

Werner Liesack

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Diversity and Structure of the Methanogenic Community in Anoxic Rice Paddy Soil Microcosms as Examined by Cultivation and Direct 16S rRNA Gene Sequence Retrieval. <i>Applied and Environmental Microbiology</i> , 1998, 64, 960-969.	1.4	679
2	Methane oxidation by an extremely acidophilic bacterium of the phylum Verrucomicrobia. <i>Nature</i> , 2007, 450, 879-882.	13.7	526
3	Microbiology of flooded rice paddies. <i>FEMS Microbiology Reviews</i> , 2000, 24, 625-645.	3.9	420
4	Succession of bacterial community structure and diversity in a paddy soil oxygen gradient. <i>Environmental Microbiology</i> , 2005, 7, 382-395.	1.8	330
5	Effects of temperature and fertilizer on activity and community structure of soil ammonia oxidizers. <i>Environmental Microbiology</i> , 2003, 5, 691-705.	1.8	303
6	Novel Euryarchaeotal Lineages Detected on Rice Roots and in the Anoxic Bulk Soil of Flooded Rice Microcosms. <i>Applied and Environmental Microbiology</i> , 1998, 64, 4983-4989.	1.4	302
7	Elemental Sulfur and Thiosulfate Disproportionation by <i>Desulfocapsa sulfoexigens</i> sp. nov., a New Anaerobic Bacterium Isolated from Marine Surface Sediment. <i>Applied and Environmental Microbiology</i> , 1998, 64, 119-125.	1.4	300
8	Phylogenetic Analysis and In Situ Identification of Bacteria Community Composition in an Acidic Sphagnum Peat Bog. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2110-2117.	1.4	262
9	Use of the T-RFLP technique to assess spatial and temporal changes in the bacterial community structure within an agricultural soil planted with transgenic and non-transgenic potato plants. <i>FEMS Microbiology Ecology</i> , 2000, 32, 241-247.	1.3	261
10	Spatial Changes in the Bacterial Community Structure along a Vertical Oxygen Gradient in Flooded Paddy Soil Cores. <i>Applied and Environmental Microbiology</i> , 2000, 66, 754-762.	1.4	259
11	<i>Methylocapsa acidiphila</i> gen. nov., sp. nov., a novel methane-oxidizing and dinitrogen-fixing acidophilic bacterium from Sphagnum bog.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 251-261.	0.8	240
12	Two isozymes of particulate methane monooxygenase with different methane oxidation kinetics are found in <i>Methylocystis</i> sp. strain SC2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10203-10208.	3.3	235
13	<i>Methyloferula stellata</i> gen. nov., sp. nov., an acidophilic, obligately methanotrophic bacterium that possesses only a soluble methane monooxygenase. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 2456-2463.	0.8	233
14	Bacterial populations and environmental factors controlling cellulose degradation in an acidic Sphagnum peat. <i>Environmental Microbiology</i> , 2011, 13, 1800-1814.	1.8	204
15	<i>Mucilaginibacter paludis</i> gen. nov., sp. nov. and <i>Mucilaginibacter gracilis</i> sp. nov., pectin-, xylan- and laminarin-degrading members of the family Sphingobacteriaceae from acidic Sphagnum peat bog. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 2349-2354.	0.8	200
16	Detection of Methanotroph Diversity on Roots of Submerged Rice Plants by Molecular Retrieval of pmoA, mmoX, mxaF, and 16S rRNA and Ribosomal DNA, Including pmoA - Based Terminal Restriction Fragment Length Polymorphism Profiling. <i>Applied and Environmental Microbiology</i> , 2001, 67, 4177-4185.	1.4	186
17	Genome of Rice Cluster I Archaea—the Key Methane Producers in the Rice Rhizosphere. <i>Science</i> , 2006, 313, 370-372.	6.0	175
