

# Junhua Li

## List of Publications by Year in descending order

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Version: 2024-02-01

72  
papers

36,458  
citations

87888

38  
h-index

102487

66  
g-index

88  
all docs

88  
docs citations

88  
times ranked

37808  
citing authors

#	ARTICLE	IF	CITATIONS
1	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	27.8	9,342
2	A metagenome-wide association study of gut microbiota in type 2 diabetes. <i>Nature</i> , 2012, 490, 55-60.	27.8	5,345
3	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	27.8	3,641
4	Dynamics and Stabilization of the Human Gut Microbiome during the First Year of Life. <i>Cell Host and Microbe</i> , 2015, 17, 690-703.	11.0	2,276
5	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	17.5	1,664
6	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	27.8	1,627
7	The oral and gut microbiomes are perturbed in rheumatoid arthritis and partly normalized after treatment. <i>Nature Medicine</i> , 2015, 21, 895-905.	30.7	1,306
8	Gut microbiome and serum metabolome alterations in obesity and after weight-loss intervention. <i>Nature Medicine</i> , 2017, 23, 859-868.	30.7	1,074
9	Gut microbiome development along the colorectal adenoma-carcinoma sequence. <i>Nature Communications</i> , 2015, 6, 6528.	12.8	1,062
10	The gut microbiome in atherosclerotic cardiovascular disease. <i>Nature Communications</i> , 2017, 8, 845.	12.8	1,029
11	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	17.5	909
12	Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer. <i>Gut</i> , 2017, 66, 70-78.	12.1	865
13	The microbiota continuum along the female reproductive tract and its relation to uterine-related diseases. <i>Nature Communications</i> , 2017, 8, 875.	12.8	572
14	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	19.0	442
15	A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2015, 33, 1103-1108.	17.5	422
16	A reference gene catalogue of the pig gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16161.	18.3	416
17	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. <i>Nature Biotechnology</i> , 2019, 37, 179-185.	17.5	402
18	Open-Source Genomic Analysis of Shiga-Toxin-Producing <i>E. coli</i> O104:H4. <i>New England Journal of Medicine</i> , 2011, 365, 718-724.	27.0	392

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19	Analyses of gut microbiota and plasma bile acids enable stratification of patients for antidiabetic treatment. <i>Nature Communications</i> , 2017, 8, 1785.	12.8	312
20	Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome. <i>Cell Systems</i> , 2016, 3, 572-584.e3.	6.2	261
21	MOCAT: A Metagenomics Assembly and Gene Prediction Toolkit. <i>PLoS ONE</i> , 2012, 7, e47656.	2.5	208
22	Connections between the human gut microbiome and gestational diabetes mellitus. <i>GigaScience</i> , 2017, 6, 1-12.	6.4	204
23	Gut microbiome-related effects of berberine and probiotics on type 2 diabetes (the PREMOTÉ study). <i>Nature Communications</i> , 2020, 11, 5015.	12.8	184
24	Prophage Hunter: an integrative hunting tool for active prophages. <i>Nucleic Acids Research</i> , 2019, 47, W74-W80.	14.5	169
25	Assessment of the cPAS-based BGISEQ-500 platform for metagenomic sequencing. <i>GigaScience</i> , 2018, 7, 1-8.	6.4	168
26	Impact of early events and lifestyle on the gut microbiota and metabolic phenotypes in young school-age children. <i>Microbiome</i> , 2019, 7, 2.	11.1	135
27	High-fat feeding rather than obesity drives taxonomical and functional changes in the gut microbiota in mice. <i>Microbiome</i> , 2017, 5, 43.	11.1	132
28	Multiple approaches for massively parallel sequencing of SARS-CoV-2 genomes directly from clinical samples. <i>Genome Medicine</i> , 2020, 12, 57.	8.2	104
29	Distinct gut metagenomics and metaproteomics signatures in prediabetics and treatment-naïve type 2 diabetics. <i>EBioMedicine</i> , 2019, 47, 373-383.	6.1	101
30	Intra-host variation and evolutionary dynamics of SARS-CoV-2 populations in COVID-19 patients. <i>Genome Medicine</i> , 2021, 13, 30.	8.2	88
31	Sex- and age-related trajectories of the adult human gut microbiota shared across populations of different ethnicities. <i>Nature Aging</i> , 2021, 1, 87-100.	11.6	86
32	The metagenome of the female upper reproductive tract. <i>GigaScience</i> , 2018, 7, .	6.4	68
33	A compromised specific humoral immune response against the SARS-CoV-2 receptor-binding domain is related to viral persistence and periodic shedding in the gastrointestinal tract. <i>Cellular and Molecular Immunology</i> , 2020, 17, 1119-1125.	10.5	67
34	A novel affordable reagent for room temperature storage and transport of fecal samples for metagenomic analyses. <i>Microbiome</i> , 2018, 6, 43.	11.1	53
35	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, .	6.4	53
36	Lipidomic profiling reveals distinct differences in plasma lipid composition in healthy, prediabetic, and type 2 diabetic individuals. <i>GigaScience</i> , 2017, 6, 1-12.	6.4	49

