

Jose A Navas-Molina

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

18
papers

8,162
citations

18
h-index

22
g-index

22
ext. papers

13,903
ext. citations

16.1
avg, IF

4.94
L-index

#	Paper	IF	Citations
18	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
17	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , 2018 , 3,	7.6	181
16	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018 ,		78
15	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018 , 15, 796-798	21.6	231
14	Balance Trees Reveal Microbial Niche Differentiation. <i>MSystems</i> , 2017 , 2,	7.6	177
13	Bringing the Dynamic Microbiome to Life with Animations. <i>Cell Host and Microbe</i> , 2017 , 21, 7-10	23.4	44
12	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017 , 2,	7.6	763
11	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	50.4	1076
10	Correcting for Microbial Blooms in Fecal Samples during Room-Temperature Shipping. <i>MSystems</i> , 2017 , 2,	7.6	44
9	Inflammation-induced IgA+ cells dismantle anti-liver cancer immunity. <i>Nature</i> , 2017 , 551, 340-345	50.4	224
8	The microbiome and big data. <i>Current Opinion in Systems Biology</i> , 2017 , 4, 92-96	3.2	7
7	Open-Source Sequence Clustering Methods Improve the State Of the Art. <i>MSystems</i> , 2016 , 1,	7.6	120
6	From Sample to Multi-Omics Conclusions in under 48 Hours. <i>MSystems</i> , 2016 , 1,	7.6	45
5	The Oral and Skin Microbiomes of Captive Komodo Dragons Are Significantly Shared with Their Habitat. <i>MSystems</i> , 2016 , 1,	7.6	41
4	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. <i>PeerJ</i> , 2014 , 2, e545	3.1	395
3	Advancing our understanding of the human microbiome using QIIME. <i>Methods in Enzymology</i> , 2013 , 531, 371-444	1.7	373
2	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36

1 QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science

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