

Alexander J Probst

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

14,944
citations

94269

37
h-index

56606

83
g-index

108
all docs

108
docs citations

108
times ranked

19134
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic diversity in terrestrial subsurface ecosystems impacted by geological degassing. <i>Nature Communications</i> , 2022, 13, 284.	5.8	11
2	Label-Free Raman Microspectroscopy for Identifying Prokaryotic Virocells. <i>MSystems</i> , 2022, 7, e0150521.	1.7	3
3	Erratum for Monsees et al., "Label-Free Raman Microspectroscopy for Identifying Prokaryotic Virocells" <i>MSystems</i> , 2022, , e0016222.	1.7	0
4	AgI24 is an ancient archaeal homolog of the eukaryotic N-glycan chitobiose synthesis enzymes. <i>ELife</i> , 2022, 11, .	2.8	2
5	Host-Associated Phages Disperse across the Extraterrestrial Analogue Antarctica. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0031522.	1.4	7
6	Plume Layer Influences the Amazon Reef Sponge Microbiome Primary Producers. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	3
7	Carbon fixation rates in groundwater similar to those in oligotrophic marine systems. <i>Nature Geoscience</i> , 2022, 15, 561-567.	5.4	28
8	Ammonium Removal in Aquaponics Indicates Participation of Comammox Nitrospira. <i>Current Microbiology</i> , 2021, 78, 894-903.	1.0	12
9	Microbial Hotspots in Lithic Microhabitats Inferred from DNA Fractionation and Metagenomics in the Atacama Desert. <i>Microorganisms</i> , 2021, 9, 1038.	1.6	19
10	Diverse Viruses Carrying Genes for Microbial Extremotolerance in the Atacama Desert Hyperarid Soil. <i>MSystems</i> , 2021, 6, .	1.7	27
11	Lytic archaeal viruses infect abundant primary producers in Earth's crust. <i>Nature Communications</i> , 2021, 12, 4642.	5.8	28
12	Virus-associated organosulfur metabolism in human and environmental systems. <i>Cell Reports</i> , 2021, 36, 109471.	2.9	38
13	Effects of a long-term anoxic warming scenario on microbial community structure and functional potential of permafrost-affected soil. <i>Permafrost and Periglacial Processes</i> , 2021, 32, 641-656.	1.5	11
14	Stable-Isotope-Informed, Genome-Resolved Metagenomics Uncovers Potential Cross-Kingdom Interactions in Rhizosphere Soil. <i>MSphere</i> , 2021, 6, e0008521.	1.3	34
15	Potential of <i>Variovorax paradoxus</i> isolate BFB1_13 for bioremediation of BTEX contaminated sites. <i>AMB Express</i> , 2021, 11, 126.	1.4	15
16	Imaging Techniques for Detecting Prokaryotic Viruses in Environmental Samples. <i>Viruses</i> , 2021, 13, 2126.	1.5	10
17	Leave no stone unturned: individually adapted xerotolerant Thaumarchaeota sheltered below the boulders of the Atacama Desert hyperarid core. <i>Microbiome</i> , 2021, 9, 234.	4.9	18
18	The economical lifestyle of CPR bacteria in groundwater allows little preference for environmental drivers. <i>Environmental Microbiomes</i> , 2021, 16, 24.	2.2	36