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37	Assessment of fecal DNA extraction protocols for metagenomic studies. <i>GigaScience</i> , 2020, 9, .	6.4	35
38	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. <i>GigaScience</i> , 2020, 9, .	6.4	35
39	Characterization of respiratory microbial dysbiosis in hospitalized COVID-19 patients. <i>Cell Discovery</i> , 2021, 7, 23.	6.7	34
40	Long-read sequencing reveals a 4.4Âkb tandem repeat region in the mitogenome of <i>Echinococcus granulosus</i> (sensu stricto) genotype G1. <i>Parasites and Vectors</i> , 2019, 12, 238.	2.5	31
41	Population Bottlenecks and Intra-host Evolution During Human-to-Human Transmission of SARS-CoV-2. <i>Frontiers in Medicine</i> , 2021, 8, 585358.	2.6	28
42	Combined berberine and probiotic treatment as an effective regimen for improving postprandial hyperlipidemia in type 2 diabetes patients: a double blinded placebo controlled randomized study. <i>Gut Microbes</i> , 2022, 14, 2003176.	9.8	27
43	Plasma cell-free RNA characteristics in COVID-19 patients. <i>Genome Research</i> , 2022, 32, 228-241.	5.5	25
44	A Path toward SARS-CoV-2 Attenuation: Metabolic Pressure on CTP Synthesis Rules the Virus Evolution. <i>Genome Biology and Evolution</i> , 2020, 12, 2467-2485.	2.5	22
45	Genomic epidemiology of SARS-CoV-2 in the UAE reveals novel virus mutation, patterns of co-infection and tissue specific host immune response. <i>Scientific Reports</i> , 2021, 11, 13971.	3.3	20
46	Genomic epidemiology of a densely sampled COVID-19 outbreak in China. <i>Virus Evolution</i> , 2021, 7, veaa102.	4.9	18
47	Global Landscape of <i>Clostridioides Difficile</i> Phylogeography, Antibiotic Susceptibility, and Toxin Polymorphisms by Post-Hoc Whole-Genome Sequencing from the MODIFY I/II Studies. <i>Infectious Diseases and Therapy</i> , 2021, 10, 853-870.	4.0	17
48	Quasispecies of SARS-CoV-2 revealed by single nucleotide polymorphisms (SNPs) analysis. <i>Virulence</i> , 2021, 12, 1209-1226.	4.4	16
49	Advances and challenges in cataloging the human gut virome. <i>Cell Host and Microbe</i> , 2022, 30, 908-916.	11.0	15
50	Genetic Association Reveals Protection against Recurrence of <i>Clostridium difficile</i> Infection with Bezlotoxumab Treatment. <i>MSphere</i> , 2020, 5, .	2.9	13
51	Comprehensive characterization of plasma cell-free <i>Echinococcus</i> spp. DNA in echinococcosis patients using ultra-high-throughput sequencing. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008148.	3.0	13
52	Genetic signatures for lineage/sublineage classification of HPV16, 18, 52 and 58 variants. <i>Virology</i> , 2021, 553, 62-69.	2.4	12
53	Chromosome-scale <i>Echinococcus granulosus</i> (genotype G1) genome reveals the Eg95 gene family and conservation of the EG95-vaccine molecule. <i>Communications Biology</i> , 2022, 5, 199.	4.4	7
54	Large-Scale Genomic Epidemiology of <i>Klebsiella pneumoniae</i> Identified Clone Divergence with Hypervirulent Plus Antimicrobial-Resistant Characteristics Causing Within-Ward Strain Transmissions. <i>Microbiology Spectrum</i> , 2022, 10, e0269821.	3.0	7

