

Fangqing Zhao

List of Publications by Year in descending order

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119
papers

10,452
citations

57719

44
h-index

36008

97
g-index

124
all docs

124
docs citations

124
times ranked

15418
citing authors

#	ARTICLE	IF	CITATIONS
1	Gut microbiota dysbiosis contributes to the development of hypertension. <i>Microbiome</i> , 2017, 5, 14.	4.9	1,086
2	CIRI: an efficient and unbiased algorithm for de novo circular RNA identification. <i>Genome Biology</i> , 2015, 16, 4.	3.8	921
3	Metagenome-wide analysis of antibiotic resistance genes in a large cohort of human gut microbiota. <i>Nature Communications</i> , 2013, 4, 2151.	5.8	606
4	Circular RNA identification based on multiple seed matching. <i>Briefings in Bioinformatics</i> , 2018, 19, 803-810.	3.2	498
5	Dysbiosis Signature of Fecal Microbiota in Colorectal Cancer Patients. <i>Microbial Ecology</i> , 2013, 66, 462-470.	1.4	408
6	Complete Khoisan and Bantu genomes from southern Africa. <i>Nature</i> , 2010, 463, 943-947.	13.7	400
7	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.	3.3	310
8	Dysbiosis of maternal and neonatal microbiota associated with gestational diabetes mellitus. <i>Gut</i> , 2018, 67, 1614-1625.	6.1	305
9	Sequencing the nuclear genome of the extinct woolly mammoth. <i>Nature</i> , 2008, 456, 387-390.	13.7	283
10	Convergent Evolution of Rumen Microbiomes in High-Altitude Mammals. <i>Current Biology</i> , 2016, 26, 1873-1879.	1.8	281
11	Metagenomic Profile of the Bacterial Communities Associated with <i>Ixodes ricinus</i> Ticks. <i>PLoS ONE</i> , 2011, 6, e25604.	1.1	261
12	CircAtlas: an integrated resource of one million highly accurate circular RNAs from 1070 vertebrate transcriptomes. <i>Genome Biology</i> , 2020, 21, 101.	3.8	256
13	Comprehensive identification of internal structure and alternative splicing events in circular RNAs. <i>Nature Communications</i> , 2016, 7, 12060.	5.8	249
14	Saccharina genomes provide novel insight into kelp biology. <i>Nature Communications</i> , 2015, 6, 6986.	5.8	222
15	Metagenomic sequencing reveals microbiota and its functional potential associated with periodontal disease. <i>Scientific Reports</i> , 2013, 3, 1843.	1.6	207
16	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, 12348-12353.	3.3	189
17	Expanded Expression Landscape and Prioritization of Circular RNAs in Mammals. <i>Cell Reports</i> , 2019, 26, 3444-3460.e5.	2.9	179
18	Comparative and Functional Genomics of Anoxygenic Green Bacteria from the Taxa <i>Chlorobi</i> , <i>Chloroflexi</i> , and <i>Acidobacteria</i> . <i>Advances in Photosynthesis and Respiration</i> , 2012, , 47-102.	1.0	145

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19	Large-Scale Comparative Analyses of Tick Genomes Elucidate Their Genetic Diversity and Vector Capacities. <i>Cell</i> , 2020, 182, 1328-1340.e13.	13.5	145
20	HTQC: a fast quality control toolkit for Illumina sequencing data. <i>BMC Bioinformatics</i> , 2013, 14, 33.	1.2	142
21	Accurate quantification of circular RNAs identifies extensive circular isoform switching events. <i>Nature Communications</i> , 2020, 11, 90.	5.8	140
22	mirTools: microRNA profiling and discovery based on high-throughput sequencing. <i>Nucleic Acids Research</i> , 2010, 38, W392-W397.	6.5	120
23	Computational Strategies for Exploring Circular RNAs. <i>Trends in Genetics</i> , 2018, 34, 389-400.	2.9	113
24	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.	3.2	112
25	Reconstruction of full-length circular RNAs enables isoform-level quantification. <i>Genome Medicine</i> , 2019, 11, 2.	3.6	112
26	Comprehensive profiling of circular RNAs with nanopore sequencing and CIRI-long. <i>Nature Biotechnology</i> , 2021, 39, 836-845.	9.4	108
27	The mitochondrial genome sequence of the Tasmanian tiger (<i>Thylacinus cynocephalus</i>). <i>Genome Research</i> , 2009, 19, 213-220.	2.4	102
28	Phage-bacteria interaction network in human oral microbiome. <i>Environmental Microbiology</i> , 2016, 18, 2143-2158.	1.8	87
29	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, 660-675.	1.2	86
30	inGAP-sv: a novel scheme to identify and visualize structural variation from paired end mapping data. <i>Nucleic Acids Research</i> , 2011, 39, W567-W575.	6.5	74
31	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.	4.3	71
32	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.	1.1	71
33	Single-cell metagenomics: challenges and applications. <i>Protein and Cell</i> , 2018, 9, 501-510.	4.8	70
34	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.	6.5	70
35	Translocation of vaginal microbiota is involved in impairment and protection of uterine health. <i>Nature Communications</i> , 2021, 12, 4191.	5.8	70
36	Deterministic transition of enterotypes shapes the infant gut microbiome at an early age. <i>Genome Biology</i> , 2021, 22, 243.	3.8	65

