

# Jun Wang

## 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.

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	Identification of antimicrobial peptides from the human gut microbiome using deep learning.. <i>Nature Biotechnology</i> , <b>2022</b> ,	44.5	11
53	alleviates dextran sulfate sodium-induced experimental colitis and promotes intestinal lymphatic vessel regeneration in mice.. <i>Annals of Translational Medicine</i> , <b>2022</b> , 10, 341	3.2	1
52	Gut microbiota and inflammatory bowel disease.. <i>WIREs Mechanisms of Disease</i> , <b>2022</b> , 14, e1540	0.3	2
51	Short- and long-read metagenomics expand individualized structural variations in gut microbiomes. <i>Nature Communications</i> , <b>2022</b> , 13,	17.4	1
50	Deficiency in X-linked inhibitor of apoptosis protein promotes susceptibility to microbial triggers of intestinal inflammation. <i>Science Immunology</i> , <b>2021</b> , 6, eabf7473	28	2
49	Targeting RNA with Next- and Third-Generation Sequencing Improves Pathogen Identification in Clinical Samples. <i>Advanced Science</i> , <b>2021</b> , 8, e2102593	13.6	4
48	Expanding the Scope of Multivariate Regression Approaches in Cross-Omics Research. <i>Engineering</i> , <b>2021</b> , 7, 1725-1725	9.7	1
47	Gut microbiota, inflammation, and molecular signatures of host response to infection. <i>Journal of Genetics and Genomics</i> , <b>2021</b> , 48, 792-802	4	21
46	Gut microbiomes of bigheaded carps and hybrids provide insights into invasion: A hologenome perspective. <i>Evolutionary Applications</i> , <b>2021</b> , 14, 735-745	4.8	4
45	Microbial characteristics across different tongue coating types in a healthy population. <i>Journal of Oral Microbiology</i> , <b>2021</b> , 13, 1946316	6.3	1
44	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , <b>2021</b> , 53, 156-165	36.3	80
43	Innate lymphoid cells and gastrointestinal disease. <i>Journal of Genetics and Genomics</i> , <b>2021</b> , 48, 763-770	4	1
42	Integrated gut virome and bacteriome dynamics in COVID-19 patients. <i>Gut Microbes</i> , <b>2021</b> , 13, 1-21	8.8	32
41	Profiling of Human Gut Virome with Oxford Nanopore Technology. <i>Medicine in Microecology</i> , <b>2020</b> , 4, 100012	4.3	9
40	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. <i>Nature Microbiology</i> , <b>2020</b> , 5, 1079-1087	26.6	55
39	Seven facts and five initiatives for gut microbiome research. <i>Protein and Cell</i> , <b>2020</b> , 11, 391-400	7.2	10
38	Strengthening the functional research on the interaction between host genes and microbiota. <i>Science China Life Sciences</i> , <b>2020</b> , 63, 929-932	8.5	3

