Jingfa Xiao

List of Publications by Year
in descending order

37 papers	3,387 citations

279798

23 h-index

315739

38 g-index

42 all docs	42 docs citations
42 times ranked	4591 citing authors

#	ARTICLE	IF	CITATIONS
1	GSA: Genome Sequence Archive *. Genomics, Proteomics and Bioinformatics, 2017, 15, 14-18.	6.9	563
2	The Genome Sequence Archive Family: Toward Explosive Data Growth and Diverse Data Types. Genomics, Proteomics and Bioinformatics, 2021, 19, 578-583.	6.9	504
3	PGAP: pan-genomes analysis pipeline. Bioinformatics, 2012, 28, 416-418.	4.1	498
4	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2022. Nucleic Acids Research, 2022, 50, D27-D38.	14.5	364
5	PanGP: A tool for quickly analyzing bacterial pan-genome profile. Bioinformatics, 2014, 30, 1297-1299.	4.1	188
6	DatabaseÂResources of the National Genomics Data Center, China National Center for Bioinformation in 2021. Nucleic Acids Research, 2021, 49, D18-D28.	14.5	168
7	Genome Warehouse: A Public Repository Housing Genome-scale Data. Genomics, Proteomics and Bioinformatics, 2021, 19, 584-589.	6.9	104
8	Genomic reconnaissance of clinical isolates of emerging human pathogen Mycobacterium abscessus reveals high evolutionary potential. Scientific Reports, 2014, 4, 4061.	3.3	96
9	The Global Landscape of SARS-CoV-2 Genomes, Variants, and Haplotypes in 2019nCoVR. Genomics, Proteomics and Bioinformatics, 2020, 18, 749-759.	6.9	88
10	Comparative genomic analysis of Streptococcus suis reveals significant genomic diversity among different serotypes. BMC Genomics, 2011, 12, 523.	2.8	71
11	A Brief Review of Software Tools for Pangenomics. Genomics, Proteomics and Bioinformatics, 2015, 13, 73-76.	6.9	66
12	Comparative Genomics Analysis of Streptomyces Species Reveals Their Adaptation to the Marine Environment and Their Diversity at the Genomic Level. Frontiers in Microbiology, 2016, 7, 998.	3.5	62
13	Comprehensive Assessment of Genotype Imputation Performance. Human Heredity, 2018, 83, 107-116.	0.8	56
14	Genome Variation Map: a data repository of genome variations in BIG Data Center. Nucleic Acids Research, 2018, 46, D944-D949.	14.5	53
15	MethBank 3.0: a database of DNA methylomes across a variety of species. Nucleic Acids Research, 2018, 46, D288-D295.	14.5	50
16	ICG: a wiki-driven knowledgebase of internal control genes for RT-qPCR normalization. Nucleic Acids Research, 2018, 46, D121-D126.	14.5	49
17	CancerSCEM: a databaseÂof single-cell expression map across various human cancers. Nucleic Acids Research, 2022, 50, D1147-D1155.	14.5	47
18	Whole Genome Analyses of Chinese Population and De Novo Assembly of A Northern Han Genome. Genomics, Proteomics and Bioinformatics, 2019, 17, 229-247.	6.9	42

#	Article	IF	Citations
19	Comparative Genomics Study of Multi-Drug-Resistance Mechanisms in the Antibiotic-Resistant Streptococcus suis R61 Strain. PLoS ONE, 2011, 6, e24988.	2.5	36
20	iDog: an integrated resource for domestic dogs and wild canids. Nucleic Acids Research, 2019, 47, D793-D800.	14.5	33
21	PGAP-X: extension on pan-genome analysis pipeline. BMC Genomics, 2018, 19, 36.	2.8	29
22	NucMap: a database of genome-wide nucleosome positioning map across species. Nucleic Acids Research, 2019, 47, D163-D169.	14.5	27
23	Pan-Genomic Analysis Provides Insights into the Genomic Variation and Evolution of Salmonella Paratyphi A. PLoS ONE, 2012, 7, e45346.	2.5	26
24	PADS Arsenal: a database of prokaryotic defense systems related genes. Nucleic Acids Research, 2020, 48, D590-D598.	14.5	25
25	PGAweb: A Web Server for Bacterial Pan-Genome Analysis. Frontiers in Microbiology, 2018, 9, 1910.	3.5	24
26	Flexibility and Symmetry of Prokaryotic Genome Rearrangement Reveal Lineage-Associated Core-Gene-Defined Genome Organizational Frameworks. MBio, 2014, 5, e01867.	4.1	22
27	Whole-genome and time-course dual RNA-Seq analyses reveal chronic pathogenicity-related gene dynamics in the ginseng rusty root rot pathogen Ilyonectria robusta. Scientific Reports, 2020, 10, 1586.	3.3	18
28	Gene Expression Nebulas (GEN): a comprehensive data portal integrating transcriptomic profiles across multiple species at both bulk and single-cell levels. Nucleic Acids Research, 2022, 50, D1016-D1024.	14.5	18
29	The Elements of Data Sharing. Genomics, Proteomics and Bioinformatics, 2020, 18, 1-4.	6.9	13
30	Compositional Variability and Mutation Spectra of Monophyletic SARS-CoV-2 Clades. Genomics, Proteomics and Bioinformatics, 2020, 18, 648-663.	6.9	8
31	Applications and challenges of high performance computing in genomics. CCF Transactions on High Performance Computing, 2021, 3, 344-352.	1.7	6
32	Evaluation of clinical impact of pharmacogenomics knowledge involved in CPIC guidelines on Chinese pediatric patients. Pharmacogenomics, 2020, 21, 209-219.	1.3	5
33	RefRGim: an intelligent reference panel reconstruction method for genotype imputation with convolutional neural networks. Briefings in Bioinformatics, 2021, 22, .	6.5	5
34	Homology modeling and molecular dynamics simulation studies of human type 1 3β-hydroxysteroid dehydrogenase: Toward the understanding of cofactor specificity. Journal of Computational Chemistry, 2011, 32, 33-42.	3.3	3
35	Exploration of the binding mode of α/β-type small acid soluble proteins (SASPs) with DNA. Journal of Molecular Modeling, 2011, 17, 3183-3193.	1.8	2
36	The C-Terminal Repeat Units of SpaA Mediate Adhesion of Erysipelothrix rhusiopathiae to Host Cells and Regulate Its Virulence. Biology, 2022, 11, 1010.	2.8	1

#	Article	IF	Citations
37	Biomedical application community based on China high-performance computing environment. CCF Transactions on High Performance Computing, 0, , .	1.7	0