

Fangqing Zhao

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.

113
papers

6,710
citations

38
h-index

81
g-index

124
ext. papers

9,000
ext. citations

10.8
avg, IF

6.15
L-index

#	Paper	IF	Citations
113	Gut microbiota dysbiosis contributes to the development of hypertension. <i>Microbiome</i> , 2017 , 5, 14	16.6	652
112	CIRI: an efficient and unbiased algorithm for de novo circular RNA identification. <i>Genome Biology</i> , 2015 , 16, 4	18.3	572
111	Metagenome-wide analysis of antibiotic resistance genes in a large cohort of human gut microbiota. <i>Nature Communications</i> , 2013 , 4, 2151	17.4	436
110	Complete Khoisan and Bantu genomes from southern Africa. <i>Nature</i> , 2010 , 463, 943-7	50.4	342
109	Dysbiosis signature of fecal microbiota in colorectal cancer patients. <i>Microbial Ecology</i> , 2013 , 66, 462-70	4.4	286
108	Circular RNA identification based on multiple seed matching. <i>Briefings in Bioinformatics</i> , 2018 , 19, 803-810	10.4	247
107	Polar and brown bear genomes reveal ancient admixture and demographic footprints of past climate change. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E2382-90	11.5	243
106	Sequencing the nuclear genome of the extinct woolly mammoth. <i>Nature</i> , 2008 , 456, 387-90	50.4	242
105	Metagenomic profile of the bacterial communities associated with <i>Ixodes ricinus</i> ticks. <i>PLoS ONE</i> , 2011 , 6, e25604	3.7	182
104	Comprehensive identification of internal structure and alternative splicing events in circular RNAs. <i>Nature Communications</i> , 2016 , 7, 12060	17.4	170
103	Dysbiosis of maternal and neonatal microbiota associated with gestational diabetes mellitus. <i>Gut</i> , 2018 , 67, 1614-1625	19.2	168
102	Genetic diversity and population structure of the endangered marsupial <i>Sarcophilus harrisii</i> (Tasmanian devil). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 12348-53	11.5	164
101	Metagenomic sequencing reveals microbiota and its functional potential associated with periodontal disease. <i>Scientific Reports</i> , 2013 , 3, 1843	4.9	158
100	Saccharina genomes provide novel insight into kelp biology. <i>Nature Communications</i> , 2015 , 6, 6986	17.4	154
99	Convergent Evolution of Rumen Microbiomes in High-Altitude Mammals. <i>Current Biology</i> , 2016 , 26, 1873-6	39.3	136
98	Expanded Expression Landscape and Prioritization of Circular RNAs in Mammals. <i>Cell Reports</i> , 2019 , 26, 3444-3460.e5	10.6	115
97	CircAtlas: an integrated resource of one million highly accurate circular RNAs from 1070 vertebrate transcriptomes. <i>Genome Biology</i> , 2020 , 21, 101	18.3	109

