

Stephane Uroz

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

6,817
citations

87723

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h-index

102304

66
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67
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67
docs citations

67
times ranked

7772
citing authors

#	ARTICLE	IF	CITATIONS
1	The mineral weathering ability of <i>Collimonas pratensis</i> PMB3(1) involves a Malleobactin-mediated iron acquisition system. <i>Environmental Microbiology</i> , 2022, 24, 784-802.	1.8	4
2	Recent progress in understanding the ecology and molecular genetics of soil mineral weathering bacteria. <i>Trends in Microbiology</i> , 2022, 30, 882-897.	3.5	17
3	Oak decaying wood harbors taxonomically and functionally different bacterial communities in sapwood and heartwood. <i>Soil Biology and Biochemistry</i> , 2021, 155, 108160.	4.2	12
4	Isotopic tracing reveals single-cell assimilation of a macroalgal polysaccharide by a few marine Flavobacteria and Gammaproteobacteria. <i>ISME Journal</i> , 2021, 15, 3062-3075.	4.4	16
5	Forest plant cover and mineral type determine the diversity and composition of mineral-colonizing fungal communities. <i>European Journal of Soil Biology</i> , 2021, 105, 103334.	1.4	5
6	<i>Acidisoma silvae</i> sp. nov. and <i>Acidisomacellulosilytica</i> sp. nov., Two Acidophilic Bacteria Isolated from Decaying Wood, Hydrolyzing Cellulose and Producing Poly-3-hydroxybutyrate. <i>Microorganisms</i> , 2021, 9, 2053.	1.6	12
7	Dual transcriptomics and proteomics analyses of the early stage of interaction between <i>Caballeronia mineralivorans</i> PML1 (12) and mineral. <i>Environmental Microbiology</i> , 2020, 22, 3838-3862.	1.8	10
8	Draft Genome Sequence of <i>Collimonas pratensis</i> Strain PMB3(1), an Effective Mineral-Weathering and Chitin-Hydrolyzing Bacterial Strain. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
9	Precipitation Partitioning Hydrologic Highways Between Microbial Communities of the Plant Microbiome?. , 2020, , 229-252.		9
10	Identification of a novel type of glucose dehydrogenase involved in the mineral weathering ability of <i>Collimonas pratensis</i> strain PMB3(1). <i>FEMS Microbiology Ecology</i> , 2020, 97, .	1.3	3
11	Orchard Conditions and Fruiting Body Characteristics Drive the Microbiome of the Black Truffle <i>Tuber aestivum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1437.	1.5	31
12	Plant Symbionts Are Engineers of the Plant-Associated Microbiome. <i>Trends in Plant Science</i> , 2019, 24, 905-916.	4.3	93
13	A microcosm approach highlights the response of soil mineral weathering bacterial communities to an increase of K and Mg availability. <i>Scientific Reports</i> , 2019, 9, 14403.	1.6	29
14	Soil parameters, land use, and geographical distance drive soil bacterial communities along a European transect. <i>Scientific Reports</i> , 2019, 9, 605.	1.6	56
15	Impact of soil pedogenesis on the diversity and composition of fungal communities across the California soil chronosequence of Mendocino. <i>Mycorrhiza</i> , 2018, 28, 343-356.	1.3	10
16	Identification, distribution, and quantification of biominerals in a deciduous forest. <i>Geobiology</i> , 2017, 15, 296-310.	1.1	14
17	Soil networks become more connected and take up more carbon as nature restoration progresses. <i>Nature Communications</i> , 2017, 8, 14349.	5.8	555
18	Ancestral alliances: Plant mutualistic symbioses with fungi and bacteria. <i>Science</i> , 2017, 356, .	6.0	333

