

Liqing Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

1,916
citations

361413

20
h-index

276875

41
g-index

52
all docs

52
docs citations

52
times ranked

2877
citing authors

#	ARTICLE	IF	CITATIONS
1	Associations between bacterial communities and microplastics from surface seawater of the Northern Patagonian area of Chile. <i>Environmental Pollution</i> , 2022, 306, 119313.	7.5	9
2	Generalizing predictions to unseen sequencing profiles via deep generative models. <i>Scientific Reports</i> , 2022, 12, 7151.	3.3	3
3	AgroSeek: a system for computational analysis of environmental metagenomic data and associated metadata. <i>BMC Bioinformatics</i> , 2021, 22, 117.	2.6	5
4	Next generation sequencing approaches to evaluate water and wastewater quality. <i>Water Research</i> , 2021, 194, 116907.	11.3	62
5	Bioinformatics analysis of a TF-miRNA-lncRNA regulatory network in major depressive disorder. <i>Psychiatry Research</i> , 2021, 299, 113842.	3.3	13
6	Data Analytics for Environmental Science and Engineering Research. <i>Environmental Science & Technology</i> , 2021, 55, 10895-10907.	10.0	44
7	MetaMLP: A Fast Word Embedding Based Classifier to Profile Target Gene Databases in Metagenomic Samples. <i>Journal of Computational Biology</i> , 2021, 28, 1063-1074.	1.6	2
8	Triclosan has a robust, yet reversible impact on human gut microbial composition in vitro. <i>PLoS ONE</i> , 2020, 15, e0234046.	2.5	6
9	DeepMicro: deep representation learning for disease prediction based on microbiome data. <i>Scientific Reports</i> , 2020, 10, 6026.	3.3	67
10	Uncovering missed indels by leveraging unmapped reads. <i>Scientific Reports</i> , 2019, 9, 11093.	3.3	8
11	Identification of discriminatory antibiotic resistance genes among environmental resistomes using extremely randomized tree algorithm. <i>Microbiome</i> , 2019, 7, 123.	11.1	35
12	Effect of antibiotic use and composting on antibiotic resistance gene abundance and resistome risks of soils receiving manure-derived amendments. <i>Environment International</i> , 2019, 128, 233-243.	10.0	101
13	Effects of Dairy Manure-Based Amendments and Soil Texture on Lettuce- and Radish-Associated Microbiota and Resistomes. <i>MSphere</i> , 2019, 4, .	2.9	35
14	vi-HMM: a novel HMM-based method for sequence variant identification in short-read data. <i>Human Genomics</i> , 2019, 13, 9.	2.9	2
15	Enhanced GII.4 human norovirus infection in gnotobiotic pigs transplanted with a human gut microbiota. <i>Journal of General Virology</i> , 2019, 100, 1530-1540.	2.9	15
16	Four targeted genes for predicting the prognosis of colorectal cancer: A bioinformatics analysis case. <i>Oncology Letters</i> , 2019, 18, 5043-5054.	1.8	18
17	A large-scale RNA interference screen identifies genes that regulate autophagy at different stages. <i>Scientific Reports</i> , 2018, 8, 2822.	3.3	12
18	Parallel Evolution of Genome Streamlining and Cellular Bioenergetics across the Marine Radiation of a Bacterial Phylum. <i>MBio</i> , 2018, 9, .	4.1	27

