

Alison Buchan

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

5,288
citations

257101

24
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182168

51
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61
all docs

61
docs citations

61
times ranked

5777
citing authors

#	ARTICLE	IF	CITATIONS
1	Plasmid-Mediated Stabilization of Prophages. <i>MSphere</i> , 2022, 7, e0093021.	1.3	2
2	Towards a mechanistic understanding of microalgae–bacteria interactions: integration of metabolomic analysis and computational models. <i>FEMS Microbiology Reviews</i> , 2022, 46, .	3.9	5
3	Microbiomes and Planctomycete diversity in large-scale aquaria habitats. <i>PLoS ONE</i> , 2022, 17, e0267881.	1.1	4
4	Breaking Barriers with Bread: Using the Sourdough Starter Microbiome to Teach High-Throughput Sequencing Techniques. <i>Journal of Microbiology and Biology Education</i> , 2022, 23, .	0.5	2
5	Revisiting the rules of life for viruses of microorganisms. <i>Nature Reviews Microbiology</i> , 2021, 19, 501-513.	13.6	77
6	Ecology of inorganic sulfur auxiliary metabolism in widespread bacteriophages. <i>Nature Communications</i> , 2021, 12, 3503.	5.8	97
7	Cyclic di-GMP Is Integrated Into a Hierarchical Quorum Sensing Network Regulating Antimicrobial Production and Biofilm Formation in Roseobacter Clade Member Rhodobacterales Strain Y4I. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	3
8	Lysogeny in the oceans: Lessons from cultivated model systems and a reanalysis of its prevalence. <i>Environmental Microbiology</i> , 2020, 22, 4919-4933.	1.8	25
9	Genetically similar temperate phages form coalitions with their shared host that lead to niche-specific fitness effects. <i>ISME Journal</i> , 2020, 14, 1688-1700.	4.4	18
10	Aerobic Hydrocarbon-Degrading Alphaproteobacteria: Rhodobacteraceae (Roseobacter)., 2019, , 1-13.		4
11	Characterization of the Interactive Effects of Labile and Recalcitrant Organic Matter on Microbial Growth and Metabolism. <i>Frontiers in Microbiology</i> , 2019, 10, 493.	1.5	11
12	Aerobic Hydrocarbon-Degrading Alphaproteobacteria: Rhodobacteraceae (Roseobacter)., 2019, , 93-104.		7
13	Functional Redundancy in the Hydroxycinnamate Catabolism Pathways of the Salt Marsh Bacterium <i>Sagittula stellata</i> E-37. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	7
14	Evidence for the Priming Effect in a Planktonic Estuarine Microbial Community. <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	31
15	Deciphering ocean carbon in a changing world. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3143-3151.	3.3	253
16	Re-examination of the relationship between marine virus and microbial cell abundances. <i>Nature Microbiology</i> , 2016, 1, 15024.	5.9	264
17	<i>Phaeobacter</i> sp. Strain Y4I Utilizes Two Separate Cell-to-Cell Communication Systems To Regulate Production of the Antimicrobial Indigoidine. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1417-1425.	1.4	19
18	A multitrophic model to quantify the effects of marine viruses on microbial food webs and ecosystem processes. <i>ISME Journal</i> , 2015, 9, 1352-1364.	4.4	223

