

Junhua Li

List of Publications by Year in descending order

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72
papers

36,458
citations

87843

38
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102432

66
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all docs

88
docs citations

88
times ranked

37808
citing authors

#	ARTICLE	IF	CITATIONS
1	Plasma cell-free RNA characteristics in COVID-19 patients. <i>Genome Research</i> , 2022, 32, 228-241.	2.4	25
2	<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.	1.0	4
3	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.	2.0	7
4	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.	4.3	27
5	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.	1.3	6
6	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.	1.2	7
7	Advances and challenges in cataloging the human gut virome. <i>Cell Host and Microbe</i> , 2022, 30, 908-916.	5.1	15
8	Genetic signatures for lineage/sublineage classification of HPV16, 18, 52 and 58 variants. <i>Virology</i> , 2021, 553, 62-69.	1.1	12
9	Genomic epidemiology of a densely sampled COVID-19 outbreak in China. <i>Virus Evolution</i> , 2021, 7, veaa102.	2.2	18
10	Quasispecies of SARS-CoV-2 revealed by single nucleotide polymorphisms (SNPs) analysis. <i>Virulence</i> , 2021, 12, 1209-1226.	1.8	16
11	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.	5.3	86
12	Population Bottlenecks and Intra-host Evolution During Human-to-Human Transmission of SARS-CoV-2. <i>Frontiers in Medicine</i> , 2021, 8, 585358.	1.2	28
13	Longitudinal Study of the Drug Resistance in <i>Klebsiella pneumoniae</i> of a Tertiary Hospital, China: Phenotypic Epidemiology Analysis (2013-2018). <i>Infection and Drug Resistance</i> , 2021, Volume 14, 613-626.	1.1	6
14	Intra-host variation and evolutionary dynamics of SARS-CoV-2 populations in COVID-19 patients. <i>Genome Medicine</i> , 2021, 13, 30.	3.6	88
15	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.	1.3	5
16	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, .	0.3	2
17	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.	1.8	17
18	Characterization of respiratory microbial dysbiosis in hospitalized COVID-19 patients. <i>Cell Discovery</i> , 2021, 7, 23.	3.1	34

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19	Mutation Profiles, Glycosylation Site Distribution and Codon Usage Bias of Human Papillomavirus Type 16. <i>Viruses</i> , 2021, 13, 1281.	1.5	3
20	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.	1.6	20
21	Cell-free DNA as a diagnostic tool for human echinococcosis. <i>Trends in Parasitology</i> , 2021, 37, 943-946.	1.5	5
22	Genetic characteristics of human papillomavirus type 16, 18, 52 and 58 in southern China. <i>Genomics</i> , 2021, 113, 3895-3906.	1.3	2
23	Bezlotoxumab for prevention of <i>Clostridium difficile</i> infection recurrence: Distinguishing relapse from reinfection with whole genome sequencing. <i>Anaerobe</i> , 2020, 61, 102137.	1.0	6
24	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.	4.8	67
25	Gut microbiome-related effects of berberine and probiotics on type 2 diabetes (the PREMOTÉ study). <i>Nature Communications</i> , 2020, 11, 5015.	5.8	184
26	Assessment of fecal DNA extraction protocols for metagenomic studies. <i>GigaScience</i> , 2020, 9, .	3.3	35
27	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.	1.1	22
28	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. <i>GigaScience</i> , 2020, 9, .	3.3	35
29	Genetic Association Reveals Protection against Recurrence of <i>Clostridium difficile</i> Infection with Bezlotoxumab Treatment. <i>MSphere</i> , 2020, 5, .	1.3	13
30	Multiple approaches for massively parallel sequencing of SARS-CoV-2 genomes directly from clinical samples. <i>Genome Medicine</i> , 2020, 12, 57.	3.6	104
31	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.	1.3	13
32	Title is missing!. , 2020, 14, e0008148.		0
33	Title is missing!. , 2020, 14, e0008148.		0
34	Title is missing!. , 2020, 14, e0008148.		0
35	Title is missing!. , 2020, 14, e0008148.		0
36	Distinct gut metagenomics and metaproteomics signatures in prediabetics and treatment-naïve type 2 diabetics. <i>EBioMedicine</i> , 2019, 47, 373-383.	2.7	101

