

Shi Huang

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.

75
papers

2,550
citations

27
h-index

49
g-index

91
ext. papers

3,422
ext. citations

8.3
avg, IF

4.86
L-index

#	Paper	IF	Citations
75	Choreography of Transcriptomes and Lipidomes of <i>Nannochloropsis</i> Reveals the Mechanisms of Oil Synthesis in Microalgae. <i>Plant Cell</i> , 2014 , 26, 1645-1665	11.6	243
74	Genome editing of model oleaginous microalgae <i>Nannochloropsis</i> spp. by CRISPR/Cas9. <i>Plant Journal</i> , 2016 , 88, 1071-1081	6.9	170
73	A cellular protein that competes with SV40 T antigen for binding to the retinoblastoma gene product. <i>Nature</i> , 1991 , 350, 160-2	50.4	148
72	Intestinal Microbiota Distinguish Gout Patients from Healthy Humans. <i>Scientific Reports</i> , 2016 , 6, 20602	4.9	142
71	Prediction of Early Childhood Caries via Spatial-Temporal Variations of Oral Microbiota. <i>Cell Host and Microbe</i> , 2015 , 18, 296-306	23.4	123
70	Age- and Sex-Dependent Patterns of Gut Microbial Diversity in Human Adults. <i>MSystems</i> , 2019 , 4,	7.6	110
69	Feed-additive probiotics accelerate yet antibiotics delay intestinal microbiota maturation in broiler chicken. <i>Microbiome</i> , 2017 , 5, 91	16.6	104
68	Genomic Foundation of Starch-to-Lipid Switch in Oleaginous <i>Chlorella</i> spp. <i>Plant Physiology</i> , 2015 , 169, 2444-61	6.6	89
67	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019 , 10, 5477	17.4	89
66	Metabolic-Activity-Based Assessment of Antimicrobial Effects by DO-Labeled Single-Cell Raman Microspectroscopy. <i>Analytical Chemistry</i> , 2017 , 89, 4108-4115	7.8	87
65	Preliminary characterization of the oral microbiota of Chinese adults with and without gingivitis. <i>BMC Oral Health</i> , 2011 , 11, 33	3.7	82
64	Phosphorylation of the translation initiation factor eIF2 β at serine 51 determines the cell fate decisions of Akt in response to oxidative stress. <i>Cell Death and Disease</i> , 2015 , 6, e1591	9.8	78
63	Impact of DNA extraction method and targeted 16S-rRNA hypervariable region on oral microbiota profiling. <i>Scientific Reports</i> , 2018 , 8, 16321	4.9	74
62	Predictive modeling of gingivitis severity and susceptibility via oral microbiota. <i>ISME Journal</i> , 2014 , 8, 1768-80	11.9	70
61	Parallel-META 3: Comprehensive taxonomical and functional analysis platform for efficient comparison of microbial communities. <i>Scientific Reports</i> , 2017 , 7, 40371	4.9	64
60	Magnetic nanoparticle-mediated isolation of functional bacteria in a complex microbial community. <i>ISME Journal</i> , 2015 , 9, 603-14	11.9	63
59	Quantitative dynamics of triacylglycerol accumulation in microalgae populations at single-cell resolution revealed by Raman microspectroscopy. <i>Biotechnology for Biofuels</i> , 2014 , 7, 58	7.8	53