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19	Comprehensive off-target analysis of dCas9-SAM-mediated HIV reactivation via long noncoding RNA and mRNA profiling. BMC Medical Genomics, 2018, 11, 78.	1.5	15
20	Identification of Differentially Methylated Sites with Weak Methylation Effects. Genes, 2018, 9, 75.	2.4	4
21	DeepARG: a deep learning approach for predicting antibiotic resistance genes from metagenomic data. Microbiome, 2018, 6, 23.	11.1	462
22	MetaCompare: a computational pipeline for prioritizing environmental resistome risk. FEMS Microbiology Ecology, 2018, 94, .	2.7	88
23	FastViromeExplorer: a pipeline for virus and phage identification and abundance profiling in metagenomics data. PeerJ, 2018, 6, e4227.	2.0	70
24	UPS-indel: a Universal Positioning System for Indels. Scientific Reports, 2017, 7, 14106.	3.3	6
25	Improving somatic variant identification through integration of genome and exome data. BMC Genomics, 2017, 18, 748.	2.8	1
26	Analysis of whole genome sequence and genome-wide SNPs in highly inbred pigs. , 2017, , .		0
27	Apigenin Impacts the Growth of the Gut Microbiota and Alters the Gene Expression of Enterococcus. Molecules, 2017, 22, 1292.	3.8	30
28	Herbicide injury induces DNA methylome alterations in <i>Arabidopsis</i> . PeerJ, 2017, 5, e3560.	2.0	27
29	MetaStorm: A Public Resource for Customizable Metagenomics Annotation. PLoS ONE, 2016, 11, e0162442.	2.5	59
30	Poster: Diagnosing and treating code-duplication problems in bioinformatics libraries. , 2016, , .		0
31	UPS-indel: A better approach for finding indel redundancy. , 2016, , .		0
32	Metagenomic profiling of historic Colorado Front Range flood impact on distribution of riverine antibiotic resistance genes. Scientific Reports, 2016, 6, 38432.	3.3	55
33	SPAI: an interactive platform for indel analysis. BMC Genomics, 2016, 17, 496.	2.8	0
34	A Bayesian Assignment Method for Ambiguous Bisulfite Short Reads. PLoS ONE, 2016, 11, e0151826.	2.5	2
35	Identification and analysis of the N6-methyladenosine in the <i>Saccharomyces cerevisiae</i> transcriptome. Scientific Reports, 2015, 5, 13859.	3.3	96
36	The pattern of DNA cleavage intensity around indels. Scientific Reports, 2015, 5, 8333.	3.3	11

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37	HMMvar-func: a new method for predicting the functional outcome of genetic variants. BMC Bioinformatics, 2015, 16, 351.	2.6	10
38	Performance evaluation of indel calling tools using real short-read data. Human Genomics, 2015, 9, 20.	2.9	75
39	PseKNC-General: a cross-platform package for generating various modes of pseudo nucleotide compositions. Bioinformatics, 2015, 31, 119-120.	4.1	210
40	Predicting the combined effect of multiple genetic variants. Human Genomics, 2015, 9, 18.	2.9	22
41	Objective and Comprehensive Evaluation of Bisulfite Short Read Mapping Tools. Advances in Bioinformatics, 2014, 2014, 1-11.	5.7	52
42	A Transcriptome Post-Scaffolding Method for Assembling High Quality Contigs. Computational Biology Journal, 2014, 2014, 1-4.	0.6	13
43	Vindel: a simple pipeline for checking indel redundancy. BMC Bioinformatics, 2014, 15, 359.	2.6	9
44	Quantitative prediction of the effect of genetic variation using hidden Markov models. BMC Bioinformatics, 2014, 15, 5.	2.6	22
45	Gene selection for classifications using Multiple PCA with Sparsity. Tsinghua Science and Technology, 2012, 17, 659-665.	6.1	2
46	A Network of SCOP Hidden Markov Models and Its Analysis. BMC Bioinformatics, 2011, 12, 191.	2.6	2
47	GPU-RMAP: Accelerating Short-Read Mapping on Graphics Processors. , 2010, , .		19
48	Towards Constructing Disease Relationship Networks Using Genome-Wide Association Studies. International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010, , .	0.0	0
49	Adaptive Evolution and Frequent Gene Conversion in the Brain Expressed X-Linked Gene Family in Mammals. Biochemical Genetics, 2008, 46, 293-311.	1.7	17
50	Note on the Computation of Critical Effective Population Sizes. Journal of Computational Biology, 2007, 14, 950-960.	1.6	2
51	Human SNPs Reveal No Evidence of Frequent Positive Selection. Molecular Biology and Evolution, 2005, 22, 2504-2507.	8.9	71