

Hendrik Schäfer

List of Publications by Year in descending order

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Version: 2024-02-01

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 | CS ₂ increasing CH ₄ -derived carbon emissions and active microbial diversity in lake sediments. <i>Environmental Research</i> , 2022, 208, 112678. | 7.5 | 8 |
| 2 | Seasonal and Zonal Succession of Bacterial Communities in North Sea Salt Marsh Sediments. <i>Microorganisms</i> , 2022, 10, 859. | 3.6 | 7 |
| 3 | 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 |
| 4 | Tree phyllospheres are a habitat for diverse populations of CO ₂ -oxidizing bacteria. <i>Environmental Microbiology</i> , 2021, 23, 6309-6327. | 3.8 | 5 |
| 5 | Longitudinal dispersion of microplastics in aquatic flows using fluorometric techniques. <i>Water Research</i> , 2020, 170, 115337. | 11.3 | 45 |
| 6 | Bedform characteristics and biofilm community development interact to modify hyporheic exchange. <i>Science of the Total Environment</i> , 2020, 749, 141397. | 8.0 | 23 |
| 7 | Seasonal Changes in Microbial Dissolved Organic Sulfur Transformations in Coastal Waters. <i>Microorganisms</i> , 2020, 8, 337. | 3.6 | 7 |
| 8 | 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 |
| 9 | Towards a systematic understanding of structure–function relationship of dimethylsulfoniopropionate–catabolizing enzymes. <i>Molecular Microbiology</i> , 2019, 111, 1399-1403. | 2.5 | 1 |
| 10 | Microbial Cycling of Methanethiol. <i>Current Issues in Molecular Biology</i> , 2019, 33, 173-182. | 2.4 | 15 |
| 11 | Mutations in SELENBP1, encoding a novel human methanethiol oxidase, cause extraoral halitosis. <i>Nature Genetics</i> , 2018, 50, 120-129. | 21.4 | 86 |
| 12 | 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 |
| 13 | Dynamical and Biological Panspermia Constraints Within Multiplanet Exosystems. <i>Astrobiology</i> , 2018, 18, 1106-1122. | 3.0 | 8 |
| 14 | 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 |
| 15 | 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 |
| 16 | O ₂ -independent demethylation of trimethylamine N-oxide by Tdm of <i>Methylocella silvestris</i> . <i>FEBS Journal</i> , 2016, 283, 3979-3993. | 4.7 | 7 |
| 17 | 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 |
| 18 | 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 |

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|----|---|------|-----------|
| 19 | 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 |
| 20 | Characterization of <i>p</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 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | 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 |
| 25 | Stable Isotope Probing to Study Functional Components of Complex Microbial Ecosystems. <i>Methods in Molecular Biology</i> , 2014, 1096, 169-180. | 0.9 | 4 |
| 26 | Transformations of Dimethylsulfide. <i>Metal Ions in Life Sciences</i> , 2014, 14, 279-313. | 2.8 | 25 |
| 27 | Non-LIV Light Influences the Degradation Rate of Crop Protection Products. <i>Environmental Science & Technology</i> , 2013, 47, 130712083104003. | 10.0 | 5 |
| 28 | Light Structures Phototroph, Bacterial and Fungal Communities at the Soil Surface. <i>PLoS ONE</i> , 2013, 8, e69048. | 2.5 | 24 |
| 29 | Diversity of methyl halide-degrading microorganisms in oceanic and coastal waters. <i>FEMS Microbiology Letters</i> , 2012, 334, 111-118. | 1.8 | 11 |
| 30 | 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 |
| 31 | Purification and Characterization of Dimethylsulfide Monooxygenase from <i>Hyphomicrobium sulfonivorans</i> . <i>Journal of Bacteriology</i> , 2011, 193, 1250-1258. | 2.2 | 79 |
| 32 | 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 |
| 33 | Genetics of the glutamate-mediated methylamine utilization pathway in the facultative methylotrophic β -proteobacterium <i>Methyloversatilis universalis</i> FAM5. <i>Molecular Microbiology</i> , 2010, 75, 426-439. | 2.5 | 77 |
| 34 | Oxidation of dimethylsulfide to tetrathionate by <i>Methylophaga thiooxydans</i> sp. nov.: a new link in the sulfur cycle. <i>Environmental Microbiology</i> , 2010, 12, 2688-2699. | 3.8 | 99 |
| 35 | $\hat{3}$ -Glutamylmethylamide Is an Essential Intermediate in the Metabolism of Methylamine by <i>Methylocella silvestris</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 4530-4537. | 3.1 | 53 |
| 36 | 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 |

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|----|---|-----|-----------|
| 37 | 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 |
| 38 | 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 |
| 39 | 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 |
| 40 | 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 |
| 41 | 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 |
| 42 | Bacterial Cycling of Methyl Halides. <i>Advances in Applied Microbiology</i> , 2007, 61, 307-346. | 2.4 | 30 |
| 43 | 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 |
| 44 | Microbial diversity in deep sediments of the Benguela Upwelling System. <i>Aquatic Microbial Ecology</i> , 2007, 50, 1-9. | 1.8 | 13 |
| 45 | 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 |
| 46 | 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 |
| 47 | Bacterial activity and genetic richness along an estuarine gradient (Rhône River plume, France). <i>Aquatic Microbial Ecology</i> , 2002, 28, 13-24. | 1.8 | 117 |
| 48 | Genetic diversity of 'satellite' bacteria present in cultures of marine diatoms. <i>FEMS Microbiology Ecology</i> , 2002, 42, 25-35. | 2.7 | 45 |
| 49 | Genetic diversity of 'satellite' bacteria present in cultures of marine diatoms. <i>FEMS Microbiology Ecology</i> , 2002, 42, 25-35. | 2.7 | 165 |
| 50 | Denaturing gradient gel electrophoresis in marine microbial ecology. <i>Methods in Microbiology</i> , 2001, 30, 425-468. | 0.8 | 212 |
| 51 | 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 |
| 52 | 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 |
| 53 | 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 |
| 54 | 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 |

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| 55 | 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 |
| 56 | Genetic diversity of total, active and culturable marine bacteria in coastal seawater. <i>Aquatic Microbial Ecology</i> , 2000, 23, 1-11. | 1.8 | 71 |
| 57 | 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 |
| 58 | 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 |
| 59 | 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 |
| 60 | 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 |