagenomics. Bioinformatics, 2025, 41, .	3.2	491
2	GenomeFISH: genome-based fluorescence in situ hybridization for strain-level visualization of microbial communities. ISME Journal, 2025, 19, .	5.9	11
3	A genome-centric view of the role of the Acropora kenti microbiome in coral health and resilience. Nature Communications, 2024, 15, .	10.8	17
4	Anaerobic oxidation of ammonium and short-chain gaseous alkanes coupled to nitrate reduction by a bacterial consortium. ISME Journal, 2024, 18, .	5.9	10
5	Microbial polyphenol metabolism is part of the thawing permafrost carbon cycle. Nature Microbiology, 2024, 9, 1454-1466.	9.9	56
6	Isolation of a Methanobrevibacter gottschalkii strain from an Eastern Gray Kangaroo. Frontiers in Microbiology, 2024, 15, .	2.9	3
7	Anaerobic methanotroph 'Candidatus Methanoperedens nitroreducens' has a pleomorphic life cycle. Nature Microbiology, 2023, 8, 321-331.	9.9	50
8	Isolation and characterisation of novel Methanocorpusculum species indicates the genus is ancestrally host-associated. BMC Biology, 2023, 21, .	3.0	24
9	Phylogenetic and metabolic diversity of microbial communities performing anaerobic ammonium and methane oxidations under different nitrogen loadings. ISME Communications, 2023, 3, .	3.8	65
10	CheckM2: a rapid, scalable and accurate tool for assessing microbial genome quality using machine learning. Nature Methods, 2023, 20, 1203-1212.	13.1	1,591
11	Multi-heme cytochrome-mediated extracellular electron transfer by the anaerobic methanotroph 'Candidatus Methanoperedens nitroreducens'. Nature Communications, 2023, 14, .	10.8	65
12	Pyrogenic Carbon Promotes Anaerobic Oxidation of Methane Coupled with Iron Reduction via the Redox-Cycling Mechanism. Environmental Science & Technology, 2023, 57, 19793-19804.	8.5	19
13	Coupling plant litter quantity to a novel metric for litter quality explains C storage changes in a thawing permafrost peatland. Global Change Biology, 2022, 28, 950-968.	7.4	26
14	Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. PLoS Biology, 2022, 20, e3001508.	3.1	176
15	Chemotaxis shapes the microscale organization of the ocean's microbiome. Nature, 2022, 605, 132-138.	30.7	143
16	Polyhydroxyalkanoate-driven current generation via acetate by an anaerobic methanotrophic consortium. Water Research, 2022, 221, 118743.	9.9	23
17	Expanding the phylogenetic distribution of cytochrome b-containing methanogenic archaea sheds light on the evolution of methanogenesis. ISME Journal, 2022, 16, 2373-2387.	5.9	53
18	Chemotaxis may assist marine heterotrophic bacterial diazotrophs to find microzones suitable for N2 fixation in the pelagic ocean. ISME Journal, 2022, 16, 2525-2534.	5.9	29

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19	Anaerobic oxidation of propane coupled to nitrate reduction by a lineage within the class Symbiobacteriia. Nature Communications, 2022, 13, .	10.8	39
20	Evidence for non-methanogenic metabolisms in globally distributed archaeal clades basal to the Methanomassiliicoccales. Environmental Microbiology, 2021, 23, 340-357.	2.6	30
21	Pregnant women who develop preeclampsia have lower abundance of the butyrate-producer Coprococcus in their gut microbiota. Pregnancy Hypertension, 2021, 23, 211-219.	0.4	92
22	Evaluation of the Microba Community Profiler for Taxonomic Profiling of Metagenomic Datasets From the Human Gut Microbiome. Frontiers in Microbiology, 2021, 12, .	2.9	49
23	Critical evaluation of faecal microbiome preservation using metagenomic analysis. ISME Communications, 2021, 1, .	3.8	37
24	Methane-dependent selenate reduction by a bacterial consortium. ISME Journal, 2021, 15, 3683-3692.	5.9	48
25	Sulfate differentially stimulates but is not respired by diverse anaerobic methanotrophic archaea. ISME Journal, 2021, 16, 168-177.	5.9	44
26	Diverse sediment microbiota shape methane emission temperature sensitivity in Arctic lakes. Nature Communications, 2021, 12, .	10.8	40