58	Candidate hematopoietic stem cells from fetal tissues, umbilical cord blood vs. adult bone marrow and mobilized peripheral blood. <i>Experimental Hematology</i> , 1998 , 26, 1162-71	3.1	46
57	Cow-to-mouse fecal transplantations suggest intestinal microbiome as one cause of mastitis. <i>Microbiome</i> , 2018 , 6, 200	16.6	38
56	Functional analysis of the cyclin-dependent kinase inhibitor Pho81 identifies a novel inhibitory domain. <i>Molecular and Cellular Biology</i> , 2001 , 21, 6695-705	4.8	37
55	Human Skin, Oral, and Gut Microbiomes Predict Chronological Age. <i>MSystems</i> , 2020 , 5,	7.6	33
54	Comparative Gut Microbiomes of Four Species Representing the Higher and the Lower Termites. <i>Journal of Insect Science</i> , 2016 , 16,	2	31
53	Translational initiation factor expression and ribosomal protein gene expression are repressed coordinately but by different mechanisms in murine lymphosarcoma cells treated with glucocorticoids. <i>Molecular and Cellular Biology</i> , 1989 , 9, 3679-84	4.8	31
52	Label-free, simultaneous quantification of starch, protein and triacylglycerol in single microalgal cells. <i>Biotechnology for Biofuels</i> , 2017 , 10, 275	7.8	30
51	Microbial basis of oral malodor development in humans. <i>Journal of Dental Research</i> , 2013 , 92, 1106-12	8.1	30
50	Improvement of hydrogen production of <i>Chlamydomonas reinhardtii</i> by co-cultivation with isolated bacteria. <i>International Journal of Hydrogen Energy</i> , 2013 , 38, 10779-10787	6.7	28
49	Ecological Effect of Arginine on Oral Microbiota. <i>Scientific Reports</i> , 2017 , 7, 7206	4.9	27
48	Changes of saliva microbiota in nasopharyngeal carcinoma patients under chemoradiation therapy. <i>Archives of Oral Biology</i> , 2014 , 59, 176-86	2.8	26
47	Variation in the Gut Microbiota of Termites (<i>Tsaitermes ampliceps</i>) Against Different Diets. <i>Applied Biochemistry and Biotechnology</i> , 2017 , 181, 32-47	3.2	22
46	Identifying and Predicting Novelty in Microbiome Studies. <i>MBio</i> , 2018 , 9,	7.8	21
45	Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , 2019 , 4,	7.6	20
44	A culture-independent approach to unravel uncultured bacteria and functional genes in a complex microbial community. <i>PLoS ONE</i> , 2012 , 7, e47530	3.7	20
43	Interleukin-1 stimulates Jun N-terminal/stress-activated protein kinase by an arachidonate-dependent mechanism in mesangial cells. <i>Kidney International</i> , 1999 , 55, 1740-9	9.9	20
42	Cetylpyridinium chloride mouth rinses alleviate experimental gingivitis by inhibiting dental plaque maturation. <i>International Journal of Oral Science</i> , 2016 , 8, 182-90	27.9	20
41	Emerging Trends for Microbiome Analysis: From Single-Cell Functional Imaging to Microbiome Big Data. <i>Engineering</i> , 2017 , 3, 66-70	9.7	19

40	Bacterial succession in paddy soils derived from different parent materials. <i>Journal of Soils and Sediments</i> , 2015 , 15, 982-992	3.4	18
39	The gut microbiome stability is altered by probiotic ingestion and improved by the continuous supplementation of galactooligosaccharide. <i>Gut Microbes</i> , 2020 , 12, 1785252	8.8	18
38	Microbiota-based Signature of Gingivitis Treatments: A Randomized Study. <i>Scientific Reports</i> , 2016 , 6, 24705	4.9	17
37	Challenges in benchmarking metagenomic profilers. <i>Nature Methods</i> , 2021 , 18, 618-626	21.6	15
36	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. <i>Microbiome</i> , 2021 , 9, 132	16.6	15
35	Diversity and resilience of the wood-feeding higher termite gut microbiota in response to temporal and diet variations. <i>Ecology and Evolution</i> , 2016 , 6, 8235-8242	2.8	14
34	Coupling metagenomics with cultivation to select host-specific probiotic micro-organisms for subtropical aquaculture. <i>Journal of Applied Microbiology</i> , 2017 , 123, 1274-1285	4.7	14
33	Exposure to soil environments during earlier life stages is distinguishable in the gut microbiome of adult mice. <i>Gut Microbes</i> , 2021 , 13, 1-13	8.8	13
32	A Microbiome-Based Index for Assessing Skin Health and Treatment Effects for Atopic Dermatitis in Children. <i>MSystems</i> , 2019 , 4,	7.6	12
31	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , 2020 , 5,	7.6	12
30	Inflammatory cytokines and peripheral mediators in the pathophysiology of pruritus in cutaneous T-cell lymphoma. <i>Journal of the European Academy of Dermatology and Venereology</i> , 2018 , 32, 1652-1656	4.6	12
29	Microbial context predicts SARS-CoV-2 prevalence in patients and the hospital built environment 2020 ,		10
28	Suppressed activities of cathepsins and metalloproteinases in the chronic model of puromycin aminonucleoside nephrosis. <i>Kidney and Blood Pressure Research</i> , 1999 , 22, 121-7	3.1	9
27	The effects of exopolysaccharides and exopolysaccharide-producing <i>Lactobacillus</i> on the intestinal microbiome of zebrafish (<i>Danio rerio</i>). <i>BMC Microbiology</i> , 2020 , 20, 300	4.5	9
26	Longitudinal Multi-omics and Microbiome Meta-analysis Identify an Asymptomatic Gingival State That Links Gingivitis, Periodontitis, and Aging. <i>MBio</i> , 2021 , 12,	7.8	9
25	Translational initiation factor expression and ribosomal protein gene expression are repressed coordinately but by different mechanisms in murine lymphosarcoma cells treated with glucocorticoids. <i>Molecular and Cellular Biology</i> , 1989 , 9, 3679-3684	4.8	7
24	OGUs enable effective, phylogeny-aware analysis of even shallow metagenome community structures		7
23	Compositional and genetic alterations in Graves' disease gut microbiome reveal specific diagnostic biomarkers. <i>ISME Journal</i> , 2021 , 15, 3399-3411	11.9	7

