

Liqing Zhang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9412662/publications.pdf>

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	DeepARG: a deep learning approach for predicting antibiotic resistance genes from metagenomic data. <i>Microbiome</i> , 2018, 6, 23.	11.1	462
2	PseKNC-General: a cross-platform package for generating various modes of pseudo nucleotide compositions. <i>Bioinformatics</i> , 2015, 31, 119-120.	4.1	210
3	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
4	Identification and analysis of the N6-methyladenosine in the <i>Saccharomyces cerevisiae</i> transcriptome. <i>Scientific Reports</i> , 2015, 5, 13859.	3.3	96
5	MetaCompare: a computational pipeline for prioritizing environmental resistome risk. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	88
6	Performance evaluation of indel calling tools using real short-read data. <i>Human Genomics</i> , 2015, 9, 20.	2.9	75
7	Human SNPs Reveal No Evidence of Frequent Positive Selection. <i>Molecular Biology and Evolution</i> , 2005, 22, 2504-2507.	8.9	71
8	FastViromeExplorer: a pipeline for virus and phage identification and abundance profiling in metagenomics data. <i>PeerJ</i> , 2018, 6, e4227.	2.0	70
9	DeepMicro: deep representation learning for disease prediction based on microbiome data. <i>Scientific Reports</i> , 2020, 10, 6026.	3.3	67
10	Next generation sequencing approaches to evaluate water and wastewater quality. <i>Water Research</i> , 2021, 194, 116907.	11.3	62
11	MetaStorm: A Public Resource for Customizable Metagenomics Annotation. <i>PLoS ONE</i> , 2016, 11, e0162442.	2.5	59
12	Metagenomic profiling of historic Colorado Front Range flood impact on distribution of riverine antibiotic resistance genes. <i>Scientific Reports</i> , 2016, 6, 38432.	3.3	55
13	Objective and Comprehensive Evaluation of Bisulfite Short Read Mapping Tools. <i>Advances in Bioinformatics</i> , 2014, 2014, 1-11.	5.7	52
14	Data Analytics for Environmental Science and Engineering Research. <i>Environmental Science & Technology</i> , 2021, 55, 10895-10907.	10.0	44
15	Identification of discriminatory antibiotic resistance genes among environmental resistomes using extremely randomized tree algorithm. <i>Microbiome</i> , 2019, 7, 123.	11.1	35
16	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
17	Apigenin Impacts the Growth of the Gut Microbiota and Alters the Gene Expression of <i>Enterococcus</i> . <i>Molecules</i> , 2017, 22, 1292.	3.8	30
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	Herbicide injury induces DNA methylome alterations in <i>Arabidopsis</i> . PeerJ, 2017, 5, e3560.	2.0	27
20	Quantitative prediction of the effect of genetic variation using hidden Markov models. BMC Bioinformatics, 2014, 15, 5.	2.6	22
21	Predicting the combined effect of multiple genetic variants. Human Genomics, 2015, 9, 18.	2.9	22
22	GPU-RMAP: Accelerating Short-Read Mapping on Graphics Processors. , 2010, , .		19
23	Four targeted genes for predicting the prognosis of colorectal cancer: A bioinformatics analysis case. Oncology Letters, 2019, 18, 5043-5054.	1.8	18
24	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
25	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
26	Enhanced GII.4 human norovirus infection in gnotobiotic pigs transplanted with a human gut microbiota. Journal of General Virology, 2019, 100, 1530-1540.	2.9	15
27	A Transcriptome Post-Scaffolding Method for Assembling High Quality Contigs. Computational Biology Journal, 2014, 2014, 1-4.	0.6	13
28	Bioinformatics analysis of a TF-miRNA-lncRNA regulatory network in major depressive disorder. Psychiatry Research, 2021, 299, 113842.	3.3	13
29	A large-scale RNA interference screen identifies genes that regulate autophagy at different stages. Scientific Reports, 2018, 8, 2822.	3.3	12
30	The pattern of DNA cleavage intensity around indels. Scientific Reports, 2015, 5, 8333.	3.3	11
31	HMMvar-func: a new method for predicting the functional outcome of genetic variants. BMC Bioinformatics, 2015, 16, 351.	2.6	10
32	Vindel: a simple pipeline for checking indel redundancy. BMC Bioinformatics, 2014, 15, 359.	2.6	9
33	Associations between bacterial communities and microplastics from surface seawater of the Northern Patagonian area of Chile. Environmental Pollution, 2022, 306, 119313.	7.5	9
34	Uncovering missed indels by leveraging unmapped reads. Scientific Reports, 2019, 9, 11093.	3.3	8
35	LPS-indel: a Universal Positioning System for Indels. Scientific Reports, 2017, 7, 14106.	3.3	6
36	Triclosan has a robust, yet reversible impact on human gut microbial composition in vitro. PLoS ONE, 2020, 15, e0234046.	2.5	6

#	ARTICLE	IF	CITATIONS
37	AgroSeek: a system for computational analysis of environmental metagenomic data and associated metadata. BMC Bioinformatics, 2021, 22, 117.	2.6	5
38	Identification of Differentially Methylated Sites with Weak Methylation Effects. Genes, 2018, 9, 75.	2.4	4
39	Generalizing predictions to unseen sequencing profiles via deep generative models. Scientific Reports, 2022, 12, 7151.	3.3	3
40	Note on the Computation of Critical Effective Population Sizes. Journal of Computational Biology, 2007, 14, 950-960.	1.6	2
41	A Network of SCOP Hidden Markov Models and Its Analysis. BMC Bioinformatics, 2011, 12, 191.	2.6	2
42	Gene selection for classifications using Multiple PCA with Sparsity. Tsinghua Science and Technology, 2012, 17, 659-665.	6.1	2
43	vi-HMM: a novel HMM-based method for sequence variant identification in short-read data. Human Genomics, 2019, 13, 9.	2.9	2
44	A Bayesian Assignment Method for Ambiguous Bisulfite Short Reads. PLoS ONE, 2016, 11, e0151826.	2.5	2
45	MetaMLP: A Fast Word Embedding Based Classifier to Profile Target Gene Databases in Metagenomic Samples. Journal of Computational Biology, 2021, 28, 1063-1074.	1.6	2
46	Improving somatic variant identification through integration of genome and exome data. BMC Genomics, 2017, 18, 748.	2.8	1
47	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
48	Poster: Diagnosing and treating code-duplication problems in bioinformatics libraries. , 2016, , .		0
49	LIPS-indel: A better approach for finding indel redundancy. , 2016, , .		0
50	SPAI: an interactive platform for indel analysis. BMC Genomics, 2016, 17, 496.	2.8	0
51	Analysis of whole genome sequence and genome-wide SNPs in highly inbred pigs. , 2017, , .		0