27	Successional dynamics and alternative stable states in a saline activated sludge microbial community over 9 years. Microbiome, 2021, 9, .	8.1	83
28	Autism-related dietary preferences mediate autism-gut microbiome associations. Cell, 2021, 184, 5916-5931.e17.	23.4	325
29	Microvolume DNA extraction methods for microscale amplicon and metagenomic studies. ISME Communications, 2021, 1, .	3.8	34
30	Accelerating microbial iron cycling promotes re-cementation of surface crusts in iron ore regions. Microbial Biotechnology, 2020, 13, 1960-1971.	3.5	12
31	Lateral Gene Transfer Drives Metabolic Flexibility in the Anaerobic Methane-Oxidizing Archaeal Family Methanoperedenaceae. MBio, 2020, 11, .	3.1	83
32	Anaerobic methane oxidation coupled to manganese reduction by members of the Methanoperedenaceae. ISME Journal, 2020, 14, 1030-1041.	5.9	337
33	The importance of designating type material for uncultured taxa. Systematic and Applied Microbiology, 2019, 42, 15-21.	1.6	163
34	Insights into the ecological roles and evolution of methyl-coenzyme M reductase-containing hot spring Archaea. Nature Communications, 2019, 10, .	10.8	153
35	A genomic view of the reef-building coral Porites lutea and its microbial symbionts. Nature Microbiology, 2019, 4, 2090-2100.	9.9	254
36	An evolving view of methane metabolism in the Archaea. Nature Reviews Microbiology, 2019, 17, 219-232.	58.2	584

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37	Acetate Production from Anaerobic Oxidation of Methane via Intracellular Storage Compounds. Environmental Science & Technology, 2019, 53, 7371-7379.	8.5	83
38	Biochar-Mediated Anaerobic Oxidation of Methane. Environmental Science & Technology, 2019, 53, 6660-6668.	8.5	159
39	Microbial Community Analyses Inform Geochemical Reaction Network Models for Predicting Pathways of Greenhouse Gas Production. Frontiers in Earth Science, 2019, 7, .	1.2	18
40	Goethite Reduction by a Neutrophilic Member of the Alphaproteobacterial Genus Telmatospirillum. Frontiers in Microbiology, 2019, 10, .	2.9	38
41	Divergent methyl-coenzyme M reductase genes in a deep-subseafloor Archaeoglobi. ISME Journal, 2019, 13, 1269-1279.	5.9	89
42	The effect of methane and odd-chain fatty acids on 3-hydroxybutyrate (3HB) and 3-hydroxyvalerate (3HV) synthesis by a Methylosinus-dominated mixed culture. Bioresources and Bioprocessing, 2019, 6, .	3.7	31
43	Biogenic Methane Cycling in a Laboratory Model of an Abandoned Bituminous Coal Mine. Geomicrobiology Journal, 2018, 35, 491-502.	1.5	4
44	A methanotrophic archaeon couples anaerobic oxidation of methane to Fe(III) reduction. ISME Journal, 2018, 12, 1929-1939.	5.9	402
45	GraftM: a tool for scalable, phylogenetically informed classification of genes within metagenomes. Nucleic Acids Research, 2018, 46, e59-e59.	10.7	180
46	Soil Viruses Are Underexplored Players in Ecosystem Carbon Processing. MSystems, 2018, 3, .	2.8	287
47	Methanotrophy across a natural permafrost thaw environment. ISME Journal, 2018, 12, 2544-2558.	5.9	150
48	Culture- and metagenomics-enabled analyses of the Methanosphaera genus reveals their monophyletic origin and differentiation according to genome size. ISME Journal, 2018, 12, 2942-2953.	5.9	38
49	Genome-centric view of carbon processing in thawing permafrost. Nature, 2018, 560, 49-54.	30.7	497
50	Host-linked soil viral ecology along a permafrost thaw gradient. Nature Microbiology, 2018, 3, 870-880.	9.9	628
51	A phylogenomic and ecological analysis of the globally abundant Marine Group II archaea (Ca. Poseidoniales ord. nov.). ISME Journal, 2018, 13, 663-675.	5.9	205
52	The effect of bituminous coal on methanogenic mixed cultures and pure cultures of Methanococcus and Methanosarcina. Fuel, 2017, 205, 60-70.	5.8	11
53	Comparison of microbial communities across sections of a corroding sewer pipe and the effects of wastewater flooding. Biofouling, 2017, 33, 780-792.	1.5	33
54	Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. Nature Microbiology, 2017, 2, 1533-1542.	9.9	1,938

