

Werner Liesack

List of Publications by Year in descending order

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93
papers

10,061
citations

34016

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45213

90
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98
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98
docs citations

98
times ranked

7567
citing authors

#	ARTICLE	IF	CITATIONS
1	Peat-vermiculite alters microbiota composition towards increased soil fertility and crop productivity. <i>Plant and Soil</i> , 2022, 470, 21-34.	1.8	19
2	Genome-Resolved Metagenomics Reveals Distinct Phosphorus Acquisition Strategies between Soil Microbiomes. <i>MSystems</i> , 2022, 7, e0110721.	1.7	64
3	Genome-resolved metagenomics identifies the particular genetic traits of phosphate-solubilizing bacteria in agricultural soil. <i>ISME Communications</i> , 2022, 2, .	1.7	15
4	Seasonality affects function and complexity but not diversity of the rhizosphere microbiome in European temperate grassland. <i>Science of the Total Environment</i> , 2021, 784, 147036.	3.9	12
5	Deciphering microbial mechanisms underlying soil organic carbon storage in a wheat-maize rotation system. <i>Science of the Total Environment</i> , 2021, 788, 147798.	3.9	23
6	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
7	Shedding light on the functional role of the Ignavibacteria in Italian rice field soil: A meta-genomic/transcriptomic analysis. <i>Soil Biology and Biochemistry</i> , 2021, 163, 108444.	4.2	12
8	Hydrogen utilization by <i>Methylocystis</i> sp. strain SC2 expands the known metabolic versatility of type IIa methanotrophs. <i>Metabolic Engineering</i> , 2020, 61, 181-196.	3.6	25
9	<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
10	Unexpected metabolic versatility among type II methanotrophs in the Alphaproteobacteria. <i>Biological Chemistry</i> , 2020, 401, 1469-1477.	1.2	27
11	Efficient Tandem LysC/Trypsin Digestion in Detergent Conditions. <i>Proteomics</i> , 2019, 19, e1900136.	1.3	7
12	Metatranscriptomics reveals climate change effects on the rhizosphere microbiomes in European grassland. <i>Soil Biology and Biochemistry</i> , 2019, 138, 107604.	4.2	33
13	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
14	Unusual Genomic Traits Suggest <i>Methylocystis bryophila</i> S285 to Be Well Adapted for Life in Peatlands. <i>Genome Biology and Evolution</i> , 2018, 10, 623-628.	1.1	18
15	Metatranscriptomics reveals the hydrolytic potential of peat-inhabiting Planctomycetes. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 801-809.	0.7	30
16	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
17	Crude-MS Strategy for in-Depth Proteome Analysis of the Methane-Oxidizing <i>Methylocystis</i> sp. strain SC2. <i>Journal of Proteome Research</i> , 2018, 17, 3086-3103.	1.8	13
18	Response of <i>Methylocystis</i> sp. Strain SC2 to Salt Stress: Physiology, Global Transcriptome, and Amino Acid Profiles. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	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. <i>Frontiers in Microbiology</i> , 2017, 8, 400.	1.5	19
20	Comparative Genomics of Four Isosphaeraceae 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
21	Unexpected Dominance of Elusive Acidobacteria in Early Industrial Soft Coal Slags. <i>Frontiers in Microbiology</i> , 2017, 8, 1023.	1.5	32
22	Identification of microbial populations driving biopolymer degradation in acidic peatlands by metatranscriptomic analysis. <i>Molecular Ecology</i> , 2016, 25, 4818-4835.	2.0	60
23	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
24	Differential Assemblage of Functional Units in Paddy Soil Microbiomes. <i>PLoS ONE</i> , 2015, 10, e0122221.	1.1	77
25	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
26	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
27	DAFGA: diversity analysis of functional gene amplicons. <i>Bioinformatics</i> , 2014, 30, 2820-2821.	1.8	3
28	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
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. <i>PLoS ONE</i> , 2013, 8, e63994.	1.1	165
30	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
31	<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
32	Complete Sequence Analysis of Two Methanotroph-Specific <i>repABC</i> -Containing Plasmids from <i>Methylocystis</i> sp. Strain SC2. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4373-4379.	1.4	16
33	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
34	Acetate utilization as a survival strategy of peat-inhabiting <i>Methylocystis</i> spp.. <i>Environmental Microbiology Reports</i> , 2011, 3, 36-46.	1.0	109
35	<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
36	Bacterial populations and environmental factors controlling cellulose degradation in an acidic <i>Sphagnum</i> peat. <i>Environmental Microbiology</i> , 2011, 13, 1800-1814.	1.8	204

