

Jun Wang

List of Publications by Citations

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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.

54
papers

28,215
citations

30
h-index

59
g-index

59
ext. papers

36,115
ext. citations

20.6
avg, IF

5.69
L-index

#	Paper	IF	Citations
54	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010 , 464, 59-65	50.4	7044
53	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011 , 473, 174-80	50.4	4240
52	A metagenome-wide association study of gut microbiota in type 2 diabetes. <i>Nature</i> , 2012 , 490, 55-60	50.4	3779
51	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013 , 500, 541-6	50.4	2584
50	Dynamics and Stabilization of the Human Gut Microbiome during the First Year of Life. <i>Cell Host and Microbe</i> , 2015 , 17, 690-703	23.4	1367
49	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016 , 352, 560-4	33.3	1120
48	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015 , 528, 262-266	50.4	1107
47	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014 , 32, 834-41	44.5	1088
46	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016 , 352, 565-9	33.3	929
45	The oral and gut microbiomes are perturbed in rheumatoid arthritis and partly normalized after treatment. <i>Nature Medicine</i> , 2015 , 21, 895-905	50.5	849
44	The neuroactive potential of the human gut microbiota in quality of life and depression. <i>Nature Microbiology</i> , 2019 , 4, 623-632	26.6	651
43	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014 , 32, 822-8	44.5	624
42	Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer. <i>Gut</i> , 2017 , 66, 70-78	19.2	488
41	Quantitative microbiome profiling links gut community variation to microbial load. <i>Nature</i> , 2017 , 551, 507-511	50.4	475
40	Genome-wide association analysis identifies variation in vitamin D receptor and other host factors influencing the gut microbiota. <i>Nature Genetics</i> , 2016 , 48, 1396-1406	36.3	369
39	Donor Species Richness Determines Faecal Microbiota Transplantation Success in Inflammatory Bowel Disease. <i>Journal of Crohns and Colitis</i> , 2016 , 10, 387-94	1.5	183
38	Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome. <i>Cell Systems</i> , 2016 , 3, 572-584.e3	10.6	172

37	Lipocalin 2 Protects from Inflammation and Tumorigenesis Associated with Gut Microbiota Alterations. <i>Cell Host and Microbe</i> , 2016 , 19, 455-69	23.4	144
36	The role of biogeography in shaping diversity of the intestinal microbiota in house mice. <i>Molecular Ecology</i> , 2013 , 22, 1904-16	5.7	121
35	Dietary history contributes to enterotype-like clustering and functional metagenomic content in the intestinal microbiome of wild mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E2703-10	11.5	107
34	Analysis of intestinal microbiota in hybrid house mice reveals evolutionary divergence in a vertebrate hologenome. <i>Nature Communications</i> , 2015 , 6, 6440	17.4	83
33	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021 , 53, 156-165	36.3	80
32	Type I interferon signalling in the intestinal epithelium affects Paneth cells, microbial ecology and epithelial regeneration. <i>Gut</i> , 2014 , 63, 1921-31	19.2	68
31	Epithelial calcineurin controls microbiota-dependent intestinal tumor development. <i>Nature Medicine</i> , 2016 , 22, 506-15	50.5	68
30	Genome-wide mapping of gene-microbiota interactions in susceptibility to autoimmune skin blistering. <i>Nature Communications</i> , 2013 , 4, 2462	17.4	62
29	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. <i>Nature Microbiology</i> , 2020 , 5, 1079-1087	26.6	55
28	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018 , 6, 101	16.6	53
27	Neutrality in the Metaorganism. <i>PLoS Biology</i> , 2019 , 17, e3000298	9.7	35
26	Low eukaryotic viral richness is associated with faecal microbiota transplantation success in patients with UC. <i>Gut</i> , 2018 , 67, 1558-1559	19.2	33
25	Integrated gut virome and bacteriome dynamics in COVID-19 patients. <i>Gut Microbes</i> , 2021 , 13, 1-21	8.8	32
24	Boolean analysis reveals systematic interactions among low-abundance species in the human gut microbiome. <i>PLoS Computational Biology</i> , 2017 , 13, e1005361	5	26
23	Of genes and microbes: solving the intricacies in host genomes. <i>Protein and Cell</i> , 2018 , 9, 446-461	7.2	21
22	Antidiabetic Effects of Gegen Qinlian Decoction via the Gut Microbiota Are Attributable to Its Key Ingredient Berberine. <i>Genomics, Proteomics and Bioinformatics</i> , 2020 , 18, 721-736	6.5	21
21	The interplay between host genetics and the gut microbiome reveals common and distinct microbiome features for complex human diseases. <i>Microbiome</i> , 2020 , 8, 145	16.6	21
20	Gut microbiota, inflammation, and molecular signatures of host response to infection. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 792-802	4	21

19	Application of the distance-based F test in an mGWAS investigating diversity of intestinal microbiota identifies variants in SLC9A8 (NHE8) and 3 other loci. <i>Gut Microbes</i> , 2018 , 9, 68-75	8.8	16
18	Identification of antimicrobial peptides from the human gut microbiome using deep learning.. <i>Nature Biotechnology</i> , 2022 ,	44.5	11
17	Seven facts and five initiatives for gut microbiome research. <i>Protein and Cell</i> , 2020 , 11, 391-400	7.2	10
16	Sucrase-isomaltase 15Phe IBS risk variant in relation to dietary carbohydrates and faecal microbiota composition. <i>Gut</i> , 2019 , 68, 177-178	19.2	10
15	Profiling of Human Gut Virome with Oxford Nanopore Technology. <i>Medicine in Microecology</i> , 2020 , 4, 100012	4.3	9
14	Large-scale association analyses identify host factors influencing human gut microbiome composition		9
13	Targeting RNA with Next- and Third-Generation Sequencing Improves Pathogen Identification in Clinical Samples. <i>Advanced Science</i> , 2021 , 8, e2102593	13.6	4
12	Neutrality in the Metaorganism		4
11	Gut microbiomes of bigheaded carps and hybrids provide insights into invasion: A hologenome perspective. <i>Evolutionary Applications</i> , 2021 , 14, 735-745	4.8	4
10	Strengthening the functional research on the interaction between host genes and microbiota. <i>Science China Life Sciences</i> , 2020 , 63, 929-932	8.5	3
9	Draft Genome Sequences of 11 Staphylococcus epidermidis Strains Isolated from Wild Mouse Species. <i>Genome Announcements</i> , 2014 , 2,		2
8	Deficiency in X-linked inhibitor of apoptosis protein promotes susceptibility to microbial triggers of intestinal inflammation. <i>Science Immunology</i> , 2021 , 6, eabf7473	28	2
7	Proinflammatory and autoimmunogenic gut microbiome in systemic lupus erythematosus		2
6	Gut microbiota and inflammatory bowel disease.. <i>WIREs Mechanisms of Disease</i> , 2022 , 14, e1540	0.3	2
5	Expanding the Scope of Multivariate Regression Approaches in Cross-Omics Research. <i>Engineering</i> , 2021 , 7, 1725-1725	9.7	1
4	Microbial characteristics across different tongue coating types in a healthy population. <i>Journal of Oral Microbiology</i> , 2021 , 13, 1946316	6.3	1
3	Innate lymphoid cells and gastrointestinal disease. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 763-770	4	1
2	alleviates dextran sulfate sodium-induced experimental colitis and promotes intestinal lymphatic vessel regeneration in mice.. <i>Annals of Translational Medicine</i> , 2022 , 10, 341	3.2	1

- 1 Short- and long-read metagenomics expand individualized structural variations in gut microbiomes. *Nature Communications*, **2022**, 13, 17.4 1