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55	Characterization of a highly efficient antibiotic-degrading metallo-β-lactamase obtained from an uncultured member of a permafrost community. Metallomics, 2017, 9, 1157-1168.	1.7	22
56	Methane-Fueled Syntrophy through Extracellular Electron Transfer: Uncovering the Genomic Traits Conserved within Diverse Bacterial Partners of Anaerobic Methanotrophic Archaea. MBio, 2017, 8, .	3.1	75
57	Adding stable carbon isotopes improves model representation of the role of microbial communities in peatland methane cycling. Journal of Advances in Modeling Earth Systems, 2017, 9, 1412-1430.	2.6	30
58	A microfluidics-based in situ chemotaxis assay to study the behaviour of aquatic microbial communities. Nature Microbiology, 2017, 2, 1344-1349.	9.9	78
59	A Phylogenomic Analysis of the Bacterial Phylum Fibrobacteres. Frontiers in Microbiology, 2016, 6, .	2.9	145
60	Genome-Centric Analysis of Microbial Populations Enriched by Hydraulic Fracture Fluid Additives in a Coal Bed Methane Production Well. Frontiers in Microbiology, 2016, 7, .	2.9	78
61	The Opportunity for High-Performance Biomaterials from Methane. Microorganisms, 2016, 4, 11.	2.7	117
62	Genome-centric resolution of microbial diversity, metabolism and interactions in anaerobic digestion. Environmental Microbiology, 2016, 18, 3144-3158.	2.6	155
63	Anode potential influences the structure and function of anodic electrode and electrolyte-associated microbiomes. Scientific Reports, 2016, 6, .	2.7	73
64	Metagenomic and metaproteomic analyses of Accumulibacter phosphatis-enriched floccular and granular biofilm. Environmental Microbiology, 2016, 18, 273-287.	2.6	53
65	Phylogenomic analysis of Candidatus 'Izimaplasma' species: free-living representatives from a Tenericutes clade found in methane seeps. ISME Journal, 2016, 10, 2679-2692.	5.9	95
66	OrfM: a fast open reading frame predictor for metagenomic data. Bioinformatics, 2016, 32, 2702-2703.	3.2	46
67	pH and Organic Carbon Dose Rates Control Microbially Driven Bioremediation Efficacy in Alkaline Bauxite Residue. Environmental Science & Technology, 2016, 50, 11164-11173.	8.5	63
68	Methylotrophic methanogenesis discovered in the archaeal phylum Verstraetearchaeota. Nature Microbiology, 2016, 1, .	9.9	554
69	The influence of hydrogeological disturbance and mining on coal seam microbial communities. Geobiology, 2016, 14, 163-175.	2.1	31
70	The effect of coal rank on biogenic methane potential and microbial composition. International Journal of Coal Geology, 2016, 154-155, 205-212.	5.0	83
71	Do You Kiss Your Mother with That Mouth? An Authentic Large-Scale Undergraduate Research Experience in Mapping the Human Oral Microbiome. Journal of Microbiology and Biology Education, 2015, 16, 50-60.	0.6	33
72	Archaeal and bacterial communities across a chronosequence of drained lake basins in arctic alaska. Scientific Reports, 2015, 5, .	2.7	18

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73	The ReFuGe 2020 Consortium—using “omics” approaches to explore the adaptability and resilience of coral holobionts to environmental change. Frontiers in Marine Science, 2015, 2, .	1.8	40
74	Habitat-specific environmental conditions primarily control the microbiomes of the coral Seriatopora hystrix. ISME Journal, 2015, 9, 1916-1927.	5.9	192
75	Chemotaxis by natural populations of coral reef bacteria. ISME Journal, 2015, 9, 1764-1777.	5.9	82
76	A laboratory investigation of interactions between denitrifying anaerobic methane oxidation (DAMO) and anammox processes in anoxic environments. Scientific Reports, 2015, 5, .	2.7	81
77	CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. Genome Research, 2015, 25, 1043-1055.	3.3	12,980
78	Selective Enrichment Establishes a Stable Performing Community for Microbial Electrosynthesis of Acetate from CO2. Environmental Science & Technology, 2015, 49, 8833-8843.	8.5	296
79	Expanding our view of genomic diversity in C andidatus	2.6	116
