

Hong-Wei Zhou

List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

7,171
citations

66234

42
h-index

64668

79
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98
all docs

98
docs citations

98
times ranked

10716
citing authors

#	ARTICLE	IF	CITATIONS
1	The gut microbial metabolite, 3,4-dihydroxyphenylpropionic acid, alleviates hepatic ischemia/reperfusion injury via mitigation of macrophage pro-inflammatory activity in mice. <i>Acta Pharmaceutica Sinica B</i> , 2022, 12, 182-196.	5.7	22
2	Comprehensive histological imaging of native microbiota in human glioma. <i>Journal of Biophotonics</i> , 2022, 15, e202100351.	1.1	14
3	Gut microbiota is causally associated with poststroke cognitive impairment through lipopolysaccharide and butyrate. <i>Journal of Neuroinflammation</i> , 2022, 19, 76.	3.1	33
4	Targeting NLRP3 inflammasome modulates gut microbiota, attenuates corticospinal tract injury and ameliorates neurobehavioral deficits after intracerebral hemorrhage in mice. <i>Biomedicine and Pharmacotherapy</i> , 2022, 149, 112797.	2.5	33
5	Outer Membrane Vesicles From <i>Fusobacterium nucleatum</i> Switch M0-Like Macrophages Toward the M1 Phenotype to Destroy Periodontal Tissues in Mice. <i>Frontiers in Microbiology</i> , 2022, 13, 815638.	1.5	20
6	è,,-è,è/2`âœ`ç¼¼èè;€æ€šè,,`â`âââ...¶â¹¶âç-‡â,çš,,æœª^¶æŽŸç`Çă,Žâº”ç””â±•æœ». <i>Scientia Sinica Vitae</i> , 2022, , . 0.1	0	0
7	The gut microbiota-bile acid axis links the positive association between chronic insomnia and cardiometabolic diseases. <i>Nature Communications</i> , 2022, 13, .	5.8	42
8	Host metabolism dysregulation and cell tropism identification in human airway and alveolar organoids upon SARS-CoV-2 infection. <i>Protein and Cell</i> , 2021, 12, 717-733.	4.8	75
9	<i>Malassezia</i> and <i>Staphylococcus</i> dominate scalp microbiome for seborrheic dermatitis. <i>Bioprocess and Biosystems Engineering</i> , 2021, 44, 965-975.	1.7	35
10	Dysbiosis of Gut Microbiota and Shortâ€Chain Fatty Acids in Acute Ischemic Stroke and the Subsequent Risk for Poor Functional Outcomes. <i>Journal of Parenteral and Enteral Nutrition</i> , 2021, 45, 518-529.	1.3	111
11	Non-nucleatum <i>Fusobacterium</i> species are dominant in the Southern Chinese population with distinctive correlations to host diseases compared with <i>F. nucleatum</i> . <i>Gut</i> , 2021, 70, 810-812.	6.1	7
12	Accuracy of a nucleocapsid protein antigen rapid test in the diagnosis of SARS-CoV-2 infection. <i>Clinical Microbiology and Infection</i> , 2021, 27, 289.e1-289.e4.	2.8	147
13	Interpretable Machine Learning Framework Reveals Robust Gut Microbiome Features Associated With Type 2 Diabetes. <i>Diabetes Care</i> , 2021, 44, 358-366.	4.3	82
14	Analysis of endometrial microbiota in intrauterine adhesion by high-throughput sequencing. <i>Annals of Translational Medicine</i> , 2021, 9, 195-195.	0.7	13
15	VirionFinder: Identification of Complete and Partial Prokaryote Virus Virion Protein From Virome Data Using the Sequence and Biochemical Properties of Amino Acids. <i>Frontiers in Microbiology</i> , 2021, 12, 615711.	1.5	9
16	Rapid gut dysbiosis induced by stroke exacerbates brain infarction in turn. <i>Gut</i> , 2021, 70, 1486-1494.	6.1	129
17	Large-scale analysis of 2,152 Ig-seq datasets reveals key features of B cell biology and the antibody repertoire. <i>Cell Reports</i> , 2021, 35, 109110.	2.9	16
18	Intestinal Flora is a Key Factor in Insulin Resistance and Contributes to the Development of Polycystic Ovary Syndrome. <i>Endocrinology</i> , 2021, 162, .	1.4	39

