

Jocelyne DiRuggiero

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

4,785
citations

109264

35
h-index

143943

57
g-index

81
all docs

81
docs citations

81
times ranked

4879
citing authors

#	ARTICLE	IF	CITATIONS
1	Adaptation of Cyanobacteria to the Endolithic Light Spectrum in Hyper-Arid Deserts. <i>Microorganisms</i> , 2022, 10, 1198.	1.6	5
2	Rock structure drives the taxonomic and functional diversity of endolithic microbial communities in extreme environments. <i>Environmental Microbiology</i> , 2021, 23, 3937-3956.	1.8	21
3	Cellular life from the three domains and viruses are transcriptionally active in a hypersaline desert community. <i>Environmental Microbiology</i> , 2021, 23, 3401-3417.	1.8	20
4	The Atacama Desert: a window into late Mars surface habitability?. , 2021, , 333-355.		2
5	Post-transcriptional regulation of redox homeostasis by the small RNA SHOxi in haloarchaea. <i>RNA Biology</i> , 2021, 18, 1867-1881.	1.5	7
6	The composition of endolithic communities in gypcrete is determined by the specific microhabitat architecture. <i>Biogeosciences</i> , 2021, 18, 993-1007.	1.3	8
7	Draft Metagenomes of Endolithic Cyanobacteria and Cohabitants from Hyper-Arid Deserts. <i>Microbiology Resource Announcements</i> , 2021, 10, e0020621.	0.3	7
8	Environmental Factors Driving Spatial Heterogeneity in Desert Halophile Microbial Communities. <i>Frontiers in Microbiology</i> , 2020, 11, 578669.	1.5	12
9	Reply to Wierzchos et al.: Microorganism-induced gypsum to anhydrite phase transformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27788-27790.	3.3	0
10	Mechanism of water extraction from gypsum rock by desert colonizing microorganisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10681-10687.	3.3	48
11	Regulatory Noncoding Small RNAs Are Diverse and Abundant in an Extremophilic Microbial Community. <i>MSystems</i> , 2020, 5, .	1.7	14
12	SnapShot: Microbial Extremophiles. <i>Cell</i> , 2020, 180, 818-818.e1.	13.5	26
13	Preandean Atacama Desert Endolithic Microbiology. , 2020, , 51-71.		3
14	Ribosome profiling in archaea reveals leaderless translation, novel translational initiation sites, and ribosome pausing at single codon resolution. <i>Nucleic Acids Research</i> , 2020, 48, 5201-5216.	6.5	57
15	Halophilic microbial community compositional shift after a rare rainfall in the Atacama Desert. <i>ISME Journal</i> , 2019, 13, 2737-2749.	4.4	62
16	Endolithic microbial communities as model systems for ecology and astrobiology. , 2019, , 145-168.		17
17	Applying Genome-Resolved Metagenomics to Deconvolute the Halophilic Microbiome. <i>Genes</i> , 2019, 10, 220.	1.0	32
18	Current State of and Future Opportunities for Prediction in Microbiome Research: Report from the Mid-Atlantic Microbiome Meet-up in Baltimore on 9 January 2019. <i>MSystems</i> , 2019, 4, .	1.7	6

