

Michael W Friedrich

List of Publications by Year in descending order

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108
papers

10,240
citations

22099

59
h-index

33814

99
g-index

116
all docs

116
docs citations

116
times ranked

9317
citing authors

#	ARTICLE	IF	CITATIONS
1	The Evolution of Ecological Diversity in Acidobacteria. <i>Frontiers in Microbiology</i> , 2022, 13, 715637.	1.5	15
2	Catabolic protein degradation in marine sediments confined to distinct archaea. <i>ISME Journal</i> , 2022, 16, 1617-1626.	4.4	12
3	Crystalline iron oxides stimulate methanogenic benzoate degradation in marine sediment-derived enrichment cultures. <i>ISME Journal</i> , 2021, 15, 965-980.	4.4	25
4	Ecological features and global distribution of Asgard archaea. <i>Science of the Total Environment</i> , 2021, 758, 143581.	3.9	12
5	Subgroup level differences of physiological activities in marine Lokiarchaeota. <i>ISME Journal</i> , 2021, 15, 848-861.	4.4	23
6	Electron Acceptor Availability Shapes Anaerobically Methane Oxidizing Archaea (ANME) Communities in South Georgia Sediments. <i>Frontiers in Microbiology</i> , 2021, 12, 617280.	1.5	11
7	Iron and sulfate reduction structure microbial communities in (sub-)Antarctic sediments. <i>ISME Journal</i> , 2021, 15, 3587-3604.	4.4	29
8	Macroalgae degradation promotes microbial iron reduction via electron shuttling in coastal Antarctic sediments. <i>Environment International</i> , 2021, 156, 106602.	4.8	9
9	Drivers of the composition of active rhizosphere bacterial communities in temperate grasslands. <i>ISME Journal</i> , 2020, 14, 463-475.	4.4	141
10	Stochastic Dispersal Rather Than Deterministic Selection Explains the Spatio-Temporal Distribution of Soil Bacteria in a Temperate Grassland. <i>Frontiers in Microbiology</i> , 2020, 11, 1391.	1.5	36
11	Creating novel specificities in a fungal nonself recognition system by single step homologous recombination events. <i>New Phytologist</i> , 2020, 228, 1001-1010.	3.5	13
12	Diverse Asgard archaea including the novel phylum Gerdarchaeota participate in organic matter degradation. <i>Science China Life Sciences</i> , 2020, 63, 886-897.	2.3	61
13	DNA and RNA Stable Isotope Probing of Methylophilic Methanogenic Archaea. <i>Methods in Molecular Biology</i> , 2019, 2046, 189-206.	0.4	4
14	Functional Traits and Spatio-Temporal Structure of a Major Group of Soil Protists (Rhizaria: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222 T	1.5	82
15	Draft Genome Sequence of <i>Streptomyces</i> sp. Strain RFCAC02, Isolated from the Gut Microflora of the Pacific Chub Mackerel <i>Scomber japonicus peruanus</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
16	CO ₂ conversion to methane and biomass in obligate methylophilic methanogens in marine sediments. <i>ISME Journal</i> , 2019, 13, 2107-2119.	4.4	26
17	Rates and Microbial Players of Iron-Driven Anaerobic Oxidation of Methane in Methanic Marine Sediments. <i>Frontiers in Microbiology</i> , 2019, 10, 3041.	1.5	51
18	Stable Isotope Probing for Microbial Iron Reduction in Chocolate Pots Hot Spring, Yellowstone National Park. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	46