80	Temperature and solids retention time control microbial population dynamics and volatile fatty acid production in replicated anaerobic digesters. Scientific Reports, 2015, 5, .	2.7	125
81	Effects of nitrate dosing on sulfidogenic and methanogenic activities in sewer sediment. Water Research, 2015, 74, 155-165.	9.9	73
82	Temporal changes in microbial community composition during culture enrichment experiments with Indonesian coals. International Journal of Coal Geology, 2015, 137, 66-76.	5.0	52
83	An Expanded Genomic Representation of the Phylum Cyanobacteria. Genome Biology and Evolution, 2014, 6, 1031-1045.	1.7	362
84	The Bio-Community Perl toolkit for microbial ecology. Bioinformatics, 2014, 30, 1926-1927.	3.2	17
85	Deterministic processes guide long-term synchronised population dynamics in replicate anaerobic digesters. ISME Journal, 2014, 8, 2015-2028.	5.9	392
86	Linking microbial community structure, interactions and function in anaerobic digesters using new molecular techniques. Current Opinion in Biotechnology, 2014, 27, 55-64.	4.7	355
87	STAMP: statistical analysis of taxonomic and functional profiles. Bioinformatics, 2014, 30, 3123-3124.	3.2	4,434
88	Methane dynamics regulated by microbial community response to permafrost thaw. Nature, 2014, 514, 478-481.	30.7	403
89	Discovery of a novel methanogen prevalent in thawing permafrost. Nature Communications, 2014, 5, .	10.8	199
90	CopyRighter: a rapid tool for improving the accuracy of microbial community profiles through lineage-specific gene copy number correction. Microbiome, 2014, 2, .	8.1	272

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91	Biomass retention on electrodes rather than electrical current enhances stability in anaerobic digestion. Water Research, 2014, 54, 211-221.	9.9	151
92	Anaerobic oxidation of methane coupled to nitrate reduction in a novel archaeal lineage. Nature, 2013, 500, 567-570.	30.7	1,317
93	Sequencing platform and library preparation choices impact viral metagenomes. BMC Genomics, 2013, 14, .	2.1	98
94	Drivers of microbial community composition in mesophilic and thermophilic temperature-phased anaerobic digestion pre-treatment reactors. Water Research, 2013, 47, 7098-7108.	9.9	120
95	Diverse populations of lake water bacteria exhibit chemotaxis towards inorganic nutrients. ISME Journal, 2013, 7, 1661-1664.	5.9	56
96	Dynamics of Cathode-Associated Microbial Communities and Metabolite Profiles in a Glycerol-Fed Bioelectrochemical System. Applied and Environmental Microbiology, 2013, 79, 4008-4014.	2.4	72
97	Spatial uniformity of microbial diversity in a continuous bioelectrochemical system. Bioresource Technology, 2013, 129, 599-605.	6.4	36
98	Coral reef invertebrate microbiomes correlate with the presence of photosymbionts. ISME Journal, 2013, 7, 1452-1458.	5.9	172
99	Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. Nature Biotechnology, 2013, 31, 533-538.	19.7	1,303
100	Shining a Light on Dark Sequencing: Characterising Errors in Ion Torrent PGM Data. PLoS Computational Biology, 2013, 9, e1003031.	1.9	288
101	Crass: identification and reconstruction of CRISPR from unassembled metagenomic data. Nucleic Acids Research, 2013, 41, e105-e105.	10.7	185
102	Future reef decalcification under a business-as-usual CO_2 emission scenario. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15342-15347.	5.2	166
103	Activation of the Jasmonic Acid Plant Defence Pathway Alters the Composition of Rhizosphere Bacterial Communities. PLoS ONE, 2013, 8, e56457.	1.5	203
104	Grinder: a versatile amplicon and shotgun sequence simulator. Nucleic Acids Research, 2012, 40, e94-e94.	10.7	198
105	Application of metatranscriptomics to soil environments. Journal of Microbiological Methods, 2012, 91, 246-251.	1.4	173
106	Fast, accurate error-correction of amplicon pyrosequences using Acacia. Nature Methods, 2012, 9, 425-426.	13.1	330
107	Des communautés de phages divergentes contrôlent-elles la microflore intestinale ?. Medecine/Sciences, 2011, 27, 229-231.	0.2	0