22	Candidate probiotic <i>Lactiplantibacillus plantarum</i> HNU082 rapidly and convergently evolves within human, mice, and zebrafish gut but differentially influences the resident microbiome. <i>Microbiome</i> , 2021 , 9, 151	16.6	5
21	Rapid comparison and correlation analysis among massive number of microbial community samples based on MDV data model. <i>Scientific Reports</i> , 2014 , 4, 6393	4.9	4
20	The Enhanced Pharmacological Effects of Modified Traditional Chinese Medicine in Attenuation of Atherosclerosis Is Driven by Modulation of Gut Microbiota. <i>Frontiers in Pharmacology</i> , 2020 , 11, 546589	5.6	4
19	Probiotic consumption influences universal adaptive mutations in indigenous human and mouse gut microbiota. <i>Communications Biology</i> , 2021 , 4, 1198	6.7	3
18	Multi-omics profiling of Earth's biomes reveals that microbial and metabolite composition are shaped by the environment		3
17	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021 , 31, 2131-2137	9.7	3
16	Parallel-Meta Suite: Interactive and rapid microbiome data analysis on multiple platforms 2022 , 1,		3
15	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy.. <i>MSystems</i> , 2022 , e0016722	7.6	3
14	Application of Meta-Mesh on the analysis of microbial communities from human associated-habitats. <i>Quantitative Biology</i> , 2015 , 3, 4-18	3.9	2
13	Fluoride profiles in dental calculus from Japanese, Chinese and British residents. <i>Archives of Oral Biology</i> , 1997 , 42, 665-71	2.8	2
12	Species-resolved sequencing of low-biomass or degraded microbiomes using 2bRAD-M.. <i>Genome Biology</i> , 2022 , 23, 36	18.3	2
11	The predictive power of saliva electrolytes exceeds that of saliva microbiomes in diagnosing early childhood caries. <i>Journal of Oral Microbiology</i> , 2021 , 13, 1921486	6.3	2
10	A 6.7µW CMOS bioamplifier for active electrode with DC rejection 2013 ,		1
9	Intra-Ramanome Correlation Analysis Unveils Metabolite Conversion Network from an Isogenic Cellular Population		1
8	Age and sex-dependent patterns of gut microbial diversity in human adults		1
7	Geographic Variation Did Not Affect the Predictive Power of Salivary Microbiota for Caries in Children With Mixed Dentition. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021 , 11, 680288	5.9	1
6	Intra-Ramanome Correlation Analysis Unveils Metabolite Conversion Network from an Isogenic Population of Cells. <i>MBio</i> , 2021 , 12, e0147021	7.8	1
5	Salivary bacterial signatures in depression-obesity comorbidity are associated with neurotransmitters and neuroactive dipeptides.. <i>BMC Microbiology</i> , 2022 , 22, 75	4.5	1

4	Nanomechanical and Molecular Characterization of Aging in Dentinal Collagen.. <i>Journal of Dental Research</i> , 2022 , 220345211072484	8.1	o
3	The Oral Microbiome Bank of China 2020 , 287-300		o
2	SARS-CoV-2 Distribution in Residential Housing Suggests Contact Deposition and Correlates with sp.. <i>MSystems</i> , 2022 , e0141121	7.6	o
1	AB1247 ELEVATED SERUM COMPLEMENT (C3/C4) LEVEL AS AN INFLAMMATORY MARKER FOR INFECTION IN PATIENTS WITH FEVER: A RETROSPECTIVE STUDY. <i>Annals of the Rheumatic Diseases</i> , 2020 , 79, 1915.2-1915	2.4	