

Fangqing Zhao

List of Publications by Year in Descending Order

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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	Screening Linear and Circular RNA Transcripts from Stress Granules.. <i>Genomics, Proteomics and Bioinformatics</i> , 2022 ,	6.5	1
112	circVAMP3 Drives CAPRIN1 Phase Separation and Inhibits Hepatocellular Carcinoma by Suppressing c-Myc Translation.. <i>Advanced Science</i> , 2022 , e2103817	13.6	3
111	Variation of the Vaginal Microbiome During and after Pregnancy in Chinese Women.. <i>Genomics, Proteomics and Bioinformatics</i> , 2022 ,	6.5	2
110	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
109	Comprehensive profiling of circular RNAs with nanopore sequencing and CIRI-long. <i>Nature Biotechnology</i> , 2021 , 39, 836-845	44.5	34
108	Reconstruction of circular RNAs using Illumina and Nanopore RNA-seq datasets. <i>Methods</i> , 2021 , 196, 17-22	4.6	1
107	Haemaphysalis longicornis. <i>Trends in Genetics</i> , 2021 , 37, 292-293	8.5	0
106	Reply to Evidence that microbes identified as tick-borne pathogens are nutritional endosymbionts. <i>Cell</i> , 2021 , 184, 2261-2262	56.2	
105	Microbiota-gut-brain axis in autism spectrum disorder. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 755-762	7.2	3
104	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	7.3	3
103	Translocation of vaginal microbiota is involved in impairment and protection of uterine health. <i>Nature Communications</i> , 2021 , 12, 4191	17.4	9
102	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	0
101	Deterministic transition of enterotypes shapes the infant gut microbiome at an early age. <i>Genome Biology</i> , 2021 , 22, 243	18.3	11
100	Characterizing Circular RNAs Using Nanopore Sequencing. <i>Trends in Biochemical Sciences</i> , 2021 , 46, 785-786	18.6	0
99	The hidden genomic diversity of ciliated protists revealed by single-cell genome sequencing.. <i>BMC Biology</i> , 2021 , 19, 264	7.3	1
98	Visualization of circular RNAs and their internal splicing events from transcriptomic data. <i>Bioinformatics</i> , 2020 , 36, 2934-2935	7.2	5
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	Accurate quantification of circular RNAs identifies extensive circular isoform switching events. <i>Nature Communications</i> , 2020 , 11, 90	17.4	58
95	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
94	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
93	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
92	Reconstruction of full-length circular RNAs enables isoform-level quantification. <i>Genome Medicine</i> , 2019 , 11, 2	14.4	59
91	Expanded Expression Landscape and Prioritization of Circular RNAs in Mammals. <i>Cell Reports</i> , 2019 , 26, 3444-3460.e5	10.6	115
90	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
89	Mining the hidden treasures from canid genomes. <i>National Science Review</i> , 2019 , 6, 124	10.8	1
88	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
87	Genetic basis for the establishment of endosymbiosis in Paramecium. <i>ISME Journal</i> , 2019 , 13, 1360-1369	11.9	17
86	Computational Strategies for Exploring Circular RNAs. <i>Trends in Genetics</i> , 2018 , 34, 389-400	8.5	82
85	Detection and Reconstruction of Circular RNAs from Transcriptomic Data. <i>Methods in Molecular Biology</i> , 2018 , 1724, 1-8	1.4	6
84	Single-cell metagenomics: challenges and applications. <i>Protein and Cell</i> , 2018 , 9, 501-510	7.2	41
83	Circular RNA identification based on multiple seed matching. <i>Briefings in Bioinformatics</i> , 2018 , 19, 803-810	13.4	247
82	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
81	Prioritization and functional assessment of noncoding variants associated with complex diseases. <i>Genome Medicine</i> , 2018 , 10, 53	14.4	13
80	Dysbiosis of maternal and neonatal microbiota associated with gestational diabetes mellitus. <i>Gut</i> , 2018 , 67, 1614-1625	19.2	168
79	The combination of direct and paired link graphs can boost repetitive genome assembly. <i>Nucleic Acids Research</i> , 2017 , 45, e43	20.1	8

