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List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8083361/publications.pdf>

Version: 2024-02-01

13
papers

605
citations

1162889

8
h-index

1372474

10
g-index

25
all docs

25
docs citations

25
times ranked

1093
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequencing 16S rRNA gene fragments using the PacBio SMRT DNA sequencing system. PeerJ, 2016, 4, e1869.	0.9	200
2	<i>Clostridium difficile</i> Colonizes Alternative Nutrient Niches during Infection across Distinct Murine Gut Microbiomes. MSystems, 2017, 2, .	1.7	130
3	<i>Clostridium difficile</i> Alters the Structure and Metabolism of Distinct Cecal Microbiomes during Initial Infection To Promote Sustained Colonization. MSphere, 2018, 3, .	1.3	73
4	Transcriptome-guided parsimonious flux analysis improves predictions with metabolic networks in complex environments. PLoS Computational Biology, 2020, 16, e1007099.	1.5	55
5	Intra- and Interindividual Variations Mask Interspecies Variation in the Microbiota of Sympatric Peromyscus Populations. Applied and Environmental Microbiology, 2015, 81, 396-404.	1.4	54
6	The Gut Microbiota Is Associated with Clearance of <i>Clostridium difficile</i> Infection Independent of Adaptive Immunity. MSphere, 2019, 4, .	1.3	26
7	Protection from Lethal <i>Clostridioides difficile</i> Infection via Intraspecies Competition for Cogerminant. MBio, 2021, 12, .	1.8	20
8	Novel Drivers of Virulence in <i>Clostridioides difficile</i> Identified via Context-Specific Metabolic Network Analysis. MSystems, 2021, 6, e0091921.	1.7	13
9	Ten simple rules to increase computational skills among biologists with Code Clubs. PLoS Computational Biology, 2020, 16, e1008119.	1.5	6
10	Quantifying cumulative phenotypic and genomic evidence for procedural generation of metabolic network reconstructions. PLoS Computational Biology, 2022, 18, e1009341.	1.5	3
11	<i>Clostridioides difficile</i> : Sometimes It Pays To Be Difficult. Cell Host and Microbe, 2020, 28, 358-359.	5.1	1
12	Conserved Virulence-Linked Metabolic Reprogramming in <i>Clostridioides Difficile</i> Identified Through Genome-Scale Metabolic Network Analysis. SSRN Electronic Journal, 0, , .	0.4	1
13	Computational approaches to understanding <i>Clostridioides difficile</i> metabolism and virulence. Current Opinion in Microbiology, 2022, 65, 108-115.	2.3	0