

# Jinzhuang 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

24  
docs citations

24  
times ranked

1814  
citing authors

#	ARTICLE	IF	CITATIONS
1	Sensei: how many samples to tell a change in cell type abundance?. BMC Bioinformatics, 2022, 23, 2.	2.6	2
2	Bi-order multimodal integration of single-cell data. Genome Biology, 2022, 23, 112.	8.8	26
3	Using off-target data from whole-exome sequencing to improve genotyping accuracy, association analysis and polygenic risk prediction. Briefings in Bioinformatics, 2021, 22, .	6.5	8
4	MEDALT: single-cell copy number lineage tracing enabling gene discovery. Genome Biology, 2021, 22, 70.	8.8	19
5	Single-cell manifold-preserving feature selection for detecting rare cell populations. Nature Computational Science, 2021, 1, 374-384.	8.0	20
6	Generation of glucocorticoid-resistant SARS-CoV-2 T cells for adoptive cell therapy. Cell Reports, 2021, 36, 109432.	6.4	24
7	Genome-Wide Association for HbA1c in Malay Identified Deletion on SLC4A1 that Influences HbA1c Independent of Glycemia. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 3854-3864.	3.6	9
8	Ab initio spillover compensation in mass cytometry data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 99, 899-909.	1.5	10
9	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. Cell, 2019, 179, 736-749.e15.	28.9	126
10	Whole-Genome Restriction Mapping by $\alpha$ -Subhaploid-Based RAD Sequencing: An Efficient and Flexible Approach for Physical Mapping and Genome Scaffolding. Genetics, 2017, 206, 1237-1250.	2.9	1
11	Scallop genome provides insights into evolution of bilaterian karyotype and development. Nature Ecology and Evolution, 2017, 1, 120.	7.8	353
12	Scallop genome reveals molecular adaptations to semi-sessile life and neurotoxins. Nature Communications, 2017, 8, 1721.	12.8	180
13	Estimation of kinship coefficient in structured and admixed populations using sparse sequencing data. PLoS Genetics, 2017, 13, e1007021.	3.5	27
14	Evaluation of the 2b-RAD method for genomic selection in scallop breeding. Scientific Reports, 2016, 6, 19244.	3.3	65
15	Construction of a High-Density Genetic Map and Quantitative Trait Locus Mapping in the Sea Cucumber <i>Apostichopus japonicus</i> . Scientific Reports, 2015, 5, 14852.	3.3	48
16	MethylRAD: a simple and scalable method for genome-wide DNA methylation profiling using methylation-dependent restriction enzymes. Open Biology, 2015, 5, 150130.	3.6	123
17	An SCD gene from the Mollusca and its upregulation in carotenoid-enriched scallops. Gene, 2015, 564, 101-108.	2.2	24
18	A Scallop IGF Binding Protein Gene: Molecular Characterization and Association of Variants with Growth Traits. PLoS ONE, 2014, 9, e89039.	2.5	33

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Reference-free SNP calling: improved accuracy by preventing incorrect calls from repetitive genomic regions. <i>Biology Direct</i> , 2012, 7, 17.	4.6	30