

# Zhang Zhang

## List of Publications by Year in descending order

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101  
papers

10,002  
citations

66343

42  
h-index

40979

93  
g-index

111  
all docs

111  
docs citations

111  
times ranked

15144  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene Expression Nebulas (GEN): a comprehensive data portal integrating transcriptomic profiles across multiple species at both bulk and single-cell levels. <i>Nucleic Acids Research</i> , 2022, 50, D1016-D1024.	14.5	18
2	LIRBase: a comprehensive database of long inverted repeats in eukaryotic genomes. <i>Nucleic Acids Research</i> , 2022, 50, D174-D182.	14.5	1
3	CompoDynamics: a comprehensive database for characterizing sequence composition dynamics. <i>Nucleic Acids Research</i> , 2022, 50, D962-D969.	14.5	6
4	LncRNAWiki 2.0: a knowledgebase of human long non-coding RNAs with enhanced curation model and database system. <i>Nucleic Acids Research</i> , 2022, 50, D190-D195.	14.5	16
5	BrainBase: a curated knowledgebase for brain diseases. <i>Nucleic Acids Research</i> , 2022, 50, D1131-D1138.	14.5	11
6	EWAS Open Platform: integrated data, knowledge and toolkit for epigenome-wide association study. <i>Nucleic Acids Research</i> , 2022, 50, D1004-D1009.	14.5	57
7	KaKs_Calculator 3.0: Calculating Selective Pressure on Coding and Non-Coding Sequences. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 536-540.	6.9	106
8	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. <i>Nucleic Acids Research</i> , 2021, 49, D212-D220.	14.5	160
9	LncExpDB: an expression database of human long non-coding RNAs. <i>Nucleic Acids Research</i> , 2021, 49, D962-D968.	14.5	55
10	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D18-D28.	14.5	168
11	Genome Warehouse: A Public Repository Housing Genome-scale Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 584-589.	6.9	104
12	The Genome Sequence Archive Family: Toward Explosive Data Growth and Diverse Data Types. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 578-583.	6.9	504
13	Genome Variation Map: a worldwide collection of genome variations across multiple species. <i>Nucleic Acids Research</i> , 2021, 49, D1186-D1191.	14.5	40
14	Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D24-D33.	14.5	165
15	CWAS Atlas: a curated resource of genome-wide variant-trait associations in plants and animals. <i>Nucleic Acids Research</i> , 2020, 48, D927-D932.	14.5	112
16	EWAS Data Hub: a resource of DNA methylation array data and metadata. <i>Nucleic Acids Research</i> , 2020, 48, D890-D895.	14.5	57
17	LSD 3.0: a comprehensive resource for the leaf senescence research community. <i>Nucleic Acids Research</i> , 2020, 48, D1069-D1075.	14.5	57
18	IC4R-2.0: Rice Genome Reannotation Using Massive RNA-seq Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 161-172.	6.9	18

