

Jingfa Xiao

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

3,387
citations

279487

23
h-index

315357

38
g-index

42
all docs

42
docs citations

42
times ranked

4591
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.	6.5	18
2	CancerSCEM: a database of single-cell expression map across various human cancers. <i>Nucleic Acids Research</i> , 2022, 50, D1147-D1155.	6.5	47
3	Database Resources of the National Genomics Data Center, China National Center for Bioinformatics in 2022. <i>Nucleic Acids Research</i> , 2022, 50, D27-D38.	6.5	364
4	The C-Terminal Repeat Units of SpaA Mediate Adhesion of <i>Erysipelothrix rhusiopathiae</i> to Host Cells and Regulate Its Virulence. <i>Biology</i> , 2022, 11, 1010.	1.3	1
5	Database Resources of the National Genomics Data Center, China National Center for Bioinformatics in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D18-D28.	6.5	168
6	Genome Warehouse: A Public Repository Housing Genome-scale Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 584-589.	3.0	104
7	RefRGim: an intelligent reference panel reconstruction method for genotype imputation with convolutional neural networks. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	5
8	The Genome Sequence Archive Family: Toward Explosive Data Growth and Diverse Data Types. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 578-583.	3.0	504
9	Applications and challenges of high performance computing in genomics. <i>CCF Transactions on High Performance Computing</i> , 2021, 3, 344-352.	1.1	6
10	PADS Arsenal: a database of prokaryotic defense systems related genes. <i>Nucleic Acids Research</i> , 2020, 48, D590-D598.	6.5	25
11	The Elements of Data Sharing. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 1-4.	3.0	13
12	Evaluation of clinical impact of pharmacogenomics knowledge involved in CPIC guidelines on Chinese pediatric patients. <i>Pharmacogenomics</i> , 2020, 21, 209-219.	0.6	5
13	Whole-genome and time-course dual RNA-Seq analyses reveal chronic pathogenicity-related gene dynamics in the ginseng rusty root rot pathogen <i>Ilyonectria robusta</i> . <i>Scientific Reports</i> , 2020, 10, 1586.	1.6	18
14	The Global Landscape of SARS-CoV-2 Genomes, Variants, and Haplotypes in 2019nCoV. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 749-759.	3.0	88
15	Compositional Variability and Mutation Spectra of Monophyletic SARS-CoV-2 Clades. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 648-663.	3.0	8
16	Whole Genome Analyses of Chinese Population and De Novo Assembly of A Northern Han Genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 229-247.	3.0	42
17	NucMap: a database of genome-wide nucleosome positioning map across species. <i>Nucleic Acids Research</i> , 2019, 47, D163-D169.	6.5	27
18	iDog: an integrated resource for domestic dogs and wild canids. <i>Nucleic Acids Research</i> , 2019, 47, D793-D800.	6.5	33

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19	Genome Variation Map: a data repository of genome variations in BIG Data Center. <i>Nucleic Acids Research</i> , 2018, 46, D944-D949.	6.5	53
20	MethBank 3.0: a database of DNA methylomes across a variety of species. <i>Nucleic Acids Research</i> , 2018, 46, D288-D295.	6.5	50
21	ICG: a wiki-driven knowledgebase of internal control genes for RT-qPCR normalization. <i>Nucleic Acids Research</i> , 2018, 46, D121-D126.	6.5	49
22	Comprehensive Assessment of Genotype Imputation Performance. <i>Human Heredity</i> , 2018, 83, 107-116.	0.4	56
23	PGAweb: A Web Server for Bacterial Pan-Genome Analysis. <i>Frontiers in Microbiology</i> , 2018, 9, 1910.	1.5	24
24	PGAP-X: extension on pan-genome analysis pipeline. <i>BMC Genomics</i> , 2018, 19, 36.	1.2	29
25	GSA: Genome Sequence Archive *. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 14-18.	3.0	563
26	Comparative Genomics Analysis of <i>Streptomyces</i> Species Reveals Their Adaptation to the Marine Environment and Their Diversity at the Genomic Level. <i>Frontiers in Microbiology</i> , 2016, 7, 998.	1.5	62
27	A Brief Review of Software Tools for Pangenomics. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 73-76.	3.0	66
28	PanGP: A tool for quickly analyzing bacterial pan-genome profile. <i>Bioinformatics</i> , 2014, 30, 1297-1299.	1.8	188
29	Flexibility and Symmetry of Prokaryotic Genome Rearrangement Reveal Lineage-Associated Core-Genes-Defined Genome Organizational Frameworks. <i>MBio</i> , 2014, 5, e01867.	1.8	22
30	Genomic reconnaissance of clinical isolates of emerging human pathogen <i>Mycobacterium abscessus</i> reveals high evolutionary potential. <i>Scientific Reports</i> , 2014, 4, 4061.	1.6	96
31	PGAP: pan-genomes analysis pipeline. <i>Bioinformatics</i> , 2012, 28, 416-418.	1.8	498
32	Pan-Genomic Analysis Provides Insights into the Genomic Variation and Evolution of <i>Salmonella Paratyphi A</i> . <i>PLoS ONE</i> , 2012, 7, e45346.	1.1	26
33	Comparative Genomics Study of Multi-Drug-Resistance Mechanisms in the Antibiotic-Resistant <i>Streptococcus suis</i> R61 Strain. <i>PLoS ONE</i> , 2011, 6, e24988.	1.1	36
34	Exploration of the binding mode of β -type small acid soluble proteins (SASPs) with DNA. <i>Journal of Molecular Modeling</i> , 2011, 17, 3183-3193.	0.8	2
35	Comparative genomic analysis of <i>Streptococcus suis</i> reveals significant genomic diversity among different serotypes. <i>BMC Genomics</i> , 2011, 12, 523.	1.2	71
36	Homology modeling and molecular dynamics simulation studies of human type 1 3β -hydroxysteroid dehydrogenase: Toward the understanding of cofactor specificity. <i>Journal of Computational Chemistry</i> , 2011, 32, 33-42.	1.5	3

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37	Biomedical application community based on China high-performance computing environment. CCF Transactions on High Performance Computing, 0, , .	1.1	0