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19	Microaerobic conditions caused the overwhelming dominance of <i>Acinetobacter</i> spp. and the marginalization of <i>Rhodococcus</i> spp. in diesel fuel/crude oil mixture-amended enrichment cultures. <i>Archives of Microbiology</i> , 2020, 202, 329-342.	1.0	33
20	Groundwater cable bacteria conserve energy by sulfur disproportionation. <i>ISME Journal</i> , 2020, 14, 623-634.	4.4	64
21	Genome-inferred spatio-temporal resolution of an uncultivated <i>Roizmanbacterium</i> reveals its ecological preferences in groundwater. <i>Environmental Microbiology</i> , 2020, 22, 726-737.	1.8	31
22	Overlooked Diversity of Ultramicrobacterial Minorities at the Air-Sea Interface. <i>Atmosphere</i> , 2020, 11, 1214.	1.0	9
23	Saccharibacteria as Organic Carbon Sinks in Hydrocarbon-Fueled Communities. <i>Frontiers in Microbiology</i> , 2020, 11, 587782.	1.5	22
24	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	5.9	115
25	Lipid analysis of CO ₂ -rich subsurface aquifers suggests an autotrophy-based deep biosphere with lysolipids enriched in CPR bacteria. <i>ISME Journal</i> , 2020, 14, 1547-1560.	4.4	29
26	Clades of huge phages from across Earth's ecosystems. <i>Nature</i> , 2020, 578, 425-431.	13.7	331
27	Are we There Yet? Understanding Interplanetary Microbial Hitchhikers using Molecular Methods. <i>Current Issues in Molecular Biology</i> , 2020, 38, 33-52.	1.0	6
28	An archaeal symbiont-host association from the deep terrestrial subsurface. <i>ISME Journal</i> , 2019, 13, 2135-2139.	4.4	39
29	Impacts of microbial assemblage and environmental conditions on the distribution of anatoxin-a producing cyanobacteria within a river network. <i>ISME Journal</i> , 2019, 13, 1618-1634.	4.4	60
30	Transitory microbial habitat in the hyperarid Atacama Desert. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2670-2675.	3.3	172
31	Genome-reconstruction for eukaryotes from complex natural microbial communities. <i>Genome Research</i> , 2018, 28, 569-580.	2.4	163
32	Assessment of UV-C-induced water disinfection by differential PCR-based quantification of bacterial DNA damage. <i>Journal of Microbiological Methods</i> , 2018, 149, 89-95.	0.7	13
33	Anaerobic degradation of 1-methylnaphthalene by a member of the <i>Thermoanaerobacteraceae</i> contained in an iron-reducing enrichment culture. <i>Biodegradation</i> , 2018, 29, 23-39.	1.5	35
34	Differential depth distribution of microbial function and putative symbionts through sediment-hosted aquifers in the deep terrestrial subsurface. <i>Nature Microbiology</i> , 2018, 3, 328-336.	5.9	227
35	Homologous Recombination and Transposon Propagation Shape the Population Structure of an Organism from the Deep Subsurface with Minimal Metabolism. <i>Genome Biology and Evolution</i> , 2018, 10, 1115-1119.	1.1	24
36	Biosynthetic capacity, metabolic variety and unusual biology in the CPR and DPANN radiations. <i>Nature Reviews Microbiology</i> , 2018, 16, 629-645.	13.6	314

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37	Recovery of genomes from metagenomes via a dereplication, aggregation and scoring strategy. <i>Nature Microbiology</i> , 2018, 3, 836-843.	5.9	906
38	Insights into the ecology, evolution, and metabolism of the widespread Woese archaeal lineages. <i>Microbiome</i> , 2018, 6, 102.	4.9	181
39	Stable isotope informed genome-resolved metagenomics reveals that Saccharibacteria utilize microbially-processed plant-derived carbon. <i>Microbiome</i> , 2018, 6, 122.	4.9	156
40	Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO ₂ concentrations. <i>Environmental Microbiology</i> , 2017, 19, 459-474.	1.8	212
41	Potential for microbial H ₂ and metal transformations associated with novel bacteria and archaea in deep terrestrial subsurface sediments. <i>ISME Journal</i> , 2017, 11, 1915-1929.	4.4	137
42	New CRISPR-Cas systems from uncultivated microbes. <i>Nature</i> , 2017, 542, 237-241.	13.7	471
43	Reply to Delmont and Eren: Strain variants and population structure during the Deepwater Horizon oil spill. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8950-E8952.	3.3	0
44	Simulation of Deepwater Horizon oil plume reveals substrate specialization within a complex community of hydrocarbon degraders. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7432-7437.	3.3	120
45	Human age and skin physiology shape diversity and abundance of Archaea on skin. <i>Scientific Reports</i> , 2017, 7, 4039.	1.6	78
46	Microbial Community Structure and the Persistence of Cyanobacterial Populations in Salt Crusts of the Hyperarid Atacama Desert from Genome-Resolved Metagenomics. <i>Frontiers in Microbiology</i> , 2017, 8, 1435.	1.5	73
47	Urban Dust Microbiome: Impact on Later Atopy and Wheezing. <i>Environmental Health Perspectives</i> , 2016, 124, 1919-1923.	2.8	41
48	Culture Independent Genomic Comparisons Reveal Environmental Adaptations for Altiarchaeales. <i>Frontiers in Microbiology</i> , 2016, 7, 1221.	1.5	25
49	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016, 7, 13219.	5.8	994
50	A new view of the tree of life. <i>Nature Microbiology</i> , 2016, 1, 16048.	5.9	1,823
51	Microbial succession in an inflated lunar/Mars analog habitat during a 30-day human occupation. <i>Microbiome</i> , 2016, 4, 22.	4.9	31
52	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. <i>Nature Communications</i> , 2016, 7, 10613.	5.8	224
53	Fungal and Bacterial Communities in Indoor Dust Follow Different Environmental Determinants. <i>PLoS ONE</i> , 2016, 11, e0154131.	1.1	86
54	Analysis of five complete genome sequences for members of the class Peribacteria in the recently recognized Peregrinibacteria bacterial phylum. <i>PeerJ</i> , 2016, 4, e1607.	0.9	57