96	HTQC: a fast quality control toolkit for Illumina sequencing data. <i>BMC Bioinformatics</i> , 2013 , 14, 33	3.6	104
95	mirTools: microRNA profiling and discovery based on high-throughput sequencing. <i>Nucleic Acids Research</i> , 2010 , 38, W392-7	20.1	98
94	Comparative and Functional Genomics of Anoxygenic Green Bacteria from the Taxa Chlorobi, Chloroflexi, and Acidobacteria. <i>Advances in Photosynthesis and Respiration</i> , 2012 , 47-102	1.7	83
93	The mitochondrial genome sequence of the Tasmanian tiger (<i>Thylacinus cynocephalus</i>). <i>Genome Research</i> , 2009 , 19, 213-20	9.7	83
92	Computational Strategies for Exploring Circular RNAs. <i>Trends in Genetics</i> , 2018 , 34, 389-400	8.5	82
91	The first metagenome of activated sludge from full-scale anaerobic/anoxic/oxic (A2O) nitrogen and phosphorus removal reactor using Illumina sequencing. <i>Journal of Environmental Sciences</i> , 2015 , 35, 181-190	6.4	73
90	Extensive lysine acetylation occurs in evolutionarily conserved metabolic pathways and parasite-specific functions during <i>Plasmodium falciparum</i> intraerythrocytic development. <i>Molecular Microbiology</i> , 2013 , 89, 660-75	4.1	67
89	Phage-bacteria interaction network in human oral microbiome. <i>Environmental Microbiology</i> , 2016 , 18, 2143-58	5.2	67
88	Characterization of the small RNA transcriptomes of androgen dependent and independent prostate cancer cell line by deep sequencing. <i>PLoS ONE</i> , 2010 , 5, e15519	3.7	64
87	inGAP-sv: a novel scheme to identify and visualize structural variation from paired end mapping data. <i>Nucleic Acids Research</i> , 2011 , 39, W567-75	20.1	63
86	Reconstruction of full-length circular RNAs enables isoform-level quantification. <i>Genome Medicine</i> , 2019 , 11, 2	14.4	59
85	Accurate quantification of circular RNAs identifies extensive circular isoform switching events. <i>Nature Communications</i> , 2020 , 11, 90	17.4	58
84	Large-Scale Comparative Analyses of Tick Genomes Elucidate Their Genetic Diversity and Vector Capacities. <i>Cell</i> , 2020 , 182, 1328-1340.e13	56.2	57
83	inGAP: an integrated next-generation genome analysis pipeline. <i>Bioinformatics</i> , 2010 , 26, 127-9	7.2	52
82	A close phylogenetic relationship between Sipuncula and Annelida evidenced from the complete mitochondrial genome sequence of <i>Phascolosoma esculenta</i> . <i>BMC Genomics</i> , 2009 , 10, 136	4.5	51
81	Composition-based classification of short metagenomic sequences elucidates the landscapes of taxonomic and functional enrichment of microorganisms. <i>Nucleic Acids Research</i> , 2013 , 41, e3	20.1	47
80	MetaSort untangles metagenome assembly by reducing microbial community complexity. <i>Nature Communications</i> , 2017 , 8, 14306	17.4	43
79	Comparative analysis of fatty acid desaturases in cyanobacterial genomes. <i>Comparative and Functional Genomics</i> , 2008 , 284508		42

78	Single-cell metagenomics: challenges and applications. <i>Protein and Cell</i> , 2018 , 9, 501-510	7.2	41
77	MagicViewer: integrated solution for next-generation sequencing data visualization and genetic variation detection and annotation. <i>Nucleic Acids Research</i> , 2010 , 38, W732-6	20.1	41
76	The complete mitochondrial genome of the ridgetail white prawn <i>Exopalaemon carinicauda</i> Holthuis, 1950 (Crustacean: Decapoda: Palaemonidae) revealed a novel rearrangement of tRNA genes. <i>Gene</i> , 2009 , 437, 1-8	3.8	38
75	Soil bacterial communities shaped by geochemical factors and land use in a less-explored area, Tibetan Plateau. <i>BMC Genomics</i> , 2013 , 14, 820	4.5	35
74	Comprehensive profiling of circular RNAs with nanopore sequencing and CIRI-long. <i>Nature Biotechnology</i> , 2021 , 39, 836-845	44.5	34
73	Sequencing and genetic variation of multidrug resistance plasmids in <i>Klebsiella pneumoniae</i> . <i>PLoS ONE</i> , 2010 , 5, e10141	3.7	33
72	Genome-wide analysis of restriction-modification system in unicellular and filamentous cyanobacteria. <i>Physiological Genomics</i> , 2006 , 24, 181-90	3.6	33
71	The meconium microbiota shares more features with the amniotic fluid microbiota than the maternal fecal and vaginal microbiota. <i>Gut Microbes</i> , 2020 , 12, 1794266	8.8	33
70	gcMeta: a Global Catalogue of Metagenomics platform to support the archiving, standardization and analysis of microbiome data. <i>Nucleic Acids Research</i> , 2019 , 47, D637-D648	20.1	33
69	Phycobilisomes linker family in cyanobacterial genomes: divergence and evolution. <i>International Journal of Biological Sciences</i> , 2007 , 3, 434-45	11.2	31
68	Population Genomics Reveals Speciation and Introgression between Brown Norway Rats and Their Sibling Species. <i>Molecular Biology and Evolution</i> , 2017 , 34, 2214-2228	8.3	30
67	Phylogenetic relationship analyses of complicated class Spirotrichea based on transcriptomes from three diverse microbial eukaryotes: <i>Uroleptopsis citrina</i> , <i>Euplotes vannus</i> and <i>Protocruzia tuzeti</i> . <i>Molecular Phylogenetics and Evolution</i> , 2018 , 129, 338-345	4.1	30
66	Genome-wide survey of putative serine/threonine protein kinases in cyanobacteria. <i>BMC Genomics</i> , 2007 , 8, 395	4.5	30
65	TCRklass: a new K-string-based algorithm for human and mouse TCR repertoire characterization. <i>Journal of Immunology</i> , 2015 , 194, 446-54	5.3	29
64	Detection, annotation and visualization of alternative splicing from RNA-Seq data with SplicingViewer. <i>Genomics</i> , 2012 , 99, 178-82	4.3	29
63	Small RNA transcriptome investigation based on next-generation sequencing technology. <i>Journal of Genetics and Genomics</i> , 2011 , 38, 505-13	4	28
62	cTFbase: a database for comparative genomics of transcription factors in cyanobacteria. <i>BMC Genomics</i> , 2007 , 8, 104	4.5	28
61	Combinational biosynthesis of a fluorescent cyanobacterial holo-alpha-phycoyanin in <i>Escherichia coli</i> by using one expression vector. <i>Applied Biochemistry and Biotechnology</i> , 2007 , 142, 52-9	3.2	28