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19	Temperature Controls Crystalline Iron Oxide Utilization by Microbial Communities in Methanic Ferruginous Marine Sediment Incubations. <i>Frontiers in Microbiology</i> , 2018, 9, 2574.	1.5	23
20	Draft Genome Sequence of a New <i>Vibrio</i> Strain with the Potential To Produce Bacteriocin-Like Inhibitory Substances, Isolated from the Gut Microflora of Scallop (<i>Argopecten purpuratus</i>). <i>Genome Announcements</i> , 2018, 6, .	0.8	8
21	Nitrogen Metabolism Genes from Temperate Marine Sediments. <i>Marine Biotechnology</i> , 2017, 19, 175-190.	1.1	30
22	Potentially Active Iron, Sulfur, and Sulfate Reducing Bacteria in Skagerrak and Bothnian Bay Sediments. <i>Geomicrobiology Journal</i> , 2017, 34, 840-850.	1.0	28
23	Metal Oxide Reduction Linked to Anaerobic Methane Oxidation. <i>Trends in Microbiology</i> , 2017, 25, 88-90.	3.5	37
24	Soil pH and plant diversity drive co-occurrence patterns of ammonia and nitrite oxidizer in soils from forest ecosystems. <i>Biology and Fertility of Soils</i> , 2017, 53, 691-700.	2.3	23
25	Draft Genome Sequence of <i>Vibrio</i> sp. Strain V1B Isolated from the Gut Microflora of the Scallop <i>Argopecten purpuratus</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	2
26	Bacterial Diversity and Biogeochemistry of Two Marine Shallow-Water Hydrothermal Systems off Dominica (Lesser Antilles). <i>Frontiers in Microbiology</i> , 2017, 8, 2400.	1.5	8
27	Diversity and abundance of sulfate-reducing microorganisms in a Mediterranean lagoonal complex (Amvrakikos Gulf, Ionian Sea) derived from <i>dsrB</i> gene. <i>Aquatic Microbial Ecology</i> , 2017, 79, 209-219.	0.9	3
28	Evaluation of Strategies to Separate Root-Associated Microbial Communities: A Crucial Choice in Rhizobiome Research. <i>Frontiers in Microbiology</i> , 2016, 7, 773.	1.5	69
29	Mössbauer spectroscopy and X-ray fluorescence studies on sediments from the methanic zone of the Helgoland mud area, North Sea. <i>Hyperfine Interactions</i> , 2016, 237, 1.	0.2	0
30	Bacterial communities potentially involved in iron-cycling in Baltic Sea and North Sea sediments revealed by pyrosequencing. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw054.	1.3	42
31	Microbial Communities and Organic Matter Composition in Surface and Subsurface Sediments of the Helgoland Mud Area, North Sea. <i>Frontiers in Microbiology</i> , 2015, 6, 1290.	1.5	102
32	Distinct microbial populations are tightly linked to the profile of dissolved iron in the methanic sediments of the Helgoland mud area, North Sea. <i>Frontiers in Microbiology</i> , 2015, 06, 365.	1.5	72
33	Isolation of microorganisms involved in reduction of crystalline iron(III) oxides in natural environments. <i>Frontiers in Microbiology</i> , 2015, 6, 386.	1.5	104
34	<i>G</i> , <i>eobacter</i> , <i>A</i> , and <i>naeromyxobacter</i> and <i>A</i> , <i>naerolineae</i> populations are enriched on anodes of root exudate-driven microbial fuel cells in rice field soil. <i>Environmental Microbiology Reports</i> , 2015, 7, 489-497.	1.0	79
35	Ultra-high sensitivity stable isotope probing of <i>rRNA</i> by high-throughput sequencing of isopycnic centrifugation gradients. <i>Environmental Microbiology Reports</i> , 2015, 7, 282-287.	1.0	63
36	Spatial Interaction of Archaeal Ammonia-Oxidizers and Nitrite-Oxidizing Bacteria in an Unfertilized Grassland Soil. <i>Frontiers in Microbiology</i> , 2015, 6, 1567.	1.5	40

