# Menghui Zhang

List of Publications by Year
in descending order



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|---|---|---|---|
| 39 papers | 8,730 citations | 218677 26 h-index | 315739 38 g-index |
| 42 all docs | 42 docs citations | 42 times ranked | 13610 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Gut bacteria selectively promoted by dietary fibers alleviate type 2 diabetes. Science, 2018, 359, 1151-1156. | 12.6 | 1,521 |
| 2 | Structural segregation of gut microbiota between colorectal cancer patients and healthy volunteers. ISME Journal, 2012, 6, 320-329. | 9.8 | 1,038 |
| 3 | Symbiotic gut microbes modulate human metabolic phenotypes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2117-2122. | 7.1 | 994 |
| 4 | Interactions between gut microbiota, host genetics and diet relevant to development of metabolic syndromes in mice. ISME Journal, 2010, 4, 232-241. | 9.8 | 845 |
| 5 | Modulation of gut microbiota by berberine and metformin during the treatment of high-fat diet-induced obesity in rats. Scientific Reports, 2015, 5, 14405. | 3.3 | 499 |
| 6 | Structural Changes of Gut Microbiota during Berberine-Mediated Prevention of Obesity and Insulin Resistance in High-Fat Diet-Fed Rats. PLoS ONE, 2012, 7, e42529. | 2.5 | 435 |
| 7 | Structural resilience of the gut microbiota in adult mice under high-fat dietary perturbations. ISME Journal, 2012, 6, 1848-1857. | 9.8 | 407 |
| 8 | Structural modulation of gut microbiota in life-long calorie-restricted mice. Nature Communications, 2013, 4, 2163. | 12.8 | 404 |
| 9 | A phylo-functional core of gut microbiota in healthy young Chinese cohorts across lifestyles, geography and ethnicities. ISME Journal, 2015, 9, 1979-1990. | 9.8 | 339 |
| 10 | A gut microbiota-targeted dietary intervention for amelioration of chronic inflammation underlying metabolic syndrome. FEMS Microbiology Ecology, 2014, 87, 357-367. | 2.7 | 338 |
| 11 | Dietary Modulation of Gut Microbiota Contributes to Alleviation of Both Genetic and Simple Obesity in Children. EBioMedicine, 2015, 2, 968-984. | 6.1 | 306 |
| 12 | The Bamboo-Eating Giant Panda Harbors a Carnivore-Like Gut Microbiota, with Excessive Seasonal Variations. MBio, 2015, 6, e00022-15. | 4.1 | 282 |
| 13 | 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. MBio, 2018, 9, . | 4.1 | 258 |
| 14 | Gut Microbial Dysbiosis Is Associated with Altered Hepatic Functions and Serum Metabolites in Chronic Hepatitis B Patients. Frontiers in Microbiology, 2017, 8, 2222. | 3.5 | 172 |
| 15 | Metabonomics Identifies Serum Metabolite Markers of Colorectal Cancer. Journal of Proteome Research, 2013, 12, 3000-3009. | 3.7 | 163 |
| 16 | Dandruff is associated with the conjoined interactions between host and microorganisms. Scientific Reports, 2016, 6, 24877. | 3.3 | 108 |
| 17 | Up-regulation of type I collagen during tumorigenesis of colorectal cancer revealed by quantitative proteomic analysis. Journal of Proteomics, 2013, 94, 473-485. | 2.4 | 92 |
| 18 | A Filifactor alocis-centered co-occurrence group associates with periodontitis across different oral habitats. Scientific Reports, 2015, 5, 9053. | 3.3 | 78 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Genetically Obese Human Gut Microbiota Induces Liver Steatosis in Germ-Free Mice Fed on Normal Diet. Frontiers in Microbiology, 2018, 9, 1602. | 3.5 | 48 |
| 20 | The abundance of fecal Faecalibacterium prausnitzii in relation to obesity and gender in Chinese adults. Archives of Microbiology, 2014, 196, 73-77. | 2.2 | 47 |