60	Phylogenomics of non-model ciliates based on transcriptomic analyses. <i>Protein and Cell</i> , 2015 , 6, 373-385.	5.2	26
59	Evidence for positive Darwinian selection of Vip gene in <i>Bacillus thuringiensis</i> . <i>Journal of Genetics and Genomics</i> , 2007 , 34, 649-60	4	25
58	Codon usage patterns and adaptive evolution of marine unicellular cyanobacteria <i>Synechococcus</i> and <i>Prochlorococcus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2012 , 62, 206-13	4.1	24
57	A new pheromone trail-based genetic algorithm for comparative genome assembly. <i>Nucleic Acids Research</i> , 2008 , 36, 3455-62	20.1	24
56	Expression of β -carotene hydroxylase gene (crtR-B) from the green alga <i>Haematococcus pluvialis</i> in chloroplasts of <i>Chlamydomonas reinhardtii</i> . <i>Journal of Applied Phycology</i> , 2007 , 19, 347-355	3.2	23
55	Scale-up of fermentation and purification of recombinant allophycocyanin over-expressed in <i>Escherichia coli</i> . <i>Process Biochemistry</i> , 2005 , 40, 3190-3195	4.8	23
54	RiboFR-Seq: a novel approach to linking 16S rRNA amplicon profiles to metagenomes. <i>Nucleic Acids Research</i> , 2016 , 44, e99	20.1	20
53	Nodeomics: pathogen detection in vertebrate lymph nodes using meta-transcriptomics. <i>PLoS ONE</i> , 2010 , 5, e13432	3.7	20
52	Tracing the accumulation of in vivo human oral microbiota elucidates microbial community dynamics at the gateway to the GI tract. <i>Gut</i> , 2020 , 69, 1355-1356	19.2	19
51	Characterization of human α CR repertoire and discovery of D-D fusion in TCR β chains. <i>Protein and Cell</i> , 2014 , 5, 603-15	7.2	18
50	Tracking the past: interspersed repeats in an extinct Afrotherian mammal, <i>Mammuthus primigenius</i> . <i>Genome Research</i> , 2009 , 19, 1384-92	9.7	18
49	Species Divergence vs. Functional Convergence Characterizes Crude Oil Microbial Community Assembly. <i>Frontiers in Microbiology</i> , 2016 , 7, 1254	5.7	18
48	Whole genomic DNA sequencing and comparative genomic analysis of <i>Arthrospira platensis</i> : high genome plasticity and genetic diversity. <i>DNA Research</i> , 2016 , 23, 325-38	4.5	17
47	Genetic basis for the establishment of endosymbiosis in <i>Paramecium</i> . <i>ISME Journal</i> , 2019 , 13, 1360-1369.	11.9	17
46	Evolutionary analysis of phycobiliproteins: implications for their structural and functional relationships. <i>Journal of Molecular Evolution</i> , 2006 , 63, 330-40	3.1	14
45	CRISPRs provide broad and robust protection to oral microbial flora of gingival health against bacteriophage challenge. <i>Protein and Cell</i> , 2015 , 6, 541-545	7.2	13
44	Prioritization and functional assessment of noncoding variants associated with complex diseases. <i>Genome Medicine</i> , 2018 , 10, 53	14.4	13
43	BreakSeek: a breakpoint-based algorithm for full spectral range INDEL detection. <i>Nucleic Acids Research</i> , 2015 , 43, 6701-13	20.1	13