18	High-Affinity Methane Oxidation by a Soil Enrichment Culture Containing a Type II Methanotroph. <i>Applied and Environmental Microbiology</i> , 1999, 65, 1009-1014.	1.4	167

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19	Disproportionation of inorganic sulfur compounds by the sulfate-reducing bacterium <i>Desulfocapsa thiozymogenes</i> gen. nov., sp. nov.. Archives of Microbiology, 1996, 166, 184-192.	1.0	165
20	Pyrosequencing-Based Assessment of the Bacteria Diversity in Surface and Subsurface Peat Layers of a Northern Wetland, with Focus on Poorly Studied Phyla and Candidate Divisions. PLoS ONE, 2013, 8, e63994.	1.1	165
21	<i>Methylocella tundrae</i> sp. nov., a novel methanotrophic bacterium from acidic tundra peatlands. International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 151-156.	0.8	156
22	<i>Holophaga foetida</i> gen. nov., sp. nov., a new, homoacetogenic bacterium degrading methoxylated aromatic compounds. Archives of Microbiology, 1994, 162, 85-90.	1.0	155
23	Comparative Phylogenetic Assignment of Environmental Sequences of Genes Encoding 16S rRNA and Numerically Abundant Culturable Bacteria from an Anoxic Rice Paddy Soil. Applied and Environmental Microbiology, 1999, 65, 5050-5058.	1.4	145
24	Structure and activity of bacterial community inhabiting rice roots and the rhizosphere. Environmental Microbiology, 2006, 8, 1351-1360.	1.8	143
25	Detection and Enumeration of Methanotrophs in Acidic Sphagnum Peat by 16S rRNA Fluorescence In Situ Hybridization, Including the Use of Newly Developed Oligonucleotide Probes for <i>Methylocella palustris</i> . Applied and Environmental Microbiology, 2001, 67, 4850-4857.	1.4	141
26	Novel Bacterial Lineages at the (Sub)Division Level as Detected by Signature Nucleotide-Targeted Recovery of 16S rRNA Genes from Bulk Soil and Rice Roots of Flooded Rice Microcosms. Applied and Environmental Microbiology, 2001, 67, 623-631.	1.4	141
27	Identification of major subgroups of ammonia-oxidizing bacteria in environmental samples by T-RFLP analysis of <i>amoA</i> PCR products. Journal of Microbiological Methods, 2000, 39, 197-204.	0.7	139
28	<i>Bryobacter aggregatus</i> gen. nov., sp. nov., a peat-inhabiting, aerobic chemo-organotroph from subdivision 3 of the Acidobacteria. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 301-306.	0.8	131
29	Characterization and Identification of Numerically Abundant Culturable Bacteria from the Anoxic Bulk Soil of Rice Paddy Microcosms. Applied and Environmental Microbiology, 1999, 65, 5042-5049.	1.4	131
30	Isolation of Acidophilic Methane-Oxidizing Bacteria from Northern Peat Wetlands. , 1998, 282, 281-284.		128
31	<i>NifH</i> and <i>NifD</i> phylogenies: an evolutionary basis for understanding nitrogen fixation capabilities of methanotrophic bacteria. Microbiology (United Kingdom), 2004, 150, 1301-1313.	0.7	123
32	<i>Methylocystis heyeri</i> sp. nov., a novel type II methanotrophic bacterium possessing a "signature" fatty acids of type I methanotrophs. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 472-479.	0.8	123
33	Substrate-induced growth and isolation of <i>Acidobacteria</i> from acidic <i>Sphagnum</i> peat. ISME Journal, 2008, 2, 551-560.	4.4	111
34	Phylogenetic identity, growth response time and rRNA operon copy number of soil bacteria indicate different stages of community succession. Environmental Microbiology, 2007, 9, 2464-2474.	1.8	109