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37	Determinants of <i>Acidobacteria</i> activity inferred from the relative abundances of 16S rRNA transcripts in German grassland and forest soils. <i>Environmental Microbiology</i> , 2014, 16, 658-675.	1.8	103
38	How sulfur beats iron. <i>Science</i> , 2014, 344, 974-975.	6.0	14
39	Environmental Factors Affect Acidobacterial Communities below the Subgroup Level in Grassland and Forest Soils. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7398-7406.	1.4	272
40	Sulfate-reducing microorganisms in wetlands – fameless actors in carbon cycling and climate change. <i>Frontiers in Microbiology</i> , 2012, 3, 72.	1.5	264
41	Bacterial Communities on Macroalgae. <i>Ecological Studies</i> , 2012, , 189-201.	0.4	13
42	Three manganese oxide-rich marine sediments harbor similar communities of acetate-oxidizing manganese-reducing bacteria. <i>ISME Journal</i> , 2012, 6, 2078-2090.	4.4	95
43	Microbial Communities, Structure, and Function. <i>Encyclopedia of Earth Sciences Series</i> , 2011, , 592-595.	0.1	7
44	The microbial ecology of electrigenic microorganisms in plant-rhizosphere based microbial fuel cells. <i>Communications in Agricultural and Applied Biological Sciences</i> , 2011, 76, 25-6.	0.0	0
45	Metagenomic Analysis of Isotopically Enriched DNA. <i>Methods in Molecular Biology</i> , 2010, 668, 67-75.	0.4	3
46	Identification of iron-reducing microorganisms in anoxic rice paddy soil by ¹³ C-acetate probing. <i>ISME Journal</i> , 2010, 4, 267-278.	4.4	237
47	A Comprehensive Investigation on Iron Cycling in a Freshwater Seep Including Microscopy, Cultivation and Molecular Community Analysis. <i>Geomicrobiology Journal</i> , 2010, 27, 15-34.	1.0	58
48	Microbial Community Analysis of Anodes from Sediment Microbial Fuel Cells Powered by Rhizodeposits of Living Rice Plants. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2002-2008.	1.4	113
49	Terminal Restriction Fragment Length Polymorphism Is a Representative Tool To Study Pulmonary Microbial Communities.., 2009, , .		0
50	Identification of novel perchloroethene-respiring microorganisms in anoxic river sediment by RNA-based stable isotope probing. <i>Environmental Microbiology</i> , 2008, 10, 31-46.	1.8	51
51	Novel uncultured <i>Chloroflexi</i> dechlorinate perchloroethene to <i>trans</i> -dichloroethene in tidal flat sediments. <i>Environmental Microbiology</i> , 2008, 10, 1557-1570.	1.8	68
52	Soil-carbon preservation through habitat constraints and biological limitations on decomposer activity. <i>Journal of Plant Nutrition and Soil Science</i> , 2008, 171, 27-35.	1.1	156
53	Shift from Acetoclastic to H ₂ -Dependent Methanogenesis in a West Siberian Peat Bog at Low pH Values and Isolation of an Acidophilic Methanobacterium Strain. <i>Applied and Environmental Microbiology</i> , 2007, 73, 2344-2348.	1.4	180
54	Identification of Acetate-Assimilating Microorganisms under Methanogenic Conditions in Anoxic Rice Field Soil by Comparative Stable Isotope Probing of RNA. <i>Applied and Environmental Microbiology</i> , 2007, 73, 101-109.	1.4	80

