

# Carl-Eric Wegner

## List of Publications by Year in descending order

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33  
papers

1,079  
citations

430754

18  
h-index

434063

31  
g-index

34  
all docs

34  
docs citations

34  
times ranked

1572  
citing authors

#	ARTICLE	IF	CITATIONS
1	Predominance of Cand. Patescibacteria 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
2	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
3	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
4	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
5	Identification of microbial populations driving biopolymer degradation in acidic peatlands by metatranscriptomic analysis. <i>Molecular Ecology</i> , 2016, 25, 4818-4835.	2.0	60
6	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
7	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
8	Cropping systems modulate the rate and magnitude of soil microbial autotrophic CO <sub>2</sub> fixation in soil. <i>Frontiers in Microbiology</i> , 2015, 6, 379.	1.5	47
9	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
10	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
11	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
12	Unexpected Dominance of Elusive Acidobacteria in Early Industrial Soft Coal Slags. <i>Frontiers in Microbiology</i> , 2017, 8, 1023.	1.5	32
13	Genome-inferred spatio-temporal resolution of an uncultivated <i>Roizmanbacterium</i> reveals its ecological preferences in groundwater. <i>Environmental Microbiology</i> , 2020, 22, 726-737.	1.8	31
14	Metatranscriptomics reveals the hydrolytic potential of peat-inhabiting Planctomycetes. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 801-809.	0.7	30
15	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
16	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
17	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
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	Lanthanide-Dependent Methyloprophs of the Family <i>Beijerinckiaceae</i> : Physiological and Genomic Insights. Applied and Environmental Microbiology, 2019, 86, .	1.4	19
20	Iron is not everything: unexpected complex metabolic responses between iron-cycling microorganisms. ISME Journal, 2020, 14, 2675-2690.	4.4	14
21	Extracellular and Intracellular Lanthanide Accumulation in the Methyloprophic <i>Beijerinckiaceae</i> Bacterium RH AL1. Applied and Environmental Microbiology, 2021, 87, e0314420.	1.4	12
22	Draft Genome Sequence of Sideroxydans sp. Strain CL21, an Fe(II)-Oxidizing Bacterium. Microbiology Resource Announcements, 2020, 9, .	0.3	9
23	Microbial diversity-ecosystem function relationships across environmental gradients. Research Ideas and Outcomes, 0, 6, .	1.0	8
24	Permanent draft genome of Rhodopirellula rubra SWK7. Marine Genomics, 2014, 13, 11-12.	0.4	6
25	Permanent draft genome of Rhodopirellula sallentina SM41. Marine Genomics, 2014, 13, 17-18.	0.4	5
26	Permanent draft genomes of the Rhodopirellula maiorica strain SM1. Marine Genomics, 2014, 13, 19-20.	0.4	5
27	Molecular Mechanisms Underpinning Aggregation in Acidiphilium sp. C61 Isolated from Iron-Rich Pelagic Aggregates. Microorganisms, 2020, 8, 314.	1.6	5
28	Permanent draft genomes of the two Rhodopirellula europaea strains 6C and SH398. Marine Genomics, 2014, 13, 15-16.	0.4	4
29	Permanent draft genomes of the three Rhodopirellula baltica strains SH28, SWK14 and WH47. Marine Genomics, 2014, 13, 13-14.	0.4	3
30	Permanent Managed Grassland at Future Climate Change: Is There a Connection between GHG Emission and Composition of Plant and Microbial Communities?. Procedia Environmental Sciences, 2015, 29, 156-157.	1.3	3
31	Insights into Autotrophic Activities and Carbon Flow in Iron-Rich Pelagic Aggregates (Iron Snow). Microorganisms, 2021, 9, 1368.	1.6	2
32	Draft Genome Sequence of Pseudomonas sp. Strain FEN, Isolated from the Fe- and Organic Matter-Rich SchlÄppnerbrunnen Fen. Microbiology Resource Announcements, 2021, 10, .	0.3	2
33	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). Microbiology Resource Announcements, 2021, 10, e0010221.	0.3	0