78	MetaSort untangles metagenome assembly by reducing microbial community complexity. <i>Nature Communications</i> , 2017 , 8, 14306	17.4	43
77	Gut microbiota dysbiosis contributes to the development of hypertension. <i>Microbiome</i> , 2017 , 5, 14	16.6	652
76	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
75	Precision Medicine: What Challenges Are We Facing?. <i>Genomics, Proteomics and Bioinformatics</i> , 2016 , 14, 253-261	6.5	9
74	A novel codon-based de Bruijn graph algorithm for gene construction from unassembled transcriptomes. <i>Genome Biology</i> , 2016 , 17, 232	18.3	11
73	Comprehensive identification of internal structure and alternative splicing events in circular RNAs. <i>Nature Communications</i> , 2016 , 7, 12060	17.4	170
72	Convergent Evolution of Rumen Microbiomes in High-Altitude Mammals. <i>Current Biology</i> , 2016 , 26, 1873-1883	17.4	136
71	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
70	RiboFR-Seq: a novel approach to linking 16S rRNA amplicon profiles to metagenomes. <i>Nucleic Acids Research</i> , 2016 , 44, e99	20.1	20
69	Species Divergence vs. Functional Convergence Characterizes Crude Oil Microbial Community Assembly. <i>Frontiers in Microbiology</i> , 2016 , 7, 1254	5.7	18
68	Phage-bacteria interaction network in human oral microbiome. <i>Environmental Microbiology</i> , 2016 , 18, 2143-58	5.2	67
67	Phylomitogenomic analyses strongly support the sister relationship of the Chaetognatha and Protostomia. <i>Zoologica Scripta</i> , 2016 , 45, 187-199	2.5	7
66	CIRI: an efficient and unbiased algorithm for de novo circular RNA identification. <i>Genome Biology</i> , 2015 , 16, 4	18.3	572
65	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
64	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
63	Saccharina genomes provide novel insight into kelp biology. <i>Nature Communications</i> , 2015 , 6, 6986	17.4	154
62	Phylogenomics of non-model ciliates based on transcriptomic analyses. <i>Protein and Cell</i> , 2015 , 6, 373-385	7.2	26
61	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

60	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
59	BreakSeek: a breakpoint-based algorithm for full spectral range INDEL detection. <i>Nucleic Acids Research</i> , 2015 , 43, 6701-13	20.1	13
58	The Value and Significance of Metagenomics of Marine Environments. Preface. <i>Genomics, Proteomics and Bioinformatics</i> , 2015 , 13, 271-4	6.5	7
57	Characterization of human TCR repertoire and discovery of D-D fusion in TCR chains. <i>Protein and Cell</i> , 2014 , 5, 603-15	7.2	18
56	Dysbiosis signature of fecal microbiota in colorectal cancer patients. <i>Microbial Ecology</i> , 2013 , 66, 462-70	4.4	286
55	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
54	HTQC: a fast quality control toolkit for Illumina sequencing data. <i>BMC Bioinformatics</i> , 2013 , 14, 33	3.6	104
53	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
52	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
51	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
50	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
49	Ancestry of the Australian termitivorous numbat. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1041-5	8.3	7
48	Metagenomic sequencing reveals microbiota and its functional potential associated with periodontal disease. <i>Scientific Reports</i> , 2013 , 3, 1843	4.9	158
47	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
46	Detection, annotation and visualization of alternative splicing from RNA-Seq data with SplicingViewer. <i>Genomics</i> , 2012 , 99, 178-82	4.3	29
45	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
44	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
43	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

