Werner Liesack

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Peat-vermiculite alters microbiota composition towards increased soil fertility and crop productivity. Plant and Soil, 2022, 470, 21-34.	3.7	19
2	Genome-Resolved Metagenomics Reveals Distinct Phosphorus Acquisition Strategies between Soil Microbiomes. MSystems, 2022, 7, e0110721.	3.8	64
3	Genome-resolved metagenomics identifies the particular genetic traits of phosphate-solubilizing bacteria in agricultural soil. ISME Communications, 2022, 2, .	4.2	15
4	Seasonality affects function and complexity but not diversity of the rhizosphere microbiome in European temperate grassland. Science of the Total Environment, 2021, 784, 147036.	8.0	12
5	Deciphering microbial mechanisms underlying soil organic carbon storage in a wheat-maize rotation system. Science of the Total Environment, 2021, 788, 147798.	8.0	23
6	Metagenomic insights into nitrogen and phosphorus cycling at the soil aggregate scale driven by organic material amendments. Science of the Total Environment, 2021, 785, 147329.	8.0	56
7	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.	8.8	12
8	Hydrogen utilization by Methylocystis sp. strain SC2 expands the known metabolic versatility of type Ila methanotrophs. Metabolic Engineering, 2020, 61, 181-196.	7.0	25
9	Limnoglobus roseus gen. nov., sp. nov., a novel freshwater planctomycete with a giant genome from the family Gemmataceae. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1240-1249.	1.7	30
10	Unexpected metabolic versatility among type II methanotrophs in the Alphaproteobacteria. Biological Chemistry, 2020, 401, 1469-1477.	2.5	27
11	Efficient Tandem LysC/Trypsin Digestion in Detergent Conditions. Proteomics, 2019, 19, e1900136.	2.2	7
12	Metatranscriptomics reveals climate change effects on the rhizosphere microbiomes in European grassland. Soil Biology and Biochemistry, 2019, 138, 107604.	8.8	33
13	Community transcriptomics reveals drainage effects on paddy soil microbiome across all three domains of life. Soil Biology and Biochemistry, 2019, 132, 131-142.	8.8	28
14	Unusual Genomic Traits Suggest Methylocystis bryophila S285 to Be Well Adapted for Life in Peatlands. Genome Biology and Evolution, 2018, 10, 623-628.	2.5	18
15	Metatranscriptomics reveals the hydrolytic potential of peat-inhabiting Planctomycetes. Antonie Van Leeuwenhoek, 2018, 111, 801-809.	1.7	30
16	Metatranscriptomics reveals a differential temperature effect on the structural and functional organization of the anaerobic food web in rice field soil. Microbiome, 2018, 6, 169.	11.1	54
17	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.	3.7	13
18	Response of Methylocystis sp. Strain SC2 to Salt Stress: Physiology, Global Transcriptome, and Amino Acid Profiles. Applied and Environmental Microbiology, 2017, 83, .	3.1	25

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19	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.	3.5	19
20	Comparative Genomics of Four Isosphaeraceae Planctomycetes: A Common Pool of Plasmids and Glycoside Hydrolase Genes Shared by Paludisphaera borealis PX4T, Isosphaera pallida IS1BT, Singulisphaera acidiphila DSM 18658T, and Strain SH-PL62. Frontiers in Microbiology, 2017, 8, 412.	3.5	47
21	Unexpected Dominance of Elusive Acidobacteria in Early Industrial Soft Coal Slags. Frontiers in Microbiology, 2017, 8, 1023.	3.5	32
22	Identification of microbial populations driving biopolymer degradation in acidic peatlands by metatranscriptomic analysis. Molecular Ecology, 2016, 25, 4818-4835.	3.9	60
23	Microbial community dynamics during the early stages of plant polymer breakdown in paddy soil. Environmental Microbiology, 2016, 18, 2825-2842.	3.8	72