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37	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.	1.0	31
38	Prophage Hunter: an integrative hunting tool for active prophages. <i>Nucleic Acids Research</i> , 2019, 47, W74-W80.	6.5	169
39	Correction: Amendments: Author Correction: A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2019, 37, 102-102.	9.4	0
40	Impact of early events and lifestyle on the gut microbiota and metabolic phenotypes in young school-age children. <i>Microbiome</i> , 2019, 7, 2.	4.9	135
41	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. <i>Nature Biotechnology</i> , 2019, 37, 179-185.	9.4	402
42	Assessment of the cPAS-based BGISEQ-500 platform for metagenomic sequencing. <i>GigaScience</i> , 2018, 7, 1-8.	3.3	168
43	A novel affordable reagent for room temperature storage and transport of fecal samples for metagenomic analyses. <i>Microbiome</i> , 2018, 6, 43.	4.9	53
44	K-mer Counting: memory-efficient strategy, parallel computing and field of application for Bioinformatics. , 2018, , .		2
45	MetaPGN: a pipeline for construction and graphical visualization of annotated pangenome networks. <i>GigaScience</i> , 2018, 7, .	3.3	6
46	The metagenome of the female upper reproductive tract. <i>GigaScience</i> , 2018, 7, .	3.3	68
47	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, .	3.3	53
48	Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer. <i>Gut</i> , 2017, 66, 70-78.	6.1	865
49	High-fat feeding rather than obesity drives taxonomical and functional changes in the gut microbiota in mice. <i>Microbiome</i> , 2017, 5, 43.	4.9	132
50	Lipidomic profiling reveals distinct differences in plasma lipid composition in healthy, prediabetic, and type 2 diabetic individuals. <i>GigaScience</i> , 2017, 6, 1-12.	3.3	49
51	Gut microbiome and serum metabolome alterations in obesity and after weight-loss intervention. <i>Nature Medicine</i> , 2017, 23, 859-868.	15.2	1,074
52	The gut microbiome in atherosclerotic cardiovascular disease. <i>Nature Communications</i> , 2017, 8, 845.	5.8	1,029
53	The microbiota continuum along the female reproductive tract and its relation to uterine-related diseases. <i>Nature Communications</i> , 2017, 8, 875.	5.8	572
54	Connections between the human gut microbiome and gestational diabetes mellitus. <i>GigaScience</i> , 2017, 6, 1-12.	3.3	204

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55	Analyses of gut microbiota and plasma bile acids enable stratification of patients for antidiabetic treatment. <i>Nature Communications</i> , 2017, 8, 1785.	5.8	312
56	Genome Wide Analysis Reveals Host Genetic Variants that Associate with Reduction in Clostridium difficile Infection Recurrence (rCDI) in Patients Treated with Bezlotoxumab. <i>Open Forum Infectious Diseases</i> , 2017, 4, S380-S380.	0.4	0
57	Bezlotoxumab (BEZ) for Prevention of Clostridium difficile Infection (CDI) Recurrence (rCDI): Distinguishing Relapse from Reinfection with Whole Genome Sequencing (WGS). <i>Open Forum Infectious Diseases</i> , 2017, 4, S388-S389.	0.4	0
58	Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome. <i>Cell Systems</i> , 2016, 3, 572-584.e3.	2.9	261
59	A reference gene catalogue of the pig gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16161.	5.9	416
60	Gut microbiome development along the colorectal adenoma→carcinoma sequence. <i>Nature Communications</i> , 2015, 6, 6528.	5.8	1,062
61	The oral and gut microbiomes are perturbed in rheumatoid arthritis and partly normalized after treatment. <i>Nature Medicine</i> , 2015, 21, 895-905.	15.2	1,306
62	Dynamics and Stabilization of the Human Gut Microbiome during the First Year of Life. <i>Cell Host and Microbe</i> , 2015, 17, 690-703.	5.1	2,276
63	A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2015, 33, 1103-1108.	9.4	422
64	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	13.7	1,627
65	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	9.4	909
66	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	9.4	1,664
67	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	13.7	3,641
68	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	9.0	442
69	A metagenome-wide association study of gut microbiota in type 2 diabetes. <i>Nature</i> , 2012, 490, 55-60.	13.7	5,345
70	MOCAT: A Metagenomics Assembly and Gene Prediction Toolkit. <i>PLoS ONE</i> , 2012, 7, e47656.	1.1	208
71	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.	13.9	392
72	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	13.7	9,342