

Sheila Podell

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

1,464
citations

516710

16
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752698

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docs citations

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times ranked

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| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Diploid genomic architecture of <i>Nitzschia inconspicua</i> , an elite biomass production diatom. <i>Scientific Reports</i> , 2021, 11, 15592. | 3.3 | 12 |
| 2 | Multi-Omic Profiling of <i>Melophlus</i> Sponges Reveals Diverse Metabolomic and Microbiome Architectures that Are Non-overlapping with Ecological Neighbors. <i>Marine Drugs</i> , 2020, 18, 124. | 4.6 | 21 |
| 3 | A genomic view of trophic and metabolic diversity in clade-specific <i>Lamellodysidea</i> sponge microbiomes. <i>Microbiome</i> , 2020, 8, 97. | 11.1 | 38 |
| 4 | Comparative Genomics of Cyanobacterial Symbionts Reveals Distinct, Specialized Metabolism in Tropical <i>Dysideidae</i> Sponges. <i>MBio</i> , 2019, 10, . | 4.1 | 31 |
| 5 | Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477. | 12.8 | 197 |
| 6 | Pangenomic comparison of globally distributed Poribacteria associated with sponge hosts and marine particles. <i>ISME Journal</i> , 2019, 13, 468-481. | 9.8 | 63 |
| 7 | 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. <i>Environmental Microbiology</i> , 2018, 20, 2727-2742. | 3.8 | 18 |
| 8 | Distinctive Archaeal Composition of an Artisanal Crystallizer Pond and Functional Insights Into Salt-Saturated Hypersaline Environment Adaptation. <i>Frontiers in Microbiology</i> , 2018, 9, 1800. | 3.5 | 14 |
| 9 | Comparative genomics uncovers the prolific and distinctive metabolic potential of the cyanobacterial genus <i>Moorea</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3198-3203. | 7.1 | 77 |
| 10 | The metabolic potential of the single cell genomes obtained from the Challenger Deep, Mariana Trench within the candidate superphylum <i>P</i> arcubacteria (<i>OD</i> >1). <i>Environmental Microbiology</i> , 2017, 19, 2769-2784. | 3.8 | 88 |
| 11 | Metagenomic discovery of polybrominated diphenyl ether biosynthesis by marine sponges. <i>Nature Chemical Biology</i> , 2017, 13, 537-543. | 8.0 | 141 |
| 12 | Sequencing rare marine actinomycete genomes reveals high density of unique natural product biosynthetic gene clusters. <i>Microbiology (United Kingdom)</i> , 2016, 162, 2075-2086. | 1.8 | 61 |
| 13 | Genome and methylome of the oleaginous diatom <i>Cyclotella cryptica</i> reveal genetic flexibility toward a high lipid phenotype. <i>Biotechnology for Biofuels</i> , 2016, 9, 258. | 6.2 | 87 |
| 14 | Genome of <i>Methanoregula boonei</i> 6A8 reveals adaptations to oligotrophic peatland environments. <i>Microbiology (United Kingdom)</i> , 2015, 161, 1572-1581. | 1.8 | 17 |
| 15 | Single Cells within the Puerto Rico Trench Suggest Hadal Adaptation of Microbial Lineages. <i>Applied and Environmental Microbiology</i> , 2015, 81, 8265-8276. | 3.1 | 43 |
| 16 | Characterization of Cyanobacterial Hydrocarbon Composition and Distribution of Biosynthetic Pathways. <i>PLoS ONE</i> , 2014, 9, e85140. | 2.5 | 190 |
| 17 | Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. <i>ISME Journal</i> , 2014, 8, 979-990. | 9.8 | 91 |
| 18 | Assembly-Driven Community Genomics of a Hypersaline Microbial Ecosystem. <i>PLoS ONE</i> , 2013, 8, e61692. | 2.5 | 101 |

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|----|---|-----|-----------|
| 19 | The phagosomal nutrient transporter (Pht) family. <i>Microbiology (United Kingdom)</i> , 2008, 154, 42-53. | 1.8 | 37 |
| 20 | DarkHorse: a method for genome-wide prediction of horizontal gene transfer. <i>Genome Biology</i> , 2007, 8, R16. | 9.6 | 137 |