24	Differential Assemblage of Functional Units in Paddy Soil Microbiomes. PLoS ONE, 2015, 10, e0122221.	2.5	77
25	Ammonium induces differential expression of methane and nitrogen metabolismâ€related genes in <scp><i>M</i></scp> <i>ethylocystis</i> sp. strain <scp>SC</scp> 2. Environmental Microbiology, 2014, 16, 3115-3127.	3.8	40
26	Gammaproteobacterial Methanotrophs Dominate Cold Methane Seeps in Floodplains of West Siberian Rivers. Applied and Environmental Microbiology, 2014, 80, 5944-5954.	3.1	27
27	DAFGA: diversity analysis of functional gene amplicons. Bioinformatics, 2014, 30, 2820-2821.	4.1	3
28	Genome Analysis Coupled with Physiological Studies Reveals a Diverse Nitrogen Metabolism in Methylocystis sp. Strain SC2. PLoS ONE, 2013, 8, e74767.	2.5	58
29	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.	2.5	165
30	Complete Genome Sequence of Methylocystis sp. Strain SC2, an Aerobic Methanotroph with High-Affinity Methane Oxidation Potential. Journal of Bacteriology, 2012, 194, 6008-6009.	2.2	55
31	Telmatocola sphagniphila gen. nov., sp. nov., a Novel Dendriform Planctomycete from Northern Wetlands. Frontiers in Microbiology, 2012, 3, 146.	3.5	64
32	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.	3.1	16
33	Linking activity, composition and seasonal dynamics of atmospheric methane oxidizers in a meadow soil. ISME Journal, 2012, 6, 1115-1126.	9.8	74
34	Acetate utilization as a survival strategy of peatâ€inhabiting <i>Methylocystis</i> spp Environmental Microbiology Reports, 2011, 3, 36-46.	2.4	109
35	Methyloferula stellata gen. nov., sp. nov., an acidophilic, obligately methanotrophic bacterium that possesses only a soluble methane monooxygenase. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 2456-2463.	1.7	233
36	Bacterial populations and environmental factors controlling cellulose degradation in an acidic <i>Sphagnum</i> peat. Environmental Microbiology, 2011, 13, 1800-1814.	3.8	204

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37	Extraction of mRNA from Soil. Applied and Environmental Microbiology, 2010, 76, 5995-6000.	3.1	96
38	Bryobacter aggregatus 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.	1.7	131
39	Phylogenetic diversity and metagenomics of candidate division OP3. Environmental Microbiology, 2010, 12, 1218-1229.	3.8	90
40	Complete Genome Sequence of the Aerobic Facultative Methanotroph <i>Methylocella silvestris</i> BL2. Journal of Bacteriology, 2010, 192, 3840-3841.	2.2	79
41	Complete Genome Sequence of <i>Beijerinckia indica</i> subsp. <i>indica</i> . Journal of Bacteriology, 2010, 192, 4532-4533.	2.2	19
42	Methanocella arvoryzae sp. nov., a hydrogenotrophic methanogen isolated from rice field soil. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 2918-2923.	1.7	78
43	Transcriptional activity of paddy soil bacterial communities. Environmental Microbiology, 2009, 11, 960-970.	3.8	72
44	Substrate-induced growth and isolation of <i>Acidobacteria</i> from acidic <i>Sphagnum</i> peat. ISME Journal, 2008, 2, 551-560.	9.8	111
45	Two isozymes of particulate methane monooxygenase with different methane oxidation kinetics are found in <i>Methylocystis</i> sp. strain SC2. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10203-10208.	7.1	235
46	Methylocystis heyeri sp. nov., a novel type II methanotrophic bacterium possessing â€~signature' fatty acids of type I methanotrophs. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 472-479.	1.7	123
47	Mucilaginibacter paludis gen. nov., sp. nov. and Mucilaginibacter gracilis sp. nov., pectin-, xylan- and laminarin-degrading members of the family Sphingobacteriaceae from acidic Sphagnum peat bog. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 2349-2354.	1.7	200
