Michael W Friedrich

List of Publications by Year
in descending order

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109 papers	10,240 citations	22132 59 h-index	33869 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. Frontiers in Microbiology, 2022, 13, 715637.	1.5	15
2	Catabolic protein degradation in marine sediments confined to distinct archaea. ISME Journal, 2022, 16, 1617-1626.	4.4	12
3	Crystalline iron oxides stimulate methanogenic benzoate degradation in marine sediment-derived enrichment cultures. ISME Journal, 2021, 15, 965-980.	4.4	25
4	Ecological features and global distribution of Asgard archaea. Science of the Total Environment, 2021, 758, 143581.	3.9	12
5	Subgroup level differences of physiological activities in marine Lokiarchaeota. ISME Journal, 2021, 15, 848-861.	4.4	23
6	Electron Acceptor Availability Shapes Anaerobically Methane Oxidizing Archaea (ANME) Communities in South Georgia Sediments. Frontiers in Microbiology, 2021, 12, 617280.	1.5	11
7	Iron and sulfate reduction structure microbial communities in (sub-)Antarctic sediments. ISME Journal, 2021, 15, 3587-3604.	4.4	29
8	Macroalgae degradation promotes microbial iron reduction via electron shuttling in coastal Antarctic sediments. Environment International, 2021, 156, 106602.	4.8	9
9	Drivers of the composition of active rhizosphere bacterial communities in temperate grasslands. ISME Journal, 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. Frontiers in Microbiology, 2020, 11, 1391.	1.5	36
11	Creating novel specificities in a fungal nonself recognition system by single step homologous recombination events. New Phytologist, 2020, 228, 1001-1010.	3.5	13
12	Diverse Asgard archaea including the novel phylum Gerdarchaeota participate in organic matter degradation. Science China Life Sciences, 2020, 63, 886-897.	2.3	61
13	DNA and RNA Stable Isotope Probing of Methylotrophic Methanogenic Archaea. Methods in Molecular Biology, 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 To	1.5	82
15	Draft Genome Sequence of Streptomyces sp. Strain RFCAC02, Isolated from the Gut Microflora of the Pacific Chub Mackerel Scomber japonicus peruanus. Microbiology Resource Announcements, 2019, 8, .	0.3	0
16	CO2 conversion to methane and biomass in obligate methylotrophic methanogens in marine sediments. ISME Journal, 2019, 13, 2107-2119.	4.4	26
17	Rates and Microbial Players of Iron-Driven Anaerobic Oxidation of Methane in Methanic Marine Sediments. Frontiers in Microbiology, 2019, 10, 3041.	1.5	51
18	Stable Isotope Probing for Microbial Iron Reduction in Chocolate Pots Hot Spring, Yellowstone National Park. Applied and Environmental Microbiology, 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. Frontiers in Microbiology, 2018, 9, 2574.	1.5	23
20	Draft Genome Sequence of a New Vibrio Strain with the Potential To Produce Bacteriocin-Like Inhibitory Substances, Isolated from the Gut Microflora of Scallop (Argopecten purpuratus). Genome Announcements, 2018, 6, .	0.8	8
21	Nitrogen Metabolism Genes from Temperate Marine Sediments. Marine Biotechnology, 2017, 19, 175-190.	1.1	30
22	Potentially Active Iron, Sulfur, and Sulfate Reducing Bacteria in Skagerrak and Bothnian Bay Sediments. Geomicrobiology Journal, 2017, 34, 840-850.	1.0	28
23	Metal Oxide Reduction Linked to Anaerobic Methane Oxidation. Trends in Microbiology, 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. Biology and Fertility of Soils, 2017, 53, 691-700.	2.3	23
25	Draft Genome Sequence of Vibrio sp. Strain V1B Isolated from the Gut Microflora of the Scallop Argopecten purpuratus. Genome Announcements, 2017, 5, .	0.8	2
26	Bacterial Diversity and Biogeochemistry of Two Marine Shallow-Water Hydrothermal Systems off Dominica (Lesser Antilles). Frontiers in Microbiology, 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 dsrB gene. Aquatic Microbial Ecology, 2017, 79, 209-219.	0.9	3
28	Evaluation of Strategies to Separate Root-Associated Microbial Communities: A Crucial Choice in Rhizobiome Research. Frontiers in Microbiology, 2016, 7, 773.	1.5	69