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19	Mineral Types and Tree Species Determine the Functional and Taxonomic Structures of Forest Soil Bacterial Communities. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	39
20	Tree roots select specific bacterial communities in the subsurface critical zone. <i>Soil Biology and Biochemistry</i> , 2017, 115, 109-123.	4.2	14
21	Taxonomic and functional shifts in the beech rhizosphere microbiome across a natural soil toposequence. <i>Scientific Reports</i> , 2017, 7, 9604.	1.6	77
22	Caballeronia mineralivorans sp. nov., isolated from oak- Scleroderma citrinum mycorrhizosphere. <i>Systematic and Applied Microbiology</i> , 2017, 40, 345-351.	1.2	14
23	Ecology of the forest microbiome: Highlights of temperate and boreal ecosystems. <i>Soil Biology and Biochemistry</i> , 2016, 103, 471-488.	4.2	140
24	Soil type determines the distribution of nutrient mobilizing bacterial communities in the rhizosphere of beech trees. <i>Soil Biology and Biochemistry</i> , 2016, 103, 429-445.	4.2	37
25	Specific impacts of beech and Norway spruce on the structure and diversity of the rhizosphere and soil microbial communities. <i>Scientific Reports</i> , 2016, 6, 27756.	1.6	101
26	Mineral Type and Solution Chemistry Affect the Structure and Composition of Actively Growing Bacterial Communities as Revealed by Bromodeoxyuridine Immunocapture and 16S rRNA Pyrosequencing. <i>Microbial Ecology</i> , 2016, 72, 428-442.	1.4	14
27	Temporal changes of bacterial communities in the Tuber melanosporum ectomycorrhizosphere during ascocarp development. <i>Mycorrhiza</i> , 2016, 26, 389-399.	1.3	75
28	Soil Parameters Drive the Structure, Diversity and Metabolic Potentials of the Bacterial Communities Across Temperate Beech Forest Soil Sequences. <i>Microbial Ecology</i> , 2016, 71, 482-493.	1.4	96
29	Draft Genome Sequence of Burkholderia sp. Strain PML1 (12), an Ectomycorrhizosphere-Inhabiting Bacterium with Effective Mineral-Weathering Ability. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
30	The Mineralosphere Concept: Mineralogical Control of the Distribution and Function of Mineral-associated Bacterial Communities. <i>Trends in Microbiology</i> , 2015, 23, 751-762.	3.5	128
31	Soil conditions and land use intensification effects on soil microbial communities across a range of European field sites. <i>Soil Biology and Biochemistry</i> , 2015, 88, 403-413.	4.2	151
32	Black truffle-associated bacterial communities during the development and maturation of Tuber melanosporum ascocarps and putative functional roles. <i>Environmental Microbiology</i> , 2014, 16, 2831-2847.	1.8	133
33	Structure and function of bacterial communities in ageing soils: Insights from the Mendocino ecological staircase. <i>Soil Biology and Biochemistry</i> , 2014, 69, 265-274.	4.2	46
34	Diversity and structure of bacterial communities associated with Phanerochaete chrysosporium during wood decay. <i>Environmental Microbiology</i> , 2014, 16, 2238-2252.	1.8	51
35	Functional Profiling and Distribution of the Forest Soil Bacterial Communities Along the Soil Mycorrhizosphere Continuum. <i>Microbial Ecology</i> , 2013, 66, 404-415.	1.4	32
36	A short-term mineral amendment impacts the mineral weathering bacterial communities in an acidic forest soil. <i>Research in Microbiology</i> , 2013, 164, 729-739.	1.0	26

