

Xiaoquan Su

List of Publications by Year in descending order

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37
papers

1,463
citations

471509

17
h-index

395702

33
g-index

37
all docs

37
docs citations

37
times ranked

1937
citing authors

#	ARTICLE	IF	CITATIONS
1	Nannochloropsis Genomes Reveal Evolution of Microalgal Oleaginous Traits. PLoS Genetics, 2014, 10, e1004094.	3.5	217
2	Feed-additive probiotics accelerate yet antibiotics delay intestinal microbiota maturation in broiler chicken. Microbiome, 2017, 5, 91.	11.1	208
3	Biological ingredient analysis of traditional Chinese medicine preparation based on high-throughput sequencing: the story for Liuwei Dihuang Wan. Scientific Reports, 2014, 4, 5147.	3.3	132
4	Genomic Foundation of Starch-to-Lipid Switch in Oleaginous <i>Chlorella</i> spp.. Plant Physiology, 2015, 169, 2444-2461.	4.8	111
5	Parallel-META 3: Comprehensive taxonomical and functional analysis platform for efficient comparison of microbial communities. Scientific Reports, 2017, 7, 40371.	3.3	96
6	Cow-to-mouse fecal transplantations suggest intestinal microbiome as one cause of mastitis. Microbiome, 2018, 6, 200.	11.1	88
7	Parallel-META 2.0: Enhanced Metagenomic Data Analysis with Functional Annotation, High Performance Computing and Advanced Visualization. PLoS ONE, 2014, 9, e89323.	2.5	70
8	Comparative Gut Microbiomes of Four Species Representing the Higher and the Lower Termites. Journal of Insect Science, 2016, 16, 97.	1.5	49
9	RNA-QC-chain: comprehensive and fast quality control for RNA-Seq data. BMC Genomics, 2018, 19, 144.	2.8	46
10	Assessment of quality control approaches for metagenomic data analysis. Scientific Reports, 2014, 4, 6957.	3.3	45
11	Meta-Storms: efficient search for similar microbial communities based on a novel indexing scheme and similarity score for metagenomic data. Bioinformatics, 2012, 28, 2493-2501.	4.1	44
12	Variation in the Gut Microbiota of Termites (<i>Tsitermes ampliceps</i>) Against Different Diets. Applied Biochemistry and Biotechnology, 2017, 181, 32-47.	2.9	29
13	Identifying and Predicting Novelty in Microbiome Studies. MBio, 2018, 9, .	4.1	28
14	Method development for cross-study microbiome data mining: Challenges and opportunities. Computational and Structural Biotechnology Journal, 2020, 18, 2075-2080.	4.1	27
15	DNA Extraction Protocol for Biological Ingredient Analysis of Liuwei Dihuang Wan. Genomics, Proteomics and Bioinformatics, 2014, 12, 137-143.	6.9	26
16	Longitudinal Multi-omics and Microbiome Meta-analysis Identify an Asymptomatic Gingival State That Links Gingivitis, Periodontitis, and Aging. MBio, 2021, 12, .	4.1	24
17	A Microbiome-Based Index for Assessing Skin Health and Treatment Effects for Atopic Dermatitis in Children. MSystems, 2019, 4, .	3.8	22
18	GPU-Meta-Storms: computing the structure similarities among massive amount of microbial community samples using GPU. Bioinformatics, 2014, 30, 1031-1033.	4.1	20

#	ARTICLE	IF	CITATIONS
19	Parallel- <i>Meta Suite</i> : Interactive and rapid microbiome data analysis on multiple platforms. , 2022, 1, .		19
20	Meta-QC-Chain: Comprehensive and Fast Quality Control Method for Metagenomic Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 52-56.	6.9	17
21	Elucidating the Beta-Diversity of the Microbiome: from Global Alignment to Local Alignment. <i>MSystems</i> , 2021, 6, e0036321.	3.8	17
22	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , 2020, 5, .	3.8	16
23	Characterization of saliva microbiota's functional feature based on metagenomic sequencing. <i>SpringerPlus</i> , 2016, 5, 2098.	1.2	15
24	Meta-Apo improves accuracy of 16S-amplicon-based prediction of microbiome function. <i>BMC Genomics</i> , 2021, 22, 9.	2.8	15
25	Microbiome Search Engine 2: a Platform for Taxonomic and Functional Search of Global Microbiomes on the Whole-Microbiome Level. <i>MSystems</i> , 2021, 6, .	3.8	14
26	MetaBoot: a machine learning framework of taxonomical biomarker discovery for different microbial communities based on metagenomic data. <i>PeerJ</i> , 2015, 3, e993.	2.0	13
27	<i>Dynamic Meta-Storms</i> enables comprehensive taxonomic and phylogenetic comparison of shotgun metagenomes at the species level. <i>Bioinformatics</i> , 2020, 36, 2308-2310.	4.1	12
28	Towards multi-label classification: Next step of machine learning for microbiome research. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2742-2749.	4.1	10
29	Comprehensive understanding to the public health risk of environmental microbes via a microbiome-based index. <i>Journal of Genetics and Genomics</i> , 2022, 49, 685-688.	3.9	9
30	<i>Hierarchical Meta-Storms</i> enables comprehensive and rapid comparison of microbiome functional profiles on a large scale using hierarchical dissimilarity metrics and parallel computing. <i>Bioinformatics Advances</i> , 2021, 1, .	2.4	7
31	QSpec: online control and data analysis system for single-cell Raman spectroscopy. <i>PeerJ</i> , 2014, 2, e436.	2.0	6
32	A Scale-Free, Fully Connected Global Transition Network Underlies Known Microbiome Diversity. <i>MSystems</i> , 2021, 6, e0039421.	3.8	5
33	Rapid comparison and correlation analysis among massive number of microbial community samples based on MDV data model. <i>Scientific Reports</i> , 2015, 4, 6393.	3.3	4
34	GPU- <i>Meta-Storms</i> : Computing the similarities among massive microbial communities using GPU. , 2013, , .		1
35	Search-based health status detection and disease classification using species-level profiles of metagenomes. <i>Medicine in Microecology</i> , 2022, 11, 100048.	1.6	1
36	Reply to Sun et al., "Identifying Composition Novelty in Microbiome Studies: Improvement of Prediction Accuracy". <i>MBio</i> , 2019, 10, .	4.1	0

#	ARTICLE	IF	CITATIONS
37	Predicting Selective RNA Processing and Stabilization Operons in Clostridium spp.. Frontiers in Microbiology, 2021, 12, 673349.	3.5	0