

# Eric D Becraft

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10928396/publications.pdf>

Version: 2024-02-01

22  
papers

3,096  
citations

471509

17  
h-index

610901

24  
g-index

27  
all docs

27  
docs citations

27  
times ranked

4228  
citing authors

#	ARTICLE	IF	CITATIONS
1	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	17.5	1,512
2	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
3	Improved genome recovery and integrated cell-size analyses of individual uncultured microbial cells and viral particles. <i>Nature Communications</i> , 2017, 8, 84.	12.8	169
4	Rokubacteria: Genomic Giants among the Uncultured Bacterial Phyla. <i>Frontiers in Microbiology</i> , 2017, 8, 2264.	3.5	142
5	Regulation of <i>nif</i> gene expression and the energetics of N <sub>2</sub> fixation over the diel cycle in a hot spring microbial mat. <i>ISME Journal</i> , 2008, 2, 364-378.	9.8	133
6	Diel metabolomics analysis of a hot spring chlorophototrophic microbial mat leads to new hypotheses of community member metabolisms. <i>Frontiers in Microbiology</i> , 2015, 6, 209.	3.5	104
7	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. <i>Nature Communications</i> , 2019, 10, 463.	12.8	87
8	Fine-Scale Distribution Patterns of <i>Synechococcus</i> Ecological Diversity in Microbial Mats of Mushroom Spring, Yellowstone National Park. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7689-7697.	3.1	72
9	The molecular dimension of microbial species: 3. Comparative genomics of <i>Synechococcus</i> strains with different light responses and in situ diel transcription patterns of associated putative ecotypes in the Mushroom Spring microbial mat. <i>Frontiers in Microbiology</i> , 2015, 6, 604.	3.5	67
10	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. <i>Frontiers in Microbiology</i> , 2020, 11, 1848.	3.5	62
11	The molecular dimension of microbial species: 2. <i>Synechococcus</i> strains representative of putative ecotypes inhabiting different depths in the Mushroom Spring microbial mat exhibit different adaptive and acclimative responses to light. <i>Frontiers in Microbiology</i> , 2015, 6, 626.	3.5	56
12	The molecular dimension of microbial species: 1. Ecological distinctions among, and homogeneity within, putative ecotypes of <i>Synechococcus</i> inhabiting the cyanobacterial mat of Mushroom Spring, Yellowstone National Park. <i>Frontiers in Microbiology</i> , 2015, 6, 590.	3.5	49
13	Single-Cell-Genomics-Facilitated Read Binning of Candidate Phylum EM19 Genomes from Geothermal Spring Metagenomes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 992-1003.	3.1	36
14	Biogeography of American Northwest Hot Spring A/B <sup>2</sup> -Lineage <i>Synechococcus</i> Populations. <i>Frontiers in Microbiology</i> , 2020, 11, 77.	3.5	24
15	Four Draft Single-Cell Genome Sequences of Novel, Nearly Identical <i>Kiritimatiellaota</i> Strains Isolated from the Continental Deep Subsurface. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	23
16	Evolutionary stasis of a deep subsurface microbial lineage. <i>ISME Journal</i> , 2021, 15, 2830-2842.	9.8	23
17	Genomic Comparison of Two Family-Level Groups of the Uncultivated NAG1 Archaeal Lineage from Chemically and Geographically Disparate Hot Springs. <i>Frontiers in Microbiology</i> , 2017, 8, 2082.	3.5	19
18	Recombination Does Not Hinder Formation or Detection of Ecological Species of <i>Synechococcus</i> Inhabiting a Hot Spring Cyanobacterial Mat. <i>Frontiers in Microbiology</i> , 2015, 6, 1540.	3.5	16

#	ARTICLE	IF	CITATIONS
19	Microbial Community in Hyperalkaline Steel Slag-Fill Emulates Serpentinizing Springs. <i>Diversity</i> , 2019, 11, 103.	1.7	8
20	Hiding in Plain Sight: The Globally Distributed Bacterial Candidate Phylum PAUC34f. <i>Frontiers in Microbiology</i> , 2020, 11, 376.	3.5	5
21	Synthase-Selective Exploration of a Tunicate Microbiome by Activity-Guided Single-Cell Genomics. <i>ACS Chemical Biology</i> , 2021, 16, 813-819.	3.4	4
22	Relationship between Microorganisms Inhabiting Alkaline Siliceous Hot Spring Mat Communities and Overflowing Water. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	1