

Carl-Eric Wegner

List of Publications by Year in descending order

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33
papers

1,079
citations

430442

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433756

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docs citations

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times ranked

1572
citing authors

#	ARTICLE	IF	CITATIONS
1	Extracellular and Intracellular Lanthanide Accumulation in the Methylophilic <i>Beijerinckiaceae</i> Bacterium RH AL1. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0314420.	1.4	12
2	Draft Genome Sequences of <i>Acidithrix</i> sp. Strain C25 and <i>Acidocella</i> sp. Strain C78, Acidophiles Isolated from Iron-Rich Pelagic Aggregates (Iron Snow). <i>Microbiology Resource Announcements</i> , 2021, 10, e0010221.	0.3	0
3	Insights into Autotrophic Activities and Carbon Flow in Iron-Rich Pelagic Aggregates (Iron Snow). <i>Microorganisms</i> , 2021, 9, 1368.	1.6	2
4	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
5	Draft Genome Sequence of <i>Pseudomonas</i> sp. Strain FEN, Isolated from the Fe- and Organic Matter-Rich SchlÄppnerbrunnen Fen. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
6	Genome-inferred spatio-temporal resolution of an uncultivated Roizmanbacterium reveals its ecological preferences in groundwater. <i>Environmental Microbiology</i> , 2020, 22, 726-737.	1.8	31
7	Iron is not everything: unexpected complex metabolic responses between iron-cycling microorganisms. <i>ISME Journal</i> , 2020, 14, 2675-2690.	4.4	14
8	Molecular Mechanisms Underpinning Aggregation in <i>Acidiphilium</i> sp. C61 Isolated from Iron-Rich Pelagic Aggregates. <i>Microorganisms</i> , 2020, 8, 314.	1.6	5
9	Draft Genome Sequence of <i>Sideroxydans</i> sp. Strain CL21, an Fe(II)-Oxidizing Bacterium. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	9
10	Iron-organic matter complexes accelerate microbial iron cycling in an iron-rich fen. <i>Science of the Total Environment</i> , 2019, 646, 972-988.	3.9	52
11	Predominance of <i>Cand. Patescibacteria</i> in Groundwater Is Caused by Their Preferential Mobilization From Soils and Flourishing Under Oligotrophic Conditions. <i>Frontiers in Microbiology</i> , 2019, 10, 1407.	1.5	160
12	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
13	Lanthanide-Dependent Methylophilic of the Family <i>Beijerinckiaceae</i> : Physiological and Genomic Insights. <i>Applied and Environmental Microbiology</i> , 2019, 86, .	1.4	19
14	Biogeochemical Regimes in Shallow Aquifers Reflect the Metabolic Coupling of the Elements Nitrogen, Sulfur, and Carbon. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	47
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	Phylogenetic and Structural Comparisons of the Three Types of Methyl Coenzyme M Reductase from Methanococcales and Methanobacteriales. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	36
18	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

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19	Unexpected Dominance of Elusive Acidobacteria in Early Industrial Soft Coal Slags. <i>Frontiers in Microbiology</i> , 2017, 8, 1023.	1.5	32
20	Ferrihydrite-associated organic matter (OM) stimulates reduction by <i>Shewanella oneidensis</i> ; MR-1 and a complex microbial consortia. <i>Biogeosciences</i> , 2017, 14, 5171-5188.	1.3	44
21	The WOPR Protein Ros1 Is a Master Regulator of Sporogenesis and Late Effector Gene Expression in the Maize Pathogen <i>Ustilago maydis</i> . <i>PLoS Pathogens</i> , 2016, 12, e1005697.	2.1	65
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	Permanent Managed Grassland at Future Climate Change: Is There a Connection between GHG Emission and Composition of Plant and Microbial Communities?. <i>Procedia Environmental Sciences</i> , 2015, 29, 156-157.	1.3	3
25	Cropping systems modulate the rate and magnitude of soil microbial autotrophic CO ₂ fixation in soil. <i>Frontiers in Microbiology</i> , 2015, 6, 379.	1.5	47
26	Permanent draft genome of <i>Rhodopirellula rubra</i> SWK7. <i>Marine Genomics</i> , 2014, 13, 11-12.	0.4	6
27	Permanent draft genome of <i>Rhodopirellula sallentina</i> SM41. <i>Marine Genomics</i> , 2014, 13, 17-18.	0.4	5
28	Gamma proteobacterial Methanotrophs Dominate Cold Methane Seeps in Floodplains of West Siberian Rivers. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5944-5954.	1.4	27
29	Permanent draft genomes of the <i>Rhodopirellula maiorica</i> strain SM1. <i>Marine Genomics</i> , 2014, 13, 19-20.	0.4	5
30	Permanent draft genomes of the two <i>Rhodopirellula europaea</i> strains 6C and SH398. <i>Marine Genomics</i> , 2014, 13, 15-16.	0.4	4
31	Permanent draft genomes of the three <i>Rhodopirellula baltica</i> strains SH28, SWK14 and WH47. <i>Marine Genomics</i> , 2014, 13, 13-14.	0.4	3
32	Expression of sulfatases in <i>Rhodopirellula baltica</i> and the diversity of sulfatases in the genus <i>Rhodopirellula</i> . <i>Marine Genomics</i> , 2013, 9, 51-61.	0.4	145
33	Microbial diversity-ecosystem function relationships across environmental gradients. <i>Research Ideas and Outcomes</i> , 0, 6, .	1.0	8