29	MÃ¶ssbauer spectroscopy and X-ray fluorescence studies on sediments from the methanic zone of the Helgoland mud area, North Sea. Hyperfine Interactions, 2016, 237, 1.	0.2	0
30	Bacterial communities potentially involved in iron-cycling in Baltic Sea and North Sea sediments revealed by pyrosequencing. FEMS Microbiology Ecology, 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. Frontiers in Microbiology, 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. Frontiers in Microbiology, 2015, 06, 365.	1.5	72
33	Isolation of microorganisms involved in reduction of crystalline iron(III) oxides in natural environments. Frontiers in Microbiology, 2015, 6, 386.	1.5	104
34	<scp><i>G</i></scp><i>eobacter</i>, <scp><i>A</i></scp><i>naeromyxobacter</i> and <scp><i>A</i></scp><i>naerolineae</i> populations are enriched on anodes of root exudateâ€driven microbial fuel cells in rice field soil. Environmental Microbiology Reports, 2015, 7, 489-497.	1.0	79
35	Ultraâ€highâ€sensitivity stableâ€isotope probing of <scp>rRNA</scp> by highâ€throughput sequencing of isopycnic centrifugation gradients. Environmental Microbiology Reports, 2015, 7, 282-287.	1.0	63
36	Spatial Interaction of Archaeal Ammonia-Oxidizers and Nitrite-Oxidizing Bacteria in an Unfertilized Grassland Soil. Frontiers in Microbiology, 2015, 6, 1567.	1.5	40

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37	Determinants of <i><scp>A</scp>cidobacteria</i> activity inferred from the relative abundances of 16<scp>S rRNA</scp> transcripts in <scp>G</scp>erman grassland and forest soils. Environmental Microbiology, 2014, 16, 658-675.	1.8	103
38	How sulfur beats iron. Science, 2014, 344, 974-975.	6.0	14
39	Environmental Factors Affect Acidobacterial Communities below the Subgroup Level in Grassland and Forest Soils. Applied and Environmental Microbiology, 2012, 78, 7398-7406.	1.4	272
40	Sulfate-reducing microorganisms in wetlands â€“ fameless actors in carbon cycling and climate change. Frontiers in Microbiology, 2012, 3, 72.	1.5	264
41	Bacterial Communities on Macroalgae. Ecological Studies, 2012, , 189-201.	0.4	13
42	Three manganese oxide-rich marine sediments harbor similar communities of acetate-oxidizing manganese-reducing bacteria. ISME Journal, 2012, 6, 2078-2090.	4.4	95
43	Microbial Communities, Structure, and Function. Encyclopedia of Earth Sciences Series, 2011, , 592-595.	0.1	7
44	The microbial ecology of electrigenic microorganisms in plant-rhizosphere based microbial fuel cells. Communications in Agricultural and Applied Biological Sciences, 2011, 76, 25-6.	0.0	0
45	Metagenomic Analysis of Isotopically Enriched DNA. Methods in Molecular Biology, 2010, 668, 67-75.	0.4	3
46	Identification of iron-reducing microorganisms in anoxic rice paddy soil by 13C-acetate probing. ISME Journal, 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. Geomicrobiology Journal, 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. Applied and Environmental Microbiology, 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 perchloroetheneâ€respiring microorganisms in anoxic river sediment by RNAâ€based stable isotope probing. Environmental Microbiology, 2008, 10, 31-46.	1.8	51
51	Novel uncultured <i>Chloroflexi</i> dechlorinate perchloroethene to <i>trans</i>â€dichloroethene in tidal flat sediments. Environmental Microbiology, 2008, 10, 1557-1570.	1.8	68
52	Soilâ€carbon preservation through habitat constraints and biological limitations on decomposer activity. Journal of Plant Nutrition and Soil Science, 2008, 171, 27-35.	1.1	156
53	Shift from Acetoclastic to H2-Dependent Methanogenesis in a West Siberian Peat Bog at Low pH Values and Isolation of an Acidophilic Methanobacterium Strain. Applied and Environmental Microbiology, 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. Applied and Environmental Microbiology, 2007, 73, 101-109.	1.4	80

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55	Methane Oxidation in Termite Hindguts: Absence of Evidence and Evidence of Absence. Applied and Environmental Microbiology, 2007, 73, 2024-2028.	1.4	30
56	DNA stable-isotope probing. Nature Protocols, 2007, 2, 860-866.	5.5	438
