

Sergio E Morales

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

3,078
citations

236925

25
h-index

182427

51
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79
all docs

79
docs citations

79
times ranked

4663
citing authors

#	ARTICLE	IF	CITATIONS
1	High viral abundance and low diversity are associated with increased CRISPR-Cas prevalence across microbial ecosystems. <i>Current Biology</i> , 2022, 32, 220-227.e5.	3.9	23
2	Nitrite accumulation and impairment of N ₂ O reduction explains contrasting soil denitrification phenotypes. <i>Soil Biology and Biochemistry</i> , 2022, 166, 108529.	8.8	8
3	Phylogenetically and functionally diverse microorganisms reside under the Ross Ice Shelf. <i>Nature Communications</i> , 2022, 13, 117.	12.8	17
4	Global and seasonal variation of marine phosphonate metabolism. <i>ISME Journal</i> , 2022, 16, 2198-2212.	9.8	22
5	Ecological drivers switch from bottomâ€“up to topâ€“down during model microbial community successions. <i>ISME Journal</i> , 2021, 15, 1085-1097.	9.8	21
6	Resolving broad patterns of prokaryotic community structure in New Zealand pasture soils. <i>New Zealand Journal of Agricultural Research</i> , 2021, 64, 143-161.	1.6	2
7	Microbial rhodopsins are increasingly favoured over chlorophyll in High Nutrient Low Chlorophyll waters. <i>Environmental Microbiology Reports</i> , 2021, 13, 401-406.	2.4	11
8	Reduced seawater pH alters marine biofilms with impacts for marine polychaete larval settlement. <i>Marine Environmental Research</i> , 2021, 167, 105291.	2.5	7
9	Seasonal Prokaryotic Community Linkages Between Surface and Deep Ocean Water. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	10
10	Competition and community succession link N transformation and greenhouse gas emissions in urine patches. <i>Science of the Total Environment</i> , 2021, 779, 146318.	8.0	6
11	Changes in microbial community phylogeny and metabolic activity along the water column uncouple at near sediment aphotic layers in fjords. <i>Scientific Reports</i> , 2021, 11, 19303.	3.3	2
12	Urea treatment decouples intrinsic pH control over N ₂ O emissions in soils. <i>Soil Biology and Biochemistry</i> , 2021, 163, 108461.	8.8	5
13	Soil Nitrogen Treatment Alters Microbiome Networks Across Farm Niches. <i>Frontiers in Microbiology</i> , 2021, 12, 786156.	3.5	3
14	Reducing the arbitrary: fuzzy detection of microbial ecotones and ecosystems â€“ focus on the pelagic environment. <i>Environmental Microbiomes</i> , 2020, 15, 16.	5.0	4
15	Correction to: Reducing the arbitrary: fuzzy detection of microbial ecotones and ecosystems â€“ focus on the pelagic environment. <i>Environmental Microbiomes</i> , 2020, 15, .	5.0	0
16	Ocean acidification affects microbial community and invertebrate settlement on biofilms. <i>Scientific Reports</i> , 2020, 10, 3274.	3.3	25
17	Soil N ₂ O emission potential falls along a denitrification phenotype gradient linked to differences in microbiome, rainfall and carbon availability. <i>Soil Biology and Biochemistry</i> , 2020, 150, 108004.	8.8	23
18	Depth and location influence prokaryotic and eukaryotic microbial community structure in New Zealand fjords. <i>Science of the Total Environment</i> , 2019, 693, 133507.	8.0	13