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37	Extraction of mRNA from Soil. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5995-6000.	1.4	96
38	<i>Bryobacter aggregatus</i> gen. nov., sp. nov., a peat-inhabiting, aerobic chemo-organotroph from subdivision 3 of the Acidobacteria. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 301-306.	0.8	131
39	Phylogenetic diversity and metagenomics of candidate division OP3. <i>Environmental Microbiology</i> , 2010, 12, 1218-1229.	1.8	90
40	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
41	Complete Genome Sequence of <i>Beijerinckia indica</i> subsp. <i>indica</i> . <i>Journal of Bacteriology</i> , 2010, 192, 4532-4533.	1.0	19
42	<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
43	Transcriptional activity of paddy soil bacterial communities. <i>Environmental Microbiology</i> , 2009, 11, 960-970.	1.8	72
44	Substrate-induced growth and isolation of <i>Acidobacteria</i> from acidic <i>Sphagnum</i> peat. <i>ISME Journal</i> , 2008, 2, 551-560.	4.4	111
45	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
46	<i>Methylocystis heyeri</i> sp. nov., a novel type II methanotrophic bacterium possessing a "signature" fatty acids of type I methanotrophs. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 472-479.	0.8	123
47	<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 <i>Sphagnum</i> peat bog. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 2349-2354.	0.8	200
48	Methane oxidation by an extremely acidophilic bacterium of the phylum Verrucomicrobia. <i>Nature</i> , 2007, 450, 879-882.	13.7	526
49	Phylogenetic identity, growth response time and rRNA operon copy number of soil bacteria indicate different stages of community succession. <i>Environmental Microbiology</i> , 2007, 9, 2464-2474.	1.8	109
50	Phylogenetic Analysis and In Situ Identification of Bacteria Community Composition in an Acidic <i>Sphagnum</i> Peat Bog. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2110-2117.	1.4	262
51	Structure and activity of bacterial community inhabiting rice roots and the rhizosphere. <i>Environmental Microbiology</i> , 2006, 8, 1351-1360.	1.8	143
52	Rice Cluster I methanogens, an important group of Archaea producing greenhouse gas in soil. <i>Current Opinion in Biotechnology</i> , 2006, 17, 262-267.	3.3	108
53	Isolation of aerobic, gliding, xylanolytic and laminarinolytic bacteria from acidic <i>Sphagnum</i> 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
54	<i>Rhodoblastus sphagnicola</i> sp. nov., a novel acidophilic purple non-sulfur bacterium from <i>Sphagnum</i> peat bog. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 1397-1402.	0.8	43

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55	Genome of Rice Cluster I Archaea—the Key Methane Producers in the Rice Rhizosphere. <i>Science</i> , 2006, 313, 370-372.	6.0	175
56	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
57	Succession of bacterial community structure and diversity in a paddy soil oxygen gradient. <i>Environmental Microbiology</i> , 2005, 7, 382-395.	1.8	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. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7472-7482.	1.4	50
59	Methylotrophic Autotrophy in <i>Beijerinckia mobilis</i> . <i>Journal of Bacteriology</i> , 2005, 187, 3884-3888.	1.0	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. <i>Microbiology (United Kingdom)</i> , 2004, 150, 1301-1313.	0.7	123
62	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
63	<i>Methylocella tundrae</i> sp. nov., a novel methanotrophic bacterium from acidic tundra peatlands. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 151-156.	0.8	156
64	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
65	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
66	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
67	Wide Distribution of a Novel pmoA -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
68	Isolation of a <i>Methylocystis</i> strain containing a novel pmoA-like gene. <i>FEMS Microbiology Ecology</i> , 2002, 41, 17-26.	1.3	56
69	<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
70	<i>Geovibrio thiophilus</i> sp. nov., a novel sulfur-reducing bacterium belonging to the phylum <i>Deferribacteres</i> .. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 1341-1347.	0.8	12
71	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
72	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

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73	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> . <i>Applied and Environmental Microbiology</i> , 2001, 67, 4850-4857.	1.4	141
74	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. <i>Applied and Environmental Microbiology</i> , 2001, 67, 623-631.	1.4	141
75	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
76	Microbiology of flooded rice paddies. <i>FEMS Microbiology Reviews</i> , 2000, 24, 625-645.	3.9	420
77	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
78	Identification of major subgroups of ammonia-oxidizing bacteria in environmental samples by T-RFLP analysis of <i>amoA</i> PCR products. <i>Journal of Microbiological Methods</i> , 2000, 39, 197-204.	0.7	139
79	Characterization and Identification of Numerically Abundant Culturable Bacteria from the Anoxic Bulk Soil of Rice Paddy Microcosms. <i>Applied and Environmental Microbiology</i> , 1999, 65, 5042-5049.	1.4	131
80	Comparative Phylogenetic Assignment of Environmental Sequences of Genes Encoding 16S rRNA and Numerically Abundant Culturable Bacteria from an Anoxic Rice Paddy Soil. <i>Applied and Environmental Microbiology</i> , 1999, 65, 5050-5058.	1.4	145
81	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
82	Isolation of Acidophilic Methane-Oxidizing Bacteria from Northern Peat Wetlands. , 1998, 282, 281-284.		128
83	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
84	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
85	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
86	<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
87	Disproportionation of inorganic sulfur compounds by the sulfate-reducing bacterium <i>Desulfocapsa thiozymogenes</i> gen. nov., sp. nov.. <i>Archives of Microbiology</i> , 1996, 166, 184-192.	1.0	165
88	Sodium-dependent succinate decarboxylation by a new anaerobic bacterium belonging to the genus <i>Peptostreptococcus</i> . <i>Antonie Van Leeuwenhoek</i> , 1996, 70, 11-20.	0.7	23
89	<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	21
90	<i>Holophaga foetida</i> gen. nov., sp. nov., a new, homoacetogenic bacterium degrading methoxylated aromatic compounds. <i>Archives of Microbiology</i> , 1994, 162, 85-90.	1.0	155

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91	<i>Clostridium viride</i> sp. nov., a strictly anaerobic bacterium using 5-aminovalerate as growth substrate, previously assigned to <i>Clostridium aminovalericum</i> . Archives of Microbiology, 1994, 162, 387-394.	1.0	3
92	Ribotyping of 16S and 23S rRNA genes and organization of <i>rrn</i> operons in members of the bacterial genera <i>Gemmata</i> , <i>Planctomyces</i> , <i>Thermotoga</i> , <i>Thermus</i> , and <i>Verrucomicrobium</i> . Archives of Microbiology, 1991, 155, 263-271.	1.0	25
93	Isolation of a <i>Methylocystis</i> strain containing a novel <i>pmo A</i> -like gene. , 0, .		2