

# Jochen A MÃ¼ller

## List of Publications by Year in descending order

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Version: 2024-02-01

48  
papers

3,136  
citations

236912

25  
h-index

206102

48  
g-index

49  
all docs

49  
docs citations

49  
times ranked

3325  
citing authors

#	ARTICLE	IF	CITATIONS
1	Aerobic naphthenic acid-degrading bacteria in petroleum-coke improve oil sands process water remediation in biofilters: DNA-stable isotope probing reveals methylotrophy in Schmutzdecke. <i>Science of the Total Environment</i> , 2022, 815, 151961.	8.0	12
2	Operational parameters optimization for remediation of crude oil-polluted water in floating treatment wetlands using response surface methodology. <i>Scientific Reports</i> , 2022, 12, 4566.	3.3	11
3	Bioaugmentation-Enhanced Remediation of Crude Oil Polluted Water in Pilot-Scale Floating Treatment Wetlands. <i>Water (Switzerland)</i> , 2021, 13, 2882.	2.7	9
4	Immobilization of metribuzin degrading bacterial consortium MB3R on biochar enhances bioremediation of potato vegetated soil and restores bacterial community structure. <i>Journal of Hazardous Materials</i> , 2020, 390, 121493.	12.4	50
5	Identification of benzene-degrading Proteobacteria in a constructed wetland by employing in situ microcosms and RNA-stable isotope probing. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 1809-1820.	3.6	8
6	Benzylsuccinate Synthase is Post-Transcriptionally Regulated in the Toluene-Degrading Denitrifier <i>Magnetospirillum</i> sp. Strain 15-1. <i>Microorganisms</i> , 2020, 8, 681.	3.6	6
7	A survey of extended-spectrum beta-lactamase-producing Enterobacteriaceae in urban wetlands in southwestern Nigeria as a step towards generating prevalence maps of antimicrobial resistance. <i>PLoS ONE</i> , 2020, 15, e0229451.	2.5	19
8	Floating treatment wetlands as a suitable option for large-scale wastewater treatment. <i>Nature Sustainability</i> , 2019, 2, 863-871.	23.7	113
9	RNA-Seq analysis of soft rush ( <i>Juncus effusus</i> ): transcriptome sequencing, de novo assembly, annotation, and polymorphism identification. <i>BMC Genomics</i> , 2019, 20, 489.	2.8	6
10	Optimizing the metribuzin degrading potential of a novel bacterial consortium based on Taguchi design of experiment. <i>Journal of Hazardous Materials</i> , 2019, 366, 1-9.	12.4	33
11	High abundances of class 1 integrase and sulfonamide resistance genes, and characterisation of class 1 integron gene cassettes in four urban wetlands in Nigeria. <i>PLoS ONE</i> , 2018, 13, e0208269.	2.5	25
12	Detection of the carbapenemase gene blaVIM-5 in members of the <i>Pseudomonas putida</i> group isolated from polluted Nigerian wetlands. <i>Scientific Reports</i> , 2018, 8, 15116.	3.3	20
13	The sulfur depot in the rhizosphere of a common wetland plant, <i>Juncus effusus</i> , can support long-term dynamics of inorganic sulfur transformations. <i>Chemosphere</i> , 2017, 184, 375-383.	8.2	12
14	Organic Micropollutants in the Environment: Ecotoxicity Potential and Methods for Remediation. , 2017, , 65-99.		16
15	Draft Genome Sequence of <i>Magnetospirillum</i> sp. Strain 15-1, a Denitrifying Toluene Degrader Isolated from a Planted Fixed-Bed Reactor. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
16	Isolation and characterization of <i>Magnetospirillum</i> sp. strain 15-1 as a representative anaerobic toluene-degrader from a constructed wetland model. <i>PLoS ONE</i> , 2017, 12, e0174750.	2.5	14
17	Injection of hydrogen gas stimulates acid mine drainage treatment in laboratory-scale hydroponic root mats. <i>Engineering in Life Sciences</i> , 2016, 16, 769-776.	3.6	8
18	<i>In situ</i> SIP highlights Burkholderiaceae as key players degrading toluene by para ring hydroxylation in a constructed wetland model. <i>Environmental Microbiology</i> , 2016, 18, 1176-1186.	3.8	81

