Zhenjiang Xu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7698183/publications.pdf Version: 2024-02-01



ΖΗΕΝΙΙΑΝΟ ΧΙΙ

#	Article	IF	CITATIONS
1	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
2	A communal catalogue reveals Earth's multiscale microbial diversity. Nature, 2017, 551, 457-463.	13.7	1,942
3	Normalization and microbial differential abundance strategies depend upon data characteristics. Microbiome, 2017, 5, 27.	4.9	1,434
4	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. MSystems, 2017, 2, .	1.7	1,339
5	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. ISME Journal, 2016, 10, 1669-1681.	4.4	593
6	Advancing Our Understanding of the Human Microbiome Using QIIME. Methods in Enzymology, 2013, 531, 371-444.	0.4	553
7	Subsistence strategies in traditional societies distinguish gut microbiomes. Nature Communications, 2015, 6, 6505.	5.8	449
8	Microbial community assembly and metabolic function during mammalian corpse decomposition. Science, 2016, 351, 158-162.	6.0	381
9	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. MSystems, 2018, 3, .	1.7	376
10	Preservation Methods Differ in Fecal Microbiome Stability, Affecting Suitability for Field Studies. MSystems, 2016, 1, .	1.7	367
11	Gut microbiota from green tea polyphenol-dosed mice improves intestinal epithelial homeostasis and ameliorates experimental colitis. Microbiome, 2021, 9, 184.	4.9	259
12	Prediction of Early Childhood Caries via Spatial-Temporal Variations of Oral Microbiota. Cell Host and Microbe, 2015, 18, 296-306.	5.1	204
13	Tiny microbes, enormous impacts: what matters in gut microbiome studies?. Genome Biology, 2016, 17, 217.	3.8	128
14	Taxon-specific aerosolization of bacteria and viruses in an experimental ocean-atmosphere mesocosm. Nature Communications, 2018, 9, 2017.	5.8	103
15	Deep sequencing-based identification of small non-coding RNAs inStreptomyces coelicolor. RNA Biology, 2011, 8, 468-477.	1.5	100
16	Vitamin D metabolites and the gut microbiome in older men. Nature Communications, 2020, 11, 5997.	5.8	88
17	Which is more important for classifying microbial communities: who's there or what they can do?. ISME Journal, 2014, 8, 2357-2359.	4.4	82
18	Microbiome Data Accurately Predicts the Postmortem Interval Using Random Forest Regression Models. Genes, 2018, 9, 104.	1.0	80

ZHENJIANG XU

#	Article	IF	CITATIONS
19	Alteration in gut microbiota is associated with dysregulation of cytokines and glucocorticoid therapy in systemic lupus erythematosus. Gut Microbes, 2020, 11, 1758-1773.	4.3	73
20	Striped UniFrac: enabling microbiome analysis at unprecedented scale. Nature Methods, 2018, 15, 847-848.	9.0	71
21	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, 6624-6629.	3.3	57
22	Lifestyle chemistries from phones for individual profiling. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7645-E7654.	3.3	55
23	Multilign: an algorithm to predict secondary structures conserved in multiple RNA sequences. Bioinformatics, 2011, 27, 626-632.	1.8	54
24	Intestinal microbiota and immune related genes in sea cucumber (Apostichopus japonicus) response to dietary Î ² -glucan supplementation. Biochemical and Biophysical Research Communications, 2015, 458, 98-103.	1.0	45
25	Puerarin Rebuilding the Mucus Layer and Regulating Mucin-Utilizing Bacteria to Relieve Ulcerative Colitis. Journal of Agricultural and Food Chemistry, 2020, 68, 11402-11411.	2.4	43
26	Trace Evidence Potential in Postmortem Skin Microbiomes: From Death Scene to Morgue. Journal of Forensic Sciences, 2019, 64, 791-798.	0.9	40
27	Guiding longitudinal sampling in IBD cohorts. Gut, 2018, 67, 1743-1745.	6.1	32
28	Chlorogenic acid attenuates cadmium-induced intestinal injury in Sprague–Dawley rats. Food and Chemical Toxicology, 2019, 133, 110751.	1.8	31
29	Calour: an Interactive, Microbe-Centric Analysis Tool. MSystems, 2019, 4, .	1.7	28
30	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. MicrobiologyOpen, 2019, 8, e939.	1.2	27
31	Discovery of Novel ncRNA Sequences in Multiple Genome Alignments on the Basis of Conserved and Stable Secondary Structures. PLoS ONE, 2015, 10, e0130200.	1.1	26
32	Air proteins control differential TRAMP substrate specificity for nuclear RNA surveillance. Rna, 2012, 18, 1934-1945.	1.6	25
33	Intermittent Hypoxia and Hypercapnia Reproducibly Change the Gut Microbiome and Metabolome across Rodent Model Systems. MSystems, 2019, 4, .	1.7	24
34	Statistical evaluation of improvement in RNA secondary structure prediction. Nucleic Acids Research, 2012, 40, e26-e26.	6.5	23
35	Microbial effects of livestock manure fertilization on freshwater aquaculture ponds rearing tilapia (<i>Oreochromis shiranus</i>) and North African catfish (<i>Clarias gariepinus</i>). MicrobiologyOpen, 2018, 7, e00716.	1.2	23
36	Cancer type classification using plasma cell-free RNAs derived from human and microbes. ELife, 0, 11, .	2.8	23