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37	Increase of apatite dissolution rate by Scots pine roots associated or not with <i>Burkholderia glathei</i> PML1(12)Rp in open-system flow microcosms. <i>Geochimica Et Cosmochimica Acta</i> , 2013, 106, 287-306.	1.6	37
38	Taxonomic and functional diversity of <i>Streptomyces</i> in a forest soil. <i>FEMS Microbiology Letters</i> , 2013, 342, 157-167.	0.7	47
39	An improved method compatible with metagenomic analyses to extract genomic DNA from soils in <i>Tuber melanosporum</i> orchards. <i>Journal of Applied Microbiology</i> , 2013, 115, 163-170.	1.4	19
40	Functional Assays and Metagenomic Analyses Reveals Differences between the Microbial Communities Inhabiting the Soil Horizons of a Norway Spruce Plantation. <i>PLoS ONE</i> , 2013, 8, e55929.	1.1	147
41	Correlation of the Abundance of Betaproteobacteria on Mineral Surfaces with Mineral Weathering in Forest Soils. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7114-7119.	1.4	84
42	Minerals Affect the Specific Diversity of Forest Soil Bacterial Communities. <i>Geomicrobiology Journal</i> , 2012, 29, 88-98.	1.0	42
43	Distinct Ectomycorrhizospheres Share Similar Bacterial Communities as Revealed by Pyrosequencing-Based Analysis of 16S rRNA Genes. <i>Applied and Environmental Microbiology</i> , 2012, 78, 3020-3024.	1.4	60
44	Bacterial weathering and its contribution to nutrient cycling in temperate forest ecosystems. <i>Research in Microbiology</i> , 2011, 162, 820-831.	1.0	98
45	<i>Pseudomonas fluorescens</i> BBc6R8 type III secretion mutants no longer promote ectomycorrhizal symbiosis. <i>Environmental Microbiology Reports</i> , 2011, 3, 203-210.	1.0	53
46	Seasons differently impact the structure of mineral weathering bacterial communities in beech and spruce stands. <i>Soil Biology and Biochemistry</i> , 2011, 43, 2012-2022.	4.2	62
47	Long term impact of mineral amendment on the distribution of the mineral weathering associated bacterial communities from the beech <i>Scleroderma citrinum</i> ectomycorrhizosphere. <i>Soil Biology and Biochemistry</i> , 2011, 43, 2275-2282.	4.2	49
48	Linking diversity to function: highlight on the mineral weathering bacteria. <i>Open Life Sciences</i> , 2011, 6, 817-820.	0.6	5
49	The role of ectomycorrhizal communities in forest ecosystem processes: New perspectives and emerging concepts. <i>Soil Biology and Biochemistry</i> , 2010, 42, 679-698.	4.2	412
50	The bacterial genus <i>Collimonas</i> : mycophagy, weathering and other adaptive solutions to life in oligotrophic soil environments. <i>Environmental Microbiology</i> , 2010, 12, 281-292.	1.8	118
51	Influence of Forest Trees on the Distribution of Mineral Weathering-Associated Bacterial Communities of the <i>Scleroderma citrinum</i> Mycorrhizosphere. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4780-4787.	1.4	69
52	Pyrosequencing reveals a contrasted bacterial diversity between oak rhizosphere and surrounding soil. <i>Environmental Microbiology Reports</i> , 2010, 2, 281-288.	1.0	309
53	Interactions between mycorrhizal fungi and mycorrhizosphere bacteria during mineral weathering: Budget analysis and bacterial quantification. <i>Soil Biology and Biochemistry</i> , 2009, 41, 1935-1942.	4.2	57
54	Efficient mineral weathering is a distinctive functional trait of the bacterial genus <i>Collimonas</i> . <i>Soil Biology and Biochemistry</i> , 2009, 41, 2178-2186.	4.2	69

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55	Quorum Sensing and Quorum Quenching: The Yin and Yang of Bacterial Communication. ChemBioChem, 2009, 10, 205-216.	1.3	273
56	454 Pyrosequencing analyses of forest soils reveal an unexpectedly high fungal diversity. New Phytologist, 2009, 184, 449-456.	3.5	908
57	Mineral weathering by bacteria: ecology, actors and mechanisms. Trends in Microbiology, 2009, 17, 378-387.	3.5	556
58	Degradation of N-acyl homoserine lactone quorum sensing signal molecules by forest root-associated fungi. FEMS Microbiology Ecology, 2008, 65, 271-278.	1.3	104
59	Simple microplate assays to measure iron mobilization and oxalate secretion by ectomycorrhizal tree roots. Soil Biology and Biochemistry, 2008, 40, 2460-2463.	4.2	25
60	A <i>Rhodococcus qsdA</i> -Encoded Enzyme Defines a Novel Class of Large-Spectrum Quorum-Quenching Lactonases. Applied and Environmental Microbiology, 2008, 74, 1357-1366.	1.4	177
61	Effect of the Mycorrhizosphere on the Genotypic and Metabolic Diversity of the Bacterial Communities Involved in Mineral Weathering in a Forest Soil. Applied and Environmental Microbiology, 2007, 73, 3019-3027.	1.4	248
62	N-acyl homoserine lactones are degraded via an amidolytic activity in Comamonas sp. strain D1. Archives of Microbiology, 2007, 187, 249-256.	1.0	61
63	N-hexanoyl-L-homoserine lactone, a mediator of bacterial quorum-sensing regulation, exhibits plant-dependent stability and may be inactivated by germinating Lotus corniculatus seedlings. FEMS Microbiology Ecology, 2005, 52, 13-20.	1.3	107
64	Bacterial populations in the rhizosphere of tobacco plants producing the quorum-sensing signals hexanoyl-homoserine lactone and 3-oxo-hexanoyl-homoserine lactone. FEMS Microbiology Ecology, 2004, 51, 19-29.	1.3	34
65	The Ti Plasmid of Agrobacterium tumefaciens Harbors an attM-Paralogous Gene, aiiB, Also Encoding N-Acyl Homoserine Lactonase Activity. Applied and Environmental Microbiology, 2003, 69, 4989-4993.	1.4	189