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19	Aerobic Toluene Degraders in the Rhizosphere of a Constructed Wetland Model Show Diurnal Polyhydroxyalkanoate Metabolism. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4126-4132.	3.1	23
20	Hydroponic root mats for wastewater treatment—a review. <i>Environmental Science and Pollution Research</i> , 2016, 23, 15911-15928.	5.3	129
21	Role of plants in nitrogen and sulfur transformations in floating hydroponic root mats: A comparison of two helophytes. <i>Journal of Environmental Management</i> , 2016, 181, 333-342.	7.8	12
22	Removal of pathogen indicators from secondary effluent using slow sand filtration: Optimization approaches. <i>Ecological Engineering</i> , 2016, 95, 635-644.	3.6	26
23	Sanitation in constructed wetlands: A review on the removal of human pathogens and fecal indicators. <i>Science of the Total Environment</i> , 2016, 541, 8-22.	8.0	193
24	Microbial Toluene Removal in Hypoxic Model Constructed Wetlands Occurs Predominantly via the Ring Monooxygenation Pathway. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6241-6252.	3.1	43
25	Selective elimination of bacterial faecal indicators in the Schmutzdecke of slow sand filtration columns. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10323-10332.	3.6	24
26	ENVIRONMENTAL POLLUTION BY WASTEWATER FROM BROWN COAL PROCESSING — A REMEDIATION CASE STUDY IN GERMANY. <i>Journal of Environmental Engineering and Landscape Management</i> , 2014, 22, 71-83.	1.0	8
27	Transcriptional profiling of <i>Gammaproteobacteria</i> in the phyllosphere: induction of pollutant degradation genes by natural plant phenolic compounds. <i>Environmental Microbiology</i> , 2014, 16, 2212-2225.	3.8	39
28	Treatment of a sulfate-rich groundwater contaminated with perchloroethene in a hydroponic plant root mat filter and a horizontal subsurface flow constructed wetland at pilot-scale. <i>Chemosphere</i> , 2014, 117, 178-184.	8.2	10
29	Sulphur transformations in constructed wetlands for wastewater treatment: A review. <i>Ecological Engineering</i> , 2013, 52, 278-289.	3.6	118
30	<i>Dehalococcoides mccartyi</i> gen. nov., sp. nov., obligately organohalide-respiring anaerobic bacteria relevant to halogen cycling and bioremediation, belong to a novel bacterial class, <i>Dehalococcoidia</i> classis nov., order <i>Dehalococcoidales</i> ord. nov. and family <i>Dehalococcoidaceae</i> fam. nov., within the phylum <i>Chloroflexi</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 625-635.	1.7	502
31	<i>ipso</i> -Hydroxylation and Subsequent Fragmentation: a Novel Microbial Strategy To Eliminate Sulfonamide Antibiotics. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5550-5558.	3.1	105
32	INFLUENCE OF NITRATE LOAD ON SULFUR TRANSFORMATIONS IN THE RHIZOSPHERE OF <i>Juncus effusus</i> IN LABORATORY-SCALE CONSTRUCTED WETLANDS TREATING ARTIFICIAL DOMESTIC WASTEWATER. <i>Environmental Engineering and Management Journal</i> , 2013, 12, 565-573.	0.6	3
33	Genome-Wide Responses of the Model Archaeon <i>Halobacterium</i> sp. Strain NRC-1 to Oxygen Limitation. <i>Journal of Bacteriology</i> , 2012, 194, 5530-5537.	2.2	38
34	Localized Plasticity in the Streamlined Genomes of Vinyl Chloride Respiring <i>Dehalococcoides</i> . <i>PLoS Genetics</i> , 2009, 5, e1000714.	3.5	162
35	Extremely Radiation-Resistant Mutants of a Halophilic Archaeon with Increased Single-Stranded DNA-Binding Protein (RPA) Gene Expression. <i>Radiation Research</i> , 2007, 168, 507.	1.5	84
36	Saline Systems highlights for 2006. <i>Saline Systems</i> , 2007, 3, 1.	2.0	48

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37	Transcriptional profiling of the model Archaeon Halobacterium sp. NRC-1: responses to changes in salinity and temperature. <i>Saline Systems</i> , 2007, 3, 6.	2.0	83
38	27 Genetic Systems for Halophilic Archaea. <i>Methods in Microbiology</i> , 2006, , 649-680.	0.8	20
39	Post-genomics of the model haloarchaeon Halobacterium sp. NRC-1. <i>Saline Systems</i> , 2006, 2, 3.	2.0	54
40	Terrestrial models for extraterrestrial life: methanogens and halophiles at Martian temperatures. <i>International Journal of Astrobiology</i> , 2006, 5, 89-97.	1.6	75
41	Genomic Analysis of Anaerobic Respiration in the Archaeon Halobacterium sp. Strain NRC-1: Dimethyl Sulfoxide and Trimethylamine N -Oxide as Terminal Electron Acceptors. <i>Journal of Bacteriology</i> , 2005, 187, 1659-1667.	2.2	102
42	UV irradiation induces homologous recombination genes in the model archaeon, Halobacterium sp. NRC-1. <i>Saline Systems</i> , 2005, 1, 3.	2.0	81
43	Molecular Identification of the Catabolic Vinyl Chloride Reductase from Dehalococcoides sp. Strain VS and Its Environmental Distribution. <i>Applied and Environmental Microbiology</i> , 2004, 70, 4880-4888.	3.1	328
44	Initiation of Anaerobic Degradation of <i>p</i> -Cresol by Formation of 4-Hydroxybenzylsuccinate in <i>Desulfobacterium cetonicum</i> . <i>Journal of Bacteriology</i> , 2001, 183, 752-757.	2.2	78
45	Initial steps in the fermentation of 3-hydroxybenzoate by <i>Sporotomaculum hydroxybenzoicum</i> . <i>Archives of Microbiology</i> , 2000, 173, 288-295.	2.2	23
46	Anaerobic Degradation of Phenolic Compounds. <i>Die Naturwissenschaften</i> , 2000, 87, 12-23.	1.6	141
47	Anaerobic degradation of <i>m</i> -cresol by <i>Desulfobacterium cetonicum</i> is initiated by formation of 3-hydroxybenzylsuccinate. <i>Archives of Microbiology</i> , 1999, 172, 287-294.	2.2	73
48	Fermentative degradation of 3-hydroxybenzoate in pure culture by a novel strictly anaerobic bacterium, <i>Sporotomaculum hydroxybenzoicum</i> gen. nov., sp. nov.. <i>International Journal of Systematic Bacteriology</i> , 1998, 48, 215-221.	2.8	54