108	Phage Encoded H-NS: A Potential Achilles Heel in the Bacterial Defence System. PLoS ONE, 2011, 6, e20095.	1.5	62

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109	Fixation-free fluorescence in situ hybridization for targeted enrichment of microbial populations. ISME Journal, 2010, 4, 1352-1356.	5.9	79
110	Widespread known and novel phosphonate utilization pathways in marine bacteria revealed by functional screening and metagenomic analyses. Environmental Microbiology, 2010, 12, 222-238.	2.6	188
111	Integrated metatranscriptomic and metagenomic analyses of stratified microbial assemblages in the open ocean. ISME Journal, 2010, 5, 999-1013.	5.9	249
112	Insights into the Diversity of Eukaryotes in Acid Mine Drainage Biofilm Communities. Applied and Environmental Microbiology, 2009, 75, 2192-2199.	2.4	112
113	Metatranscriptomics reveals unique microbial small RNAs in the ocean's water column. Nature, 2009, 459, 266-269.	30.7	258
114	Rapidly evolving CRISPRs implicated in acquired resistance of microorganisms to viruses. Environmental Microbiology, 2008, 10, 200-207.	2.6	317
115	Microbial community gene expression in ocean surface waters. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3805-3810.	5.2	726
116	Genome dynamics in a natural archaeal population. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1883-1888.	5.2	126
117	Genetic Exchange Across a Species Boundary in the Archaeal Genus Ferroplasma. Genetics, 2007, 177, 407-416.	3.3	70
118	Strain-resolved community proteomics reveals recombining genomes of acidophilic bacteria. Nature, 2007, 446, 537-541.	30.7	212
119	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.	6.6	13
120	Genome-Directed Isolation of the Key Nitrogen Fixer Leptospirillum ferrodiazotrophum sp. nov. from an Acidophilic Microbial Community. Applied and Environmental Microbiology, 2005, 71, 6319-6324.	2.4	244
121	Cultivating the uncultivated: a community genomics perspective. Trends in Microbiology, 2005, 13, 411-415.	7.0	98
122	Community structure and metabolism through reconstruction of microbial genomes from the environment. Nature, 2004, 428, 37-43.	30.7	2,252
123	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 16S rDNA), X84565 (strain SBR2022 16S rDNA), X84576 (strain SBR2037 16S rDNA) and X84607 (strain SBR2076 16S rDNA). Microbiology (United Kingdom), 2002, 148, 2309-2318.	2.4	278
124	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.	2.4	335
125	GroopM: an automated tool for the recovery of population genomes from related metagenomes. PeerJ, 0, 2, e603.	0.0	290
126	Marine microbial communities of the Great Barrier Reef lagoon are influenced by riverine floodwaters and seasonal weather events. PeerJ, 0, 4, e1511.	0.0	65

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127	Diuron tolerance and potential degradation by pelagic microbiomes in the Great Barrier Reef lagoon. PeerJ, 0, 4, e1758.	0.0	8
128	Validation of picogram- and femtogram-input DNA libraries for microscale metagenomics. PeerJ, 0, 4, e2486.	0.0	86
129	Title is missing!. , 0, .		40
130	First genomic insights into members of a candidate bacterial phylum responsible for wastewater bulking. PeerJ, 0, 3, e740.	0.0	157
131	Back from the dead; the curious tale of the predatory cyanobacterium Vampirovibrio chlorellavorus. PeerJ, 0, 3, e968.	0.0	130
132	Comprehensive taxonomic identification of microbial species in metagenomic data using SingleM and Sandpiper. Nature Biotechnology, 0, 44, 948-953.	19.7	110
133	Potential for aerobic hydrocarbon oxidation in archaea. Nature Communications, 0, 16, .	10.8	3
134	Bin Chicken: targeted metagenomic coassembly for the efficient recovery of novel genomes. Nature Methods, 0, 22, 2516-2524.	13.1	6
135	Gut microbiota is different before the development of preeclampsia. Pregnancy Hypertension, 0, 43, 101415.	0.4	0
136	Carbon monoxide metabolism in freshwater anaerobic methanotrophic archaea. Nature Communications, 0, 17, .	10.8	6