Luis H Orellana

List of Publications by Year in descending order

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567144 677027 23 882 15 22 citations h-index g-index papers 25 25 25 1239 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Detecting Nitrous Oxide Reductase (<i>nosZ</i>) Genes in Soil Metagenomes: Method Development and Implications for the Nitrogen Cycle. MBio, 2014, 5, e01193-14.	1.8	142
2	Year-Round Shotgun Metagenomes Reveal Stable Microbial Communities in Agricultural Soils and Novel Ammonia Oxidizers Responding to Fertilization. Applied and Environmental Microbiology, 2018, 84, .	1.4	121
3	Transcriptional and Functional Studies of <i>Acidithiobacillus ferrooxidans</i> Genes Related to Survival in the Presence of Copper. Applied and Environmental Microbiology, 2009, 75, 6102-6109.	1.4	73
4	A genomic island provides Acidithiobacillus ferrooxidans ATCC 53993 additional copper resistance: a possible competitive advantage. Applied Microbiology and Biotechnology, 2011, 92, 761-767.	1.7	69
5	The low diverse gastric microbiome of the jellyfish <i>Cotylorhiza tuberculata</i> is dominated by four novel taxa. Environmental Microbiology, 2017, 19, 3039-3058.	1.8	62
6	<i>Verrucomicrobiota</i> are specialist consumers of sulfated methyl pentoses during diatom blooms. ISME Journal, 2022, 16, 630-641.	4.4	62
7	Detection and Diversity of Fungal Nitric Oxide Reductase Genes (<i>p450nor</i>) in Agricultural Soils. Applied and Environmental Microbiology, 2016, 82, 2919-2928.	1.4	55
8	Niche differentiation among annually recurrent coastal Marine Group II Euryarchaeota. ISME Journal, 2019, 13, 3024-3036.	4.4	41
9	ROCker: accurate detection and quantification of target genes in short-read metagenomic data sets by modeling sliding-window bitscores. Nucleic Acids Research, 2017, 45, gkw900.	6.5	37
10	Global response of Acidithiobacillus ferrooxidans ATCC 53993 to high concentrations of copper: A quantitative proteomics approach. Journal of Proteomics, 2016, 145, 37-45.	1.2	34
11	Genomic comparison between members of the Salinibacteraceae family, and description of a new species of Salinibacter (Salinibacter altiplanensis sp. nov.) isolated from high altitude hypersaline environments of the Argentinian Altiplano. Systematic and Applied Microbiology, 2018, 41, 198-212.	1.2	29
12	Metagenomics as a Public Health Risk Assessment Tool in a Study of Natural Creek Sediments Influenced by Agricultural and Livestock Runoff: Potential and Limitations. Applied and Environmental Microbiology, 2020, 86, .	1.4	27
13	Candidatus Abditibacter, a novel genus within the Cryomorphaceae, thriving in the North Sea. Systematic and Applied Microbiology, 2020, 43, 126088.	1.2	21
14	Predominance of deterministic microbial community dynamics in salterns exposed to different light intensities. Environmental Microbiology, 2019, 21, 4300-4315.	1.8	20
15	Comparing DNA, RNA and protein levels for measuring microbial dynamics in soil microcosms amended with nitrogen fertilizer. Scientific Reports, 2019, 9, 17630.	1.6	18
16	Effects of timber harvesting on the genetic potential for carbon and nitrogen cycling in five North American forest ecozones. Scientific Reports, 2018, 8, 3142.	1.6	17
17	Distinct ecotypes within a natural haloarchaeal population enable adaptation to changing environmental conditions without causing population sweeps. ISME Journal, 2021, 15, 1178-1191.	4.4	14
18	Microbial metagenome-assembled genomes of the Fram Strait from short and long read sequencing platforms. Peerl, 2021, 9, e11721.	0.9	14

#	Article	IF	CITATIONS
19	Diversity of microbial communities and genes involved in nitrous oxide emissions in Antarctic soils impacted by marine animals as revealed by metagenomics and 100 metagenome-assembled genomes. Science of the Total Environment, 2021, 788, 147693.	3.9	12
20	Metagenomic Characterization of Soil Microbial Communities in the Luquillo Experimental Forest (Puerto Rico) and Implications for Nitrogen Cycling. Applied and Environmental Microbiology, 2021, 87, e0054621.	1.4	8
21	The influence of alfalfaâ€switchgrass intercropping on microbial community structure and function. Environmental Microbiology, 2021, 23, 6828-6843.	1.8	5
22	ROCker Models for Reliable Detection and Typing of Short-Read Sequences Carrying \hat{l}^2 -Lactamase Genes. MSystems, 2022, 7, .	1.7	1
23	Transcriptomic and rRNA:rDNA Signatures of Environmental versus Enteric Enterococcus faecalis Isolates under Oligotrophic Freshwater Conditions. Microbiology Spectrum, 2021, 9, e0081721.	1.2	0