

Michael W Friedrich

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6250257/publications.pdf>

Version: 2024-02-01

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	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
2	DNA stable-isotope probing. <i>Nature Protocols</i> , 2007, 2, 860-866.	5.5	438
3	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
4	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
5	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. <i>Applied and Environmental Microbiology</i> , 2003, 69, 320-326.	1.4	301
6	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
7	Sulfate-reducing microorganisms in wetlands – “fameless actors in carbon cycling and climate change. <i>Frontiers in Microbiology</i> , 2012, 3, 72.	1.5	264
8	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. <i>Environmental Microbiology</i> , 2001, 3, 194-204.	1.8	259
9	Archaeal Population Dynamics during Sequential Reduction Processes in Rice Field Soil. <i>Applied and Environmental Microbiology</i> , 2000, 66, 2732-2742.	1.4	255
10	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
11	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
12	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
13	Microecology of the termite gut: structure and function on a microscale. <i>Current Opinion in Microbiology</i> , 2000, 3, 263-269.	2.3	208
14	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
15	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
16	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
17	Phylogenetic Analysis Reveals Multiple Lateral Transfers of Adenosine-5'-Phosphosulfate Reductase Genes among Sulfate-Reducing Microorganisms. <i>Journal of Bacteriology</i> , 2002, 184, 278-289.	1.0	180
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	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
22	Lateral Gene Transfer of Dissimilatory (Bi)Sulfite Reductase Revisited. <i>Journal of Bacteriology</i> , 2005, 187, 2203-2208.	1.0	153
23	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
24	Physicochemical Conditions and Microbial Activities in the Highly Alkaline Gut of the Humus-Feeding Larva of <i>Pachnoda ephippiata</i> (Coleoptera: Scarabaeidae). <i>Applied and Environmental Microbiology</i> , 2003, 69, 6650-6658.	1.4	145
25	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
26	Drivers of the composition of active rhizosphere bacterial communities in temperate grasslands. <i>ISME Journal</i> , 2020, 14, 463-475.	4.4	141
27	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
28	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
29	Detecting active methanogenic populations on rice roots using stable isotope probing. <i>Environmental Microbiology</i> , 2005, 7, 326-336.	1.8	127
30	Phosphite oxidation by sulphate reduction. <i>Nature</i> , 2000, 406, 37-37.	13.7	124
31	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
32	Denitrification with methane as electron donor in oxygen-limited bioreactors. <i>Applied Microbiology and Biotechnology</i> , 2000, 53, 754-762.	1.7	118
33	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
34	<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
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	Archaeal Community Structure and Pathway of Methane Formation on Rice Roots. <i>Microbial Ecology</i> , 2004, 47, 59-67.	1.4	104
39	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
40	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
41	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
42	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
43	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
44	Functional Marker Genes for Identification of Sulfate-Reducing Prokaryotes. <i>Methods in Enzymology</i> , 2005, 397, 469-489.	0.4	86
45	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
46	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
47	Functional Traits and Spatio-Temporal Structure of a Major Group of Soil Protists (Rhizaria: Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tj 5	1.5	82
48	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
49	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
50	<i>Gyrobacter</i> , <i>Aeromyxobacter</i> and <i>Aerolineae</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
51	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
52	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
53	<i>Methanobacterium aarhusense</i> sp. nov., a novel methanogen isolated from a marine sediment (Aarhus) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tj 5	0.8	70
54	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

#	ARTICLE	IF	CITATIONS
55	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
56	Energetics of syntrophic fatty acid oxidation. <i>FEMS Microbiology Reviews</i> , 1994, 15, 85-94.	3.9	66
57	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
58	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
59	Diversity and ubiquity of thermophilic methanogenic archaea in temperate anoxic soils. <i>Environmental Microbiology</i> , 2006, 8, 394-404.	1.8	62
60	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
61	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
62	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
63	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
64	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
65	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
66	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
67	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
68	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
69	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
70	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
71	Metal Oxide Reduction Linked to Anaerobic Methane Oxidation. <i>Trends in Microbiology</i> , 2017, 25, 88-90.	3.5	37
72	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

