

Fernando Santos

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

962
citations

566801

15
h-index

752256

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21
all docs

21
docs citations

21
times ranked

1067
citing authors

#	ARTICLE	IF	CITATIONS
1	Environmental dissolved <sc>DNA</sc> harbours meaningful biological information on microbial community structure. Environmental Microbiology, 2021, 23, 2669-2682.	1.8	3
2	Ancient saltern metagenomics: tracking changes in microbes and their viruses from the underground to the surface. Environmental Microbiology, 2021, 23, 3477-3498.	1.8	6
3	Inverted microbial community stratification and spatialâ€“temporal stability in hypersaline anaerobic sediments from the Sâ€™Avall solar salterns. Systematic and Applied Microbiology, 2021, 44, 126231.	1.2	5
4	Unveiling Ecological and Genetic Novelty within Lytic and Lysogenic Viral Communities of Hot Spring Phototrophic Microbial Mats. Microbiology Spectrum, 2021, , e0069421.	1.2	4
5	Prokaryotic and viral community of the sulfateâ€™rich crust from PeÃ±ahueca ephemeral lake, an astrobiology analogue. Environmental Microbiology, 2019, 21, 3577-3600.	1.8	9
6	Recovering microbial genomes from metagenomes in hypersaline environments: The Good, the Bad and the Ugly. Systematic and Applied Microbiology, 2019, 42, 30-40.	1.2	29
7	Characterization of ecologically diverse viruses infecting co-occurring strains of cosmopolitan hyperhalophilic <i>Bacteroidetes</i>. ISME Journal, 2018, 12, 424-437.	4.4	29
8	Seasonal dynamics of extremely halophilic microbial communities in three Argentinian salterns. FEMS Microbiology Ecology, 2016, 92, fiw184.	1.3	34
9	Structure and temporal dynamics of the bacterial communities associated to microhabitats of the coral <sc><i>O</i></sc> <i>culina patagonica</i>. Environmental Microbiology, 2016, 18, 4564-4578.	1.8	37
10	Interactions between Closely Related Bacterial Strains Are Revealed by Deep Transcriptome Sequencing. Applied and Environmental Microbiology, 2015, 81, 8445-8456.	1.4	40
11	From community approaches to single-cell genomics: the discovery of ubiquitous hyperhalophilic <i>Bacteroidetes</i> generalists. ISME Journal, 2015, 9, 16-31.	4.4	51
12	Unveiling viralâ€™host interactions within the â€™microbial dark matterâ€™. Nature Communications, 2014, 5, 4542.	5.8	69
13	Culture-Independent Approaches for Studying Viruses from Hypersaline Environments. Applied and Environmental Microbiology, 2012, 78, 1635-1643.	1.4	70
14	Virioplankton Community Structure in Tunisian Solar Salterns. Applied and Environmental Microbiology, 2012, 78, 7429-7437.	1.4	51
15	Spatial and seasonal prokaryotic community dynamics in ponds of increasing salinity of Sfax solar saltern in Tunisia. Antonie Van Leeuwenhoek, 2012, 101, 845-857.	0.7	59
16	Reconstructing Viral Genomes from the Environment Using Fosmid Clones: The Case of Haloviruses. PLoS ONE, 2012, 7, e33802.	1.1	78
17	Metatranscriptomic analysis of extremely halophilic viral communities. ISME Journal, 2011, 5, 1621-1633.	4.4	36
18	The metavirome of a hypersaline environment. Environmental Microbiology, 2010, 12, 2965-2976.	1.8	78

#	ARTICLE	IF	CITATIONS
19	Prokaryotic diversity in Tuz Lake, a hypersaline environment in Inland Turkey. FEMS Microbiology Ecology, 2008, 65, 474-483.	1.3	90
20	Microbial Diversity in Maras Salterns, a Hypersaline Environment in the Peruvian Andes. Applied and Environmental Microbiology, 2006, 72, 3887-3895.	1.4	184