

Menghui Zhang

List of Publications by Year in Descending Order

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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.

38 papers	5,993 citations	23 h-index	42 g-index
42 ext. papers	7,745 ext. citations	6.7 avg, IF	4.97 L-index

#	Paper	IF	Citations
38	Rifaximin Ameliorates Non-alcoholic Steatohepatitis in Mice Through Regulating gut Microbiome-Related Bile Acids.. <i>Frontiers in Pharmacology</i> , 2022 , 13, 841132	5.6	1
37	Gut Microbial SNPs Induced by High-Fiber Diet Dominate Nutrition Metabolism and Environmental Adaption of in Obese Children. <i>Frontiers in Microbiology</i> , 2021 , 12, 683714	5.7	0
36	The deletion of <i>Schizosaccharomyces pombe</i> decreased the production of flavor-related metabolites during traditional Baijiu fermentation. <i>Food Research International</i> , 2021 , 140, 109872	7	2
35	Suppressed inflammation in obese children induced by a high-fiber diet is associated with the attenuation of gut microbial virulence factor genes. <i>Virulence</i> , 2021 , 12, 1754-1770	4.7	3
34	miRNA-Gene Regulatory Network in Gnotobiotic Mice Stimulated by Dysbiotic Gut Microbiota Transplanted From a Genetically Obese Child. <i>Frontiers in Microbiology</i> , 2019 , 10, 1517	5.7	5
33	Gastrointestinal Microbiology in the Normal Host 2019 , 362-362		
32	can Reduce Acetic Acid Produced by Spontaneous Fermentation Microbiota. <i>Microorganisms</i> , 2019 , 7,	4.9	10
31	Gut bacteria selectively promoted by dietary fibers alleviate type 2 diabetes. <i>Science</i> , 2018 , 359, 1151-1156	35.9	904
30	Genetically Obese Human Gut Microbiota Induces Liver Steatosis in Germ-Free Mice Fed on Normal Diet. <i>Frontiers in Microbiology</i> , 2018 , 9, 1602	5.7	25
29	Structural Alteration of Gut Microbiota during the Amelioration of Human Type 2 Diabetes with Hyperlipidemia by Metformin and a Traditional Chinese Herbal Formula: a Multicenter, Randomized, Open Label Clinical Trial. <i>MBio</i> , 2018 , 9,	7.8	139
28	Genomic Microdiversity of Underlying Differential Strain-Level Responses to Dietary Carbohydrate Intervention. <i>MBio</i> , 2017 , 8,	7.8	31
27	Systematic identification of the protein substrates of UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase-T1/T2/T3 using a human proteome microarray. <i>Proteomics</i> , 2017 , 17, 1600485	4.8	8
26	Gut Microbial Dysbiosis Is Associated with Altered Hepatic Functions and Serum Metabolites in Chronic Hepatitis B Patients. <i>Frontiers in Microbiology</i> , 2017 , 8, 2222	5.7	97
25	The structural alteration of gut microbiota in low-birth-weight mice undergoing accelerated postnatal growth. <i>Scientific Reports</i> , 2016 , 6, 27780	4.9	18
24	Diminution of the gut resistome after a gut microbiota-targeted dietary intervention in obese children. <i>Scientific Reports</i> , 2016 , 6, 24030	4.9	22
23	Dandruff is associated with the conjoined interactions between host and microorganisms. <i>Scientific Reports</i> , 2016 , 6, 24877	4.9	67
22	Draft genome sequence of <i>Thauera</i> sp. DTG from a denitrifying quinoline degrading microbial consortium. <i>Applied Environmental Biotechnology</i> , 2016 , 1, 38	1.8	2

21	Regulated Inflammation and Lipid Metabolism in Colon mRNA Expressions of Obese Germfree Mice Responding to B29 Combined with the High Fat Diet. <i>Frontiers in Microbiology</i> , 2016 , 7, 1786	5.7	7
20	Dietary Modulation of Gut Microbiota Contributes to Alleviation of Both Genetic and Simple Obesity in Children. <i>EBioMedicine</i> , 2015 , 2, 968-84	8.8	198
19	A Filifactor alocis-centered co-occurrence group associates with periodontitis across different oral habitats. <i>Scientific Reports</i> , 2015 , 5, 9053	4.9	45
18	Modulation of gut microbiota by berberine and metformin during the treatment of high-fat diet-induced obesity in rats. <i>Scientific Reports</i> , 2015 , 5, 14405	4.9	363
17	The bamboo-eating giant panda harbors a carnivore-like gut microbiota, with excessive seasonal variations. <i>MBio</i> , 2015 , 6, e00022-15	7.8	142
16	A phylo-functional core of gut microbiota in healthy young Chinese cohorts across lifestyles, geography and ethnicities. <i>ISME Journal</i> , 2015 , 9, 1979-90	11.9	231
15	A gut microbiota-targeted dietary intervention for amelioration of chronic inflammation underlying metabolic syndrome. <i>FEMS Microbiology Ecology</i> , 2014 , 87, 357-67	4.3	224
14	The abundance of fecal <i>Faecalibacterium prausnitzii</i> in relation to obesity and gender in Chinese adults. <i>Archives of Microbiology</i> , 2014 , 196, 73-7	3	33
13	Structural modulation of gut microbiota in life-long calorie-restricted mice. <i>Nature Communications</i> , 2013 , 4, 2163	17.4	305
12	Up-regulation of type I collagen during tumorigenesis of colorectal cancer revealed by quantitative proteomic analysis. <i>Journal of Proteomics</i> , 2013 , 94, 473-85	3.9	71
11	Metabonomics identifies serum metabolite markers of colorectal cancer. <i>Journal of Proteome Research</i> , 2013 , 12, 3000-9	5.6	125
10	Structural segregation of gut microbiota between colorectal cancer patients and healthy volunteers. <i>ISME Journal</i> , 2012 , 6, 320-9	11.9	720
9	Structural changes of gut microbiota during berberine-mediated prevention of obesity and insulin resistance in high-fat diet-fed rats. <i>PLoS ONE</i> , 2012 , 7, e42529	3.7	339
8	Structural resilience of the gut microbiota in adult mice under high-fat dietary perturbations. <i>ISME Journal</i> , 2012 , 6, 1848-57	11.9	294
7	Development of a fluorophore-ribosomal DNA restriction typing method for monitoring structural shifts of microbial communities. <i>Archives of Microbiology</i> , 2011 , 193, 341-50	3	4
6	Structural shifts of gut microbiota as surrogate endpoints for monitoring host health changes induced by carcinogen exposure. <i>FEMS Microbiology Ecology</i> , 2010 , 73, 577-86	4.3	40
5	Interactions between gut microbiota, host genetics and diet relevant to development of metabolic syndromes in mice. <i>ISME Journal</i> , 2010 , 4, 232-41	11.9	633
4	Pattern extraction of structural responses of gut microbiota to rotavirus infection via multivariate statistical analysis of clone library data. <i>FEMS Microbiology Ecology</i> , 2009 , 70, 21-9	4.3	20

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| 3 | Symbiotic gut microbes modulate human metabolic phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 2117-22 | 11.5 | 825 |
| 2 | Evaluation of boosted regression trees (BRTs) and two-step BRT procedures to model and predict blood-brain barrier passage. <i>Journal of Chemometrics</i> , 2007 , 21, 280-291 | 1.6 | 11 |
| 1 | Minimizing spurious features in 16S rRNA gene amplicon sequencing | | 5 |