48	Methane oxidation by an extremely acidophilic bacterium of the phylum Verrucomicrobia. Nature, 2007, 450, 879-882.	27.8	526
49	Phylogenetic identity, growthâ€response time and rRNA operon copy number of soil bacteria indicate different stages of community succession. Environmental Microbiology, 2007, 9, 2464-2474.	3.8	109
50	Phylogenetic Analysis and In Situ Identification of Bacteria Community Composition in an Acidic Sphagnum Peat Bog. Applied and Environmental Microbiology, 2006, 72, 2110-2117.	3.1	262
51	Structure and activity of bacterial community inhabiting rice roots and the rhizosphere. Environmental Microbiology, 2006, 8, 1351-1360.	3.8	143
52	Rice Cluster I methanogens, an important group of Archaea producing greenhouse gas in soil. Current Opinion in Biotechnology, 2006, 17, 262-267.	6.6	108
53	Isolation of aerobic, gliding, xylanolytic and laminarinolytic bacteria from acidic Sphagnum peatlands and emended description of Chitinophaga arvensicola KĂmpfer et al. 2006. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 2761-2764.	1.7	36
54	Rhodoblastus sphagnicola sp. nov., a novel acidophilic purple non-sulfur bacterium from Sphagnum peat bog. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 1397-1402.	1.7	43

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55	Genome of Rice Cluster I Archaeathe Key Methane Producers in the Rice Rhizosphere. Science, 2006, 313, 370-372.	12.6	175
56	Retrieval of first genome data for rice cluster I methanogens by a combination of cultivation and molecular techniques. FEMS Microbiology Ecology, 2005, 53, 187-204.	2.7	44
57	Succession of bacterial community structure and diversity in a paddy soil oxygen gradient. Environmental Microbiology, 2005, 7, 382-395.	3.8	330
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. Applied and Environmental Microbiology, 2005, 71, 7472-7482.	3.1	50
59	Methylotrophic Autotrophy in Beijerinckia mobilis. Journal of Bacteriology, 2005, 187, 3884-3888.	2.2	53
60	T-RFLP Analysis. , 2004, , 23-37.		6
61	NifH and NifD phylogenies: an evolutionary basis for understanding nitrogen fixation capabilities of methanotrophic bacteria. Microbiology (United Kingdom), 2004, 150, 1301-1313.	1.8	123
62	Comparative Analysis of the Conventional and Novel pmo (Particulate Methane Monooxygenase) Operons from Methylocystis Strain SC2. Applied and Environmental Microbiology, 2004, 70, 3055-3063.	3.1	38
63	Methylocella tundrae sp. nov., a novel methanotrophic bacterium from acidic tundra peatlands. International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 151-156.	1.7	156
64	Strain FAc12, a dissimilatory iron-reducing member of the Anaeromyxobacter subgroup of Myxococcales. FEMS Microbiology Ecology, 2003, 44, 261-269.	2.7	95
65	Effects of temperature and fertilizer on activity and community structure of soil ammonia oxidizers. Environmental Microbiology, 2003, 5, 691-705.	3.8	303
66	Differential detection of type II methanotrophic bacteria in acidic peatlands using newly developed 16S rRNA-targeted fluorescent oligonucleotide probes. FEMS Microbiology Ecology, 2003, 43, 299-308.	2.7	80
67	Wide Distribution of a Novel pmoA -Like Gene Copy among Type II Methanotrophs, and Its Expression in Methylocystis Strain SC2. Applied and Environmental Microbiology, 2003, 69, 5593-5602.	3.1	94
68	Isolation of a Methylocystis strain containing a novel pmoA-like gene. FEMS Microbiology Ecology, 2002, 41, 17-26.	2.7	56
69	Isolation of a Methylocystis strain containing a novel pmoA-like gene. FEMS Microbiology Ecology, 2002, 41, 17-26.	2.7	2