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37	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.	1.2	60
38	inGAP: an integrated next-generation genome analysis pipeline. <i>Bioinformatics</i> , 2010, 26, 127-129.	1.8	58
39	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-e3.	6.5	54
40	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.	6.1	53
41	Sequencing and Genetic Variation of Multidrug Resistance Plasmids in <i>Klebsiella pneumoniae</i> . <i>PLoS ONE</i> , 2010, 5, e10141.	1.1	52
42	MetaSort untangles metagenome assembly by reducing microbial community complexity. <i>Nature Communications</i> , 2017, 8, 14306.	5.8	52
43	Soil bacterial communities shaped by geochemical factors and land use in a less-explored area, Tibetan Plateau. <i>BMC Genomics</i> , 2013, 14, 820.	1.2	51
44	Comparative Analysis of Fatty Acid Desaturases in Cyanobacterial Genomes. <i>Comparative and Functional Genomics</i> , 2008, 2008, 1-25.	2.0	48
45	Population Genomics Reveals Speciation and Introgression between Brown Norway Rats and Their Sibling Species. <i>Molecular Biology and Evolution</i> , 2017, 34, 2214-2228.	3.5	47
46	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.	3.1	47
47	MagicViewer: integrated solution for next-generation sequencing data visualization and genetic variation detection and annotation. <i>Nucleic Acids Research</i> , 2010, 38, W732-W736.	6.5	45
48	Detection, annotation and visualization of alternative splicing from RNA-Seq data with SplicingViewer. <i>Genomics</i> , 2012, 99, 178-182.	1.3	43
49	TCRklass: A New K-String-Based Algorithm for Human and Mouse TCR Repertoire Characterization. <i>Journal of Immunology</i> , 2015, 194, 446-454.	0.4	43
50	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.	1.0	42
51	Phycobilisomes linker family in cyanobacterial genomes: divergence and evolution. <i>International Journal of Biological Sciences</i> , 2007, 3, 434-445.	2.6	40
52	Genome-wide survey of putative Serine/Threonine protein kinases in cyanobacteria. <i>BMC Genomics</i> , 2007, 8, 395.	1.2	38
53	circVAMP3 Drives CAPRIN1 Phase Separation and Inhibits Hepatocellular Carcinoma by Suppressing c-Myc Translation. <i>Advanced Science</i> , 2022, 9, e2103817.	5.6	38
54	Genome-wide analysis of restriction-modification system in unicellular and filamentous cyanobacteria. <i>Physiological Genomics</i> , 2006, 24, 181-190.	1.0	37