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19	The Association of Gut Microbiota With Osteoporosis Is Mediated by Amino Acid Metabolism: Multiomics in a Large Cohort. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, e3852-e3864.	1.8	59
20	Dysbiosis of Gut Microbiota Is an Independent Risk Factor of Stroke-Associated Pneumonia: A Chinese Pilot Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 715475.	1.8	19
21	Postnatal age is strongly correlated with the early development of the gut microbiome in preterm infants. <i>Translational Pediatrics</i> , 2021, 10, 2313-2324.	0.5	3
22	A Virtual Machine Platform for Non-Computer Professionals for Using Deep Learning to Classify Biological Sequences of Metagenomic Data. <i>Journal of Visualized Experiments</i> , 2021, , .	0.2	0
23	Fecal Transplantation from db/db Mice Treated with Sodium Butyrate Attenuates Ischemic Stroke Injury. <i>Microbiology Spectrum</i> , 2021, 9, e0004221.	1.2	32
24	Targeting RNA with Next- and Third-Generation Sequencing Improves Pathogen Identification in Clinical Samples. <i>Advanced Science</i> , 2021, 8, e2102593.	5.6	23
25	Gut microbiota dysbiosis in patients with preeclampsia: A systematic review. <i>Medicine in Microecology</i> , 2021, 10, 100047.	0.7	6
26	Large-scale characterisation of the pregnancy vaginal microbiome and sialidase activity in a low-risk Chinese population. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 89.	2.9	10
27	Tools for fundamental analysis functions of TCR repertoires: a systematic comparison. <i>Briefings in Bioinformatics</i> , 2020, 21, 1706-1716.	3.2	18
28	Vaginal dysbiosis dominated by miscellaneous bacteria correlates with more severe clinical symptoms. <i>Infection, Genetics and Evolution</i> , 2020, 79, 104138.	1.0	0
29	Interpretable Machine Learning Algorithm Reveals Novel Gut Microbiome Features in Predicting Type 2 Diabetes. <i>Current Developments in Nutrition</i> , 2020, 4, nzaa062_016.	0.1	3
30	Dietary fruit and vegetable intake, gut microbiota, and type 2 diabetes: results from two large human cohort studies. <i>BMC Medicine</i> , 2020, 18, 371.	2.3	74
31	The Interactions of Airway Bacterial and Fungal Communities in Clinically Stable Asthma. <i>Frontiers in Microbiology</i> , 2020, 11, 1647.	1.5	22
32	A Refined View of Airway Microbiome in Chronic Obstructive Pulmonary Disease at Species and Strain-Levels. <i>Frontiers in Microbiology</i> , 2020, 11, 1758.	1.5	36
33	Association of sputum microbiome with clinical outcome of initial antibiotic treatment in hospitalized patients with acute exacerbations of COPD. <i>Pharmacological Research</i> , 2020, 160, 105095.	3.1	19
34	Multi-omic meta-analysis identifies functional signatures of airway microbiome in chronic obstructive pulmonary disease. <i>ISME Journal</i> , 2020, 14, 2748-2765.	4.4	43
35	The Biological Significance of Multi-copy Regions and Their Impact on Variant Discovery. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 516-524.	3.0	1
36	Associations of Gut Microbiota with Osteoporosis in Elderly Chinese: A Cohort Study. <i>Current Developments in Nutrition</i> , 2020, 4, nzaa040_048.	0.1	1