35	Acetate utilization as a survival strategy of peat-inhabiting <i>Methylocystis</i> spp.. Environmental Microbiology Reports, 2011, 3, 36-46.	1.0	109
36	Rice Cluster I methanogens, an important group of Archaea producing greenhouse gas in soil. Current Opinion in Biotechnology, 2006, 17, 262-267.	3.3	108

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37	Extraction of mRNA from Soil. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5995-6000.	1.4	96
38	Strain FAc12, a dissimilatory iron-reducing member of the <i>Anaeromyxobacter</i> subgroup of <i>Myxococcales</i> . <i>FEMS Microbiology Ecology</i> , 2003, 44, 261-269.	1.3	95
39	Wide Distribution of a Novel <i>pmoA</i> -Like Gene Copy among Type II Methanotrophs, and Its Expression in <i>Methylocystis</i> Strain SC2. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5593-5602.	1.4	94
40	Phylogenetic diversity and metagenomics of candidate division OP3. <i>Environmental Microbiology</i> , 2010, 12, 1218-1229.	1.8	90
41	Differential detection of type II methanotrophic bacteria in acidic peatlands using newly developed 16S rRNA-targeted fluorescent oligonucleotide probes. <i>FEMS Microbiology Ecology</i> , 2003, 43, 299-308.	1.3	80
42	Complete Genome Sequence of the Aerobic Facultative Methanotroph <i>Methylocella silvestris</i> BL2. <i>Journal of Bacteriology</i> , 2010, 192, 3840-3841.	1.0	79
43	<i>Methanocella arvoryzae</i> sp. nov., a hydrogenotrophic methanogen isolated from rice field soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 2918-2923.	0.8	78
44	Differential Assemblage of Functional Units in Paddy Soil Microbiomes. <i>PLoS ONE</i> , 2015, 10, e0122221.	1.1	77
45	Linking activity, composition and seasonal dynamics of atmospheric methane oxidizers in a meadow soil. <i>ISME Journal</i> , 2012, 6, 1115-1126.	4.4	74
46	Transcriptional activity of paddy soil bacterial communities. <i>Environmental Microbiology</i> , 2009, 11, 960-970.	1.8	72
47	Microbial community dynamics during the early stages of plant polymer breakdown in paddy soil. <i>Environmental Microbiology</i> , 2016, 18, 2825-2842.	1.8	72
48	<i>Telmatocola sphagniphila</i> gen. nov., sp. nov., a Novel Dendriform Planctomycete from Northern Wetlands. <i>Frontiers in Microbiology</i> , 2012, 3, 146.	1.5	64
49	Genome-Resolved Metagenomics Reveals Distinct Phosphorus Acquisition Strategies between Soil Microbiomes. <i>MSystems</i> , 2022, 7, e0110721.	1.7	64
50	Identification of microbial populations driving biopolymer degradation in acidic peatlands by metatranscriptomic analysis. <i>Molecular Ecology</i> , 2016, 25, 4818-4835.	2.0	60
51	<i>Desulfospira joergensenii</i> , gen. nov., sp. nov., a new Sulfate-reducing Bacterium Isolated from Marine Surface Sediment. <i>Systematic and Applied Microbiology</i> , 1997, 20, 201-208.	1.2	58
52	Genome Analysis Coupled with Physiological Studies Reveals a Diverse Nitrogen Metabolism in <i>Methylocystis</i> sp. Strain SC2. <i>PLoS ONE</i> , 2013, 8, e74767.	1.1	58
53	Isolation of a <i>Methylocystis</i> strain containing a novel <i>pmoA</i> -like gene. <i>FEMS Microbiology Ecology</i> , 2002, 41, 17-26.	1.3	56
54	Metagenomic insights into nitrogen and phosphorus cycling at the soil aggregate scale driven by organic material amendments. <i>Science of the Total Environment</i> , 2021, 785, 147329.	3.9	56

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55	Complete Genome Sequence of <i>Methylocystis</i> sp. Strain SC2, an Aerobic Methanotroph with High-Affinity Methane Oxidation Potential. <i>Journal of Bacteriology</i> , 2012, 194, 6008-6009.	1.0	55
