Zhenjiang Xu

List of Publications by Year in Descending Order

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	Gut Microbiome-Targeted Modulations Regulate Metabolic Profiles and Alleviate Altitude-Related Cardiac Hypertrophy in Rats.. *Microbiology Spectrum*, **2022**, e0105321	8.9	2
51	Green Banana Flour Contributes to Gut Microbiota Recovery and Improves Colonic Barrier Integrity in Mice Following Antibiotic Perturbation.. *Frontiers in Nutrition*, **2022**, 9, 832848	6.2	0
50	Alterations in gut microbiota and metabolites associated with altitude-induced cardiac hypertrophy in rats during hypobaric hypoxia challenge.. *Science China Life Sciences*, **2022**, 1	8.5	0
49	Zebrafish model for human gut microbiome-related studies: advantages and limitations. *Medicine in Microecology*, **2021**, 8, 100042	4.3	0
48	Toxicant substitutes in immunological assays for mycotoxins detection: A mini review. *Food Chemistry*, **2021**, 344, 128589	8.5	5
47	PM2RA: A Framework for Detecting and Quantifying Relationship Alterations in Microbial Community. *Genomics, Proteomics and Bioinformatics*, **2021**, 19, 154-167	6.5	2
46	A Pilot Study of Microbial Succession in Human Rib Skeletal Remains during Terrestrial Decomposition. *MSphere*, **2021**, 6, e0045521	5	1
45	Gut microbiota from green tea polyphenol-dosed mice improves intestinal epithelial homeostasis and ameliorates experimental colitis. *Microbiome*, **2021**, 9, 184	16.6	39
44	Alteration in gut microbiota is associated with dysregulation of cytokines and glucocorticoid therapy in systemic lupus erythematosus. *Gut Microbes*, **2020**, 11, 1758-1773	8.8	24
43	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. *MSystems*, **2020**, 5,	7.6	12
42	Vitamin D metabolites and the gut microbiome in older men. *Nature Communications*, **2020**, 11, 5997	17.4	33
41	Puerarin Rebuilding the Mucus Layer and Regulating Mucin-Utilizing Bacteria to Relieve Ulcerative Colitis. *Journal of Agricultural and Food Chemistry*, **2020**, 68, 11402-11411	5.7	18
40	Intermittent Hypoxia and Hypercapnia Reproducibly Change the Gut Microbiome and Metabolome across Rodent Model Systems. *MSystems*, **2019**, 4,	7.6	13
39	Calour: an Interactive, Microbe-Centric Analysis Tool. *MSystems*, **2019**, 4,	7.6	20
38	Chlorogenic acid attenuates cadmium-induced intestinal injury in Sprague-Dawley rats. *Food and Chemical Toxicology*, **2019**, 133, 110751	4.7	16
37	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, **2019**, 37, 852-857	44.5	4050
36	An examination of data from the American Gut Project reveals that the dominance of the genus Bifidobacterium is associated with the diversity and robustness of the gut microbiota. *MicrobiologyOpen*, **2019**, 8, e939	3.4	12

35	Trace Evidence Potential in Postmortem Skin Microbiomes: From Death Scene to Morgue. *Journal of Forensic Sciences*, **2019**, 64, 791-798	1.8	19
34	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. *MSystems*, **2018**, 3,	7.6	181
33	Guiding longitudinal sampling in IBD cohorts. *Gut*, **2018**, 67, 1743-1745	19.2	23
32	Microbiome Data Accurately Predicts the Postmortem Interval Using Random Forest Regression Models. *Genes*, **2018**, 9,	4.2	42
31	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science **2018**,		78
30	Striped UniFrac: enabling microbiome analysis at unprecedented scale. *Nature Methods*, **2018**, 15, 847-848	28.6	40
29	Microbial effects of livestock manure fertilization on freshwater aquaculture ponds rearing tilapia (Oreochromis shiranus) and North African catfish (Clarias gariepinus). *MicrobiologyOpen*, **2018**, 7, e00716	3.4	13
28	Taxon-specific aerosolization of bacteria and viruses in an experimental ocean-atmosphere mesocosm. *Nature Communications*, **2018**, 9, 2017	17.4	61
27	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. *MSystems*, **2017**, 2,	7.6	763
26	Normalization and microbial differential abundance strategies depend upon data characteristics. *Microbiome*, **2017**, 5, 27	16.6	840
25	A communal catalogue reveals Earth's multiscale microbial diversity. *Nature*, **2017**, 551, 457-463	50.4	1076
24	Lifestyle chemistries from phones for individual profiling. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E7645-E7654	11.5	41
23	Tiny microbes, enormous impacts: what matters in gut microbiome studies?. *Genome Biology*, **2016**, 17, 217	18.3	86
22	Microbial community assembly and metabolic function during mammalian corpse decomposition. *Science*, **2016**, 351, 158-62	33.3	256
21	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. *ISME Journal*, **2016**, 10, 1669-81	11.9	365
20	Preservation Methods Differ in Fecal Microbiome Stability, Affecting Suitability for Field Studies. *MSystems*, **2016**, 1,	7.6	250
19	Experiment-Assisted Secondary Structure Prediction with RNAstructure. *Methods in Molecular Biology*, **2016**, 1490, 163-76	1.4	17
18	Secondary Structure Prediction of Single Sequences Using RNAstructure. *Methods in Molecular Biology*, **2016**, 1490, 15-34	1.4	13

17	Prediction of Secondary Structures Conserved in Multiple RNA Sequences. *Methods in Molecular Biology*, **2016**, 1490, 35-50	1.4	3
16	Ribosomal RNA, the lens into life. *Rna*, **2015**, 21, 692-4	5.8	3
15	Subsistence strategies in traditional societies distinguish gut microbiomes. *Nature Communications*, **2015**, 6, 6505	17.4	304
14	Prediction of Early Childhood Caries via Spatial-Temporal Variations of Oral Microbiota. *Cell Host and Microbe*, **2015**, 18, 296-306	23.4	123
13	Discovery of Novel ncRNA Sequences in Multiple Genome Alignments on the Basis of Conserved and Stable Secondary Structures. *PLoS ONE*, **2015**, 10, e0130200	3.7	21
12	Intestinal microbiota and immune related genes in sea cucumber (Apostichopus japonicus) response to dietary β-glucan supplementation. *Biochemical and Biophysical Research Communications*, **2015**, 458, 98-103	3.4	26
11	Which is more important for classifying microbial communities: who's there or what they can do?. *ISME Journal*, **2014**, 8, 2357-9	11.9	65
10	Structural basis for diversity in the SAM clan of riboswitches. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 6624-9	11.5	45
9	Advancing our understanding of the human microbiome using QIIME. *Methods in Enzymology*, **2013**, 531, 371-444	1.7	373
8	Statistical evaluation of improvement in RNA secondary structure prediction. *Nucleic Acids Research* , **2012**, 40, e26	20.1	22
7	Air proteins control differential TRAMP substrate specificity for nuclear RNA surveillance. *Rna*, **2012**, 18, 1934-45	5.8	23
6	Deep sequencing-based identification of small non-coding RNAs in Streptomyces coelicolor. *RNA Biology*, **2011**, 8, 468-77	4.8	71
5	Multilign: an algorithm to predict secondary structures conserved in multiple RNA sequences. *Bioinformatics*, **2011**, 27, 626-32	7.2	42
4	Effects of library size variance, sparsity, and compositionality on the analysis of microbiome data		5
3	Effects of library size variance, sparsity, and compositionality on the analysis of microbiome data		23
2	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
1	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138