ZHENJIANG XU

#	Article	lF	CITATIONS
37	Secondary Structure Prediction of Single Sequences Using RNAstructure. Methods in Molecular Biology, 2016, 1490, 15-34.	0.4	21
38	Experiment-Assisted Secondary Structure Prediction with RNAstructure. Methods in Molecular Biology, 2016, 1490, 163-176.	0.4	20
39	Alterations in gut microbiota and metabolites associated with altitude-induced cardiac hypertrophy in rats during hypobaric hypoxia challenge. Science China Life Sciences, 2022, 65, 2093-2113.	2.3	19
40	Zebrafish model for human gut microbiome-related studies: advantages and limitations. Medicine in Microecology, 2021, 8, 100042.	0.7	17
41	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. MSystems, 2020, 5, .	1.7	16
42	Toxicant substitutes in immunological assays for mycotoxins detection: A mini review. Food Chemistry, 2021, 344, 128589.	4.2	14
43	A Pilot Study of Microbial Succession in Human Rib Skeletal Remains during Terrestrial Decomposition. MSphere, 2021, 6, e0045521.	1.3	12
44	Microbial and Nonvolatile Chemical Diversities of Chinese Dark Teas Are Differed by Latitude and Pile Fermentation. Journal of Agricultural and Food Chemistry, 2022, 70, 5701-5714.	2.4	11
45	Gut Microbiome-Targeted Modulations Regulate Metabolic Profiles and Alleviate Altitude-Related Cardiac Hypertrophy in Rats. Microbiology Spectrum, 2022, 10, e0105321.	1.2	10
46	Prediction of Secondary Structures Conserved in Multiple RNA Sequences. Methods in Molecular Biology, 2016, 1490, 35-50.	0.4	7
47	Green Banana Flour Contributes to Gut Microbiota Recovery and Improves Colonic Barrier Integrity in Mice Following Antibiotic Perturbation. Frontiers in Nutrition, 2022, 9, 832848.	1.6	5
48	PM2RA: A Framework for Detecting and Quantifying Relationship Alterations in Microbial Community. Genomics, Proteomics and Bioinformatics, 2021, 19, 154-167.	3.0	4
49	Ribosomal RNA, the lens into life. Rna, 2015, 21, 692-694.	1.6	3
50	Diurnal and eating-associated microbial patterns revealed via high-frequency saliva sampling. Genome Research, 2022, 32, 1112-1123.	2.4	3
51	SEQEL: a tool for biological sequence manipulation in Emacs. Bioinformatics Advances, 0, , .	0.9	0