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19	Diverse hydrogen production and consumption pathways influence methane production in ruminants. ISME Journal, 2019, 13, 2617-2632.	9.8	132
20	Impact of nitrogen compounds on fungal and bacterial contributions to codenitrification in a pasture soil. Scientific Reports, 2019, 9, 13371.	3.3	14
21	Global Structuring of Phylogenetic and Functional Diversity of Pelagic Fungi by Depth and Temperature. Frontiers in Marine Science, 2019, 6, .	2.5	39
22	Occurrence and expression of genes encoding methyl-compound production in rumen bacteria. Animal Microbiome, 2019, 1, 15.	3.8	27
23	Identifying accurate metagenome and amplicon software via a meta-analysis of sequence to taxonomy benchmarking studies. PeerJ, 2019, 7, e6160.	2.0	34
24	Are oceanic fronts ecotones? Seasonal changes along the subtropical front show fronts as bacterioplankton transition zones but not diversity hotspots. Environmental Microbiology Reports, 2018, 10, 184-189.	2.4	18
25	Shifts in prokaryotic communities under forest and grassland within a tropical mosaic landscape. Applied Soil Ecology, 2018, 125, 156-161.	4.3	2
26	Fungal and bacterial contributions to codenitrification emissions of N ₂ O and N ₂ following urea deposition to soil. Nutrient Cycling in Agroecosystems, 2018, 110, 135-149.	2.2	34
27	Specific Effect of Trace Metals on Marine Heterotrophic Microbial Activity and Diversity: Key Role of Iron and Zinc and Hydrocarbon-Degrading Bacteria. Frontiers in Microbiology, 2018, 9, 3190.	3.5	15
28	Towards robust and repeatable sampling methods in <sc>eDNA</sc>-based studies. Molecular Ecology Resources, 2018, 18, 940-952.	4.8	137
29	Conditionally Rare Taxa Contribute but Do Not Account for Changes in Soil Prokaryotic Community Structure. Frontiers in Microbiology, 2018, 9, 809.	3.5	12
30	Novel Autotrophic Organisms Contribute Significantly to the Internal Carbon Cycling Potential of a Boreal Lake. MBio, 2018, 9, .	4.1	18
31	Methods for the extraction, storage, amplification and sequencing of DNA from environmental samples. , 2018, , .		58
32	Influence of soil moisture on codenitrification fluxes from a urea-affected pasture soil. Scientific Reports, 2017, 7, 2185.	3.3	44
33	Response to nitrogen addition reveals metabolic and ecological strategies of soil bacteria. Molecular Ecology, 2017, 26, 5500-5514.	3.9	26
34	Soil classification predicts differences in prokaryotic communities across a range of geographically distant soils once pH is accounted for. Scientific Reports, 2017, 7, 45369.	3.3	19
35	The methanogenic redox cofactor F420 is widely synthesized by aerobic soil bacteria. ISME Journal, 2017, 11, 125-137.	9.8	66
36	Physical Factors Correlate to Microbial Community Structure and Nitrogen Cycling Gene Abundance in a Nitrate Fed Eutrophic Lagoon. Frontiers in Microbiology, 2016, 7, 1691.	3.5	17

