

Huijue Jia

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.

74
papers

9,976
citations

33
h-index

87
g-index

87
ext. papers

13,468
ext. citations

15.1
avg, IF

5.41
L-index

#	Paper	IF	Citations
74	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
73	Taxonomic structure and functional association of foxtail millet root microbiome. <i>GigaScience</i> , 2017 , 6, 1-12	7.6	1155
72	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014 , 32, 834-41	44.5	1088
71	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
70	Gut microbiome and serum metabolome alterations in obesity and after weight-loss intervention. <i>Nature Medicine</i> , 2017 , 23, 859-868	50.5	627
69	Gut microbiome development along the colorectal adenoma-carcinoma sequence. <i>Nature Communications</i> , 2015 , 6, 6528	17.4	614
68	The gut microbiome in atherosclerotic cardiovascular disease. <i>Nature Communications</i> , 2017 , 8, 845	17.4	575
67	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
66	The microbiota continuum along the female reproductive tract and its relation to uterine-related diseases. <i>Nature Communications</i> , 2017 , 8, 875	17.4	308
65	A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2015 , 33, 1103-8	44.5	295
64	Metagenome-wide association studies: fine-mining the microbiome. <i>Nature Reviews Microbiology</i> , 2016 , 14, 508-22	22.2	244
63	AID/APOBEC deaminases disfavor modified cytosines implicated in DNA demethylation. <i>Nature Chemical Biology</i> , 2012 , 8, 751-8	11.7	238
62	A reference gene catalogue of the pig gut microbiome. <i>Nature Microbiology</i> , 2016 , 1, 16161	26.6	233
61	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. <i>Nature Biotechnology</i> , 2019 , 37, 179-185	44.5	213
60	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
59	Transplantation of microbiota from drug-free patients with schizophrenia causes schizophrenia-like abnormal behaviors and dysregulated kynurenine metabolism in mice. <i>Molecular Psychiatry</i> , 2020 , 25, 2905-2918	15.1	82
58	Influenza H7N9 and H9N2 viruses: coexistence in poultry linked to human H7N9 infection and genome characteristics. <i>Journal of Virology</i> , 2014 , 88, 3423-31	6.6	78

57	The RNA helicase Mtr4p modulates polyadenylation in the TRAMP complex. <i>Cell</i> , 2011 , 145, 890-901	56.2	76
56	Metagenome-wide association of gut microbiome features for schizophrenia. <i>Nature Communications</i> , 2020 , 11, 1612	17.4	73
55	Unwinding by local strand separation is critical for the function of DEAD-box proteins as RNA chaperones. <i>Journal of Molecular Biology</i> , 2009 , 389, 674-93	6.5	72
54	Function of the C-terminal domain of the DEAD-box protein Mss116p analyzed in vivo and in vitro. <i>Journal of Molecular Biology</i> , 2008 , 375, 1344-64	6.5	68
53	Degradation of hypomodified tRNA(iMet) in vivo involves RNA-dependent ATPase activity of the DEXH helicase Mtr4p. <i>Rna</i> , 2008 , 14, 107-16	5.8	65
52	A single bacterium restores the microbiome dysbiosis to protect bones from destruction in a rat model of rheumatoid arthritis. <i>Microbiome</i> , 2019 , 7, 107	16.6	55
51	RNA unwinding by the Trf4/Air2/Mtr4 polyadenylation (TRAMP) complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 7292-7	11.5	50
50	Distinct gut metagenomics and metaproteomics signatures in prediabetics and treatment-naïve type 2 diabetics. <i>EBioMedicine</i> , 2019 , 47, 373-383	8.8	44
49	A metagenome-wide association study of gut microbiota in asthma in UK adults. <i>BMC Microbiology</i> , 2018 , 18, 114	4.5	44
48	The metagenome of the female upper reproductive tract. <i>GigaScience</i> , 2018 , 7,	7.6	43
47	A gene catalogue of the Sprague-Dawley rat gut metagenome. <i>GigaScience</i> , 2018 , 7,	7.6	41
46	Two distinct metacommunities characterize the gut microbiota in Crohn's disease patients. <i>GigaScience</i> , 2017 , 6, 1-11	7.6	40
45	Septin1, a new interaction partner for human serine/threonine kinase aurora-B. <i>Biochemical and Biophysical Research Communications</i> , 2005 , 336, 994-1000	3.4	40
44	Metagenomic profiling of the pro-inflammatory gut microbiota in ankylosing spondylitis. <i>Journal of Autoimmunity</i> , 2020 , 107, 102360	15.5	37
43	Division of Labor in an Oligomer of the DEAD-Box RNA Helicase Ded1p. <i>Molecular Cell</i> , 2015 , 59, 541-52	17.6	34
42	A novel affordable reagent for room temperature storage and transport of fecal samples for metagenomic analyses. <i>Microbiome</i> , 2018 , 6, 43	16.6	33
41	Establishment of a <i>Macaca fascicularis</i> gut microbiome gene catalog and comparison with the human, pig, and mouse gut microbiomes. <i>GigaScience</i> , 2018 , 7,	7.6	27
40	The Baseline Gut Microbiota Directs Dieting-Induced Weight Loss Trajectories. <i>Gastroenterology</i> , 2021 , 160, 2029-2042.e16	13.3	19