| 21 | Structural shifts of gut microbiota as surrogate endpoints for monitoring host health changes induced by carcinogen exposure. FEMS Microbiology Ecology, 2010, 73, no-no. | 2.7 | 44 |
| 22 | Genomic Microdiversity of Bifidobacterium pseudocatenulatum Underlying Differential Strain-Level Responses to Dietary Carbohydrate Intervention. MBio, 2017, 8, . | 4.1 | 43 |
| 23 | Pattern extraction of structural responses of gut microbiota to rotavirus infection via multivariate statistical analysis of clone library data. FEMS Microbiology Ecology, 2009, 70, 177-185. | 2.7 | 34 |
| 24 | The structural alteration of gut microbiota in low-birth-weight mice undergoing accelerated postnatal growth. Scientific Reports, 2016, 6, 27780. | 3.3 | 34 |
| 25 | Diminution of the gut resistome after a gut microbiota-targeted dietary intervention in obese children. Scientific Reports, 2016, 6, 24030. | 3.3 | 33 |
| 26 | Schizosaccharomyces pombe Can Reduce Acetic Acid Produced by Baijiu Spontaneous Fermentation Microbiota. Microorganisms, 2019, 7, 606. | 3.6 | 20 |
| 27 | Regulated Inflammation and Lipid Metabolism in Colon mRNA Expressions of Obese Germfree Mice Responding to Enterobacter cloacae B29 Combined with the High Fat Diet. Frontiers in Microbiology, 2016, 7, 1786. | 3.5 | 18 |
| 28 | Rifaximin Ameliorates Non-alcoholic Steatohepatitis in Mice Through Regulating gut Microbiome-Related Bile Acids. Frontiers in Pharmacology, 2022, 13, 841132. | 3.5 | 14 |
| 29 | Evaluation of boosted regression trees (BRTs) and twoâ€step BRT procedures to model and predict bloodâ€brain barrier passage. Journal of Chemometrics, 2007, 21, 280-291. | 1.3 | 13 |
| 30 | Systematic identification of the protein substrates of UDPâ€GalNAc:polypeptide Nâ€acetylgalactosaminyltransferaseâ€T1/T2/T3 using a human proteome microarray. Proteomics, 2017, 17, 1600485. | 2.2 | 10 |
| 31 | The deletion of Schizosaccharomyces pombe decreased the production of flavor-related metabolites during traditional Baijiu fermentation. Food Research International, 2021, 140, 109872. | 6.2 | 10 |
| 32 | miRNA-Gene Regulatory Network in Gnotobiotic Mice Stimulated by Dysbiotic Gut Microbiota Transplanted From a Genetically Obese Child. Frontiers in Microbiology, 2019, 10, 1517. | 3.5 | 8 |
| 33 | Gut Microbial SNPs Induced by High-Fiber Diet Dominate Nutrition Metabolism and Environmental Adaption of Faecalibacterium prausnitzii in Obese Children. Frontiers in Microbiology, 2021, 12, 683714. | 3.5 | 8 |
| 34 | Suppressed inflammation in obese children induced by a high-fiber diet is associated with the attenuation of gut microbial virulence factor genes. Virulence, 2021, 12, 1754-1770. | 4.4 | 6 |
| 35 | Draft genome sequence of Thauera sp. DTG from a denitrifying quinoline degrading microbial consortium. Applied Environmental Biotechnology, 2016, 1, 38. | 2.4 | 5 |
| 36 | Development of a fluorophore-ribosomal DNA restriction typing method for monitoring structural shifts of microbial communities. Archives of Microbiology, 2011, 193, 341-50. | 2.2 | 4 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | Metagenome-Scale Metabolic Network Suggests Folate Produced by Bifidobacterium longum Might Contribute to High-Fiber-Diet-Induced Weight Loss in a Praderâ€“Willi Syndrome Child. Microorganisms, 2021, 9, 2493. | 3.6 | 1 |
| 38 | Microbiota profiling on itchy scalp with undetermined origin. Archives of Microbiology, 2022, 204, . | 2.2 | 1 |
| 39 | Gastrointestinal Microbiology in the Normal Host. , 2019, , 362-362. | | 0 |