Xiaoquan Su

List of Publications by Year
in descending order

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	Comprehensive understanding to the public health risk of environmental microbes via a microbiome-based index. Journal of Genetics and Genomics, 2022, 49, 685-688.	3.9	9
2	Search-based health status detection and disease classification using species-level profiles of metagenomes. Medicine in Microecology, 2022, 11, 100048.	1.6	1
3	Parallel‑Meta Suite: Interactive and rapid microbiome data analysis on multiple platforms. , 2022, 1, .		19
4	<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. Bioinformatics Advances, 2021, 1, .	2.4	7
5	Meta-Apo improves accuracy of 16S-amplicon-based prediction of microbiome function. BMC Genomics, 2021, 22, 9.	2.8	15
6	Towards multi-label classification: Next step of machine learning for microbiome research. Computational and Structural Biotechnology Journal, 2021, 19, 2742-2749.	4.1	10
7	Microbiome Search Engine 2: a Platform for Taxonomic and Functional Search of Global Microbiomes on the Whole-Microbiome Level. MSystems, 2021, 6, .	3.8	14
8	Longitudinal Multi-omics and Microbiome Meta-analysis Identify an Asymptomatic Gingival State That Links Gingivitis, Periodontitis, and Aging. MBio, 2021, 12, .	4.1	24
9	Predicting Selective RNA Processing and Stabilization Operons in Clostridium spp.. Frontiers in Microbiology, 2021, 12, 673349.	3.5	0
10	Elucidating the Beta-Diversity of the Microbiome: from Global Alignment to Local Alignment. MSystems, 2021, 6, e0036321.	3.8	17
11	A Scale-Free, Fully Connected Global Transition Network Underlies Known Microbiome Diversity. MSystems, 2021, 6, e0039421.	3.8	5
12	<i>Dynamic Meta-Storms</i> enables comprehensive taxonomic and phylogenetic comparison of shotgun metagenomes at the species level. Bioinformatics, 2020, 36, 2308-2310.	4.1	12
13	Method development for cross-study microbiome data mining: Challenges and opportunities. Computational and Structural Biotechnology Journal, 2020, 18, 2075-2080.	4.1	27
14	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. MSystems, 2020, 5, .	3.8	16
15	Reply to Sun et al., â€œIdentifying Composition Novelty in Microbiome Studies: Improvement of Prediction Accuracyâ€. MBio, 2019, 10, .	4.1	0
16	A Microbiome-Based Index for Assessing Skin Health and Treatment Effects for Atopic Dermatitis in Children. MSystems, 2019, 4, .	3.8	22
17	RNA-QC-chain: comprehensive and fast quality control for RNA-Seq data. BMC Genomics, 2018, 19, 144.	2.8	46
18	Cow-to-mouse fecal transplantations suggest intestinal microbiome as one cause of mastitis. Microbiome, 2018, 6, 200.	11.1	88

#	Article	IF	Citations
19	Identifying and Predicting Novelty in Microbiome Studies. MBio, 2018, 9, .	4.1	28
20	Parallel-META 3: Comprehensive taxonomical and functional analysis platform for efficient comparison of microbial communities. Scientific Reports, 2017, 7, 40371.	3.3	96
21	Variation in the Gut Microbiota of Termites (Tsaitermes ampliceps) Against Different Diets. Applied Biochemistry and Biotechnology, 2017, 181, 32-47.	2.9	29
22	Feed-additive probiotics accelerate yet antibiotics delay intestinal microbiota maturation in broiler chicken. Microbiome, 2017, 5, 91.	11.1	208
23	Characterization of saliva microbiotaâ€™s functional feature based on metagenomic sequencing. SpringerPlus, 2016, 5, 2098.	1.2	15
24	Comparative Gut Microbiomes of Four Species Representing the Higher and the Lower Termites. Journal of Insect Science, 2016, 16, 97.	1.5	49
25	Genomic Foundation of Starch-to-Lipid Switch in Oleaginous <i>Chlorella</i> spp.. Plant Physiology, 2015, 169, 2444-2461.	4.8	111
26	Rapid comparison and correlation analysis among massive number of microbial community samples based on MDV data model. Scientific Reports, 2015, 4, 6393.	3.3	4
27	MetaBoot: a machine learning framework of taxonomical biomarker discovery for different microbial communities based on metagenomic data. PeerJ, 2015, 3, e993.	2.0	13
28	GPU-Meta-Storms: computing the structure similarities among massive amount of microbial community samples using GPU. Bioinformatics, 2014, 30, 1031-1033.	4.1	20
29	Nannochloropsis Genomes Reveal Evolution of Microalgal Oleaginous Traits. PLoS Genetics, 2014, 10, e1004094.	3.5	217
30	Meta-QC-Chain: Comprehensive and Fast Quality Control Method for Metagenomic Data. Genomics, Proteomics and Bioinformatics, 2014, 12, 52-56.	6.9	17
31	DNA Extraction Protocol for Biological Ingredient Analysis of Liuwei Dihuang Wan. Genomics, Proteomics and Bioinformatics, 2014, 12, 137-143.	6.9	26
32	Assessment of quality control approaches for metagenomic data analysis. Scientific Reports, 2014, 4, 6957.	3.3	45
33	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
34	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
35	QSpec: online control and data analysis system for single-cell Raman spectroscopy. PeerJ, 2014, 2, e436.	2.0	6
36	GPU-Meta-Storms: Computing the similarities among massive microbial communities using GPU. , 2013, , .		1

#	Article	IF	Citations
37	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