42	Argonaute proteins from human gastrointestinal bacteria catalyze DNA-guided cleavage of single- and double-stranded DNA at 37 °C. <i>Cell Discovery</i> , 2019 , 5, 38	22.3	12
41	Comparative molecular population genetics of phycoerythrin locus in <i>Prochlorococcus</i> . <i>Genetica</i> , 2007 , 129, 291-9	1.5	12
40	Adaptive evolution of cry genes in <i>Bacillus thuringiensis</i> : implications for their specificity determination. <i>Genomics, Proteomics and Bioinformatics</i> , 2007 , 5, 102-10	6.5	12
39	A novel codon-based de Bruijn graph algorithm for gene construction from unassembled transcriptomes. <i>Genome Biology</i> , 2016 , 17, 232	18.3	11
38	Deterministic transition of enterotypes shapes the infant gut microbiome at an early age. <i>Genome Biology</i> , 2021 , 22, 243	18.3	11
37	Complete mitochondrial genome of <i>Membranipora grandicella</i> (Bryozoa: Cheilostomatida) determined with next-generation sequencing: the first representative of the suborder Malacostegina. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2012 , 7, 248-53	2	10
36	PGA4genomics for comparative genome assembly based on genetic algorithm optimization. <i>Genomics</i> , 2009 , 94, 284-6	4.3	10
35	Precision Medicine: What Challenges Are We Facing?. <i>Genomics, Proteomics and Bioinformatics</i> , 2016 , 14, 253-261	6.5	9
34	Translocation of vaginal microbiota is involved in impairment and protection of uterine health. <i>Nature Communications</i> , 2021 , 12, 4191	17.4	9
33	The combination of direct and paired link graphs can boost repetitive genome assembly. <i>Nucleic Acids Research</i> , 2017 , 45, e43	20.1	8
32	Lineage-specific domain fusion in the evolution of purine nucleotide cyclases in cyanobacteria. <i>Journal of Molecular Evolution</i> , 2008 , 67, 85-94	3.1	8
31	The Value and Significance of Metagenomics of Marine Environments. Preface. <i>Genomics, Proteomics and Bioinformatics</i> , 2015 , 13, 271-4	6.5	7
30	Ancestry of the Australian termitivorous numbat. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1041-5	8.3	7
29	Comparison of envelope-related genes in unicellular and filamentous cyanobacteria. <i>Comparative and Functional Genomics</i> , 2007 , 2007, 25751		7
28	Phylomitogenomic analyses strongly support the sister relationship of the Chaetognatha and Protostomia. <i>Zoologica Scripta</i> , 2016 , 45, 187-199	2.5	7
27	Detection and Reconstruction of Circular RNAs from Transcriptomic Data. <i>Methods in Molecular Biology</i> , 2018 , 1724, 1-8	1.4	6
26	Evidence for positive selection in phycoerythrin genes of red algae and cyanobacteria <i>Prochlorococcus</i> and <i>Synechococcus</i> . <i>Photosynthetica</i> , 2005 , 43, 141-146	2.2	6
25	Visualization of circular RNAs and their internal splicing events from transcriptomic data. <i>Bioinformatics</i> , 2020 , 36, 2934-2935	7.2	5

