

# Hendrik Schäfer

## List of Publications by Year in descending order

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60  
papers

3,763  
citations

117625

34  
h-index

128289

60  
g-index

60  
all docs

60  
docs citations

60  
times ranked

4622  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of and Spatio-Temporal Differences between Microbial Assemblages from Two Neighboring Sulfurous Lakes: Comparison by Microscopy and Denaturing Gradient Gel Electrophoresis. <i>Applied and Environmental Microbiology</i> , 2000, 66, 499-508.	3.1	392
2	Carnitine metabolism to trimethylamine by an unusual Rieske-type oxygenase from human microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4268-4273.	7.1	264
3	Denaturing gradient gel electrophoresis in marine microbial ecology. <i>Methods in Microbiology</i> , 2001, 30, 425-468.	0.8	212
4	Stable-isotope probing implicates <i>Methylophaga</i> spp and novel <i>Gammaproteobacteria</i> in marine methanol and methylamine metabolism. <i>ISME Journal</i> , 2007, 1, 480-491.	9.8	177
5	Microbial community dynamics in Mediterranean nutrient-enriched seawater mesocosms: changes in the genetic diversity of bacterial populations. <i>FEMS Microbiology Ecology</i> , 2001, 34, 243-253.	2.7	168
6	Genetic diversity of $\phi$ -satellite $\phi^{\text{TM}}$ bacteria present in cultures of marine diatoms. <i>FEMS Microbiology Ecology</i> , 2002, 42, 25-35.	2.7	165
7	Microbial degradation of dimethylsulphide and related C1-sulphur compounds: organisms and pathways controlling fluxes of sulphur in the biosphere. <i>Journal of Experimental Botany</i> , 2010, 61, 315-334.	4.8	158
8	Bacterial activity and genetic richness along an estuarine gradient (Rhone River plume, France). <i>Aquatic Microbial Ecology</i> , 2002, 28, 13-24.	1.8	117
9	Isolation of <i>Methylophaga</i> spp. from Marine Dimethylsulfide-Degrading Enrichment Cultures and Identification of Polypeptides Induced during Growth on Dimethylsulfide. <i>Applied and Environmental Microbiology</i> , 2007, 73, 2580-2591.	3.1	103
10	Oxidation of dimethylsulfide to tetrathionate by <i>Methylophaga thiooxidans</i> sp. nov.: a new link in the sulfur cycle. <i>Environmental Microbiology</i> , 2010, 12, 2688-2699.	3.8	99
11	Refinement of biodegradation tests methodologies and the proposed utility of new microbial ecology techniques. <i>Ecotoxicology and Environmental Safety</i> , 2015, 111, 9-22.	6.0	91
12	The Response of the Microbial Community of Marine Sediments to Organic Carbon Input under Anaerobic Conditions. <i>Systematic and Applied Microbiology</i> , 1999, 22, 237-248.	2.8	89
13	Successional changes in the genetic diversity of a marine bacterial assemblage during confinement. <i>Archives of Microbiology</i> , 2000, 173, 138-145.	2.2	88
14	Mutations in SELENBP1, encoding a novel human methanethiol oxidase, cause extraoral halitosis. <i>Nature Genetics</i> , 2018, 50, 120-129.	21.4	86
15	changes in bacterial community structure in seawater mesocosms differing in their nutrient status. <i>Aquatic Microbial Ecology</i> , 1999, 19, 255-267.	1.8	85
16	Substrate-Specific Clades of Active Marine Methylotrophs Associated with a Phytoplankton Bloom in a Temperate Coastal Environment. <i>Applied and Environmental Microbiology</i> , 2008, 74, 7321-7328.	3.1	80
17	Purification and Characterization of Dimethylsulfide Monooxygenase from <i>Hyphomicrobium sulfonivorans</i> . <i>Journal of Bacteriology</i> , 2011, 193, 1250-1258.	2.2	79
18	Microbial community dynamics in Mediterranean nutrient-enriched seawater mesocosms: changes in abundances, activity and composition. <i>FEMS Microbiology Ecology</i> , 2001, 34, 255-266.	2.7	78