56	Metatranscriptomics reveals a differential temperature effect on the structural and functional organization of the anaerobic food web in rice field soil. <i>Microbiome</i> , 2018, 6, 169.	4.9	54
57	Methylotrophic Autotrophy in <i>Beijerinckia mobilis</i> . <i>Journal of Bacteriology</i> , 2005, 187, 3884-3888.	1.0	53
58	First Genome Data from Uncultured Upland Soil Cluster Alpha Methanotrophs Provide Further Evidence for a Close Phylogenetic Relationship to <i>Methylocapsa acidiphila</i> B2 and for High-Affinity Methanotrophy Involving Particulate Methane Monooxygenase. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7472-7482.	1.4	50
59	Comparative Genomics of Four <i>Isosphaeraceae</i> Planctomycetes: A Common Pool of Plasmids and Glycoside Hydrolase Genes Shared by <i>Paludisphaera borealis</i> PX4T, <i>Isosphaera pallida</i> IS1BT, <i>Singulisphaera acidiphila</i> DSM 18658T, and Strain SH-PL62. <i>Frontiers in Microbiology</i> , 2017, 8, 412.	1.5	47
60	Retrieval of first genome data for rice cluster I methanogens by a combination of cultivation and molecular techniques. <i>FEMS Microbiology Ecology</i> , 2005, 53, 187-204.	1.3	44
61	<i>Rhodoblastus sphagnicola</i> sp. nov., a novel acidophilic purple non-sulfur bacterium from Sphagnum peat bog. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 1397-1402.	0.8	43
62	Ammonium induces differential expression of methane and nitrogen metabolism-related genes in <i>Methylocystis</i> sp. strain SC2. <i>Environmental Microbiology</i> , 2014, 16, 3115-3127.	1.8	40
63	Comparative Analysis of the Conventional and Novel pmo (Particulate Methane Monooxygenase) Operons from <i>Methylocystis</i> Strain SC2. <i>Applied and Environmental Microbiology</i> , 2004, 70, 3055-3063.	1.4	38
64	Isolation of aerobic, gliding, xylanolytic and laminarinolytic bacteria from acidic Sphagnum peatlands and emended description of <i>Chitinophaga arvensicola</i> Kämpfer et al. 2006. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 2761-2764.	0.8	36
65	A novel pmoA lineage represented by the acidophilic methanotrophic bacterium <i>Methylocapsa acidiphila</i> B2. <i>Archives of Microbiology</i> , 2001, 177, 117-121.	1.0	34
66	Metatranscriptomics reveals climate change effects on the rhizosphere microbiomes in European grassland. <i>Soil Biology and Biochemistry</i> , 2019, 138, 107604.	4.2	33
67	Unexpected Dominance of Elusive Acidobacteria in Early Industrial Soft Coal Slags. <i>Frontiers in Microbiology</i> , 2017, 8, 1023.	1.5	32
68	Metatranscriptomics reveals the hydrolytic potential of peat-inhabiting Planctomycetes. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 801-809.	0.7	30
69	<i>Limnoglobus roseus</i> gen. nov., sp. nov., a novel freshwater planctomycete with a giant genome from the family Gemmataceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1240-1249.	0.8	30
70	Community transcriptomics reveals drainage effects on paddy soil microbiome across all three domains of life. <i>Soil Biology and Biochemistry</i> , 2019, 132, 131-142.	4.2	28
71	Gammaproteobacterial Methanotrophs Dominate Cold Methane Seeps in Floodplains of West Siberian Rivers. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5944-5954.	1.4	27
72	Unexpected metabolic versatility among type II methanotrophs in the Alphaproteobacteria. <i>Biological Chemistry</i> , 2020, 401, 1469-1477.	1.2	27