24	Evidence of extensive homologous recombination in the core genome of rickettsia. <i>Comparative and Functional Genomics</i> , 2009 , 510270		5
23	MBRidge: an accurate and cost-effective method for profiling DNA methylome at single-base resolution. <i>Journal of Molecular Cell Biology</i> , 2015 , 7, 299-313	6.3	4
22	Genome-wide identification and divergent transcriptional expression of StAR-related lipid transfer (START) genes in teleosts. <i>Gene</i> , 2013 , 519, 18-25	3.8	4
21	PlasmoGF: an integrated system for comparative genomics and phylogenetic analysis of Plasmodium gene families. <i>Bioinformatics</i> , 2008 , 24, 1217-20	7.2	4
20	The recombination and expression of the allophycocyanin beta subunit gene in the chloroplast of Chlamydomonas reinhardtii. <i>World Journal of Microbiology and Biotechnology</i> , 2006 , 22, 101-103	4.4	4
19	The repertoire and evolution of ATP-binding cassette systems in Synechococcus and Prochlorococcus. <i>Journal of Molecular Evolution</i> , 2009 , 69, 300-10	3.1	3
18	circVAMP3 Drives CAPRIN1 Phase Separation and Inhibits Hepatocellular Carcinoma by Suppressing c-Myc Translation.. <i>Advanced Science</i> , 2022 , e2103817	13.6	3
17	Microbiota-gut-brain axis in autism spectrum disorder. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 755-762		3
16	Genomic analysis of field pennycress (Thlaspi arvense) provides insights into mechanisms of adaptation to high elevation. <i>BMC Biology</i> , 2021 , 19, 143	7.3	3
15	FlyPhy: a phylogenomic analysis platform for Drosophila genes and gene families. <i>BMC Bioinformatics</i> , 2009 , 10, 123	3.6	2
14	Cloning, expression and characterization of phycoerythrin gene from Ceramium boydenn. <i>DNA Sequence</i> , 2006 , 17, 129-35		2
13	Heterologous Expression and Purification of Recombinant Allophycocyanin in Marine Streptomyces sp. Isolate M097. <i>World Journal of Microbiology and Biotechnology</i> , 2006 , 22, 525-529	4.4	2
12	Variation of the Vaginal Microbiome During and after Pregnancy in Chinese Women.. <i>Genomics, Proteomics and Bioinformatics</i> , 2022 ,	6.5	2
11	Changes to gut amino acid transporters and microbiome associated with increased E/I ratio in Chd8 mouse model of ASD-like behavior.. <i>Nature Communications</i> , 2022 , 13, 1151	17.4	2
10	Mining the hidden treasures from canid genomes. <i>National Science Review</i> , 2019 , 6, 124	10.8	1
9	Screening Linear and Circular RNA Transcripts from Stress Granules.. <i>Genomics, Proteomics and Bioinformatics</i> , 2022 ,	6.5	1
8	Reconstruction of circular RNAs using Illumina and Nanopore RNA-seq datasets. <i>Methods</i> , 2021 , 196, 17-22	4.6	1
7	The hidden genomic diversity of ciliated protists revealed by single-cell genome sequencing.. <i>BMC Biology</i> , 2021 , 19, 264	7.3	1

6	Large-scale microbiome data integration enables robust biomarker identification. <i>Nature Computational Science</i> ,		1
5	Haemaphysalis longicornis. <i>Trends in Genetics</i> , 2021 , 37, 292-293	8.5	o
4	An efficient metatranscriptomic approach for capturing RNA virome and its application to SARS-CoV-2. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 860-862	4	o
3	Characterizing Circular RNAs Using Nanopore Sequencing. <i>Trends in Biochemical Sciences</i> , 2021 , 46, 785-786	18.3	o
2	Colorectal Cancer Patient-Derived 2D and 3D Models Efficiently Recapitulate Inter- and Intratumoral Heterogeneity. <i>Advanced Science</i> , 2201539	13.6	o
1	Reply to Evidence that microbes identified as tick-borne pathogens are nutritional endosymbionts. <i>Cell</i> , 2021 , 184, 2261-2262	56.2	