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55	Methane Oxidation in Termite Hindguts: Absence of Evidence and Evidence of Absence. <i>Applied and Environmental Microbiology</i> , 2007, 73, 2024-2028.	1.4	30
56	DNA stable-isotope probing. <i>Nature Protocols</i> , 2007, 2, 860-866.	5.5	438
57	Diversity and ubiquity of thermophilic methanogenic archaea in temperate anoxic soils. <i>Environmental Microbiology</i> , 2006, 8, 394-404.	1.8	62
58	Stable-isotope probing of DNA: insights into the function of uncultivated microorganisms from isotopically labeled metagenomes. <i>Current Opinion in Biotechnology</i> , 2006, 17, 59-66.	3.3	175
59	Characterization of the psychrotolerant acetogen strain SyrA5 and the emended description of the species <i>Acetobacterium carbinolicum</i> . <i>Antonie Van Leeuwenhoek</i> , 2006, 89, 55-69.	0.7	30
60	Identification of Bacterial Micropredators Distinctively Active in a Soil Microbial Food Web. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5342-5348.	1.4	191
61	Detecting active methanogenic populations on rice roots using stable isotope probing. <i>Environmental Microbiology</i> , 2005, 7, 326-336.	1.8	127
62	Structure and Topology of Microbial Communities in the Major Gut Compartments of <i>Melolontha melolontha</i> Larvae (Coleoptera: Scarabaeidae). <i>Applied and Environmental Microbiology</i> , 2005, 71, 4556-4566.	1.4	104
63	Lateral Gene Transfer of Dissimilatory (Bi)Sulfite Reductase Revisited. <i>Journal of Bacteriology</i> , 2005, 187, 2203-2208.	1.0	153
64	Methyl-Coenzyme M Reductase Genes: Unique Functional Markers for Methanogenic and Anaerobic Methane-Oxidizing Archaea. <i>Methods in Enzymology</i> , 2005, 397, 428-442.	0.4	160
65	Post-amplification Klenow fragment treatment alleviates PCR bias caused by partially single-stranded amplicons. <i>Journal of Microbiological Methods</i> , 2005, 61, 69-75.	0.7	30
66	Functional Marker Genes for Identification of Sulfate-Reducing Prokaryotes. <i>Methods in Enzymology</i> , 2005, 397, 469-489.	0.4	86
67	pmoA-Based Analysis of Methanotrophs in a Littoral Lake Sediment Reveals a Diverse and Stable Community in a Dynamic Environment. <i>Applied and Environmental Microbiology</i> , 2004, 70, 3138-3142.	1.4	85
68	<i>Methanobacterium aarhusense</i> sp. nov., a novel methanogen isolated from a marine sediment (Aarhus) Tj ETQq0 0 0 rgBT /Overlock 10	0.8	70
69	Stable-Isotope Probing of Microorganisms Thriving at Thermodynamic Limits: Syntrophic Propionate Oxidation in Flooded Soil. <i>Applied and Environmental Microbiology</i> , 2004, 70, 5778-5786.	1.4	191
70	Archaeal Community Structure and Pathway of Methane Formation on Rice Roots. <i>Microbial Ecology</i> , 2004, 47, 59-67.	1.4	104
71	Molecular profiling of 16S rRNA genes reveals diet-related differences of microbial communities in soil, gut, and casts of <i>Lumbricus terrestris</i> L. (Oligochaeta: Lumbricidae). <i>FEMS Microbiology Ecology</i> , 2004, 48, 187-197.	1.3	141
72	Methanol utilization by a novel thermophilic homoacetogenic bacterium, <i>Moorella mulderi</i> sp. nov., isolated from a bioreactor. <i>Archives of Microbiology</i> , 2003, 179, 315-320.	1.0	54