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37	Phylogenetic and functional potential links pH and N ₂ O emissions in pasture soils. <i>Scientific Reports</i> , 2016, 6, 35990.	3.3	67
38	Oceanic fronts: transition zones for bacterioplankton community composition. <i>Environmental Microbiology Reports</i> , 2016, 8, 132-138.	2.4	65
39	H ₂ metabolism is widespread and diverse among human colonic microbes. <i>Gut Microbes</i> , 2016, 7, 235-245.	9.8	105
40	CRISPRDetect: A flexible algorithm to define CRISPR arrays. <i>BMC Genomics</i> , 2016, 17, 356.	2.8	277
41	Genomic and metagenomic surveys of hydrogenase distribution indicate H ₂ is a widely utilised energy source for microbial growth and survival. <i>ISME Journal</i> , 2016, 10, 761-777.	9.8	503
42	High-Resolution Denitrification Kinetics in Pasture Soils Link N ₂ O Emissions to pH, and Denitrification to C Mineralization. <i>PLoS ONE</i> , 2016, 11, e0151713.	2.5	62
43	Biogeography and biophysicochemical traits link N ₂ O emissions, N ₂ O emission potential and microbial communities across New Zealand pasture soils. <i>Soil Biology and Biochemistry</i> , 2015, 82, 87-98.	8.8	34
44	Atmospheric Hydrogen Scavenging: from Enzymes to Ecosystems. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1190-1199.	3.1	81
45	Bacterioplankton carbon cycling along the Subtropical Frontal Zone off New Zealand. <i>Progress in Oceanography</i> , 2015, 135, 168-175.	3.2	40
46	Impact of urine and the application of the nitrification inhibitor DCD on microbial communities in dairy-grazed pasture soils. <i>Soil Biology and Biochemistry</i> , 2015, 88, 344-353.	8.8	26
47	Persistence of the dominant soil phylum <i>Acidobacteria</i> by trace gas scavenging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10497-10502.	7.1	117
48	Simulated geologic carbon storage leak reduces bacterial richness and alters bacterial community composition in surface soil. <i>Soil Biology and Biochemistry</i> , 2014, 76, 286-296.	8.8	11
49	Functional Response of a Near-Surface Soil Microbial Community to a Simulated Underground CO ₂ Storage Leak. <i>PLoS ONE</i> , 2013, 8, e81742.	2.5	38
50	Linking bacterial identities and ecosystem processes: can ¹³ C analyses be more than the sum of their parts?. <i>FEMS Microbiology Ecology</i> , 2011, 75, 2-16.	2.7	102
51	Use of Microcalorimetry To Determine the Costs and Benefits to <i>Pseudomonas putida</i> Strain KT2440 of Harboring Cadmium Efflux Genes. <i>Applied and Environmental Microbiology</i> , 2011, 77, 108-113.	3.1	24
52	Bacterial gene abundances as indicators of greenhouse gas emission in soils. <i>ISME Journal</i> , 2010, 4, 799-808.	9.8	265
53	Enhanced detection of groundwater contamination from a leaking waste disposal site by microbial community profiles. <i>Water Resources Research</i> , 2010, 46, .	4.2	21
54	Empirical Testing of 16S rRNA Gene PCR Primer Pairs Reveals Variance in Target Specificity and Efficacy Not Suggested by In Silico Analysis. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2677-2683.	3.1	81

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55	Extensive Phylogenetic Analysis of a Soil Bacterial Community Illustrates Extreme Taxon Evenness and the Effects of Amplicon Length, Degree of Coverage, and DNA Fractionation on Classification and Ecological Parameters. <i>Applied and Environmental Microbiology</i> , 2009, 75, 668-675.	3.1	56
56	Geographic variation in nutrient availability, stoichiometry, and metal concentrations of plants and pore-water in ombrotrophic bogs in New England, USA. <i>Wetlands</i> , 2008, 28, 827-840.	1.5	20
57	Supplemental programs for enhanced recovery of data from the DOTUR application. <i>Journal of Microbiological Methods</i> , 2008, 75, 572-575.	1.6	4
58	Comparison of Bacterial Communities in New England Sphagnum Bogs Using Terminal Restriction Fragment Length Polymorphism (T-RFLP). <i>Microbial Ecology</i> , 2006, 52, 34-44.	2.8	64
59	Transcriptional Regulation of the <i>pdt</i> Gene Cluster of <i>Pseudomonas stutzeri</i> KC Involves an AraC/XylS Family Transcriptional Activator (PdtC) and the Cognate Siderophore Pyridine-2,6-Bis(Thiocarboxylic) Tj ETQq1 1 0.384314 rgBT /Over	1.7	37
60	Analysis of cell-cycle specific localization of the Rdi1p RhoGDI and the structural determinants required for Cdc42p membrane localization and clustering at sites of polarized growth. <i>Current Genetics</i> , 2004, 45, 339-349.	1.7	37
61	Physiological and molecular genetic evaluation of the dechlorination agent, pyridine-2,6-bis(monothiocarboxylic acid) (PDTC) as a secondary siderophore of <i>Pseudomonas</i> . <i>Environmental Microbiology</i> , 2004, 6, 159-169.	3.8	37
62	Elevating soil pH does not reduce N ₂ O emissions from urine deposited onto pastoral soils. <i>New Zealand Journal of Agricultural Research</i> , 0, , 1-23.	1.6	2