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19	Trophic Selective Pressures Organize the Composition of Endolithic Microbial Communities From Global Deserts. <i>Frontiers in Microbiology</i> , 2019, 10, 2952.	1.5	26
20	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
21	Transcriptional Landscape and Regulatory Roles of Small Noncoding RNAs in the Oxidative Stress Response of the Haloarchaeon <i>Haloferax volcanii</i> . <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	48
22	Fundamental drivers for endolithic microbial community assemblies in the hyperarid Atacama Desert. <i>Environmental Microbiology</i> , 2018, 20, 1765-1781.	1.8	82
23	MetaWRAP—a flexible pipeline for genome-resolved metagenomic data analysis. <i>Microbiome</i> , 2018, 6, 158.	4.9	1,098
24	The Non-Coding Regulatory RNA Revolution in Archaea. <i>Genes</i> , 2018, 9, 141.	1.0	41
25	Comparative activity and functional ecology of permafrost soils and lithic niches in a hyperarid polar desert. <i>Environmental Microbiology</i> , 2017, 19, 443-458.	1.8	77
26	Across the tree of life, radiation resistance is governed by antioxidant Mn ²⁺ , gauged by paramagnetic resonance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9253-E9260.	3.3	94
27	Phylogenetic and Functional Substrate Specificity for Endolithic Microbial Communities in Hyper-Arid Environments. <i>Frontiers in Microbiology</i> , 2016, 7, 301.	1.5	60
28	Functional interactions of archaea, bacteria and viruses in a hypersaline endolithic community. <i>Environmental Microbiology</i> , 2016, 18, 2064-2077.	1.8	107
29	Adaptation strategies of endolithic chlorophototrophs to survive the hyperarid and extreme solar radiation environment of the Atacama Desert. <i>Frontiers in Microbiology</i> , 2015, 6, 934.	1.5	108
30	In situ metabolism in halite endolithic microbial communities of the hyperarid Atacama Desert. <i>Frontiers in Microbiology</i> , 2015, 6, 1035.	1.5	50
31	Microbial diversity and the presence of algae in halite endolithic communities are correlated to atmospheric moisture in the hyperarid zone of the Atacama Desert. <i>Environmental Microbiology</i> , 2015, 17, 299-315.	1.8	108
32	Effects of intracellular Mn on the radiation resistance of the halophilic archaeon <i>Halobacterium salinarum</i> . <i>Extremophiles</i> , 2013, 17, 485-497.	0.9	42
33	Radiation Resistance in Extremophiles: Fending Off Multiple Attacks. <i>Cellular Origin and Life in Extreme Habitats</i> , 2013, , 249-267.	0.3	5
34	Colonization patterns of soil microbial communities in the Atacama Desert. <i>Microbiome</i> , 2013, 1, 28.	4.9	215
35	Erratum to “Role of Mn ²⁺ and Compatible Solutes in the Radiation Resistance of Thermophilic Bacteria and Archaea”. <i>Archaea</i> , 2013, 2013, 1-1.	2.3	7
36	DNA Replication and Repair in Halophiles. , 2012, , 163-198.		8