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73	Isolation and Characterization of New Strains of Methanogens from Cold Terrestrial Habitats. <i>Systematic and Applied Microbiology</i> , 2003, 26, 312-318.	1.2	123
74	Stable isotope probing of rRNA and DNA reveals a dynamic methylotroph community and trophic interactions with fungi and protozoa in oxic rice field soil. <i>Environmental Microbiology</i> , 2003, 6, 60-72.	1.8	221
75	Enhanced sensitivity of DNA- and rRNA-based stable isotope probing by fractionation and quantitative analysis of isopycnic centrifugation gradients. <i>Environmental Microbiology</i> , 2003, 6, 73-78.	1.8	530
76	Formation of Pseudo-Terminal Restriction Fragments, a PCR-Related Bias Affecting Terminal Restriction Fragment Length Polymorphism Analysis of Microbial Community Structure. <i>Applied and Environmental Microbiology</i> , 2003, 69, 2555-2562.	1.4	250
77	Evaluation of PCR Amplification Bias by Terminal Restriction Fragment Length Polymorphism Analysis of Small-Subunit rRNA and <i>mcrA</i> Genes by Using Defined Template Mixtures of Methanogenic Pure Cultures and Soil DNA Extracts. <i>Applied and Environmental Microbiology</i> , 2003, 69, 320-326.	1.4	301
78	Phylogenetic Diversity, Abundance, and Axial Distribution of Bacteria in the Intestinal Tract of Two Soil-Feeding Termites (<i>Cubitermes</i> spp.). <i>Applied and Environmental Microbiology</i> , 2003, 69, 6007-6017.	1.4	136
79	Physicochemical Conditions and Microbial Activities in the Highly Alkaline Gut of the Humus-Feeding Larva of <i>Pachnoda ehippiata</i> (Coleoptera: Scarabaeidae). <i>Applied and Environmental Microbiology</i> , 2003, 69, 6650-6658.	1.4	145
80	Microbial Community Structure in Midgut and Hindgut of the Humus-Feeding Larva of <i>Pachnoda ehippiata</i> (Coleoptera: Scarabaeidae). <i>Applied and Environmental Microbiology</i> , 2003, 69, 6659-6668.	1.4	186
81	Axial Dynamics, Stability, and Interspecies Similarity of Bacterial Community Structure in the Highly Compartmentalized Gut of Soil-Feeding Termites (<i>Cubitermes</i> spp.). <i>Applied and Environmental Microbiology</i> , 2003, 69, 6018-6024.	1.4	81
82	Effects of Amendment with Ferrihydrite and Gypsum on the Structure and Activity of Methanogenic Populations in Rice Field Soil. <i>Applied and Environmental Microbiology</i> , 2002, 68, 2484-2494.	1.4	133
83	Phylogenetic Analysis Reveals Multiple Lateral Transfers of Adenosine-5â€²-Phosphosulfate Reductase Genes among Sulfate-Reducing Microorganisms. <i>Journal of Bacteriology</i> , 2002, 184, 278-289.	1.0	180
84	<i>Desulfotignum phosphitoxidans</i> sp. nov., a new marine sulfate reducer that oxidizes phosphite to phosphate. <i>Archives of Microbiology</i> , 2002, 177, 381-391.	1.0	113
85	A balance of KIF1A-like kinesin and dynein organizes early endosomes in the fungus <i>Ustilago maydis</i> . <i>EMBO Journal</i> , 2002, 21, 2946-2957.	3.5	150
86	Multiple Lateral Transfers of Dissimilatory Sulfite Reductase Genes between Major Lineages of Sulfate-Reducing Prokaryotes. <i>Journal of Bacteriology</i> , 2001, 183, 6028-6035.	1.0	309
87	Molecular analyses of methyl-coenzyme M reductase alpha-subunit (<i>mcrA</i>) genes in rice field soil and enrichment cultures reveal the methanogenic phenotype of a novel archaeal lineage. <i>Environmental Microbiology</i> , 2001, 3, 194-204.	1.8	259
88	Archaeal community structures in rice soils from different geographical regions before and after initiation of methane production. <i>FEMS Microbiology Ecology</i> , 2001, 37, 175-186.	1.3	108
89	Methanogenic populations involved in the degradation of rice straw in anoxic paddy soil. <i>FEMS Microbiology Ecology</i> , 2001, 38, 11-20.	1.3	63
90	Dissimilatory Sulfite Reductase (Desulfovirdin) of the Taurine-Degrading, Non-Sulfate-Reducing Bacterium <i>Bilophila wadsworthia</i> RZATAU Contains a Fused DsrB-DsrD Subunit. <i>Journal of Bacteriology</i> , 2001, 183, 1727-1733.	1.0	82

