

Dominik Schneider

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

1,885
citations

394421
19
h-index

302126
39
g-index

79
all docs

79
docs citations

79
times ranked

2708
citing authors

#	ARTICLE	IF	CITATIONS
1	Land-use choices follow profitability at the expense of ecological functions in Indonesian smallholder landscapes. <i>Nature Communications</i> , 2016, 7, 13137.	12.8	186
2	Phylogenetic Analysis of a Microbialite-Forming Microbial Mat from a Hypersaline Lake of the Kiritimati Atoll, Central Pacific. <i>PLoS ONE</i> , 2013, 8, e66662.	2.5	160
3	Trade-offs between multifunctionality and profit in tropical smallholder landscapes. <i>Nature Communications</i> , 2020, 11, 1186.	12.8	156
4	Direct and cascading impacts of tropical land-use change on multi-trophic biodiversity. <i>Nature Ecology and Evolution</i> , 2017, 1, 1511-1519.	7.8	137
5	Impact of Lowland Rainforest Transformation on Diversity and Composition of Soil Prokaryotic Communities in Sumatra (Indonesia). <i>Frontiers in Microbiology</i> , 2015, 6, 1339.	3.5	92
6	Intensive tropical land use massively shifts soil fungal communities. <i>Scientific Reports</i> , 2019, 9, 3403.	3.3	86
7	Tree Species Shape Soil Bacterial Community Structure and Function in Temperate Deciduous Forests. <i>Frontiers in Microbiology</i> , 2019, 10, 1519.	3.5	71
8	Drylands soil bacterial community is affected by land use change and different irrigation practices in the Mezquital Valley, Mexico. <i>Scientific Reports</i> , 2018, 8, 1413.	3.3	58
9	Changes in Trophic Groups of Protists With Conversion of Rainforest Into Rubber and Oil Palm Plantations. <i>Frontiers in Microbiology</i> , 2019, 10, 240.	3.5	48
10	How Rainforest Conversion to Agricultural Systems in Sumatra (Indonesia) Affects Active Soil Bacterial Communities. <i>Frontiers in Microbiology</i> , 2018, 9, 2381.	3.5	44
11	Unravelling the effects of tropical land use conversion on the soil microbiome. <i>Environmental Microbiomes</i> , 2020, 15, 5.	5.0	37
12	Microbial functional changes mark irreversible course of Tibetan grassland degradation. <i>Nature Communications</i> , 2022, 13, 2681.	12.8	37
13	Nitrile-Degrading Bacteria Isolated from Compost. <i>Frontiers in Environmental Science</i> , 2017, 5, .	3.3	33
14	Globally Abundant <i>Candidatus</i> <i>Udaeobacter</i> Benefits from Release of Antibiotics in Soil and Potentially Performs Trace Gas Scavenging. <i>MSphere</i> , 2020, 5, .	2.9	32
15	Active metabolic pathways of anaerobic methane oxidation in paddy soils. <i>Soil Biology and Biochemistry</i> , 2021, 156, 108215.	8.8	32
16	Calcium dynamics in microbialite-forming exopolymer-rich mats on the atoll of Kiritimati, Republic of Kiribati, Central Pacific. <i>Geobiology</i> , 2015, 13, 170-180.	2.4	30
17	Nitrogen Metabolism Genes from Temperate Marine Sediments. <i>Marine Biotechnology</i> , 2017, 19, 175-190.	2.4	30
18	The influence of microbial mats on travertine precipitation in active hydrothermal systems (Central Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.7	30

