

Benjamin D Kaehler

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

15,932
citations

1170033

9
h-index

1336881

12
g-index

23
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23
docs citations

23
times ranked

17735
citing authors

#	ARTICLE	IF	CITATIONS
1	Beating Naive Bayes at Taxonomic Classification of 16S rRNA Gene Sequences. <i>Frontiers in Microbiology</i> , 2021, 12, 644487.	1.5	12
2	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , 2021, 17, e1009056.	1.5	2
3	RESCRIPT: Reproducible sequence taxonomy reference database management. <i>PLoS Computational Biology</i> , 2021, 17, e1009581.	1.5	277
4	Measuring the microbiome: Best practices for developing and benchmarking microbiomics methods. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 4048-4062.	1.9	37
5	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
6	Species abundance information improves sequence taxonomy classification accuracy. <i>Nature Communications</i> , 2019, 10, 4643.	5.8	86
7	redbiom: a Rapid Sample Discovery and Feature Characterization System. <i>MSystems</i> , 2019, 4, .	1.7	35
8	Did aculeate silk evolve as an antifouling material?. <i>PLoS ONE</i> , 2018, 13, e0203948.	1.1	3
9	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. <i>Microbiome</i> , 2018, 6, 90.	4.9	3,159
10	q2-sample-classifier: machine-learning tools for microbiome classification and regression. <i>Journal of Open Source Software</i> , 2018, 3, 934.	2.0	116
11	Standard Codon Substitution Models Overestimate Purifying Selection for Non-Stationary Data. <i>Genome Biology and Evolution</i> , 2017, 9, evw308.	1.1	9
12	Full reconstruction of non-stationary strand-symmetric models on rooted phylogenies. <i>Journal of Theoretical Biology</i> , 2017, 420, 144-151.	0.8	2