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37	Gut dysbiosis induces the development of pre-eclampsia through bacterial translocation. <i>Gut</i> , 2020, 69, 513-522.	6.1	173
38	Soyasaponin II protects against acute liver failure through diminishing YB-1 phosphorylation and Nlrp3-inflammasome priming in mice. <i>Theranostics</i> , 2020, 10, 2714-2726.	4.6	35
39	Human Skin, Oral, and Gut Microbiomes Predict Chronological Age. <i>MSystems</i> , 2020, 5, .	1.7	80
40	Dynamic Changes and Prognostic Value of Gut Microbiota-Dependent Trimethylamine-N-Oxide in Acute Ischemic Stroke. <i>Frontiers in Neurology</i> , 2020, 11, 29.	1.1	33
41	Identification of the conjugative and mobilizable plasmid fragments in the plasmidome using sequence signatures. <i>Microbial Genomics</i> , 2020, 6, .	1.0	6
42	Regional distribution of <i>Christensenellaceae</i> and its associations with metabolic syndrome based on a population-level analysis. <i>PeerJ</i> , 2020, 8, e9591.	0.9	34
43	Characterization of <i>Peptacetobacter hominis</i> gen. nov., sp. nov., isolated from human faeces, and proposal for the reclassification of <i>Clostridium hiranonis</i> within the genus <i>Peptacetobacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2988-2997.	0.8	18
44	Enteric dysbiosis is associated with sepsis in patients. <i>FASEB Journal</i> , 2019, 33, 12299-12310.	0.2	67
45	Altered composition and function of intestinal microbiota in autism spectrum disorders: a systematic review. <i>Translational Psychiatry</i> , 2019, 9, 43.	2.4	194
46	Gut microbiota partially mediates the effects of fine particulate matter on type 2 diabetes: Evidence from a population-based epidemiological study. <i>Environment International</i> , 2019, 130, 104882.	4.8	89
47	Dysbiosis of the intestinal microbiota in neurocritically ill patients and the risk for death. <i>Critical Care</i> , 2019, 23, 195.	2.5	84
48	Stroke Dysbiosis Index (SDI) in Gut Microbiome Are Associated With Brain Injury and Prognosis of Stroke. <i>Frontiers in Neurology</i> , 2019, 10, 397.	1.1	152
49	Disordered intestinal microbes are associated with the activity of Systemic Lupus Erythematosus. <i>Clinical Science</i> , 2019, 133, 821-838.	1.8	119
50	Higher Risk of Stroke Is Correlated With Increased Opportunistic Pathogen Load and Reduced Levels of Butyrate-Producing Bacteria in the Gut. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 4.	1.8	134
51	Septic patients in the intensive care unit present different nasal microbiotas. <i>Future Microbiology</i> , 2019, 14, 383-395.	1.0	4
52	Fasting challenges human gut microbiome resilience and reduces <i>Fusobacterium</i> . <i>Medicine in Microecology</i> , 2019, 1-2, 100003.	0.7	10
53	Intestinal Microbiota Mediates the Susceptibility to Polymicrobial Sepsis-Induced Liver Injury by Granisetron Generation in Mice. <i>Hepatology</i> , 2019, 69, 1751-1767.	3.6	102
54	Gut microbiota mediates diurnal variation of acetaminophen induced acute liver injury in mice. <i>Journal of Hepatology</i> , 2018, 69, 51-59.	1.8	178

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55	Distinct shifts in the oral microbiota are associated with the progression and aggravation of mucositis during radiotherapy. <i>Radiotherapy and Oncology</i> , 2018, 129, 44-51.	0.3	72
56	Gut Microbiota Offers Universal Biomarkers across Ethnicity in Inflammatory Bowel Disease Diagnosis and Infliximab Response Prediction. <i>MSystems</i> , 2018, 3, .	1.7	204
57	Linking gut microbiota, metabolic syndrome and economic status based on a population-level analysis. <i>Microbiome</i> , 2018, 6, 172.	4.9	131
58	Gut microbiota in patients with Parkinson's disease in southern China. <i>Parkinsonism and Related Disorders</i> , 2018, 53, 82-88.	1.1	184
59	<i>Bacteroides fragilis</i> Protects Against Antibiotic-Associated Diarrhea in Rats by Modulating Intestinal Defenses. <i>Frontiers in Immunology</i> , 2018, 9, 1040.	2.2	80
60	Light exposure influences the diurnal oscillation of gut microbiota in mice. <i>Biochemical and Biophysical Research Communications</i> , 2018, 501, 16-23.	1.0	68
61	Regional variation limits applications of healthy gut microbiome reference ranges and disease models. <i>Nature Medicine</i> , 2018, 24, 1532-1535.	15.2	629
62	iCRISPR hESCs for inducible and multiplex orthogonal gene knockout and activation. <i>FEBS Letters</i> , 2018, 592, 2238-2247.	1.3	7
63	Gut Microbial Compositions in Four Age Groups of Tibetan Minipigs. <i>Polish Journal of Microbiology</i> , 2018, 67, 383-388.	0.6	3
64	The Potential Effect of Oral Microbiota in the Prediction of Mucositis During Radiotherapy for Nasopharyngeal Carcinoma. <i>EBioMedicine</i> , 2017, 18, 23-31.	2.7	109
65	Impaired renal function and dysbiosis of gut microbiota contribute to increased trimethylamine-N-oxide in chronic kidney disease patients. <i>Scientific Reports</i> , 2017, 7, 1445.	1.6	201
66	Alteration of the gut microbiota in Chinese population with chronic kidney disease. <i>Scientific Reports</i> , 2017, 7, 2870.	1.6	192
67	Long-term consumption of caffeine-free high sucrose cola beverages aggravates the pathogenesis of EAE in mice. <i>Cell Discovery</i> , 2017, 3, 17020.	3.1	21
68	Enteric dysbiosis-linked gut barrier disruption triggers early renal injury induced by chronic high salt feeding in mice. <i>Experimental and Molecular Medicine</i> , 2017, 49, e370-e370.	3.2	77
69	Fructooligosaccharide (FOS) and Galactooligosaccharide (GOS) Increase Bifidobacterium but Reduce Butyrate Producing Bacteria with Adverse Glycemic Metabolism in healthy young population. <i>Scientific Reports</i> , 2017, 7, 11789.	1.6	181
70	Bacterial distribution pattern in the surface sediments distinctive among shelf, slope and basin across the western Arctic Ocean. <i>Polar Biology</i> , 2017, 40, 423-436.	0.5	11
71	Open-Source Sequence Clustering Methods Improve the State Of the Art. <i>MSystems</i> , 2016, 1, .	1.7	155
72	Intron V, not intron I of human thrombopoietin, improves expression in the milk of transgenic mice regulated by goat beta-casein promoter. <i>Scientific Reports</i> , 2015, 5, 16051.	1.6	0

