

# Dominik Schneider

## List of Publications by Year in descending order

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Version: 2024-02-01

68  
papers

1,885  
citations

393982

19  
h-index

301761

39  
g-index

79  
all docs

79  
docs citations

79  
times ranked

2708  
citing authors

#	ARTICLE	IF	CITATIONS
1	The influence of microbial mats on travertine precipitation in active hydrothermal systems (Central Tj ETQq1 1 0.784314 rgBT /Overlo	0.8	30
2	Characterization of glyphosate-resistant <i>Burkholderia anthina</i> and <i>Burkholderia cenocepacia</i> isolates from a commercial Roundup® solution. Environmental Microbiology Reports, 2022, 14, 70-84.	1.0	11
3	Transcriptional Landscape of Ectomycorrhizal Fungi and Their Host Provides Insight into N Uptake from Forest Soil. MSystems, 2022, 7, e0095721.	1.7	11
4	Dietary shifts and social interactions drive temporal fluctuations of the gut microbiome from wild redfronted lemurs. ISME Communications, 2022, 2, .	1.7	16
5	Early Effects of Fertilizer and Herbicide Reduction on Root-Associated Biota in Oil Palm Plantations. Agronomy, 2022, 12, 199.	1.3	4
6	Bovine Rumen Microbiome: Impact of DNA Extraction Methods and Comparison of Non-Invasive Sampling Sites. Ruminants, 2022, 2, 112-132.	0.4	4
7	Drivers of gut microbiome variation within and between groups of a wild Malagasy primate. Microbiome, 2022, 10, 28.	4.9	19
8	Thermophilic Composting of Human Feces: Development of Bacterial Community Composition and Antimicrobial Resistance Gene Pool. Frontiers in Microbiology, 2022, 13, 824834.	1.5	8
9	Metagenomic Insights Into the Changes of Antibiotic Resistance and Pathogenicity Factor Pools Upon Thermophilic Composting of Human Excreta. Frontiers in Microbiology, 2022, 13, 826071.	1.5	6
10	DNA- and RNA-based bacterial communities and geochemical zonation under changing sediment porewater dynamics on the Aldabra Atoll. Scientific Reports, 2022, 12, 4257.	1.6	4
11	Microbial functional changes mark irreversible course of Tibetan grassland degradation. Nature Communications, 2022, 13, 2681.	5.8	37
12	Draft Genome Sequence of <i>Saccharomyces cerevisiae</i> LW2591Y, a Laboratory Strain for <i>In Vivo</i> Multigene Assemblies. Microbiology Resource Announcements, 2021, 10, .	0.3	1
13	Shifts in root and soil chemistry drive the assembly of belowground fungal communities in tropical land-use systems. Soil Biology and Biochemistry, 2021, 154, 108140.	4.2	22
14	Active metabolic pathways of anaerobic methane oxidation in paddy soils. Soil Biology and Biochemistry, 2021, 156, 108215.	4.2	32
15	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.. Applied Microbiology, 2021, 1, 38-59.	0.7	20
16	Morphological and Metabolite Responses of Potatoes under Various Phosphorus Levels and Their Amelioration by Plant Growth-Promoting Rhizobacteria. International Journal of Molecular Sciences, 2021, 22, 5162.	1.8	17
17	Metagenome-Assembled Genome Sequences from Different Wastewater Treatment Stages in Germany. Microbiology Resource Announcements, 2021, 10, e0050421.	0.3	6
18	<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. PLoS ONE, 2021, 16, e0256639.	1.1	2

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19	The ubiquitous soil verrucomicrobial clade <i>Candidatus</i> Udaeobacter™ shows preferences for acidic <math>pH</math>. Environmental Microbiology Reports, 2021, 13, 878-883.	1.0	13
20	Impact of nitrogen and phosphorus addition on resident soil and root mycobiomes in beech forests. Biology and Fertility of Soils, 2021, 57, 1031-1052.	2.3	18
21	Tree species composition and soil properties in pure and mixed beech-conifer stands drive soil fungal communities. Forest Ecology and Management, 2021, 502, 119709.	1.4	15
22	Soil Layers Matter: Vertical Stratification of Root-Associated Fungal Assemblages in Temperate Forests Reveals Differences in Habitat Colonization. Microorganisms, 2021, 9, 2131.	1.6	6
23	Metagenome Sequences of a Wastewater Treatment Plant Digester Sludge-Derived Enrichment Culture. Microbiology Resource Announcements, 2020, 9, .	0.3	2
24	Complete Genome of Roseobacter ponti DSM 106830T. Genome Biology and Evolution, 2020, 12, 1013-1018.	1.1	3
25	First Complete Genome Sequences of Janthinobacterium lividum EIF1 and EIF2 and Their Comparative Genome Analysis. Genome Biology and Evolution, 2020, 12, 1782-1788.	1.1	15
26	Novel Antimicrobial Cellulose Fleece Inhibits Growth of Human-Derived Biofilm-Forming Staphylococci During the SIRIUS19 Simulated Space Mission. Frontiers in Microbiology, 2020, 11, 1626.	1.5	3
27	Globally Abundant <i>Candidatus</i> Udaeobacter™ Benefits from Release of Antibiotics in Soil and Potentially Performs Trace Gas Scavenging. MSphere, 2020, 5, .	1.3	32
28	Production of the Fragrance Geraniol in Peroxisomes of a Product-Tolerant Baker's Yeast. Frontiers in Bioengineering and Biotechnology, 2020, 8, 582052.	2.0	22
29	Soil bacterial community structures in relation to different oil palm management practices. Scientific Data, 2020, 7, 421.	2.4	11
30	Legacy Effects Overshadow Tree Diversity Effects on Soil Fungal Communities in Oil Palm-Enrichment Plantations. Microorganisms, 2020, 8, 1577.	1.6	9
31	Soil and root nutrient chemistry structure root-associated fungal assemblages in temperate forests. Environmental Microbiology, 2020, 22, 3081-3095.	1.8	21
32	Saprotrophic and Ectomycorrhizal Fungi Contribute Differentially to Organic P Mobilization in Beech-Dominated Forest Ecosystems. Frontiers in Forests and Global Change, 2020, 3, .	1.0	11
33	Maize root and shoot litter quality controls short-term CO <sub>2</sub> and N <sub>2</sub> O emissions and bacterial community structure of arable soil. Biogeosciences, 2020, 17, 1181-1198.	1.3	20
34	Formation of Siderite in Microbial Microcosms Derived from a Marine Sediment. Geomicrobiology Journal, 2020, 37, 475-485.	1.0	6
35	Trade-offs between multifunctionality and profit in tropical smallholder landscapes. Nature Communications, 2020, 11, 1186.	5.8	156
36	Unravelling the effects of tropical land use conversion on the soil microbiome. Environmental Microbiomes, 2020, 15, 5.	2.2	37