57	Diversity and ubiquity of thermophilic methanogenic archaea in temperate anoxic soils. Environmental Microbiology, 2006, 8, 394-404.	1.8	62
58	Stable-isotope probing of DNA: insights into the function of uncultivated microorganisms from isotopically labeled metagenomes. Current Opinion in Biotechnology, 2006, 17, 59-66.	3.3	175
59	Characterization of the psychrotolerant acetogen strain SyrA5 and the emended description of the species Acetobacterium carbinolicum. Antonie Van Leeuwenhoek, 2006, 89, 55-69.	0.7	30
60	Identification of Bacterial Micropredators Distinctively Active in a Soil Microbial Food Web. Applied and Environmental Microbiology, 2006, 72, 5342-5348.	1.4	191
61	Detecting active methanogenic populations on rice roots using stable isotope probing. Environmental Microbiology, 2005, 7, 326-336.	1.8	127
62	Structure and Topology of Microbial Communities in the Major Gut Compartments of Melolontha melolontha Larvae (Coleoptera: Scarabaeidae). Applied and Environmental Microbiology, 2005, 71, 4556-4566.	1.4	104
63	Lateral Gene Transfer of Dissimilatory (Bi)Sulfite Reductase Revisited. Journal of Bacteriology, 2005, 187, 2203-2208.	1.0	153
64	Methylâ€Coenzyme M Reductase Genes: Unique Functional Markers for Methanogenic and Anaerobic Methaneâ€Oxidizing Archaea. Methods in Enzymology, 2005, 397, 428-442.	0.4	160
65	Post-amplification Klenow fragment treatment alleviates PCR bias caused by partially single-stranded amplicons. Journal of Microbiological Methods, 2005, 61, 69-75.	0.7	30
66	Functional Marker Genes for Identification of Sulfateâ€Reducing Prokaryotes. Methods in Enzymology, 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. Applied and Environmental Microbiology, 2004, 70, 3138-3142.	1.4	85
68	Methanobacterium aarhusense 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. Applied and Environmental Microbiology, 2004, 70, 5778-5786.	1.4	191
70	Archaeal Community Structure and Pathway of Methane Formation on Rice Roots. Microbial Ecology, 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 Lumbricus terrestris L. (Oligochaeta: Lumbricidae). FEMS Microbiology Ecology, 2004, 48, 187-197.	1.3	141
72	Methanol utilization by a novel thermophilic homoacetogenic bacterium, Moorella mulderi sp. nov., isolated from a bioreactor. Archives of Microbiology, 2003, 179, 315-320.	1.0	54

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73	Isolation and Characterization of New Strains of Methanogens from Cold Terrestrial Habitats. Systematic and Applied Microbiology, 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. Environmental Microbiology, 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. Environmental Microbiology, 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. Applied and Environmental Microbiology, 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 mcrA Genes by Using Defined Template Mixtures of Methanogenic Pure Cultures and Soil DNA Extracts. Applied and Environmental Microbiology, 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 (Cubitermes spp.). Applied and Environmental Microbiology, 2003, 69, 6007-6017.	1.4	136
79	Physicochemical Conditions and Microbial Activities in the Highly Alkaline Gut of the Humus-Feeding Larva of Pachnoda ephippiata (Coleoptera: Scarabaeidae). Applied and Environmental Microbiology, 2003, 69, 6650-6658.	1.4	145
80	Microbial Community Structure in Midgut and Hindgut of the Humus-Feeding Larva of Pachnoda ephippiata (Coleoptera: Scarabaeidae). Applied and Environmental Microbiology, 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 (Cubitermes spp.). Applied and Environmental Microbiology, 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. Applied and Environmental Microbiology, 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. Journal of Bacteriology, 2002, 184, 278-289.	1.0	180
84	Desulfotignum phosphitoxidans sp. nov., a new marine sulfate reducer that oxidizes phosphite to phosphate. Archives of Microbiology, 2002, 177, 381-391.	1.0	113
