Sheila Podell

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/992301/publications.pdf

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20 papers 1,464 citations

16 h-index 752698 20 g-index

22 all docs 22 docs citations

22 times ranked 2622 citing authors

#	Article	IF	CITATIONS
1	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. Nature Communications, 2019, 10, 5477.	12.8	197
2	Characterization of Cyanobacterial Hydrocarbon Composition and Distribution of Biosynthetic Pathways. PLoS ONE, 2014, 9, e85140.	2.5	190
3	Metagenomic discovery of polybrominated diphenyl ether biosynthesis by marine sponges. Nature Chemical Biology, 2017, 13, 537-543.	8.0	141
4	DarkHorse: a method for genome-wide prediction of horizontal gene transfer. Genome Biology, 2007, 8, R16.	9.6	137
5	Assembly-Driven Community Genomics of a Hypersaline Microbial Ecosystem. PLoS ONE, 2013, 8, e61692.	2.5	101
6	Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. ISME Journal, 2014, 8, 979-990.	9.8	91
7	The metabolic potential of the single cell genomes obtained from the Challenger Deep, <scp>M</scp> ariana <scp>T</scp> rench within the candidate superphylum <scp>P</scp> arcubacteria (<scp>OD</scp> 1). Environmental Microbiology, 2017, 19, 2769-2784.	3.8	88
8	Genome and methylome of the oleaginous diatom Cyclotella cryptica reveal genetic flexibility toward a high lipid phenotype. Biotechnology for Biofuels, 2016, 9, 258.	6.2	87
9	Comparative genomics uncovers the prolific and distinctive metabolic potential of the cyanobacterial genus <i>Moorea</i> . Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3198-3203.	7.1	77
10	Pangenomic comparison of globally distributed Poribacteria associated with sponge hosts and marine particles. ISME Journal, 2019, 13, 468-481.	9.8	63
11	Sequencing rare marine actinomycete genomes reveals high density of unique natural product biosynthetic gene clusters. Microbiology (United Kingdom), 2016, 162, 2075-2086.	1.8	61
12	Single Cells within the Puerto Rico Trench Suggest Hadal Adaptation of Microbial Lineages. Applied and Environmental Microbiology, 2015, 81, 8265-8276.	3.1	43
13	A genomic view of trophic and metabolic diversity in clade-specific Lamellodysidea sponge microbiomes. Microbiome, 2020, 8, 97.	11.1	38
14	The phagosomal nutrient transporter (Pht) family. Microbiology (United Kingdom), 2008, 154, 42-53.	1.8	37
15	Comparative Genomics of Cyanobacterial Symbionts Reveals Distinct, Specialized Metabolism in Tropical <i>Dysideidae</i> Sponges. MBio, 2019, 10, .	4.1	31
16	Multi-Omic Profiling of Melophlus Sponges Reveals Diverse Metabolomic and Microbiome Architectures that Are Non-overlapping with Ecological Neighbors. Marine Drugs, 2020, 18, 124.	4.6	21
17	Metabolic potential and <i>in situ</i> transcriptomic profiles of previously uncharacterized key microbial groups involved in coupled carbon, nitrogen and sulfur cycling in anoxic marine zones. Environmental Microbiology, 2018, 20, 2727-2742.	3.8	18
18	Genome of Methanoregula boonei 6A8 reveals adaptations to oligotrophic peatland environments. Microbiology (United Kingdom), 2015, 161, 1572-1581.	1.8	17

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#	Article	IF	CITATIONS
19	Distinctive Archaeal Composition of an Artisanal Crystallizer Pond and Functional Insights Into Salt-Saturated Hypersaline Environment Adaptation. Frontiers in Microbiology, 2018, 9, 1800.	3.5	14
20	Diploid genomic architecture of Nitzschia inconspicua, an elite biomass production diatom. Scientific Reports, 2021, 11, 15592.	3.3	12