

Zhenjiang Xu

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

52 papers	9,870 citations	26 h-index	59 g-index
59 ext. papers	16,308 ext. citations	10.6 avg, IF	5.53 L-index

#	Paper	IF	Citations
52	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
51	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	50.4	1076
50	Normalization and microbial differential abundance strategies depend upon data characteristics. <i>Microbiome</i> , 2017 , 5, 27	16.6	840
49	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017 , 2,	7.6	763
48	Advancing our understanding of the human microbiome using QIIME. <i>Methods in Enzymology</i> , 2013 , 531, 371-444	1.7	373
47	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016 , 10, 1669-81	11.9	365
46	Subsistence strategies in traditional societies distinguish gut microbiomes. <i>Nature Communications</i> , 2015 , 6, 6505	17.4	304
45	Microbial community assembly and metabolic function during mammalian corpse decomposition. <i>Science</i> , 2016 , 351, 158-62	33.3	256
44	Preservation Methods Differ in Fecal Microbiome Stability, Affecting Suitability for Field Studies. <i>MSystems</i> , 2016 , 1,	7.6	250
43	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , 2018 , 3,	7.6	181
42	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
41	Prediction of Early Childhood Caries via Spatial-Temporal Variations of Oral Microbiota. <i>Cell Host and Microbe</i> , 2015 , 18, 296-306	23.4	123
40	Tiny microbes, enormous impacts: what matters in gut microbiome studies?. <i>Genome Biology</i> , 2016 , 17, 217	18.3	86
39	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018 ,		78
38	Deep sequencing-based identification of small non-coding RNAs in <i>Streptomyces coelicolor</i> . <i>RNA Biology</i> , 2011 , 8, 468-77	4.8	71
37	Which is more important for classifying microbial communities: who's there or what they can do?. <i>ISME Journal</i> , 2014 , 8, 2357-9	11.9	65
36	Taxon-specific aerosolization of bacteria and viruses in an experimental ocean-atmosphere mesocosm. <i>Nature Communications</i> , 2018 , 9, 2017	17.4	61

35	Structural basis for diversity in the SAM clan of riboswitches. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 6624-9	11.5	45
34	Microbiome Data Accurately Predicts the Postmortem Interval Using Random Forest Regression Models. <i>Genes</i> , 2018 , 9,	4.2	42
33	Multilign: an algorithm to predict secondary structures conserved in multiple RNA sequences. <i>Bioinformatics</i> , 2011 , 27, 626-32	7.2	42
32	Lifestyle chemistries from phones for individual profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E7645-E7654	11.5	41
31	Striped UniFrac: enabling microbiome analysis at unprecedented scale. <i>Nature Methods</i> , 2018 , 15, 847-848	11.6	40
30	Gut microbiota from green tea polyphenol-dosed mice improves intestinal epithelial homeostasis and ameliorates experimental colitis. <i>Microbiome</i> , 2021 , 9, 184	16.6	39
29	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
28	Vitamin D metabolites and the gut microbiome in older men. <i>Nature Communications</i> , 2020 , 11, 5997	17.4	33
27	Intestinal microbiota and immune related genes in sea cucumber (<i>Apostichopus japonicus</i>) response to dietary β -glucan supplementation. <i>Biochemical and Biophysical Research Communications</i> , 2015 , 458, 98-103	3.4	26
26	Alteration in gut microbiota is associated with dysregulation of cytokines and glucocorticoid therapy in systemic lupus erythematosus. <i>Gut Microbes</i> , 2020 , 11, 1758-1773	8.8	24
25	Guiding longitudinal sampling in IBD cohorts. <i>Gut</i> , 2018 , 67, 1743-1745	19.2	23
24	Air proteins control differential TRAMP substrate specificity for nuclear RNA surveillance. <i>Rna</i> , 2012 , 18, 1934-45	5.8	23
23	Effects of library size variance, sparsity, and compositionality on the analysis of microbiome data		23
22	Statistical evaluation of improvement in RNA secondary structure prediction. <i>Nucleic Acids Research</i> , 2012 , 40, e26	20.1	22
21	Discovery of Novel ncRNA Sequences in Multiple Genome Alignments on the Basis of Conserved and Stable Secondary Structures. <i>PLoS ONE</i> , 2015 , 10, e0130200	3.7	21
20	Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , 2019 , 4,	7.6	20
19	Trace Evidence Potential in Postmortem Skin Microbiomes: From Death Scene to Morgue. <i>Journal of Forensic Sciences</i> , 2019 , 64, 791-798	1.8	19
18	Puerarin Rebuilding the Mucus Layer and Regulating Mucin-Utilizing Bacteria to Relieve Ulcerative Colitis. <i>Journal of Agricultural and Food Chemistry</i> , 2020 , 68, 11402-11411	5.7	18