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19	Potentially Active Iron, Sulfur, and Sulfate Reducing Bacteria in Skagerrak and Bothnian Bay Sediments. <i>Geomicrobiology Journal</i> , 2017, 34, 840-850.	2.0	28
20	Bacterial succession along a sediment porewater gradient at Lake Neusiedl in Austria. <i>Scientific Data</i> , 2019, 6, 163.	5.3	23
21	Production of the Fragrance Geraniol in Peroxisomes of a Product-Tolerant Baker's Yeast. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 582052.	4.1	22
22	Shifts in root and soil chemistry drive the assembly of belowground fungal communities in tropical land-use systems. <i>Soil Biology and Biochemistry</i> , 2021, 154, 108140.	8.8	22
23	A novel, versatile family IV carboxylesterase exhibits high stability and activity in a broad pH spectrum. <i>Biotechnology Letters</i> , 2017, 39, 577-587.	2.2	21
24	Soil and root nutrient chemistry structure root-associated fungal assemblages in temperate forests. <i>Environmental Microbiology</i> , 2020, 22, 3081-3095.	3.8	21
25	Authigenic formation of Ca-Mg carbonates in the shallow alkaline Lake Neusiedl, Austria. <i>Biogeosciences</i> , 2020, 17, 2085-2106.	3.3	21
26	Maize root and shoot litter quality controls short-term CO ₂ and N ₂ O emissions and bacterial community structure of arable soil. <i>Biogeosciences</i> , 2020, 17, 1181-1198.	3.3	20
27	Living in a Puddle of Mud: Isolation and Characterization of Two Novel Caulobacteraceae Strains <i>Brevundimonas pondensis</i> sp. nov. and <i>Brevundimonas goettingensis</i> sp. nov.. <i>Applied Microbiology</i> , 2021, 1, 38-59.	1.6	20
28	Metagenomic and Metatranscriptomic Analyses of Bacterial Communities Derived From a Calcifying Karst Water Creek Biofilm and Tufa. <i>Geomicrobiology Journal</i> , 2015, 32, 316-331.	2.0	19
29	Drivers of gut microbiome variation within and between groups of a wild Malagasy primate. <i>Microbiome</i> , 2022, 10, 28.	11.1	19
30	Impact of Nitriles on Bacterial Communities. <i>Frontiers in Environmental Science</i> , 2019, 7, .	3.3	18
31	One size fits all? Relationships among group size, health, and ecology indicate a lack of an optimal group size in a wild lemur population. <i>Behavioral Ecology and Sociobiology</i> , 2019, 73, 1.	1.4	18
32	Impact of nitrogen and phosphorus addition on resident soil and root mycobiomes in beech forests. <i>Biology and Fertility of Soils</i> , 2021, 57, 1031-1052.	4.3	18
33	Comparative Genomic Analysis of Members of the Genera <i>Methanosphaera</i> and <i>Methanobrevibacter</i> Reveals Distinct Clades with Specific Potential Metabolic Functions. <i>Archaea</i> , 2018, 2018, 1-9.	2.3	17
34	Morphological and Metabolite Responses of Potatoes under Various Phosphorus Levels and Their Amelioration by Plant Growth-Promoting Rhizobacteria. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5162.	4.1	17
35	Dietary shifts and social interactions drive temporal fluctuations of the gut microbiome from wild redfronted lemurs. <i>ISME Communications</i> , 2022, 2, .	4.2	16
36	Gut bacterial communities of diarrheic patients with indications of <i>Clostridioides difficile</i> infection. <i>Scientific Data</i> , 2017, 4, 170152.	5.3	15

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37	Land Use Change and Water Quality Use for Irrigation Alters Drylands Soil Fungal Community in the Mezquital Valley, Mexico. <i>Frontiers in Microbiology</i> , 2019, 10, 1220.	3.5	15
38	First Complete Genome Sequences of <i>Janthinobacterium lividum</i> EIF1 and EIF2 and Their Comparative Genome Analysis. <i>Genome Biology and Evolution</i> , 2020, 12, 1782-1788.	2.5	15
39	Tree species composition and soil properties in pure and mixed beech-conifer stands drive soil fungal communities. <i>Forest Ecology and Management</i> , 2021, 502, 119709.	3.2	15
40	Bacteriohopanepolyols in a stratified cyanobacterial mat from Kiritimati (Christmas Island, Kiribati). <i>Organic Geochemistry</i> , 2013, 55, 55-62.	1.8	14
41	Extraction of Total DNA and RNA from Marine Filter Samples and Generation of a cDNA as Universal Template for Marker Gene Studies. <i>Methods in Molecular Biology</i> , 2017, 1539, 13-22.	0.9	13
42	The ubiquitous soil verrucomicrobial clade <i>Candidatus</i> <i>Udaeobacter</i> ™ shows preferences for acidic pH. <i>Environmental Microbiology Reports</i> , 2021, 13, 878-883.	2.4	13
43	Cold-water corals and hydrocarbon-rich seepage in Pompeia Province (Gulf of Cádiz) “living on the edge. <i>Biogeosciences</i> , 2019, 16, 1607-1627.	3.3	12
44	Metagenomes of Wastewater at Different Treatment Stages in Central Germany. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	12
45	Soil bacterial community structures in relation to different oil palm management practices. <i>Scientific Data</i> , 2020, 7, 421.	5.3	11
46	Saprotrophic and Ectomycorrhizal Fungi Contribute Differentially to Organic P Mobilization in Beech-Dominated Forest Ecosystems. <i>Frontiers in Forests and Global Change</i> , 2020, 3, .	2.3	11
47	Characterization of glyphosate-resistant <i>Burkholderia anthina</i> and <i>Burkholderia cenocepacia</i> isolates from a commercial Roundup® solution. <i>Environmental Microbiology Reports</i> , 2022, 14, 70-84.	2.4	11
48	Transcriptional Landscape of Ectomycorrhizal Fungi and Their Host Provides Insight into N Uptake from Forest Soil. <i>MSystems</i> , 2022, 7, e0095721.	3.8	11
49	Legacy Effects Overshadow Tree Diversity Effects on Soil Fungal Communities in Oil Palm-Enrichment Plantations. <i>Microorganisms</i> , 2020, 8, 1577.	3.6	9
50	Thermophilic Composting of Human Feces: Development of Bacterial Community Composition and Antimicrobial Resistance Gene Pool. <i>Frontiers in Microbiology</i> , 2022, 13, 824834.	3.5	8
51	Bioleaching potential of bacterial communities in historic mine waste areas. <i>Environmental Earth Sciences</i> , 2018, 77, 1.	2.7	7
52	Formation of Siderite in Microbial Microcosms Derived from a Marine Sediment. <i>Geomicrobiology Journal</i> , 2020, 37, 475-485.	2.0	6
53	Metagenome-Assembled Genome Sequences from Different Wastewater Treatment Stages in Germany. <i>Microbiology Resource Announcements</i> , 2021, 10, e0050421.	0.6	6
54	Soil Layers Matter: Vertical Stratification of Root-Associated Fungal Assemblages in Temperate Forests Reveals Differences in Habitat Colonization. <i>Microorganisms</i> , 2021, 9, 2131.	3.6	6