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19	Genetics of the glutamate-mediated methylamine utilization pathway in the facultative methylotrophic beta-proteobacterium <i>Methyloversatilis universalis</i> FAM5. <i>Molecular Microbiology</i> , 2010, 75, 426-439.	2.5	77
20	Genetic diversity of total, active and culturable marine bacteria in coastal seawater. <i>Aquatic Microbial Ecology</i> , 2000, 23, 1-11.	1.8	71
21	SIP metagenomics identifies uncultivated <i>Methylophilaceae</i> as dimethylsulphide degrading bacteria in soil and lake sediment. <i>ISME Journal</i> , 2015, 9, 2336-2348.	9.8	66
22	Analysis of Methane Monooxygenase Genes in Mono Lake Suggests That Increased Methane Oxidation Activity May Correlate with a Change in Methanotroph Community Structure. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6458-6462.	3.1	65
23	Comparison of Bacterioneuston and Bacterioplankton Dynamics during a Phytoplankton Bloom in a Fjord Mesocosm. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7173-7181.	3.1	63
24	A mechanism for bacterial transformation of dimethylsulfide to dimethylsulfoxide: a missing link in the marine organic sulfur cycle. <i>Environmental Microbiology</i> , 2016, 18, 2754-2766.	3.8	63
25	Bacterial SBP56 identified as a Cu-dependent methanethiol oxidase widely distributed in the biosphere. <i>ISME Journal</i> , 2018, 12, 145-160.	9.8	62
26	Evidence for the presence of a CmuA methyltransferase pathway in novel marine methyl halide-oxidizing bacteria. <i>Environmental Microbiology</i> , 2005, 7, 839-852.	3.8	57
27	$\beta$ -Glutamylmethylamide Is an Essential Intermediate in the Metabolism of Methylamine by <i>Methyloccella silvestris</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 4530-4537.	3.1	53
28	Phylogenetic and functional gene analysis of the bacterial and archaeal communities associated with the surface microlayer of an estuary. <i>ISME Journal</i> , 2008, 2, 776-789.	9.8	50
29	Comparison and validation of sampling strategies for the molecular microbial analysis of surface microlayers. <i>Aquatic Microbial Ecology</i> , 2009, 57, 69-77.	1.8	49
30	Comparative genomics defines the core genome of the growing N4-like phage genus and identifies N4-like Roseophage specific genes. <i>Frontiers in Microbiology</i> , 2014, 5, 506.	3.5	48
31	Genetic diversity of 'satellite' bacteria present in cultures of marine diatoms. <i>FEMS Microbiology Ecology</i> , 2002, 42, 25-35.	2.7	45
32	Longitudinal dispersion of microplastics in aquatic flows using fluorometric techniques. <i>Water Research</i> , 2020, 170, 115337.	11.3	45
33	Draft Genome Sequence of the Chemolithoheterotrophic, Halophilic Methylotroph <i>Methylophaga thiooxydans</i> DMS010. <i>Journal of Bacteriology</i> , 2011, 193, 3154-3155.	2.2	37
34	A new approach to determine the genetic diversity of viable and active bacteria in aquatic ecosystems. <i>Cytometry</i> , 2001, 43, 314-321.	1.8	36
35	Dimethylsulfide is an energy source for the heterotrophic marine bacterium <i>Sagittula stellata</i> . <i>FEMS Microbiology Letters</i> , 2011, 322, 188-193.	1.8	35
36	Characterization of <i>para</i> -Nitrophenol-Degrading Bacterial Communities in River Water by Using Functional Markers and Stable Isotope Probing. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6890-6900.	3.1	33