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19	Protist 10,000 Genomes Project. <i>Innovation(China)</i> , 2020, 1, 100058.	9.1	14
20	Computational identification and characterization of glioma candidate biomarkers through multi-omics integrative profiling. <i>Biology Direct</i> , 2020, 15, 10.	4.6	22
21	The Elements of Data Sharing. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 1-4.	6.9	13
22	SR4R: An Integrative SNP Resource for Genomic Breeding and Population Research in Rice. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 173-185.	6.9	18
23	The Global Landscape of SARS-CoV-2 Genomes, Variants, and Haplotypes in 2019nCoV. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 749-759.	6.9	88
24	Compositional Variability and Mutation Spectra of Monophyletic SARS-CoV-2 Clades. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 648-663.	6.9	8
25	Multi-omics annotation of human long non-coding RNAs. <i>Biochemical Society Transactions</i> , 2020, 48, 1545-1556.	3.4	6
26	The 2019 novel coronavirus resource. <i>Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji</i> , 2020, 42, 212-221.	0.2	152
27	An online coronavirus analysis platform from the National Genomics Data Center. <i>Zoological Research</i> , 2020, 41, 705-708.	2.1	62
28	Community Curation and Expert Curation of Human Long Noncoding RNAs with LncRNAWiki and LncBook. <i>Current Protocols in Bioinformatics</i> , 2019, 67, e82.	25.8	6
29	Database Resources in BIG Data Center: Submission, Archiving, and Integration of Big Data in Plant Science. <i>Molecular Plant</i> , 2019, 12, 279-281.	8.3	6
30	Computational determination of gene age and characterization of evolutionary dynamics in human. <i>Briefings in Bioinformatics</i> , 2019, 20, 2141-2149.	6.5	1
31	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229.	14.5	153
32	Characterization and identification of long non-coding RNAs based on feature relationship. <i>Bioinformatics</i> , 2019, 35, 2949-2956.	4.1	64
33	NucMap: a database of genome-wide nucleosome positioning map across species. <i>Nucleic Acids Research</i> , 2019, 47, D163-D169.	14.5	27
34	EWAS Atlas: a curated knowledgebase of epigenome-wide association studies. <i>Nucleic Acids Research</i> , 2019, 47, D983-D988.	14.5	193
35	Plant editosome database: a curated database of RNA editosome in plants. <i>Nucleic Acids Research</i> , 2019, 47, D170-D174.	14.5	38
36	iDog: an integrated resource for domestic dogs and wild canids. <i>Nucleic Acids Research</i> , 2019, 47, D793-D800.	14.5	33

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37	Editome Disease Knowledgebase (EDK): a curated knowledgebase of editome-disease associations in human. <i>Nucleic Acids Research</i> , 2019, 47, D78-D83.	14.5	28
38	LncBook: a curated knowledgebase of human long non-coding RNAs. <i>Nucleic Acids Research</i> , 2019, 47, D128-D134.	14.5	177
39	Genome Variation Map: a data repository of genome variations in BIG Data Center. <i>Nucleic Acids Research</i> , 2018, 46, D944-D949.	14.5	53
40	MethBank 3.0: a database of DNA methylomes across a variety of species. <i>Nucleic Acids Research</i> , 2018, 46, D288-D295.	14.5	50
41	ICG: a wiki-driven knowledgebase of internal control genes for RT-qPCR normalization. <i>Nucleic Acids Research</i> , 2018, 46, D121-D126.	14.5	49
42	Rice Genomics: over the Past Two Decades and into the Future. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 397-404.	6.9	46
43	Database Resources of the BIG Data Center in 2018. <i>Nucleic Acids Research</i> , 2018, 46, D14-D20.	14.5	128
44	Bioinformatics Commons: The Cornerstone of Life and Health Sciences. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 223-225.	6.9	2
45	CloudPhylo: a fast and scalable tool for phylogeny reconstruction. <i>Bioinformatics</i> , 2017, 33, 438-440.	4.1	7
46	Rice Expression Database (RED): An integrated RNA-Seq-derived gene expression database for rice. <i>Journal of Genetics and Genomics</i> , 2017, 44, 235-241.	3.9	114
47	GSA: Genome Sequence Archive *. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 14-18.	6.9	563
48	DES-ncRNA: A knowledgebase for exploring information about human micro and long noncoding RNAs based on literature-mining. <i>RNA Biology</i> , 2017, 14, 963-971.	3.1	21
49	Detection of Regional Variation in Selection Intensity within Protein-Coding Genes Using DNA Sequence Polymorphism and Divergence. <i>Molecular Biology and Evolution</i> , 2017, 34, 3006-3022.	8.9	10
50	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017, 45, D128-D134.	14.5	174
51	Comparative Genomics Analysis of Streptomyces Species Reveals Their Adaptation to the Marine Environment and Their Diversity at the Genomic Level. <i>Frontiers in Microbiology</i> , 2016, 7, 998.	3.5	62
52	Pangenome Evidence for Higher Codon Usage Bias and Stronger Translational Selection in Core Genes of Escherichia coli. <i>Frontiers in Microbiology</i> , 2016, 7, 1180.	3.5	18
53	Randomness in Sequence Evolution Increases over Time. <i>PLoS ONE</i> , 2016, 11, e0155935.	2.5	9
54	Transcriptome analyses provide insights into the phylogeny and adaptive evolution of the mangrove fern genus <i>Acrostichum</i> . <i>Scientific Reports</i> , 2016, 6, 35634.	3.3	25