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55	MetaPGN: a pipeline for construction and graphical visualization of annotated pangenome networks. <i>GigaScience</i> , 2018, 7, .	6.4	6
56	Bezlotoxumab for prevention of <i>Clostridium difficile</i> infection recurrence: Distinguishing relapse from reinfection with whole genome sequencing. <i>Anaerobe</i> , 2020, 61, 102137.	2.1	6
57	Longitudinal Study of the Drug Resistance in <i>Klebsiella pneumoniae</i> of a Tertiary Hospital, China: Phenotypic Epidemiology Analysis (2013â€“2018). <i>Infection and Drug Resistance</i> , 2021, Volume 14, 613-626.	2.7	6
58	Distinct Functional Metagenomic Markers Predict the Responsiveness to Anti-PD-1 Therapy in Chinese Non-Small Cell Lung Cancer Patients. <i>Frontiers in Oncology</i> , 2022, 12, 837525.	2.8	6
59	Characterizing dynamic changes of plasma cell-free <i>Echinococcus granulosus</i> DNA before and after cystic echinococcosis treatment initiation. <i>Genomics</i> , 2021, 113, 576-582.	2.9	5
60	Cell-free DNA as a diagnostic tool for human echinococcosis. <i>Trends in Parasitology</i> , 2021, 37, 943-946.	3.3	5
61	<i>Echinococcus</i> spp. and genotypes infecting humans in Tibet Autonomous Region of China: a molecular investigation with near-complete/complete mitochondrial sequences. <i>Parasites and Vectors</i> , 2022, 15, 75.	2.5	4
62	Mutation Profiles, Glycosylation Site Distribution and Codon Usage Bias of Human Papillomavirus Type 16. <i>Viruses</i> , 2021, 13, 1281.	3.3	3
63	K-mer Counting: memory-efficient strategy, parallel computing and field of application for <i>Bioinformatics</i> . , 2018, , .		2
64	Draft Genome Sequence of a Polymyxin-Resistant <i>Klebsiella pneumoniae</i> Clinical Strain Carrying mcr-8.1 and bla NDM-5. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	2
65	Genetic characteristics of human papillomavirus type 16, 18, 52 and 58 in southern China. <i>Genomics</i> , 2021, 113, 3895-3906.	2.9	2
66	Genome Wide Analysis Reveals Host Genetic Variants that Associate with Reduction in <i>Clostridium difficile</i> Infection Recurrence (rCDI) in Patients Treated with Bezlotoxumab. <i>Open Forum Infectious Diseases</i> , 2017, 4, S380-S380.	0.9	0
67	Bezlotoxumab (BEZ) for Prevention of <i>Clostridium difficile</i> Infection (CDI) Recurrence (rCDI): Distinguishing Relapse from Reinfection with Whole Genome Sequencing (WGS). <i>Open Forum Infectious Diseases</i> , 2017, 4, S388-S389.	0.9	0
68	Correction: Amendments: Author Correction: A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2019, 37, 102-102.	17.5	0
69	Title is missing!. , 2020, 14, e0008148.		0
70	Title is missing!. , 2020, 14, e0008148.		0
71	Title is missing!. , 2020, 14, e0008148.		0
72	Title is missing!. , 2020, 14, e0008148.		0