

# Zhenjiang Xu

## List of Publications by Year in descending order

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Version: 2024-02-01

51  
papers

21,464  
citations

186209

28  
h-index

182361

51  
g-index

59  
all docs

59  
docs citations

59  
times ranked

24987  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gut Microbiome-Targeted Modulations Regulate Metabolic Profiles and Alleviate Altitude-Related Cardiac Hypertrophy in Rats. <i>Microbiology Spectrum</i> , 2022, 10, e0105321.	1.2	10
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.	1.6	5
3	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, 65, 2093-2113.	2.3	19
4	Microbial and Nonvolatile Chemical Diversities of Chinese Dark Teas Are Differed by Latitude and Pile Fermentation. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 5701-5714.	2.4	11
5	Diurnal and eating-associated microbial patterns revealed via high-frequency saliva sampling. <i>Genome Research</i> , 2022, 32, 1112-1123.	2.4	3
6	Toxicant substitutes in immunological assays for mycotoxins detection: A mini review. <i>Food Chemistry</i> , 2021, 344, 128589.	4.2	14
7	PM2RA: A Framework for Detecting and Quantifying Relationship Alterations in Microbial Community. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 154-167.	3.0	4
8	Zebrafish model for human gut microbiome-related studies: advantages and limitations. <i>Medicine in Microecology</i> , 2021, 8, 100042.	0.7	17
9	A Pilot Study of Microbial Succession in Human Rib Skeletal Remains during Terrestrial Decomposition. <i>MSphere</i> , 2021, 6, e0045521.	1.3	12
10	Gut microbiota from green tea polyphenol-dosed mice improves intestinal epithelial homeostasis and ameliorates experimental colitis. <i>Microbiome</i> , 2021, 9, 184.	4.9	259
11	Vitamin D metabolites and the gut microbiome in older men. <i>Nature Communications</i> , 2020, 11, 5997.	5.8	88
12	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.	2.4	43
13	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.	4.3	73
14	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , 2020, 5, .	1.7	16
15	Chlorogenic acid attenuates cadmium-induced intestinal injury in Sprague-Dawley rats. <i>Food and Chemical Toxicology</i> , 2019, 133, 110751.	1.8	31
16	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
17	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.	1.2	27
18	Intermittent Hypoxia and Hypercapnia Reproducibly Change the Gut Microbiome and Metabolome across Rodent Model Systems. <i>MSystems</i> , 2019, 4, .	1.7	24

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19	Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , 2019, 4, .	1.7	28
20	Trace Evidence Potential in Postmortem Skin Microbiomes: From Death Scene to Morgue. <i>Journal of Forensic Sciences</i> , 2019, 64, 791-798.	0.9	40
21	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , 2018, 3, .	1.7	376
22	Guiding longitudinal sampling in IBD cohorts. <i>Gut</i> , 2018, 67, 1743-1745.	6.1	32
23	Striped UniFrac: enabling microbiome analysis at unprecedented scale. <i>Nature Methods</i> , 2018, 15, 847-848.	9.0	71
24	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.	1.2	23
25	Taxon-specific aerosolization of bacteria and viruses in an experimental ocean-atmosphere mesocosm. <i>Nature Communications</i> , 2018, 9, 2017.	5.8	103
26	Microbiome Data Accurately Predicts the Postmortem Interval Using Random Forest Regression Models. <i>Genes</i> , 2018, 9, 104.	1.0	80
27	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017, 2, .	1.7	1,339
28	Normalization and microbial differential abundance strategies depend upon data characteristics. <i>Microbiome</i> , 2017, 5, 27.	4.9	1,434
29	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
30	Preservation Methods Differ in Fecal Microbiome Stability, Affecting Suitability for Field Studies. <i>MSystems</i> , 2016, 1, .	1.7	367
31	Experiment-Assisted Secondary Structure Prediction with RNAstructure. <i>Methods in Molecular Biology</i> , 2016, 1490, 163-176.	0.4	20
32	Secondary Structure Prediction of Single Sequences Using RNAstructure. <i>Methods in Molecular Biology</i> , 2016, 1490, 15-34.	0.4	21
33	Prediction of Secondary Structures Conserved in Multiple RNA Sequences. <i>Methods in Molecular Biology</i> , 2016, 1490, 35-50.	0.4	7
34	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.	3.3	55
35	Tiny microbes, enormous impacts: what matters in gut microbiome studies?. <i>Genome Biology</i> , 2016, 17, 217.	3.8	128
36	Microbial community assembly and metabolic function during mammalian corpse decomposition. <i>Science</i> , 2016, 351, 158-162.	6.0	381

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37	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016, 10, 1669-1681.	4.4	593
38	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.	1.1	26
39	Intestinal microbiota and immune related genes in sea cucumber ( <i>Apostichopus japonicus</i> ) response to dietary $\beta$ -glucan supplementation. <i>Biochemical and Biophysical Research Communications</i> , 2015, 458, 98-103.	1.0	45
40	Ribosomal RNA, the lens into life. <i>Rna</i> , 2015, 21, 692-694.	1.6	3
41	Subsistence strategies in traditional societies distinguish gut microbiomes. <i>Nature Communications</i> , 2015, 6, 6505.	5.8	449
42	Prediction of Early Childhood Caries via Spatial-Temporal Variations of Oral Microbiota. <i>Cell Host and Microbe</i> , 2015, 18, 296-306.	5.1	204
43	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, 6624-6629.	3.3	57
44	Which is more important for classifying microbial communities: who's there or what they can do?. <i>ISME Journal</i> , 2014, 8, 2357-2359.	4.4	82
45	Advancing Our Understanding of the Human Microbiome Using QIIME. <i>Methods in Enzymology</i> , 2013, 531, 371-444.	0.4	553
46	Statistical evaluation of improvement in RNA secondary structure prediction. <i>Nucleic Acids Research</i> , 2012, 40, e26-e26.	6.5	23
47	Air proteins control differential TRAMP substrate specificity for nuclear RNA surveillance. <i>Rna</i> , 2012, 18, 1934-1945.	1.6	25
48	Deep sequencing-based identification of small non-coding RNAs in <i>Streptomyces coelicolor</i> . <i>RNA Biology</i> , 2011, 8, 468-477.	1.5	100
49	Multalign: an algorithm to predict secondary structures conserved in multiple RNA sequences. <i>Bioinformatics</i> , 2011, 27, 626-632.	1.8	54
50	SEQEL: a tool for biological sequence manipulation in Emacs. <i>Bioinformatics Advances</i> , 0, , .	0.9	0
51	Cancer type classification using plasma cell-free RNAs derived from human and microbes. <i>ELife</i> , 0, 11, .	2.8	23