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55	Metagenomic Insights Into the Changes of Antibiotic Resistance and Pathogenicity Factor Pools Upon Thermophilic Composting of Human Excreta. <i>Frontiers in Microbiology</i> , 2022, 13, 826071.	3.5	6
56	First Insights Into Bacterial Gastrointestinal Tract Communities of the Eurasian Beaver (<i>Castor fiber</i>). <i>Frontiers in Microbiology</i> , 2019, 10, 1646.	3.5	4
57	Early Effects of Fertilizer and Herbicide Reduction on Root-Associated Biota in Oil Palm Plantations. <i>Agronomy</i> , 2022, 12, 199.	3.0	4
58	Bovine Rumen Microbiome: Impact of DNA Extraction Methods and Comparison of Non-Invasive Sampling Sites. <i>Ruminants</i> , 2022, 2, 112-132.	1.1	4
59	DNA- and RNA-based bacterial communities and geochemical zonation under changing sediment porewater dynamics on the Aldabra Atoll. <i>Scientific Reports</i> , 2022, 12, 4257.	3.3	4
60	Complete Genome of <i>Roseobacter ponti</i> DSM 106830T. <i>Genome Biology and Evolution</i> , 2020, 12, 1013-1018.	2.5	3
61	Novel Antimicrobial Cellulose Fleece Inhibits Growth of Human-Derived Biofilm-Forming <i>Staphylococci</i> During the SIRIUS19 Simulated Space Mission. <i>Frontiers in Microbiology</i> , 2020, 11, 1626.	3.5	3
62	Metagenome Sequences of a Wastewater Treatment Plant Digester Sludge-Derived Enrichment Culture. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
63	<i>Pontibacillus</i> sp. ALD_SL1 and <i>Psychroflexus</i> sp. ALD_RP9, two novel moderately halophilic bacteria isolated from sediment and water from the Aldabra Atoll, Seychelles. <i>PLoS ONE</i> , 2021, 16, e0256639.	2.5	2
64	Draft Genome Sequence of <i>Saccharomyces cerevisiae</i> LW2591Y, a Laboratory Strain for <i>In Vivo</i> Multigene Assemblies. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
65	Metagenomic Screening for Lipolytic Genes Reveals an Ecology-Clustered Distribution Pattern. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
66	Complete Genome Sequence of <i>Escherichia coli</i> GW-AmxH19, Isolated from Hospital Wastewater in Greifswald, Germany. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
67	Optimising High-Throughput Sequencing Data Analysis, from Gene Database Selection to the Analysis of Compositional Data: A Case Study on Tropical Soil Nematodes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
68	Decoupling of Pore Water Chemistry, Bacterial Community Profiles, and Carbonate Mud Diagenesis in a Land-Locked Pool on Aldabra (Seychelles, Indian Ocean). <i>Geomicrobiology Journal</i> , 0, , 1-19.	2.0	0