85	A balance of KIF1A-like kinesin and dynein organizes early endosomes in the fungus Ustilago maydis. EMBO Journal, 2002, 21, 2946-2957.	3.5	150
86	Multiple Lateral Transfers of Dissimilatory Sulfite Reductase Genes between Major Lineages of Sulfate-Reducing Prokaryotes. Journal of Bacteriology, 2001, 183, 6028-6035.	1.0	309
87	Molecular analyses of methyl-coenzyme M reductase alpha-subunit (mcrA) genes in rice field soil and enrichment cultures reveal the methanogenic phenotype of a novel archaeal lineage. Environmental Microbiology, 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. FEMS Microbiology Ecology, 2001, 37, 175-186.	1.3	108
89	Methanogenic populations involved in the degradation of rice straw in anoxic paddy soil. FEMS Microbiology Ecology, 2001, 38, 11-20.	1.3	63
90	Dissimilatory Sulfite Reductase (Desulfoviridin) of the Taurine-Degrading, Non-Sulfate-Reducing Bacterium Bilophila wadsworthia RZATAU Contains a Fused DsrB-DsrD Subunit. Journal of Bacteriology, 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 Cubitermes orthognathus. Applied and Environmental Microbiology, 2001, 67, 4880-4890.	1.4	114
92	Archaeal community structures in rice soils from different geographical regions before and after initiation of methane production. FEMS Microbiology Ecology, 2001, 37, 175-186.	1.3	5
93	Phosphite oxidation by sulphate reduction. Nature, 2000, 406, 37-37.	13.7	124
94	Effect of soil aggregate size on methanogenesis and archaeal community structure in anoxic rice field soil. FEMS Microbiology Ecology, 2000, 32, 261-270.	1.3	45
95	Denitrification with methane as electron donor in oxygen-limited bioreactors. Applied Microbiology and Biotechnology, 2000, 53, 754-762.	1.7	118
96	Effect of Model Sorptive Phases on Phenanthrene Biodegradation: Molecular Analysis of Enrichments and Isolates Suggests Selection Based on Bioavailability. Applied and Environmental Microbiology, 2000, 66, 2703-2710.	1.4	59
97	Effect of Model Sorptive Phases on Phenanthrene Biodegradation: Different Enrichment Conditions Influence Bioavailability and Selection of Phenanthrene-Degrading Isolates. Applied and Environmental Microbiology, 2000, 66, 2695-2702.	1.4	71
98	Archaeal Population Dynamics during Sequential Reduction Processes in Rice Field Soil. Applied and Environmental Microbiology, 2000, 66, 2732-2742.	1.4	255
99	Microecology of the termite gut: structure and function on a microscale. Current Opinion in Microbiology, 2000, 3, 263-269.	2.3	208
100	Effect of soil aggregate size on methanogenesis and archaeal community structure in anoxic rice field soil. FEMS Microbiology Ecology, 2000, 32, 261-270.	1.3	2
101	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. Applied and Environmental Microbiology, 1999, 65, 1980-1990.	1.4	302
102	Phylogenetic Positions of Desulfofustis glycolicus gen. nov., sp. nov. and Syntrophobotulus glycolicus gen. nov., sp. nov., Two New Strict Anaerobes Growing with Glycolic Acid. International Journal of Systematic Bacteriology, 1996, 46, 1065-1069.	2.8	107
103	Isolation and characterization of a desulforubidin-containing sulfate-reducing bacterium growing with glycolate. Archives of Microbiology, 1995, 164, 271-279.	1.0	25
104	Electron transport phosphorylation driven by glyoxylate respiration with hydrogen as electron donor in membrane vesicles of a glyoxylate-fermenting bacterium. Archives of Microbiology, 1995, 163, 268-275.	1.0	0
105	Energetics of syntrophic fatty acid oxidation. FEMS Microbiology Reviews, 1994, 15, 85-94.	3.9	66
106	Hydrogen formation from glycolate driven by reversed electron transport in membrane vesicles of a syntrophic glycolate-oxidizing bacterium. FEBS Journal, 1993, 217, 233-240.	0.2	43
107	Fermentative degradation of glyoxylate by a new strictly anaerobic bacterium. Archives of Microbiology, 1991, 156, 392-397.	1.0	10
108	Fermentative degradation of glycolic acid by defined syntrophic cocultures. Archives of Microbiology, 1991, 156, 398-404.	1.0	30

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109	Trophic Interactions in Microbial Communities and Food Webs Traced by Stable Isotope Probing of Nucleic Acids. , 0, , 203-232.		0