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55	What Signatures Dominantly Associate with Gene Age?. <i>Genome Biology and Evolution</i> , 2016, 8, 3083-3089.	2.5	39
56	Precision Medicine: What Challenges Are We Facing?. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 253-261.	6.9	15
57	Old genes experience stronger translational selection than young genes. <i>Gene</i> , 2016, 590, 29-34.	2.2	11
58	Information Commons for Rice (IC4R). <i>Nucleic Acids Research</i> , 2016, 44, D1172-D1180.	14.5	41
59	De Novo Assembly of Coding Sequences of the Mangrove Palm ( <i>Nypa fruticans</i> ) Using RNA-Seq and Discovery of Whole-Genome Duplications in the Ancestor of Palms. <i>PLoS ONE</i> , 2015, 10, e0145385.	2.5	27
60	MethBank: a database integrating next-generation sequencing single-base-resolution DNA methylation programming data. <i>Nucleic Acids Research</i> , 2015, 43, D54-D58.	14.5	31
61	LncRNAWiki: harnessing community knowledge in collaborative curation of human long non-coding RNAs. <i>Nucleic Acids Research</i> , 2015, 43, D187-D192.	14.5	110
62	DoGSD: the dog and wolf genome SNP database. <i>Nucleic Acids Research</i> , 2015, 43, D777-D783.	14.5	76
63	Biological Databases for Human Research. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 55-63.	6.9	84
64	Transcriptome analysis of the Holly mangrove <i>Acanthus ilicifolius</i> and its terrestrial relative, <i>Acanthus leucostachyus</i> , provides insights into adaptation to intertidal zones. <i>BMC Genomics</i> , 2015, 16, 605.	2.8	46
65	PanGP: A tool for quickly analyzing bacterial pan-genome profile. <i>Bioinformatics</i> , 2014, 30, 1297-1299.	4.1	188
66	Bringing Biocuration to China. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 153-155.	6.9	8
67	RiceWiki: a wiki-based database for community curation of rice genes. <i>Nucleic Acids Research</i> , 2014, 42, D1222-D1228.	14.5	19
68	Flexibility and Symmetry of Prokaryotic Genome Rearrangement Reveal Lineage-Associated Core-Gene-Defined Genome Organizational Frameworks. <i>MBio</i> , 2014, 5, e01867.	4.1	22
69	Ribogenomics: the Science and Knowledge of RNA. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 57-63.	6.9	38
70	Evaluation of Five Methods for Genome-Wide Circadian Gene Identification. <i>Journal of Biological Rhythms</i> , 2014, 29, 231-242.	2.6	41
71	The quest for a unified view of bacterial land colonization. <i>ISME Journal</i> , 2014, 8, 1358-1369.	9.8	21
72	Translational selection in human: more pronounced in housekeeping genes. <i>Biology Direct</i> , 2014, 9, 17.	4.6	45