70	Methylocapsa acidiphila gen. nov., sp. nov., a novel methane-oxidizing and dinitrogen-fixing acidophilic bacterium from Sphagnum bog International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 251-261.	1.7	240
71	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.	1.7	12
72	A novel pmoA lineage represented by the acidophilic methanotrophic bacterium Methylocapsa acidophila B2. Archives of Microbiology, 2001, 177, 117-121.	2.2	34

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73	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. Applied and Environmental Microbiology, 2001, 67, 4177-4185.	3.1	186
74	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 Methylocella palustris. Applied and Environmental Microbiology, 2001, 67, 4850-4857.	3.1	141
75	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.	3.1	141
76	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. FEMS Microbiology Ecology, 2000, 32, 241-247.	2.7	261
77	Microbiology of flooded rice paddies. FEMS Microbiology Reviews, 2000, 24, 625-645.	8.6	420
78	Spatial Changes in the Bacterial Community Structure along a Vertical Oxygen Gradient in Flooded Paddy Soil Cores. Applied and Environmental Microbiology, 2000, 66, 754-762.	3.1	259
79	Identification of major subgroups of ammonia-oxidizing bacteria in environmental samples by T-RFLP analysis of amoA PCR products. Journal of Microbiological Methods, 2000, 39, 197-204.	1.6	139
80	Microbiology of flooded rice paddies. FEMS Microbiology Reviews, 2000, 24, 625-645.	8.6	9
81	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.	3.1	131
82	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.	3.1	145
83	High-Affinity Methane Oxidation by a Soil Enrichment Culture Containing a Type II Methanotroph. Applied and Environmental Microbiology, 1999, 65, 1009-1014.	3.1	167
84	Isolation of Acidophilic Methane-Oxidizing Bacteria from Northern Peat Wetlands. , 1998, 282, 281-284.		128
85	Elemental Sulfur and Thiosulfate Disproportionation by <i>Desulfocapsa sulfoexigens</i> sp. nov., a New Anaerobic Bacterium Isolated from Marine Surface Sediment. Applied and Environmental Microbiology, 1998, 64, 119-125.	3.1	300
86	Diversity and Structure of the Methanogenic Community in Anoxic Rice Paddy Soil Microcosms as Examined by Cultivation and Direct 16S rRNA Gene Sequence Retrieval. Applied and Environmental Microbiology, 1998, 64, 960-969.	3.1	679
87	Novel Euryarchaeotal Lineages Detected on Rice Roots and in the Anoxic Bulk Soil of Flooded Rice Microcosms. Applied and Environmental Microbiology, 1998, 64, 4983-4989.	3.1	302
88	Desulfospira joergensenii, gen. nov., sp. nov., a new Sulfate-reducing Bacterium Isolated from Marine Surface Sediment. Systematic and Applied Microbiology, 1997, 20, 201-208.	2.8	58
89	Disproportionation of inorganic sulfur compounds by the sulfate-reducing bacterium Desulfocapsa thiozymogenes gen. nov., sp. nov Archives of Microbiology, 1996, 166, 184-192.	2.2	165
90	Sodium-dependent succinate decarboxylation by a new anaerobic bacterium belonging to the genus Peptostreptococcus. Antonie Van Leeuwenhoek, 1996, 70, 11-20.	1.7	23

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91	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.	2.2	21
92	Holophaga foetida gen. nov., sp. nov., a new, homoacetogenic bacterium degrading methoxylated aromatic compounds. Archives of Microbiology, 1994, 162, 85-90.	2.2	155
93	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.	2.2	3
94	Ribotyping of 16S and 23S rRNA genes and organization of rrn operons in members of the bacterial genera Gemmata, Planctomyces, Thermotoga, Thermus, and Verrucomicrobium. Archives of Microbiology, 1991, 155, 263-271.	2.2	25