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55	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.	1.2	36
56	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, 206-213.	1.2	35
57	Changes to gut amino acid transporters and microbiome associated with increased E/I ratio in <i>Chd8+/-</i> mouse model of ASD-like behavior. <i>Nature Communications</i> , 2022, 13, 1151.	5.8	35
58	Prioritization and functional assessment of noncoding variants associated with complex diseases. <i>Genome Medicine</i> , 2018, 10, 53.	3.6	33
59	Nodeomics: Pathogen Detection in Vertebrate Lymph Nodes Using Meta-Transcriptomics. <i>PLoS ONE</i> , 2010, 5, e13432.	1.1	33
60	Small RNA transcriptome investigation based on next-generation sequencing technology. <i>Journal of Genetics and Genomics</i> , 2011, 38, 505-513.	1.7	32
61	Combinational Biosynthesis of a Fluorescent Cyanobacterial Holo- β -Phycocyanin in <i>Escherichia coli</i> by Using One Expression Vector. <i>Applied Biochemistry and Biotechnology</i> , 2007, 142, 52-59.	1.4	31
62	Phylogenomics of non-model ciliates based on transcriptomic analyses. <i>Protein and Cell</i> , 2015, 6, 373-385.	4.8	31
63	Expression of β -carotene hydroxylase gene (<i>crtR-B</i>) 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.	1.5	30
64	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, 325-338.	1.5	30
65	Genetic basis for the establishment of endosymbiosis in <i>Paramecium</i> . <i>ISME Journal</i> , 2019, 13, 1360-1369.	4.4	30
66	Large-scale microbiome data integration enables robust biomarker identification. <i>Nature Computational Science</i> , 2022, 2, 307-316.	3.8	30
67	Evidence for Positive Darwinian Selection of <i>Vip</i> Gene in <i>Bacillus thuringiensis</i> . <i>Journal of Genetics and Genomics</i> , 2007, 34, 649-660.	1.7	28
68	cTFbase: a database for comparative genomics of transcription factors in cyanobacteria. <i>BMC Genomics</i> , 2007, 8, 104.	1.2	28
69	A new pheromone trail-based genetic algorithm for comparative genome assembly. <i>Nucleic Acids Research</i> , 2008, 36, 3455-3462.	6.5	28
70	Characterization of human β TCR repertoire and discovery of D-D fusion in β chains. <i>Protein and Cell</i> , 2014, 5, 603-615.	4.8	27
71	Unfavourable intrauterine environment contributes to abnormal gut microbiome and metabolome in twins. <i>Gut</i> , 2022, 71, 2451-2462.	6.1	25
72	Exploring the cellular landscape of circular RNAs using full-length single-cell RNA sequencing. <i>Nature Communications</i> , 2022, 13, .	5.8	25

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73	Scale-up of fermentation and purification of recombinant allophycocyanin over-expressed in <i>Escherichia coli</i> . <i>Process Biochemistry</i> , 2005, 40, 3190-3195.	1.8	24
74	Species Divergence vs. Functional Convergence Characterizes Crude Oil Microbial Community Assembly. <i>Frontiers in Microbiology</i> , 2016, 7, 1254.	1.5	24
75	RiboFR-Seq: a novel approach to linking 16S rRNA amplicon profiles to metagenomes. <i>Nucleic Acids Research</i> , 2016, 44, e99-e99.	6.5	24
76	Genomic analysis of field pennycress (<i>Thlaspi arvense</i>) provides insights into mechanisms of adaptation to high elevation. <i>BMC Biology</i> , 2021, 19, 143.	1.7	23
77	A novel peptide protects against diet-induced obesity by suppressing appetite and modulating the gut microbiota. <i>Gut</i> , 2023, 72, 686-698.	6.1	23
78	Microbiota-gut-brain axis in autism spectrum disorder. <i>Journal of Genetics and Genomics</i> , 2021, 48, 755-762.	1.7	21
79	Tracking the past: Interspersed repeats in an extinct Afrotherian mammal, <i>Mammuthus primigenius</i> . <i>Genome Research</i> , 2009, 19, 1384-1392.	2.4	20
80	Adaptive Evolution of cry Genes in <i>Bacillus thuringiensis</i> : Implications for Their Specificity Determination. <i>Genomics, Proteomics and Bioinformatics</i> , 2007, 5, 102-110.	3.0	17
81	Evolutionary Analysis of Phycobiliproteins: Implications for Their Structural and Functional Relationships. <i>Journal of Molecular Evolution</i> , 2006, 63, 330-340.	0.8	16
82	Comparison of Envelope-Related Genes in Unicellular and Filamentous Cyanobacteria. <i>Comparative and Functional Genomics</i> , 2007, 2007, 1-10.	2.0	15
83	BreakSeek: a breakpoint-based algorithm for full spectral range INDEL detection. <i>Nucleic Acids Research</i> , 2015, 43, 6701-6713.	6.5	15
84	Precision Medicine: What Challenges Are We Facing?. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 253-261.	3.0	15
85	Visualization of circular RNAs and their internal splicing events from transcriptomic data. <i>Bioinformatics</i> , 2020, 36, 2934-2935.	1.8	15
86	Variation of the Vaginal Microbiome During and After Pregnancy in Chinese Women. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 322-333.	3.0	15
87	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.	4.8	14
88	The Value and Significance of Metagenomics of Marine Environments. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 271-274.	3.0	13
89	Comparative molecular population genetics of phycoerythrin locus in <i>Prochlorococcus</i> . <i>Genetica</i> , 2007, 129, 291-299.	0.5	12
90	A novel codon-based de Bruijn graph algorithm for gene construction from unassembled transcriptomes. <i>Genome Biology</i> , 2016, 17, 232.	3.8	12