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73	Stability of operational taxonomic units: an important but neglected property for analyzing microbial diversity. <i>Microbiome</i> , 2015, 3, 20.	4.9	115
74	Sputum Bacterial and Fungal Dynamics during Exacerbations of Severe COPD. <i>PLoS ONE</i> , 2015, 10, e0130736.	1.1	49
75	Different Dynamic Patterns of β -Lactams, Quinolones, Glycopeptides and Macrolides on Mouse Gut Microbial Diversity. <i>PLoS ONE</i> , 2015, 10, e0126712.	1.1	26
76	Homogeneity of the Vaginal Microbiome at the Cervix, Posterior Fornix, and Vaginal Canal in Pregnant Chinese Women. <i>Microbial Ecology</i> , 2015, 69, 407-414.	1.4	60
77	Dysbiosis of Gut Microbiota With Reduced Trimethylamine-N-Oxide Level in Patients With Large-Artery Atherosclerotic Stroke or Transient Ischemic Attack. <i>Journal of the American Heart Association</i> , 2015, 4, .	1.6	486
78	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. <i>PeerJ</i> , 2014, 2, e545.	0.9	535
79	Comparison of direct boiling method with commercial kits for extracting fecal microbiome DNA by Illumina sequencing of 16S rRNA tags. <i>Journal of Microbiological Methods</i> , 2013, 95, 455-462.	0.7	82
80	Comparison of microbial diversity determined with the same variable tag sequence extracted from two different PCR amplicons. <i>BMC Microbiology</i> , 2013, 13, 208.	1.3	55
81	Illumina Sequencing of 16S rRNA Tag Revealed Spatial Variations of Bacterial Communities in a Mangrove Wetland. <i>Microbial Ecology</i> , 2013, 66, 96-104.	1.4	314
82	Diverse Vaginal Microbiomes in Reproductive-Age Women with Vulvovaginal Candidiasis. <i>PLoS ONE</i> , 2013, 8, e79812.	1.1	108
83	Two-Stage Clustering (TSC): A Pipeline for Selecting Operational Taxonomic Units for the High-Throughput Sequencing of PCR Amplicons. <i>PLoS ONE</i> , 2012, 7, e30230.	1.1	19
84	BIPES, a cost-effective high-throughput method for assessing microbial diversity. <i>ISME Journal</i> , 2011, 5, 741-749.	4.4	160
85	Integrated lysis procedures reduce extraction biases of microbial DNA from mangrove sediment. <i>Journal of Bioscience and Bioengineering</i> , 2011, 111, 153-157.	1.1	17
86	The Effect of Trifluoroethanol on Tyrosinase Activity and Conformation: Inhibition Kinetics and Computational Simulations. <i>Applied Biochemistry and Biotechnology</i> , 2010, 160, 1896-1908.	1.4	30
87	Cloning and functional study of a novel aromatic-ring-hydroxylating dioxygenase gene. <i>Nan Fang Yi Ke Da Xue Xue Bao = Journal of Southern Medical University</i> , 2007, 27, 717-9.	0.4	0