

Sina Beier

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6333990/publications.pdf>

Version: 2024-02-01

9
papers

1,771
citations

1307594

7
h-index

1588992

8
g-index

11
all docs

11
docs citations

11
times ranked

3595
citing authors

#	ARTICLE	IF	CITATIONS
1	A Computational Model of Bacterial Population Dynamics in Gastrointestinal <i>Yersinia enterocolitica</i> Infections in Mice. <i>Biology</i> , 2022, 11, 297.	2.8	0
2	Panakeia - a universal tool for bacterial pangenome analysis. <i>BMC Genomics</i> , 2022, 23, 265.	2.8	5
3	Introduction to the Analysis of Environmental Sequences: Metagenomics with MEGAN. <i>Methods in Molecular Biology</i> , 2019, 1910, 591-604.	0.9	23
4	Annotated bacterial chromosomes from frame-shift-corrected long-read metagenomic data. <i>Microbiome</i> , 2019, 7, 61.	11.1	69
5	Flagellin hypervariable region determines symbiotic properties of commensal <i>Escherichia coli</i> strains. <i>PLoS Biology</i> , 2019, 17, e3000334.	5.6	22
6	Genome Sequence of <i>Galleria mellonella</i> (Greater Wax Moth). <i>Genome Announcements</i> , 2018, 6, .	0.8	76
7	<i>Galleria mellonella</i> : A Novel Invertebrate Model to Distinguish Intestinal Symbionts From Pathobionts. <i>Frontiers in Immunology</i> , 2018, 9, 2114.	4.8	37
8	Extensive Mobilome-Driven Genome Diversification in Mouse Gut-Associated <i>Bacteroides vulgatus</i> mpk. <i>Genome Biology and Evolution</i> , 2016, 8, 1197-1207.	2.5	37
9	MEGAN Community Edition - Interactive Exploration and Analysis of Large-Scale Microbiome Sequencing Data. <i>PLoS Computational Biology</i> , 2016, 12, e1004957.	3.2	1,500