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73	Does the Genetic Code Have A Eukaryotic Origin?. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 41-55.	6.9	2
74	On the classification of long non-coding RNAs. <i>RNA Biology</i> , 2013, 10, 924-933.	3.1	1,040
75	Systematic analysis of intron size and abundance parameters in diverse lineages. <i>Science China Life Sciences</i> , 2013, 56, 968-974.	4.9	43
76	AuthorReward: increasing community curation in biological knowledge wikis through automated authorship quantification. <i>Bioinformatics</i> , 2013, 29, 1837-1839.	4.1	10
77	Community Intelligence in Knowledge Curation: An Application to Managing Scientific Nomenclature. <i>PLoS ONE</i> , 2013, 8, e56961.	2.5	7
78	Distinct Contributions of Replication and Transcription to Mutation Rate Variation of Human Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 4-10.	6.9	31
79	ParaAT: A parallel tool for constructing multiple protein-coding DNA alignments. <i>Biochemical and Biophysical Research Communications</i> , 2012, 419, 779-781.	2.1	377
80	Codon Deviation Coefficient: a novel measure for estimating codon usage bias and its statistical significance. <i>BMC Bioinformatics</i> , 2012, 13, 43.	2.6	53
81	Bioinformatics clouds for big data manipulation. <i>Biology Direct</i> , 2012, 7, 43; discussion 43.	4.6	121
82	Comparative Analyses of H3K4 and H3K27 Trimethylations Between the Mouse Cerebrum and Testis. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 82-93.	6.9	22
83	Strand-biased Gene Distribution in Bacteria Is Related to both Horizontal Gene Transfer and Strand-biased Nucleotide Composition. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 186-196.	6.9	11
84	The Pendulum Model for Genome Compositional Dynamics: from the Four Nucleotides to the Twenty Amino Acids. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 175-180.	6.9	8
85	On the molecular mechanism of GC content variation among eubacterial genomes. <i>Biology Direct</i> , 2012, 7, 2.	4.6	121
86	On the Organizational Dynamics of the Genetic Code. <i>Genomics, Proteomics and Bioinformatics</i> , 2011, 9, 21-29.	6.9	20
87	LOX: inferring Level Of eXpression from diverse methods of census sequencing. <i>Bioinformatics</i> , 2010, 26, 1918-1919.	4.1	30
88	Modeling compositional dynamics based on GC and purine contents of protein-coding sequences. <i>Biology Direct</i> , 2010, 5, 63.	4.6	13
89	The filamentous fungal gene expression database (FFGED). <i>Fungal Genetics and Biology</i> , 2010, 47, 199-204.	2.1	32
90	Nucleotide compositional asymmetry between the leading and lagging strands of eubacterial genomes. <i>Research in Microbiology</i> , 2010, 161, 838-846.	2.1	19

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91	KaKs_Calculator 2.0: A Toolkit Incorporating Gamma-Series Methods and Sliding Window Strategies. <i>Genomics, Proteomics and Bioinformatics</i> , 2010, 8, 77-80.	6.9	1,301
92	Maximum-Likelihood Model Averaging To Profile Clustering of Site Types across Discrete Linear Sequences. <i>PLoS Computational Biology</i> , 2009, 5, e1000421.	3.2	17
93	Correlation Between Ka/Ks and Ks is Related to Substitution Model and Evolutionary Lineage. <i>Journal of Molecular Evolution</i> , 2009, 68, 414-423.	1.8	71
94	Bringing Web 2.0 to bioinformatics. <i>Briefings in Bioinformatics</i> , 2008, 10, 1-10.	6.5	66
95	Compositional dynamics of guanine and cytosine content in prokaryotic genomes. <i>Research in Microbiology</i> , 2007, 158, 363-370.	2.1	31
96	GC content variability of eubacteria is governed by the pol III $\beta'$ subunit. <i>Biochemical and Biophysical Research Communications</i> , 2007, 356, 20-25.	2.1	40
97	Evaluation of Six Methods for Estimating Synonymous and Nonsynonymous Substitution Rates. <i>Genomics, Proteomics and Bioinformatics</i> , 2006, 4, 173-181.	6.9	34
98	KaKs_Calculator: Calculating Ka and Ks Through Model Selection and Model Averaging. <i>Genomics, Proteomics and Bioinformatics</i> , 2006, 4, 259-263.	6.9	940
99	Computing Ka and Ks with a consideration of unequal transitional substitutions. <i>BMC Evolutionary Biology</i> , 2006, 6, 44.	3.2	78
100	TreeFam: a curated database of phylogenetic trees of animal gene families. <i>Nucleic Acids Research</i> , 2006, 34, D572-D580.	14.5	465
101	Data Integration in Bioinformatics: Current Efforts and Challenges. , 0, , .		18