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37	Role of Mn ²⁺ and Compatible Solutes in the Radiation Resistance of Thermophilic Bacteria and Archaea. <i>Archaea</i> , 2012, 2012, 1-11.	2.3	63
38	A Major Role for Nonenzymatic Antioxidant Processes in the Radioresistance of <i>Halobacterium salinarum</i> . <i>Journal of Bacteriology</i> , 2011, 193, 1653-1662.	1.0	59
39	Coordination of frontline defense mechanisms under severe oxidative stress. <i>Molecular Systems Biology</i> , 2010, 6, 393.	3.2	55
40	MutS and MutL Are Dispensable for Maintenance of the Genomic Mutation Rate in the Halophilic Archaeon <i>Halobacterium salinarum</i> NRC-1. <i>PLoS ONE</i> , 2010, 5, e9045.	1.1	31
41	Salt shield: intracellular salts provide cellular protection against ionizing radiation in the halophilic archaeon, <i>Halobacterium salinarum</i> NRC-1. <i>Environmental Microbiology</i> , 2009, 11, 1066-1078.	1.8	58
42	Rad50 Is Not Essential for the Mre11-Dependent Repair of DNA Double-Strand Breaks in <i>Halobacterium</i> sp. Strain NRC-1. <i>Journal of Bacteriology</i> , 2008, 190, 5210-5216.	1.0	33
43	Extensive Genome Rearrangements and Multiple Horizontal Gene Transfers in a Population of <i>Pyrococcus</i> Isolates from Vulcano Island, Italy. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6447-6451.	1.4	33
44	A Predictive Model for Transcriptional Control of Physiology in a Free Living Cell. <i>Cell</i> , 2007, 131, 1354-1365.	13.5	284
45	Microarray analysis of the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> exposed to gamma irradiation. <i>Extremophiles</i> , 2007, 11, 19-29.	0.9	83
46	An integrated systems approach for understanding cellular responses to gamma radiation. <i>Molecular Systems Biology</i> , 2006, 2, 47.	3.2	78
47	Physiological responses of the halophilic archaeon <i>Halobacterium</i> sp. strain NRC1 to desiccation and gamma irradiation. <i>Extremophiles</i> , 2005, 9, 219-227.	0.9	174
48	Evidence for Genetic Drift in the Diversification of a Geographically Isolated Population of the Hyperthermophilic Archaeon <i>Pyrococcus</i> . <i>Molecular Biology and Evolution</i> , 2005, 22, 2297-2303.	3.5	42
49	A proposal to rename the hyperthermophile <i>Pyrococcus woesei</i> as <i>Pyrococcus furiosus</i> subsp. <i>woesei</i> . <i>Archaea</i> , 2004, 1, 277-283.	2.3	30
50	Systems Level Insights Into the Stress Response to UV Radiation in the Halophilic Archaeon <i>Halobacterium</i> NRC-1. <i>Genome Research</i> , 2004, 14, 1025-1035.	2.4	130
51	Characterization of Plasmid pRT1 from <i>Pyrococcus</i> sp. Strain JT1. <i>Journal of Bacteriology</i> , 2002, 184, 2561-2566.	1.0	30
52	Microbial survival of space vacuum and extreme ultraviolet irradiation: strain isolation and analysis during a rocket flight. <i>FEMS Microbiology Letters</i> , 2002, 215, 163-168.	0.7	72
53	Genomic sequence of hyperthermophile, <i>Pyrococcus furiosus</i> : Implications for physiology and enzymology. <i>Methods in Enzymology</i> , 2001, 330, 134-157.	0.4	201
54	Evidence of recent lateral gene transfer among hyperthermophilic Archaea. <i>Molecular Microbiology</i> , 2000, 38, 684-693.	1.2	107

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55	Both RadA and RadB Are Involved in Homologous Recombination in <i>Pyrococcus furiosus</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 33782-33790.	1.6	111
56	Cloning and Sequence Analysis of the Mercury Resistance Operon of <i>Streptomyces</i> sp. Strain CHR28 Reveals a Novel Putative Second Regulatory Gene. <i>Journal of Bacteriology</i> , 2000, 182, 2345-2349.	1.0	30
57	Molecular and Biochemical Analysis of Malk, the ATP-hydrolyzing Subunit of the Trehalose/Maltose Transport System of the Hyperthermophilic Archaeon <i>Thermococcus litoralis</i> . <i>Journal of Biological Chemistry</i> , 1999, 274, 20259-20264.	1.6	60
58	DNA Repair Systems in Archaea: Mementos from the Last Universal Common Ancestor?. <i>Journal of Molecular Evolution</i> , 1999, 49, 474-484.	0.8	59
59	Divergence of the Hyperthermophilic Archaea <i>Pyrococcus furiosus</i> and <i>P. horikoshii</i> Inferred From Complete Genomic Sequences. <i>Genetics</i> , 1999, 152, 1299-1305.	1.2	115
60	Archaeal Binding Protein-Dependent ABC Transporter: Molecular and Biochemical Analysis of the Trehalose/Maltose Transport System of the Hyperthermophilic Archaeon <i>Thermococcus litoralis</i> . <i>Journal of Bacteriology</i> , 1998, 180, 680-689.	1.0	116
61	Enzymes of Central Nitrogen Metabolism from Hyperthermophiles: Characterization, Thermostability, and Genetics. <i>Advances in Protein Chemistry</i> , 1996, 48, 311-339.	4.4	10