

Justin D Silverman

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3862326/publications.pdf>

Version: 2024-02-01

13
papers

3,066
citations

759233

12
h-index

1058476

14
g-index

28
all docs

28
docs citations

28
times ranked

7654
citing authors

#	ARTICLE	IF	CITATIONS
1	Estimated transmissibility and impact of SARS-CoV-2 lineage B.1.1.7 in England. <i>Science</i> , 2021, 372, .	12.6	2,103
2	DNA Extraction and Host Depletion Methods Significantly Impact and Potentially Bias Bacterial Detection in a Biological Fluid. <i>MSystems</i> , 2021, 6, e0061921.	3.8	21
3	Measuring and mitigating PCR bias in microbiota datasets. <i>PLoS Computational Biology</i> , 2021, 17, e1009113.	3.2	43
4	Short-Chain Fatty Acid Production by Gut Microbiota from Children with Obesity Differs According to Prebiotic Choice and Bacterial Community Composition. <i>MBio</i> , 2020, 11, .	4.1	49
5	Naught all zeros in sequence count data are the same. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2789-2798.	4.1	87
6	Using influenza surveillance networks to estimate state-specific prevalence of SARS-CoV-2 in the United States. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	91
7	Interindividual Variation in Dietary Carbohydrate Metabolism by Gut Bacteria Revealed with Droplet Microfluidic Culture. <i>MSystems</i> , 2020, 5, .	3.8	34
8	Modeling the temporal dynamics of the gut microbial community in adults and infants. <i>PLoS Computational Biology</i> , 2019, 15, e1006960.	3.2	42
9	Phylofactorization: a graph partitioning algorithm to identify phylogenetic scales of ecological data. <i>Ecological Monographs</i> , 2019, 89, e01353.	5.4	52
10	Dynamic linear models guide design and analysis of microbiota studies within artificial human guts. <i>Microbiome</i> , 2018, 6, 202.	11.1	54
11	Human Gut Microbiota Predicts Susceptibility to <i>Vibrio cholerae</i> Infection. <i>Journal of Infectious Diseases</i> , 2018, 218, 645-653.	4.0	60
12	A phylogenetic transform enhances analysis of compositional microbiota data. <i>ELife</i> , 2017, 6, .	6.0	247
13	Phylogenetic factorization of compositional data yields lineage-level associations in microbiome datasets. <i>PeerJ</i> , 2017, 5, e2969.	2.0	105