37	Antidiabetic Effects of Gegen Qinlian Decoction via the Gut Microbiota Are Attributable to Its Key Ingredient Berberine. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2020</b> , 18, 721-736	6.5	21
36	The interplay between host genetics and the gut microbiome reveals common and distinct microbiome features for complex human diseases. <i>Microbiome</i> , <b>2020</b> , 8, 145	16.6	21
35	Neutrality in the Metaorganism. <i>PLoS Biology</i> , <b>2019</b> , 17, e3000298	9.7	35
34	The neuroactive potential of the human gut microbiota in quality of life and depression. <i>Nature Microbiology</i> , <b>2019</b> , 4, 623-632	26.6	651
33	Sucrase-isomaltase 15Phe IBS risk variant in relation to dietary carbohydrates and faecal microbiota composition. <i>Gut</i> , <b>2019</b> , 68, 177-178	19.2	10
32	Of genes and microbes: solving the intricacies in host genomes. <i>Protein and Cell</i> , <b>2018</b> , 9, 446-461	7.2	21
31	Low eukaryotic viral richness is associated with faecal microbiota transplantation success in patients with UC. <i>Gut</i> , <b>2018</b> , 67, 1558-1559	19.2	33
30	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , <b>2018</b> , 6, 101	16.6	53
29	Application of the distance-based F test in an mGWAS investigating α diversity of intestinal microbiota identifies variants in SLC9A8 (NHE8) and 3 other loci. <i>Gut Microbes</i> , <b>2018</b> , 9, 68-75	8.8	16
28	Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer. <i>Gut</i> , <b>2017</b> , 66, 70-78	19.2	488
27	Quantitative microbiome profiling links gut community variation to microbial load. <i>Nature</i> , <b>2017</b> , 551, 507-511	50.4	475
26	Boolean analysis reveals systematic interactions among low-abundance species in the human gut microbiome. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005361	5	26
25	Donor Species Richness Determines Faecal Microbiota Transplantation Success in Inflammatory Bowel Disease. <i>Journal of Crohns and Colitis</i> , <b>2016</b> , 10, 387-94	1.5	183
24	Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome. <i>Cell Systems</i> , <b>2016</b> , 3, 572-584.e3	10.6	172
23	Epithelial calcineurin controls microbiota-dependent intestinal tumor development. <i>Nature Medicine</i> , <b>2016</b> , 22, 506-15	50.5	68
22	Lipocalin 2 Protects from Inflammation and Tumorigenesis Associated with Gut Microbiota Alterations. <i>Cell Host and Microbe</i> , <b>2016</b> , 19, 455-69	23.4	144
21	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , <b>2016</b> , 352, 565-9	33.3	929
20	Population-level analysis of gut microbiome variation. <i>Science</i> , <b>2016</b> , 352, 560-4	33.3	1120

19	Genome-wide association analysis identifies variation in vitamin D receptor and other host factors influencing the gut microbiota. <i>Nature Genetics</i> , <b>2016</b> , 48, 1396-1406	36.3	369
18	The oral and gut microbiomes are perturbed in rheumatoid arthritis and partly normalized after treatment. <i>Nature Medicine</i> , <b>2015</b> , 21, 895-905	50.5	849
17	Dynamics and Stabilization of the Human Gut Microbiome during the First Year of Life. <i>Cell Host and Microbe</i> , <b>2015</b> , 17, 690-703	23.4	1367
16	Analysis of intestinal microbiota in hybrid house mice reveals evolutionary divergence in a vertebrate hologenome. <i>Nature Communications</i> , <b>2015</b> , 6, 6440	17.4	83
15	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , <b>2015</b> , 528, 262-266	50.4	1107
14	Type I interferon signalling in the intestinal epithelium affects Paneth cells, microbial ecology and epithelial regeneration. <i>Gut</i> , <b>2014</b> , 63, 1921-31	19.2	68
13	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 822-8	44.5	624
12	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 834-41	44.5	1088
11	Draft Genome Sequences of 11 Staphylococcus epidermidis Strains Isolated from Wild Mouse Species. <i>Genome Announcements</i> , <b>2014</b> , 2,		2
10	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> , <b>2014</b> , 111, E2703-10	11.5	107
9	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , <b>2013</b> , 500, 541-6	50.4	2584
8	Genome-wide mapping of gene-microbiota interactions in susceptibility to autoimmune skin blistering. <i>Nature Communications</i> , <b>2013</b> , 4, 2462	17.4	62
7	The role of biogeography in shaping diversity of the intestinal microbiota in house mice. <i>Molecular Ecology</i> , <b>2013</b> , 22, 1904-16	5.7	121
6	A metagenome-wide association study of gut microbiota in type 2 diabetes. <i>Nature</i> , <b>2012</b> , 490, 55-60	50.4	3779
5	Enterotypes of the human gut microbiome. <i>Nature</i> , <b>2011</b> , 473, 174-80	50.4	4240
4	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , <b>2010</b> , 464, 59-65	50.4	7044
3	Large-scale association analyses identify host factors influencing human gut microbiome composition		9
2	Neutrality in the Metaorganism		4

1 Proinflammatory and autoimmunogenic gut microbiome in systemic lupus erythematosus

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