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19	Big data - a 21st century science Maginot Line? No-boundary thinking: shifting from the big data paradigm. <i>BioData Mining</i> , 2015, 8, 7.	2.2	6
20	Novel N4 Bacteriophages Prevail in the Cold Biosphere. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5196-5202.	1.4	19
21	Phage infection of an environmentally relevant marine bacterium alters host metabolism and lysate composition. <i>ISME Journal</i> , 2014, 8, 1089-1100.	4.4	127
22	Genome Sequence of the Sulfitobacter sp. Strain 2047-Infecting Lytic Phage Î CB2047-B. <i>Genome Announcements</i> , 2014, 2, .	0.8	13
23	Draft Genome Sequence of <i>Sulfitobacter</i> sp. CB2047, a Member of the <i>Roseobacter</i> Clade of Marine Bacteria, Isolated from an <i>Emiliana huxleyi</i> Bloom. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
24	The elemental composition of virus particles: implications for marine biogeochemical cycles. <i>Nature Reviews Microbiology</i> , 2014, 12, 519-528.	13.6	273
25	Master recyclers: features and functions of bacteria associated with phytoplankton blooms. <i>Nature Reviews Microbiology</i> , 2014, 12, 686-698.	13.6	947
26	Genome Sequences of Two Temperate Phages, Î CB2047-A and Î CB2047-C, Infecting <i>Sulfitobacter</i> sp. Strain 2047. <i>Genome Announcements</i> , 2014, 2, .	0.8	16
27	No-boundary thinking in bioinformatics research. <i>BioData Mining</i> , 2013, 6, 19.	2.2	10
28	Simultaneous Catabolism of Plant-Derived Aromatic Compounds Results in Enhanced Growth for Members of the Roseobacter Lineage. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3716-3723.	1.4	24
29	Acyl-homoserine lactone-based quorum sensing in the Roseobacter clade: complex cell-to-cell communication controls multiple physiologies. <i>Frontiers in Microbiology</i> , 2013, 4, 336.	1.5	67
30	Production of the Antimicrobial Secondary Metabolite Indigoidine Contributes to Competitive Surface Colonization by the Marine Roseobacter Phaeobacter sp. Strain Y4l. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4771-4780.	1.4	114
31	De-MetaST-BLAST: A Tool for the Validation of Degenerate Primer Sets and Data Mining of Publicly Available Metagenomes. <i>PLoS ONE</i> , 2012, 7, e50362.	1.1	11
32	Marivita roseacus sp. nov., of the family Rhodobacteraceae, isolated from a temperate estuary and an emended description of the genus Marivita. <i>Journal of General and Applied Microbiology</i> , 2011, 57, 259-267.	0.4	15
33	<i>In situ</i> activity of NAC11â€7 roseobacters in coastal waters off the Chesapeake Bay based on <i>ftsZ</i> expression. <i>Environmental Microbiology</i> , 2011, 13, 1032-1041.	1.8	7
34	A protocol for enumeration of aquatic viruses by epifluorescence microscopy using Anodiscâ„¢ 13 membranes. <i>BMC Microbiology</i> , 2011, 11, 168.	1.3	14
35	T-RFPred: a nucleotide sequence size prediction tool for microbial community description based on terminal-restriction fragment length polymorphism chromatograms. <i>BMC Microbiology</i> , 2010, 10, 262.	1.3	8
36	Temporal dynamics and genetic diversity of chemotacticâ€competent microbial populations in the rhizosphere. <i>Environmental Microbiology</i> , 2010, 12, 3171-3184.	1.8	33

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37	Estimating Virus Production Rates in Aquatic Systems. <i>Journal of Visualized Experiments</i> , 2010, , .	0.2	2
38	Development and Application of Quantitative-PCR Tools for Subgroups of the <i>Roseobacter</i> Clade. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7542-7547.	1.4	16
39	Surface Colonization by Marine Roseobacters: Integrating Genotype and Phenotype. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6027-6037.	1.4	145
40	Gene transfer agent (GTA) genes reveal diverse and dynamic <i>Roseobacter</i> and <i>Rhodobacter</i> populations in the Chesapeake Bay. <i>ISME Journal</i> , 2009, 3, 364-373.	4.4	37
41	Comparison of chitinolytic enzymes from an alkaline, hypersaline lake and an estuary. <i>Environmental Microbiology</i> , 2007, 9, 197-205.	1.8	52
42	Bacterial Taxa That Limit Sulfur Flux from the Ocean. <i>Science</i> , 2006, 314, 649-652.	6.0	296
43	When Coupled to Natural Transformation in <i>Acinetobacter</i> sp. Strain ADP1, PCR Mutagenesis Is Made Less Random by Mismatch Repair. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7610-7612.	1.4	6
44	Overview of the Marine Roseobacter Lineage. <i>Applied and Environmental Microbiology</i> , 2005, 71, 5665-5677.	1.4	753
45	Analysis of Microbial Gene Transcripts in Environmental Samples. <i>Applied and Environmental Microbiology</i> , 2005, 71, 4121-4126.	1.4	211
46	Chitinase Gene Sequences Retrieved from Diverse Aquatic Habitats Reveal Environment-Specific Distributions. <i>Applied and Environmental Microbiology</i> , 2004, 70, 6977-6983.	1.4	86
47	Genome sequence of <i>Silicibacter pomeroyi</i> reveals adaptations to the marine environment. <i>Nature</i> , 2004, 432, 910-913.	13.7	415
48	<i>Silicibacter pomeroyi</i> sp. nov. and <i>Roseovarius nubinhibens</i> sp. nov., dimethylsulfoniopropionate-demethylating bacteria from marine environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 1261-1269.	0.8	231
49	Strain-specific differentiation of environmental <i>Escherichia coli</i> isolates via denaturing gradient gel electrophoresis (DGGE) analysis of the 16S-23S intergenic spacer region. <i>FEMS Microbiology Ecology</i> , 2001, 35, 313-321.	1.3	37
50	Diversity of the Ring-Cleaving Dioxygenase Gene <i>pcaH</i> in a Salt Marsh Bacterial Community. <i>Applied and Environmental Microbiology</i> , 2001, 67, 5801-5809.	1.4	58
51	Key Aromatic-Ring-Cleaving Enzyme, Protocatechuate 3,4-Dioxygenase, in the Ecologically Important Marine Roseobacter Lineage. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4662-4672.	1.4	132