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91	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, 248-253.	0.4	11
92	Ancestry of the Australian Termitivorous Numbat. <i>Molecular Biology and Evolution</i> , 2013, 30, 1041-1045.	3.5	11
93	The hidden genomic diversity of ciliated protists revealed by single-cell genome sequencing. <i>BMC Biology</i> , 2021, 19, 264.	1.7	11
94	PGA4genomics for comparative genome assembly based on genetic algorithm optimization. <i>Genomics</i> , 2009, 94, 284-286.	1.3	10
95	Colorectal Cancer Patientâ€Derived 2D and 3D Models Efficiently Recapitulate Interâ€and Intratumoral Heterogeneity. <i>Advanced Science</i> , 2022, 9, .	5.6	10
96	Lineage-Specific Domain Fusion in the Evolution of Purine Nucleotide Cyclases in Cyanobacteria. <i>Journal of Molecular Evolution</i> , 2008, 67, 85-94.	0.8	9
97	The combination of direct and paired link graphs can boost repetitive genome assembly. <i>Nucleic Acids Research</i> , 2017, 45, e43-e43.	6.5	9
98	Reconstruction of circular RNAs using Illumina and Nanopore RNA-seq datasets. <i>Methods</i> , 2021, 196, 17-22.	1.9	9
99	Characterizing Circular RNAs Using Nanopore Sequencing. <i>Trends in Biochemical Sciences</i> , 2021, 46, 785-786.	3.7	8
100	Screening Linear and Circular RNA Transcripts from Stress Granules. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 886-893.	3.0	8
101	Evidence of Extensive Homologous Recombination in the Core Genome of <i>Rickettsia</i> . <i>Comparative and Functional Genomics</i> , 2009, 2009, 1-5.	2.0	7
102	Phylomitogenomic analyses strongly support the sister relationship of the <i>Cyrtognatha</i> and <i>Protostomia</i> . <i>Zoologica Scripta</i> , 2016, 45, 187-199.	0.7	7
103	Detection and Reconstruction of Circular RNAs from Transcriptomic Data. <i>Methods in Molecular Biology</i> , 2018, 1724, 1-8.	0.4	7
104	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.	0.9	6
105	<i>Haemaphysalis longicornis</i> . <i>Trends in Genetics</i> , 2021, 37, 292-293.	2.9	6
106	The recombination and expression of the allophycocyanin beta subunit gene in the chloroplast of <i>Chlamydomonas reinhardtii</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2006, 22, 101-103.	1.7	5
107	Heterologous Expression and Purification of Recombinant Allophycocyanin in Marine <i>Streptomyces</i> sp. Isolate M097. <i>World Journal of Microbiology and Biotechnology</i> , 2006, 22, 525-529.	1.7	5
108	PlasmoGF: an integrated system for comparative genomics and phylogenetic analysis of <i>Plasmodium</i> gene families. <i>Bioinformatics</i> , 2008, 24, 1217-1220.	1.8	5

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109	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.	1.5	5
110	Genome-wide identification and divergent transcriptional expression of StAR-related lipid transfer (START) genes in teleosts. <i>Gene</i> , 2013, 519, 18-25.	1.0	4
111	An Extremely Streamlined Macronuclear Genome in the Free-Living Protozoan <i>Fabrea salina</i> . <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	4
112	Cloning, expression and characterization of phycoerythrin gene from <i>Ceramium boydenn</i> . <i>DNA Sequence</i> , 2006, 17, 129-135.	0.7	3
113	The Repertoire and Evolution of ATP-Binding Cassette Systems in <i>Synechococcus</i> and <i>Prochlorococcus</i> . <i>Journal of Molecular Evolution</i> , 2009, 69, 300-310.	0.8	3
114	FlyPhy: a phylogenomic analysis platform for <i>Drosophila</i> genes and gene families. <i>BMC Bioinformatics</i> , 2009, 10, 123.	1.2	2
115	Bioinformatics Commons: The Cornerstone of Life and Health Sciences. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 223-225.	3.0	2
116	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.	1.7	2
117	Mining the hidden treasures from canid genomes. <i>National Science Review</i> , 2019, 6, 124-124.	4.6	1
118	Current status and challenges in biological big data visualization. <i>Chinese Science Bulletin</i> , 2015, 60, 547-557.	0.4	1
119	Reply to Evidence that microbes identified as tick-borne pathogens are nutritional endosymbionts. <i>Cell</i> , 2021, 184, 2261-2262.	13.5	0