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37	Bacterial Cycling of Methyl Halides. <i>Advances in Applied Microbiology</i> , 2007, 61, 307-346.	2.4	30
38	Transformations of Dimethylsulfide. <i>Metal Ions in Life Sciences</i> , 2014, 14, 279-313.	2.8	25
39	Light Structures Phototroph, Bacterial and Fungal Communities at the Soil Surface. <i>PLoS ONE</i> , 2013, 8, e69048.	2.5	24
40	Bedform characteristics and biofilm community development interact to modify hyporheic exchange. <i>Science of the Total Environment</i> , 2020, 749, 141397.	8.0	23
41	DNA-, RNA-, and Protein-Based Stable-Isotope Probing for High-Throughput Biomarker Analysis of Active Microorganisms. <i>Methods in Molecular Biology</i> , 2017, 1539, 57-74.	0.9	21
42	Identification and characterization of trimethylamine <i>N</i> -oxide (TMAO) demethylase and TMAO permease in <i>Methylocella silvestris</i> . <i>Environmental Microbiology</i> , 2014, 16, 3318-3330.	3.8	18
43	Microbial Cycling of Methanethiol. <i>Current Issues in Molecular Biology</i> , 2019, 33, 173-182.	2.4	15
44	Microbial diversity in deep sediments of the Benguela Upwelling System. <i>Aquatic Microbial Ecology</i> , 2007, 50, 1-9.	1.8	13
45	Culture-dependent and culture-independent methods reveal diverse methylotrophic communities in terrestrial environments. <i>Archives of Microbiology</i> , 2016, 198, 17-26.	2.2	12
46	Diversity of methyl halide-degrading microorganisms in oceanic and coastal waters. <i>FEMS Microbiology Letters</i> , 2012, 334, 111-118.	1.8	11
47	Identification of Proteins and Genes Expressed by <i>Methylophaga thiooxydans</i> During Growth on Dimethylsulfide and Their Presence in Other Members of the Genus. <i>Frontiers in Microbiology</i> , 2019, 10, 1132.	3.5	11
48	Dynamical and Biological Panspermia Constraints Within Multiplanet Exosystems. <i>Astrobiology</i> , 2018, 18, 1106-1122.	3.0	8
49	Contrasting Responses of Rhizosphere Bacterial, Fungal, Protist, and Nematode Communities to Nitrogen Fertilization and Crop Genotype in Field Grown Oilseed Rape ( <i>Brassica napus</i> ). <i>Frontiers in Sustainable Food Systems</i> , 2021, 5, .	3.9	8
50	CS <sub>2</sub> increasing CH <sub>4</sub> -derived carbon emissions and active microbial diversity in lake sediments. <i>Environmental Research</i> , 2022, 208, 112678.	7.5	8
51	O <sub>2</sub> -independent demethylation of trimethylamine <i>N</i> -oxide by Tdm of <i>Methylocella silvestris</i> . <i>FEBS Journal</i> , 2016, 283, 3979-3993.	4.7	7
52	Seasonal Changes in Microbial Dissolved Organic Sulfur Transformations in Coastal Waters. <i>Microorganisms</i> , 2020, 8, 337.	3.6	7
53	Seasonal and Zonal Succession of Bacterial Communities in North Sea Salt Marsh Sediments. <i>Microorganisms</i> , 2022, 10, 859.	3.6	7
54	Non-UV Light Influences the Degradation Rate of Crop Protection Products. <i>Environmental Science &amp; Technology</i> , 2013, 47, 130712083104003.	10.0	5

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55	Spatial and temporal variability in the potential of river water biofilms to degrade p-nitrophenol. <i>Chemosphere</i> , 2016, 164, 355-362.	8.2	5
56	Tree phyllospheres are a habitat for diverse populations of $\text{CO}_2$ -oxidizing bacteria. <i>Environmental Microbiology</i> , 2021, 23, 6309-6327.	3.8	5
57	A new approach to determine the genetic diversity of viable and active bacteria in aquatic ecosystems. <i>Cytometry</i> , 2001, 43, 314-321.	1.8	5
58	Stable Isotope Probing to Study Functional Components of Complex Microbial Ecosystems. <i>Methods in Molecular Biology</i> , 2014, 1096, 169-180.	0.9	4
59	Microbial community dynamics in Mediterranean nutrient-enriched seawater mesocosms: changes in abundances, activity and composition. <i>FEMS Microbiology Ecology</i> , 2001, 34, 255-266.	2.7	4
60	Towards a systematic understanding of structure–function relationship of dimethylsulfoniopropionate–catabolizing enzymes. <i>Molecular Microbiology</i> , 2019, 111, 1399-1403.	2.5	1