

Yongzhuang Liu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3627537/publications.pdf>

Version: 2024-02-01

20
papers

482
citations

840776

11
h-index

940533

16
g-index

22
all docs

22
docs citations

22
times ranked

967
citing authors

#	ARTICLE	IF	CITATIONS
1	Long-read-based human genomic structural variation detection with cuteSV. <i>Genome Biology</i> , 2020, 21, 189.	8.8	164
2	A Bayesian framework for <i>de novo</i> mutation calling in parents-offspring trios. <i>Bioinformatics</i> , 2015, 31, 1375-1381.	4.1	87
3	A gradient-boosting approach for filtering <i>de novo</i> mutations in parent-offspring trios. <i>Bioinformatics</i> , 2014, 30, 1830-1836.	4.1	33
4	A deep learning approach for filtering structural variants in short read sequencing data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	32
5	A pipeline for RNA-seq based eQTL analysis with automated quality control procedures. <i>BMC Bioinformatics</i> , 2021, 22, 403.	2.6	27
6	InteGO2: a web tool for measuring and visualizing gene semantic similarities using Gene Ontology. <i>BMC Genomics</i> , 2016, 17, 530.	2.8	26
7	Disease Module Identification Based on Representation Learning of Complex Networks Integrated From GWAS, eQTL Summaries, and Human Interactome. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 418.	4.1	22
8	abPOA: an SIMD-based C library for fast partial order alignment using adaptive band. <i>Bioinformatics</i> , 2021, 37, 2209-2211.	4.1	20
9	Joint detection of copy number variations in parent-offspring trios. <i>Bioinformatics</i> , 2016, 32, 1130-1137.	4.1	18
10	eQTLMAPT: Fast and Accurate eQTL Mediation Analysis With Efficient Permutation Testing Approaches. <i>Frontiers in Genetics</i> , 2019, 10, 1309.	2.3	17
11	Sexually Dimorphic Gene Expression Associated with Growth and Reproduction of Tongue Sole (<i>Cynoglossus semilaevis</i>) Revealed by Brain Transcriptome Analysis. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1402.	4.1	15
12	Enhancing discoveries of molecular QTL studies with small sample size using summary statistic imputation. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	15
13	MGMIN: A Normalization Method for Correcting Probe Design Bias in Illumina Infinium HumanMethylation450 BeadChips. <i>Frontiers in Genetics</i> , 2020, 11, 538492.	2.3	2
14	Fast and Accurate Classification of Meta-Genomics Long Reads With deSAMBA. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 643645.	3.7	1
15	PocaCNV: A Tool to Detect Copy Number Variants from Population-Scale Genome Sequencing Data. , 2021, , .		1
16	Joint detection of germline and somatic copy number events in matched tumor-normal sample pairs. <i>Bioinformatics</i> , 2019, 35, 4955-4961.	4.1	0
17	DNMFilter_Indel: Filtering <i>de novo</i> Indels in Parent-Offspring Trios. , 2019, , .		0
18	An integrated approach for copy number variation discovery in parent-offspring trios. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	0

#	ARTICLE	IF	CITATIONS
19	Filtering de novo indels in parent-offspring trios. BMC Bioinformatics, 2020, 21, 547.	2.6	0
20	Ontology-based annotation and retrieval for large-scale VCF data. , 2021, , .		0