42	Small RNA transcriptome investigation based on next-generation sequencing technology. <i>Journal of Genetics and Genomics</i> , 2011 , 38, 505-13	4	28
41	Metagenomic profile of the bacterial communities associated with Ixodes ricinus ticks. <i>PLoS ONE</i> , 2011 , 6, e25604	3.7	182
40	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
39	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
38	Complete Khoisan and Bantu genomes from southern Africa. <i>Nature</i> , 2010 , 463, 943-7	50.4	342
37	Sequencing and genetic variation of multidrug resistance plasmids in <i>Klebsiella pneumoniae</i> . <i>PLoS ONE</i> , 2010 , 5, e10141	3.7	33
36	mirTools: microRNA profiling and discovery based on high-throughput sequencing. <i>Nucleic Acids Research</i> , 2010 , 38, W392-7	20.1	98
35	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
34	inGAP: an integrated next-generation genome analysis pipeline. <i>Bioinformatics</i> , 2010 , 26, 127-9	7.2	52
33	Nodeomics: pathogen detection in vertebrate lymph nodes using meta-transcriptomics. <i>PLoS ONE</i> , 2010 , 5, e13432	3.7	20
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	3.7	64
31	Evidence of extensive homologous recombination in the core genome of rickettsia. <i>Comparative and Functional Genomics</i> , 2009 , 510270		5
30	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
29	FlyPhy: a phylogenomic analysis platform for <i>Drosophila</i> genes and gene families. <i>BMC Bioinformatics</i> , 2009 , 10, 123	3.6	2
28	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
27	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, 300-10	3.1	3
26	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
25	PGA4genomics for comparative genome assembly based on genetic algorithm optimization. <i>Genomics</i> , 2009 , 94, 284-6	4.3	10

24	The mitochondrial genome sequence of the Tasmanian tiger (<i>Thylacinus cynocephalus</i>). <i>Genome Research</i> , 2009 , 19, 213-20	9.7	83
23	Sequencing the nuclear genome of the extinct woolly mammoth. <i>Nature</i> , 2008 , 456, 387-90	50.4	242
22	A new pheromone trail-based genetic algorithm for comparative genome assembly. <i>Nucleic Acids Research</i> , 2008 , 36, 3455-62	20.1	24
21	Comparative analysis of fatty acid desaturases in cyanobacterial genomes. <i>Comparative and Functional Genomics</i> , 2008 , 284508		42
20	PlasmoGF: an integrated system for comparative genomics and phylogenetic analysis of Plasmodium gene families. <i>Bioinformatics</i> , 2008 , 24, 1217-20	7.2	4
19	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
18	cTFbase: a database for comparative genomics of transcription factors in cyanobacteria. <i>BMC Genomics</i> , 2007 , 8, 104	4.5	28
17	Genome-wide survey of putative serine/threonine protein kinases in cyanobacteria. <i>BMC Genomics</i> , 2007 , 8, 395	4.5	30
16	Comparative molecular population genetics of phycoerythrin locus in <i>Prochlorococcus</i> . <i>Genetica</i> , 2007 , 129, 291-9	1.5	12
15	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	3.2	23
14	Combinational biosynthesis of a fluorescent cyanobacterial holo- α -phycoerythrin in <i>Escherichia coli</i> by using one expression vector. <i>Applied Biochemistry and Biotechnology</i> , 2007 , 142, 52-9	3.2	28
13	Comparison of envelope-related genes in unicellular and filamentous cyanobacteria. <i>Comparative and Functional Genomics</i> , 2007 , 2007, 25751		7
12	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
11	Evidence for positive Darwinian selection of <i>Vip</i> gene in <i>Bacillus thuringiensis</i> . <i>Journal of Genetics and Genomics</i> , 2007 , 34, 649-60	4	25
10	Phycobilisomes linker family in cyanobacterial genomes: divergence and evolution. <i>International Journal of Biological Sciences</i> , 2007 , 3, 434-45	11.2	31
9	Evolutionary analysis of phycobiliproteins: implications for their structural and functional relationships. <i>Journal of Molecular Evolution</i> , 2006 , 63, 330-40	3.1	14
8	Cloning, expression and characterization of phycoerythrin gene from <i>Ceramium boydenn</i> . <i>DNA Sequence</i> , 2006 , 17, 129-35		2
7	Genome-wide analysis of restriction-modification system in unicellular and filamentous cyanobacteria. <i>Physiological Genomics</i> , 2006 , 24, 181-90	3.6	33

6	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	4.4	4
5	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	4.4	2
4	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
3	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
2	Large-scale microbiome data integration enables robust biomarker identification. <i>Nature Computational Science</i> ,		1
1	Colorectal Cancer Patient-Derived 2D and 3D Models Efficiently Recapitulate Inter- and Intratumoral Heterogeneity. <i>Advanced Science</i> , 2201539	13.6	0