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73	Ribotyping of 16S and 23S rRNA genes and organization of <i>rrn</i> operons in members of the bacterial genera Gemmata, Planctomyces, Thermotoga, Thermus, and Verrucomicrobium. Archives of Microbiology, 1991, 155, 263-271.	1.0	25
74	Response of Methylocystis sp. Strain SC2 to Salt Stress: Physiology, Global Transcriptome, and Amino Acid Profiles. Applied and Environmental Microbiology, 2017, 83, .	1.4	25
75	Hydrogen utilization by Methylocystis sp. strain SC2 expands the known metabolic versatility of type Ila methanotrophs. Metabolic Engineering, 2020, 61, 181-196.	3.6	25
76	Sodium-dependent succinate decarboxylation by a new anaerobic bacterium belonging to the genus Peptostreptococcus. Antonie Van Leeuwenhoek, 1996, 70, 11-20.	0.7	23
77	Deciphering microbial mechanisms underlying soil organic carbon storage in a wheat-maize rotation system. Science of the Total Environment, 2021, 788, 147798.	3.9	23
78	Clostridium viride sp. nov., a strictly anaerobic bacterium using 5-aminovalerate as growth substrate, previously assigned to Clostridium aminovalericum. Archives of Microbiology, 1994, 162, 387-394.	1.0	21
79	Complete Genome Sequence of <i>Beijerinckia indica</i> subsp. <i>indica</i> . Journal of Bacteriology, 2010, 192, 4532-4533.	1.0	19
80	Short-Term Exposure of Paddy Soil Microbial Communities to Salt Stress Triggers Different Transcriptional Responses of Key Taxonomic Groups. Frontiers in Microbiology, 2017, 8, 400.	1.5	19
81	Peat-vermiculite alters microbiota composition towards increased soil fertility and crop productivity. Plant and Soil, 2022, 470, 21-34.	1.8	19
82	Unusual Genomic Traits Suggest Methylocystis bryophila S285 to Be Well Adapted for Life in Peatlands. Genome Biology and Evolution, 2018, 10, 623-628.	1.1	18
83	Complete Sequence Analysis of Two Methanotroph-Specific <i>repABC</i> -Containing Plasmids from Methylocystis sp. Strain SC2. Applied and Environmental Microbiology, 2012, 78, 4373-4379.	1.4	16
84	Genome-resolved metagenomics identifies the particular genetic traits of phosphate-solubilizing bacteria in agricultural soil. ISME Communications, 2022, 2, .	1.7	15
85	Crude-MS Strategy for in-Depth Proteome Analysis of the Methane-Oxidizing <i>Methylocystis</i> sp. strain SC2. Journal of Proteome Research, 2018, 17, 3086-3103.	1.8	13
86	Seasonality affects function and complexity but not diversity of the rhizosphere microbiome in European temperate grassland. Science of the Total Environment, 2021, 784, 147036.	3.9	12
87	Geovibrio thiophilus sp. nov., a novel sulfur-reducing bacterium belonging to the phylum Deferribacteres.. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 1341-1347.	0.8	12
88	Shedding light on the functional role of the Ignavibacteria in Italian rice field soil: A meta-genomic/transcriptomic analysis. Soil Biology and Biochemistry, 2021, 163, 108444.	4.2	12
89	Efficient Tandem LysC/Trypsin Digestion in Detergent Conditions. Proteomics, 2019, 19, e1900136.	1.3	7
90	T-RFLP Analysis. , 2004, , 23-37.		6

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91	DAFGA: diversity analysis of functional gene amplicons. <i>Bioinformatics</i> , 2014, 30, 2820-2821.	1.8	3
92	<i>Clostridium viride</i> sp. nov., a strictly anaerobic bacterium using 5-aminovalerate as growth substrate, previously assigned to <i>Clostridium aminovalericum</i> . <i>Archives of Microbiology</i> , 1994, 162, 387-394.	1.0	3
93	Isolation of a <i>Methylocystis</i> strain containing a novel <i>pmo A</i> -like gene. , 0, .		2