39	A genome-wide association study for gut metagenome in Chinese adults illuminates complex diseases. <i>Cell Discovery</i> , 2021 , 7, 9	22.3	17
38	Sequencing of the MHC region defines as the major genetic risk for seropositive rheumatoid arthritis in Han Chinese population. <i>Annals of the Rheumatic Diseases</i> , 2019 , 78, 773-780	2.4	16
37	A transomic cohort as a reference point for promoting a healthy human gut microbiome. <i>Medicine in Microecology</i> , 2021 , 8, 100039	4.3	13
36	Gut Microbiota Perturbation in IgA Deficiency Is Influenced by IgA-Autoantibody Status. <i>Gastroenterology</i> , 2021 , 160, 2423-2434.e5	13.3	11
35	Mendelian randomization analyses support causal relationships between blood metabolites and the gut microbiome.. <i>Nature Genetics</i> , 2022 ,	36.3	10
34	Life History Recorded in the Vagino-cervical Microbiome Along with Multi-omics. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 ,	6.5	8
33	Fecal microbiota transplantation results in bacterial strain displacement in patients with inflammatory bowel diseases. <i>FEBS Open Bio</i> , 2020 , 10, 41-55	2.7	8
32	A multi-omic cohort as a reference point for promoting a healthy human gut microbiome		7
31	Integrated genetic analyses revealed novel human longevity loci and reduced risks of multiple diseases in a cohort study of 15,651 Chinese individuals. <i>Aging Cell</i> , 2021 , 20, e13323	9.9	7
30	Over 50,000 Metagenomically Assembled Draft Genomes for the Human Oral Microbiome Reveal New Taxa. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 ,	6.5	7
29	Inter-determination of blood metabolite levels and gut microbiome supported by Mendelian randomization		5
28	M-GWAS for the Gut Microbiome in Chinese Adults Illuminates on Complex Diseases. <i>SSRN Electronic Journal</i> ,	1	4
27	The vagino-cervical microbiome as a woman's life history		4
26	MetaPGN: a pipeline for construction and graphical visualization of annotated pangenome networks. <i>GigaScience</i> , 2018 , 7,	7.6	4
25	Cervicovaginal microbiome dynamics after taking oral probiotics. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 716-726	4	4
24	The female urinary microbiota in relation to the reproductive tract microbiota. <i>GigaByte</i> , 2020 , 1-9		3
23	Over 50000 metagenomically assembled draft genomes for the human oral microbiome reveal new taxa		3
22	Metagenome-genome-wide association studies reveal human genetic impact on the oral microbiome. <i>Cell Discovery</i> , 2021 , 7, 117	22.3	3

21	Metagenome-genome-wide association studies reveal human genetic impact on the oral microbiome		2
20	New genetic variants associated with major adverse cardiovascular events in patients with acute coronary syndromes and treated with clopidogrel and aspirin. <i>Pharmacogenomics Journal</i> , 2021 , 21, 664-672	3.5	2
19	Linking gut microbiome to bone mineral density: a shotgun metagenomic dataset from 361 elderly women. <i>GigaByte</i> , 2021, 1-7		2
18	Dairy consumption and physical fitness tests associated with fecal microbiome in a Chinese cohort. <i>Medicine in Microecology</i> , 2021 , 100038	4.3	2
17	Disease trends in a young Chinese cohort according to fecal metagenome and plasma metabolites. <i>Medicine in Microecology</i> , 2021 , 100037	4.3	2
16	The complete mitochondrial genome of the Hoffmann's two-toed sloth (<i>Choloepus hoffmanni</i>). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3661-2	1.3	1
15	Network of Interactions Between Gut Microbiome, Host Biomarkers, and Urine Metabolome in Carotid Atherosclerosis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021 , 11, 708088	5.9	1
14	Shotgun Metagenomics of 361 elderly women reveals gut microbiome change in bone mass loss		1
13	M-GWAS for the gut microbiome in Chinese adults illuminates on complex diseases		1
12	Identification of gut microbiome markers for schizophrenia delineates a potential role of <i>Streptococcus</i>		1
11	New genetic variants associated with major adverse cardiovascular events in patients with acute coronary syndromes and treated with clopidogrel and aspirin		1
10	Amendments: Author Correction: A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2019 , 37, 102	44.5	
9	Mining the Microbiome for Drug Targets. <i>Methods in Enzymology</i> , 2018 , 610, 59-72	1.7	
8	The supraorganism 2022 , 1-19		
7	The evolving microbial taxonomy 2022 , 109-132		
6	Metagenomics from bench to bedside and from bedside to bench 2022 , 157-187		
5	Microbiota 2022 , 21-56		
4	Epidemiology in the human body 2022 , 83-107		

3 Collecting samples for metagenomics **2022**, 57-81

2 Blurring the line between opportunistic pathogens and commensals **2022**, 133-155

1 A microbiome record for life **2022**, 189-213