

Yungang Xu

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

579
citations

687363

13
h-index

839539

18
g-index

21
all docs

21
docs citations

21
times ranked

683
citing authors

#	ARTICLE	IF	CITATIONS
1	Machine learning meets omics: applications and perspectives. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	50
2	Establishment of a micropropagation supporting technology for the <i>Fraxinus mandshurica</i> Å– <i>Fraxinus sogdiana</i> . <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2021, 57, 307-318.	2.1	6
3	Detecting Allele-Specific Alternative Splicing from Population-Scale RNA-Seq Data. <i>American Journal of Human Genetics</i> , 2020, 107, 461-472.	6.2	14
4	sclGANs: single-cell RNA-seq imputation using generative adversarial networks. <i>Nucleic Acids Research</i> , 2020, 48, e85-e85.	14.5	93
5	Integrative analysis of DNA methylation and gene expression profiles identifies MIR4435-2HG as an oncogenic lncRNA for glioma progression. <i>Gene</i> , 2019, 715, 144012.	2.2	23
6	Applications of Single-Cell Sequencing for Multiomics. <i>Methods in Molecular Biology</i> , 2018, 1754, 327-374.	0.9	18
7	Genome-Wide Association and Mechanistic Studies Indicate That Immune Response Contributes to Alzheimerâ€™s Disease Development. <i>Frontiers in Genetics</i> , 2018, 9, 410.	2.3	50
8	Alternative splicing links histone modifications to stem cell fate decision. <i>Genome Biology</i> , 2018, 19, 133.	8.8	53
9	Deep learning of the splicing (epi)genetic code reveals a novel candidate mechanism linking histone modifications to ESC fate decision. <i>Nucleic Acids Research</i> , 2017, 45, 12100-12112.	14.5	66
10	Machine learning and graph analytics in computational biomedicine. <i>Artificial Intelligence in Medicine</i> , 2017, 83, 1.	6.5	26
11	Scalable Data Mining Algorithms in Computational Biology and Biomedicine. <i>BioMed Research International</i> , 2017, 2017, 1-3.	1.9	20
12	Identify bilayer modules via pseudo-3D clustering: applications to miRNA-gene bilayer networks. <i>Nucleic Acids Research</i> , 2016, 44, gkw679.	14.5	20
13	SoyFN: a knowledge database of soybean functional networks. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau019.	3.0	20
14	Inferring the soybean (<i>Glycine max</i>) microRNA functional network based on target gene network. <i>Bioinformatics</i> , 2014, 30, 94-103.	4.1	39
15	System-Level Insights into the Cellular Interactome of a Non-Model Organism: Inferring, Modelling and Analysing Functional Gene Network of Soybean (<i>Glycine max</i>). <i>PLoS ONE</i> , 2014, 9, e113907.	2.5	9
16	A novel insight into Gene Ontology semantic similarity. <i>Genomics</i> , 2013, 101, 368-375.	2.9	57
17	Survey on the Numbers and Catches of Weirs in Honghu Lake. <i>Hupo Kexue/Journal of Lake Sciences</i> , 1998, 10, 68-74.	0.8	1