Pablo Yarza

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11322608/publications.pdf

Version: 2024-02-01

20 papers 28,966 citations

430754 18 h-index 19 g-index

21 all docs

21 docs citations

times ranked

21

34591 citing authors

#	Article	IF	CITATIONS
1	The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. Nucleic Acids Research, 2012, 41, D590-D596.	6.5	21,425
2	The SILVA and "All-species Living Tree Project (LTP)―taxonomic frameworks. Nucleic Acids Research, 2014, 42, D643-D648.	6.5	2,667
3	Uniting the classification of cultured and uncultured bacteria and archaea using 16S rRNA gene sequences. Nature Reviews Microbiology, 2014, 12, 635-645.	13.6	2,000
4	The All-Species Living Tree project: A 16S rRNA-based phylogenetic tree of all sequenced type strains. Systematic and Applied Microbiology, 2008, 31, 241-250.	1.2	884
5	25 years of serving the community with ribosomal RNA gene reference databases and tools. Journal of Biotechnology, 2017, 261, 169-176.	1.9	679
6	Update of the All-Species Living Tree Project based on 16S and 23S rRNA sequence analyses. Systematic and Applied Microbiology, 2010, 33, 291-299.	1.2	441
7	Release LTPs104 of the All-Species Living Tree. Systematic and Applied Microbiology, 2011, 34, 169-170.	1.2	146
8	Expanding the World of Marine Bacterial and Archaeal Clades. Frontiers in Microbiology, 2015, 6, 1524.	1.5	122
9	Fine-scale evolution: genomic, phenotypic and ecological differentiation in two coexisting <i>Salinibacter ruber</i> strains. ISME Journal, 2010, 4, 882-895.	4.4	81
10	The metavirome of a hypersaline environment. Environmental Microbiology, 2010, 12, 2965-2976.	1.8	78
11	Culture-Independent Approaches for Studying Viruses from Hypersaline Environments. Applied and Environmental Microbiology, 2012, 78, 1635-1643.	1.4	70
12	Response of sulfateâ€reducing bacteria to an artificial oilâ€spill in a coastal marine sediment. Environmental Microbiology, 2011, 13, 1488-1499.	1.8	55
13	New insights into <i>Oculina patagonica</i> coral diseases and their associated <i>Vibrio</i> spp. communities. ISME Journal, 2014, 8, 1794-1807.	4.4	54
14	Taxonomic and Functional Metagenomic Profiling of the Microbial Community in the Anoxic Sediment of a Sub-saline Shallow Lake (Laguna de Carrizo, Central Spain). Microbial Ecology, 2011, 62, 824-837.	1.4	51
15	Virioplankton Community Structure in Tunisian Solar Salterns. Applied and Environmental Microbiology, 2012, 78, 7429-7437.	1.4	51
16	Complete genome sequence of Marinobacter adhaerens type strain (HP15), a diatom-interacting marine microorganism. Standards in Genomic Sciences, 2010, 3, 97-107.	1.5	50
17	A phylogenetic framework for the kingdom Fungi based on 18S rRNA gene sequences. Marine Genomics, 2017, 36, 33-39.	0.4	47
18	Extremely halophilic microbial communities in anaerobic sediments from a solar saltern. Environmental Microbiology Reports, 2010, 2, 258-271.	1.0	44

#	Article	IF	CITATIONS
19	The All-Species Living Tree Project. Methods in Microbiology, 2014, 41, 45-59.	0.4	10
20	Harmonized Phylogenetic Trees for The Prokaryotes. , 2014, , 1-3.		10