#	ARTICLE	IF	CITATIONS
73	Fermentative degradation of glycolic acid by defined syntrophic cocultures. Archives of Microbiology, 1991, 156, 398-404.	1.0	30
74	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
75	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
76	Methane Oxidation in Termite Hindguts: Absence of Evidence and Evidence of Absence. Applied and Environmental Microbiology, 2007, 73, 2024-2028.	1.4	30
77	Nitrogen Metabolism Genes from Temperate Marine Sediments. Marine Biotechnology, 2017, 19, 175-190.	1.1	30
78	Iron and sulfate reduction structure microbial communities in (sub-)Antarctic sediments. ISME Journal, 2021, 15, 3587-3604.	4.4	29
79	Potentially Active Iron, Sulfur, and Sulfate Reducing Bacteria in Skagerrak and Bothnian Bay Sediments. Geomicrobiology Journal, 2017, 34, 840-850.	1.0	28
80	CO ₂ conversion to methane and biomass in obligate methylotrophic methanogens in marine sediments. ISME Journal, 2019, 13, 2107-2119.	4.4	26
81	Isolation and characterization of a desulforubidin-containing sulfate-reducing bacterium growing with glycolate. Archives of Microbiology, 1995, 164, 271-279.	1.0	25
82	Crystalline iron oxides stimulate methanogenic benzoate degradation in marine sediment-derived enrichment cultures. ISME Journal, 2021, 15, 965-980.	4.4	25
83	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
84	Temperature Controls Crystalline Iron Oxide Utilization by Microbial Communities in Methanic Ferruginous Marine Sediment Incubations. Frontiers in Microbiology, 2018, 9, 2574.	1.5	23
85	Subgroup level differences of physiological activities in marine Lokiarchaeota. ISME Journal, 2021, 15, 848-861.	4.4	23
86	The Evolution of Ecological Diversity in Acidobacteria. Frontiers in Microbiology, 2022, 13, 715637.	1.5	15
87	How sulfur beats iron. Science, 2014, 344, 974-975.	6.0	14
88	Bacterial Communities on Macroalgae. Ecological Studies, 2012, , 189-201.	0.4	13
89	Creating novel specificities in a fungal nonself recognition system by single step homologous recombination events. New Phytologist, 2020, 228, 1001-1010.	3.5	13
90	Ecological features and global distribution of Asgard archaea. Science of the Total Environment, 2021, 758, 143581.	3.9	12

#	ARTICLE	IF	CITATIONS
91	Catabolic protein degradation in marine sediments confined to distinct archaea. <i>ISME Journal</i> , 2022, 16, 1617-1626.	4.4	12
92	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
93	Fermentative degradation of glyoxylate by a new strictly anaerobic bacterium. <i>Archives of Microbiology</i> , 1991, 156, 392-397.	1.0	10
94	Macroalgae degradation promotes microbial iron reduction via electron shuttling in coastal Antarctic sediments. <i>Environment International</i> , 2021, 156, 106602.	4.8	9
95	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
96	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
97	Microbial Communities, Structure, and Function. <i>Encyclopedia of Earth Sciences Series</i> , 2011, , 592-595.	0.1	7
98	Archaeal community structures in rice soils from different geographical regions before and after initiation of methane production. , 0, .		5
99	DNA and RNA Stable Isotope Probing of Methylotrophic Methanogenic Archaea. <i>Methods in Molecular Biology</i> , 2019, 2046, 189-206.	0.4	4
100	Metagenomic Analysis of Isotopically Enriched DNA. <i>Methods in Molecular Biology</i> , 2010, 668, 67-75.	0.4	3
101	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
102	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
103	Terminal Restriction Fragment Length Polymorphism Is a Representative Tool To Study Pulmonary Microbial Communities.. , 2009, , .		0
104	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
105	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
106	Trophic Interactions in Microbial Communities and Food Webs Traced by Stable Isotope Probing of Nucleic Acids. , 0, , 203-232.		0
107	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
108	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