

Jin Zhuang Dou

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11754421/publications.pdf>

Version: 2024-02-01

21
papers

1,411
citations

567281

15
h-index

713466

21
g-index

24
all docs

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docs citations

24
times ranked

1814
citing authors

#	ARTICLE	IF	CITATIONS
1	Scallop genome provides insights into evolution of bilaterian karyotype and development. <i>Nature Ecology and Evolution</i> , 2017, 1, 120.	7.8	353
2	Scallop genome reveals molecular adaptations to semi-sessile life and neurotoxins. <i>Nature Communications</i> , 2017, 8, 1721.	12.8	180
3	High-Resolution Linkage and Quantitative Trait Locus Mapping Aided by Genome Survey Sequencing: Building Up An Integrative Genomic Framework for a Bivalve Mollusc. <i>DNA Research</i> , 2014, 21, 85-101.	3.4	173
4	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. <i>Cell</i> , 2019, 179, 736-749.e15.	28.9	126
5	MethylRAD: a simple and scalable method for genome-wide DNA methylation profiling using methylation-dependent restriction enzymes. <i>Open Biology</i> , 2015, 5, 150130.	3.6	123
6	RADtyping: An Integrated Package for Accurate De Novo Codominant and Dominant RAD Genotyping in Mapping Populations. <i>PLoS ONE</i> , 2013, 8, e79960.	2.5	102
7	Evaluation of the 2b-RAD method for genomic selection in scallop breeding. <i>Scientific Reports</i> , 2016, 6, 19244.	3.3	65
8	Construction of a High-Density Genetic Map and Quantitative Trait Locus Mapping in the Sea Cucumber <i>Apostichopus japonicus</i> . <i>Scientific Reports</i> , 2015, 5, 14852.	3.3	48
9	A Scallop IGF Binding Protein Gene: Molecular Characterization and Association of Variants with Growth Traits. <i>PLoS ONE</i> , 2014, 9, e89039.	2.5	33
10	Reference-free SNP calling: improved accuracy by preventing incorrect calls from repetitive genomic regions. <i>Biology Direct</i> , 2012, 7, 17.	4.6	30
11	Estimation of kinship coefficient in structured and admixed populations using sparse sequencing data. <i>PLoS Genetics</i> , 2017, 13, e1007021.	3.5	27
12	Bi-order multimodal integration of single-cell data. <i>Genome Biology</i> , 2022, 23, 112.	8.8	26
13	An SCD gene from the Mollusca and its upregulation in carotenoid-enriched scallops. <i>Gene</i> , 2015, 564, 101-108.	2.2	24
14	Generation of glucocorticoid-resistant SARS-CoV-2 T ^h 1 cells for adoptive cell therapy. <i>Cell Reports</i> , 2021, 36, 109432.	6.4	24
15	Single-cell manifold-preserving feature selection for detecting rare cell populations. <i>Nature Computational Science</i> , 2021, 1, 374-384.	8.0	20
16	MEDALT: single-cell copy number lineage tracing enabling gene discovery. <i>Genome Biology</i> , 2021, 22, 70.	8.8	19
17	Ab initio spillover compensation in mass cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 99, 899-909.	1.5	10
18	Genome-Wide Association for HbA1c in Malay Identified Deletion on SLC4A1 that Influences HbA1c Independent of Glycemia. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, 3854-3864.	3.6	9

#	ARTICLE	IF	CITATIONS
19	Using off-target data from whole-exome sequencing to improve genotyping accuracy, association analysis and polygenic risk prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	8
20	Sensei: how many samples to tell a change in cell type abundance?. <i>BMC Bioinformatics</i> , 2022, 23, 2.	2.6	2
21	Whole-Genome Restriction Mapping by "Subhaploid"-Based RAD Sequencing: An Efficient and Flexible Approach for Physical Mapping and Genome Scaffolding. <i>Genetics</i> , 2017, 206, 1237-1250.	2.9	1