17	Experiment-Assisted Secondary Structure Prediction with RNAstructure. <i>Methods in Molecular Biology</i> , 2016 , 1490, 163-76	1.4	17
16	Chlorogenic acid attenuates cadmium-induced intestinal injury in Sprague-Dawley rats. <i>Food and Chemical Toxicology</i> , 2019 , 133, 110751	4.7	16
15	Intermittent Hypoxia and Hypercapnia Reproducibly Change the Gut Microbiome and Metabolome across Rodent Model Systems. <i>MSystems</i> , 2019 , 4,	7.6	13
14	Secondary Structure Prediction of Single Sequences Using RNAstructure. <i>Methods in Molecular Biology</i> , 2016 , 1490, 15-34	1.4	13
13	Microbial effects of livestock manure fertilization on freshwater aquaculture ponds rearing tilapia (<i>Oreochromis shiranus</i>) and North African catfish (<i>Clarias gariepinus</i>). <i>MicrobiologyOpen</i> , 2018 , 7, e00716	3.4	13
12	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , 2020 , 5,	7.6	12
11	An examination of data from the American Gut Project reveals that the dominance of the genus <i>Bifidobacterium</i> is associated with the diversity and robustness of the gut microbiota. <i>MicrobiologyOpen</i> , 2019 , 8, e939	3.4	12
10	Effects of library size variance, sparsity, and compositionality on the analysis of microbiome data		5
9	Toxicant substitutes in immunological assays for mycotoxins detection: A mini review. <i>Food Chemistry</i> , 2021 , 344, 128589	8.5	5
8	Ribosomal RNA, the lens into life. <i>Rna</i> , 2015 , 21, 692-4	5.8	3
7	Prediction of Secondary Structures Conserved in Multiple RNA Sequences. <i>Methods in Molecular Biology</i> , 2016 , 1490, 35-50	1.4	3
6	Gut Microbiome-Targeted Modulations Regulate Metabolic Profiles and Alleviate Altitude-Related Cardiac Hypertrophy in Rats.. <i>Microbiology Spectrum</i> , 2022 , e0105321	8.9	2
5	PM2RA: A Framework for Detecting and Quantifying Relationship Alterations in Microbial Community. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 , 19, 154-167	6.5	2
4	A Pilot Study of Microbial Succession in Human Rib Skeletal Remains during Terrestrial Decomposition. <i>MSphere</i> , 2021 , 6, e0045521	5	1
3	Zebrafish model for human gut microbiome-related studies: advantages and limitations. <i>Medicine in Microecology</i> , 2021 , 8, 100042	4.3	0
2	Green Banana Flour Contributes to Gut Microbiota Recovery and Improves Colonic Barrier Integrity in Mice Following Antibiotic Perturbation.. <i>Frontiers in Nutrition</i> , 2022 , 9, 832848	6.2	0
1	Alterations in gut microbiota and metabolites associated with altitude-induced cardiac hypertrophy in rats during hypobaric hypoxia challenge.. <i>Science China Life Sciences</i> , 2022 , 1	8.5	0