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91	Axial Differences in Community Structure of Crenarchaeota and Euryarchaeota in the Highly Compartmentalized Gut of the Soil-Feeding Termite <i>Cubitermes orthognathus</i> . <i>Applied and Environmental Microbiology</i> , 2001, 67, 4880-4890.	1.4	114
92	Phosphite oxidation by sulphate reduction. <i>Nature</i> , 2000, 406, 37-37.	13.7	124
93	Effect of soil aggregate size on methanogenesis and archaeal community structure in anoxic rice field soil. <i>FEMS Microbiology Ecology</i> , 2000, 32, 261-270.	1.3	45
94	Denitrification with methane as electron donor in oxygen-limited bioreactors. <i>Applied Microbiology and Biotechnology</i> , 2000, 53, 754-762.	1.7	118
95	Effect of Model Sorptive Phases on Phenanthrene Biodegradation: Molecular Analysis of Enrichments and Isolates Suggests Selection Based on Bioavailability. <i>Applied and Environmental Microbiology</i> , 2000, 66, 2703-2710.	1.4	59
96	Effect of Model Sorptive Phases on Phenanthrene Biodegradation: Different Enrichment Conditions Influence Bioavailability and Selection of Phenanthrene-Degrading Isolates. <i>Applied and Environmental Microbiology</i> , 2000, 66, 2695-2702.	1.4	71
97	Archaeal Population Dynamics during Sequential Reduction Processes in Rice Field Soil. <i>Applied and Environmental Microbiology</i> , 2000, 66, 2732-2742.	1.4	255
98	Microecology of the termite gut: structure and function on a microscale. <i>Current Opinion in Microbiology</i> , 2000, 3, 263-269.	2.3	208
99	Molecular Analyses of the Methane-Oxidizing Microbial Community in Rice Field Soil by Targeting the Genes of the 16S rRNA, Particulate Methane Monooxygenase, and Methanol Dehydrogenase. <i>Applied and Environmental Microbiology</i> , 1999, 65, 1980-1990.	1.4	302
100	Phylogenetic Positions of <i>Desulfofustis glycolicus</i> gen. nov., sp. nov. and <i>Syntrophobotulus glycolicus</i> gen. nov., sp. nov., Two New Strict Anaerobes Growing with Glycolic Acid. <i>International Journal of Systematic Bacteriology</i> , 1996, 46, 1065-1069.	2.8	107
101	Isolation and characterization of a desulforubidin-containing sulfate-reducing bacterium growing with glycolate. <i>Archives of Microbiology</i> , 1995, 164, 271-279.	1.0	25
102	Electron transport phosphorylation driven by glyoxylate respiration with hydrogen as electron donor in membrane vesicles of a glyoxylate-fermenting bacterium. <i>Archives of Microbiology</i> , 1995, 163, 268-275.	1.0	0
103	Energetics of syntrophic fatty acid oxidation. <i>FEMS Microbiology Reviews</i> , 1994, 15, 85-94.	3.9	66
104	Hydrogen formation from glycolate driven by reversed electron transport in membrane vesicles of a syntrophic glycolate-oxidizing bacterium. <i>FEBS Journal</i> , 1993, 217, 233-240.	0.2	43
105	Fermentative degradation of glyoxylate by a new strictly anaerobic bacterium. <i>Archives of Microbiology</i> , 1991, 156, 392-397.	1.0	10
106	Fermentative degradation of glycolic acid by defined syntrophic cocultures. <i>Archives of Microbiology</i> , 1991, 156, 398-404.	1.0	30
107	Archaeal community structures in rice soils from different geographical regions before and after initiation of methane production. , 0, .		5
108	Trophic Interactions in Microbial Communities and Food Webs Traced by Stable Isotope Probing of Nucleic Acids. , 0, , 203-232.		0