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55	Proteogenomic analyses indicate bacterial methylotrophy and archaeal heterotrophy are prevalent below the grass root zone. <i>PeerJ</i> , 2016, 4, e2687.	0.9	124
56	Microbiomes of the dust particles collected from the International Space Station and Spacecraft Assembly Facilities. <i>Microbiome</i> , 2015, 3, 50.	4.9	175
57	A viability-linked metagenomic analysis of cleanroom environments: eukarya, prokaryotes, and viruses. <i>Microbiome</i> , 2015, 3, 62.	4.9	56
58	Altarchaeales: Uncultivated Archaea from the Subsurface. <i>Life</i> , 2015, 5, 1381-1395.	1.1	40
59	S-layers at second glance? Altarchaeal grappling hooks (hami) resemble archaeal S-layer proteins in structure and sequence. <i>Frontiers in Microbiology</i> , 2015, 6, 543.	1.5	31
60	Cleanroom Maintenance Significantly Reduces Abundance but Not Diversity of Indoor Microbiomes. <i>PLoS ONE</i> , 2015, 10, e0134848.	1.1	56
61	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. <i>ISME Journal</i> , 2015, 9, 2697-2711.	4.4	35
62	Quo vadis? Microbial profiling revealed strong effects of cleanroom maintenance and routes of contamination in indoor environments. <i>Scientific Reports</i> , 2015, 5, 9156.	1.6	52
63	An <i>in vitro</i> culture model to study the dynamics of colonic microbiota in Syrian golden hamsters and their susceptibility to infection with <i>Clostridium difficile</i> . <i>ISME Journal</i> , 2015, 9, 321-332.	4.4	17
64	New Perspectives on Microbial Community Distortion after Whole-Genome Amplification. <i>PLoS ONE</i> , 2015, 10, e0124158.	1.1	35
65	Coupling Genetic and Chemical Microbiome Profiling Reveals Heterogeneity of Archaeome and Bacteriome in Subsurface Biofilms That Are Dominated by the Same Archaeal Species. <i>PLoS ONE</i> , 2014, 9, e99801.	1.1	28
66	Grappling archaea: ultrastructural analyses of an uncultivated, cold-loving archaeon, and its biofilm. <i>Frontiers in Microbiology</i> , 2014, 5, 397.	1.5	26
67	Biology of a widespread uncultivated archaeon that contributes to carbon fixation in the subsurface. <i>Nature Communications</i> , 2014, 5, 5497.	5.8	119
68	Microbial Community Structures of Novel Icelandic Hot Spring Systems Revealed by PhyloChip G3 Analysis. <i>Astrobiology</i> , 2014, 14, 229-240.	1.5	16
69	Quantification of Encapsulated Bioburden in Spacecraft Polymer Materials by Cultivation-Dependent and Molecular Methods. <i>PLoS ONE</i> , 2014, 9, e94265.	1.1	4
70	New perspectives on viable microbial communities in low-biomass cleanroom environments. <i>ISME Journal</i> , 2013, 7, 312-324.	4.4	126
71	Lessons Learned from the Microbial Analysis of the Herschel Spacecraft during Assembly, Integration, and Test Operations. <i>Astrobiology</i> , 2013, 13, 1125-1139.	1.5	25
72	Tackling the minority: sulfate-reducing bacteria in an archaea-dominated subsurface biofilm. <i>ISME Journal</i> , 2013, 7, 635-651.	4.4	57

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73	Archaea on Human Skin. PLoS ONE, 2013, 8, e65388.	1.1	166
74	Positive, Neutral and Negative Interactions in Cocultures between <i>Pyrococcus furiosus</i> and Different Methanogenic Archaea. Microbiology Insights, 2012, 5, MBI.S8516.	0.9	11
75	Detecting inactivated endospores in fluorescence microscopy using propidium monoazide. International Journal of Astrobiology, 2012, 11, 117-123.	0.9	15
76	An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. ISME Journal, 2012, 6, 610-618.	4.4	4,581
77	Comparison of Innovative Molecular Approaches and Standard Spore Assays for Assessment of Surface Cleanliness. Applied and Environmental Microbiology, 2011, 77, 5438-5444.	1.4	27
78	Recovery of Bacillus Spore Contaminants from Rough Surfaces: a Challenge to Space Mission Cleanliness Control. Applied and Environmental Microbiology, 2011, 77, 1628-1637.	1.4	33
79	The Mode of Cell Wall Growth in Selected Archaea Is Similar to the General Mode of Cell Wall Growth in Bacteria as Revealed by Fluorescent Dye Analysis. Applied and Environmental Microbiology, 2011, 77, 1556-1562.	1.4	39
80	Validation of a Nylon-Flocked-Swab Protocol for Efficient Recovery of Bacterial Spores from Smooth and Rough Surfaces. Applied and Environmental Microbiology, 2010, 76, 5148-5158.	1.4	76
81	Diversity of Anaerobic Microbes in Spacecraft Assembly Clean Rooms. Applied and Environmental Microbiology, 2010, 76, 2837-2845.	1.4	50
82	Bacillus horneckiae sp. nov., isolated from a spacecraft-assembly clean room. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 1031-1037.	0.8	81
83	Deep-Sea Oil Plume Enriches Indigenous Oil-Degrading Bacteria. Science, 2010, 330, 204-208.	6.0	1,109