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37	Metagenomes of Wastewater at Different Treatment Stages in Central Germany. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	12
38	Authigenic formation of Ca-Mg carbonates in the shallow alkaline Lake Neusiedl, Austria. <i>Biogeosciences</i> , 2020, 17, 2085-2106.	1.3	21
39	Complete Genome Sequence of <i>Escherichia coli</i> GW-AmxH19, Isolated from Hospital Wastewater in Greifswald, Germany. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
40	Impact of Nitriles on Bacterial Communities. <i>Frontiers in Environmental Science</i> , 2019, 7, .	1.5	18
41	First Insights Into Bacterial Gastrointestinal Tract Communities of the Eurasian Beaver ( <i>Castor fiber</i> ). <i>Frontiers in Microbiology</i> , 2019, 10, 1646.	1.5	4
42	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.	1.5	15
43	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.	0.6	18
44	Bacterial succession along a sediment porewater gradient at Lake Neusiedl in Austria. <i>Scientific Data</i> , 2019, 6, 163.	2.4	23
45	Tree Species Shape Soil Bacterial Community Structure and Function in Temperate Deciduous Forests. <i>Frontiers in Microbiology</i> , 2019, 10, 1519.	1.5	71
46	Cold-water corals and hydrocarbon-rich seepage in Pompeia Province (Gulf of Cádiz) – living on the edge. <i>Biogeosciences</i> , 2019, 16, 1607-1627.	1.3	12
47	Intensive tropical land use massively shifts soil fungal communities. <i>Scientific Reports</i> , 2019, 9, 3403.	1.6	86
48	Changes in Trophic Groups of Protists With Conversion of Rainforest Into Rubber and Oil Palm Plantations. <i>Frontiers in Microbiology</i> , 2019, 10, 240.	1.5	48
49	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.	1.6	58
50	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
51	How Rainforest Conversion to Agricultural Systems in Sumatra (Indonesia) Affects Active Soil Bacterial Communities. <i>Frontiers in Microbiology</i> , 2018, 9, 2381.	1.5	44
52	Bioleaching potential of bacterial communities in historic mine waste areas. <i>Environmental Earth Sciences</i> , 2018, 77, 1.	1.3	7
53	Nitrogen Metabolism Genes from Temperate Marine Sediments. <i>Marine Biotechnology</i> , 2017, 19, 175-190.	1.1	30
54	A novel, versatile family IV carboxylesterase exhibits high stability and activity in a broad pH spectrum. <i>Biotechnology Letters</i> , 2017, 39, 577-587.	1.1	21

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55	Potentially Active Iron, Sulfur, and Sulfate Reducing Bacteria in Skagerrak and Bothnian Bay Sediments. <i>Geomicrobiology Journal</i> , 2017, 34, 840-850.	1.0	28
56	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.	0.4	13
57	Gut bacterial communities of diarrheic patients with indications of <i>Clostridioides difficile</i> infection. <i>Scientific Data</i> , 2017, 4, 170152.	2.4	15
58	Direct and cascading impacts of tropical land-use change on multi-trophic biodiversity. <i>Nature Ecology and Evolution</i> , 2017, 1, 1511-1519.	3.4	137
59	Nitrile-Degrading Bacteria Isolated from Compost. <i>Frontiers in Environmental Science</i> , 2017, 5, .	1.5	33
60	Land-use choices follow profitability at the expense of ecological functions in Indonesian smallholder landscapes. <i>Nature Communications</i> , 2016, 7, 13137.	5.8	186
61	Impact of Lowland Rainforest Transformation on Diversity and Composition of Soil Prokaryotic Communities in Sumatra (Indonesia). <i>Frontiers in Microbiology</i> , 2015, 6, 1339.	1.5	92
62	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.	1.0	19
63	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.	1.1	30
64	Bacteriohopanepolyols in a stratified cyanobacterial mat from Kiritimati (Christmas Island, Kiribati). <i>Organic Geochemistry</i> , 2013, 55, 55-62.	0.9	14
65	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.	1.1	160
66	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
67	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.	1.0	0
68	Metagenomic Screening for Lipolytic Genes Reveals an Ecology-Clustered Distribution Pattern. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1