

Shi-Ping Liu

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

7,137
citations

257101

24
h-index

454577

30
g-index

35
all docs

35
docs citations

35
times ranked

10923
citing authors

#	ARTICLE	IF	CITATIONS
1	Cell transcriptomic atlas of the non-human primate <i>Macaca fascicularis</i> . <i>Nature</i> , 2022, 604, 723-731.	13.7	81
2	Incomplete lineage sorting and phenotypic evolution in marsupials. <i>Cell</i> , 2022, 185, 1646-1660.e18.	13.5	43
3	Spatiotemporal transcriptomic atlas of mouse organogenesis using DNA nanoball-patterned arrays. <i>Cell</i> , 2022, 185, 1777-1792.e21.	13.5	437
4	Single-cell landscape of the ecosystem in early-relapse hepatocellular carcinoma. <i>Cell</i> , 2021, 184, 404-421.e16.	13.5	399
5	scDPN for High-throughput Single-cell CNV Detection to Uncover Clonal Evolution During HCC Recurrence. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 346-357.	3.0	3
6	Dissecting spatial heterogeneity and the immune-evasion mechanism of CTCs by single-cell RNA-seq in hepatocellular carcinoma. <i>Nature Communications</i> , 2021, 12, 4091.	5.8	90
7	Embryonic liver developmental trajectory revealed by single-cell RNA sequencing in the <i>Foxa2eGFP</i> mouse. <i>Communications Biology</i> , 2020, 3, 642.	2.0	24
8	Single-cell RNA profiling links ncRNAs to spatiotemporal gene expression during <i>C. elegans</i> embryogenesis. <i>Scientific Reports</i> , 2020, 10, 18863.	1.6	2
9	The evolutionary history of extinct and living lions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10927-10934.	3.3	70
10	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. <i>Nature Communications</i> , 2019, 10, 470.	5.8	156
11	Single-cell transcriptomic landscape of nucleated cells in umbilical cord blood. <i>GigaScience</i> , 2019, 8, .	3.3	24
12	Comparative analysis of sequencing technologies for single-cell transcriptomics. <i>Genome Biology</i> , 2019, 20, 70.	3.8	82
13	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018, 2, 659-668.	3.4	124
14	High Throughput Single Cell RNA Sequencing, Bioinformatics Analysis and Applications. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1068, 33-43.	0.8	50
15	Red fox genome assembly identifies genomic regions associated with tame and aggressive behaviours. <i>Nature Ecology and Evolution</i> , 2018, 2, 1479-1491.	3.4	113
16	Construction of Red Fox Chromosomal Fragments from the Short-Read Genome Assembly. <i>Genes</i> , 2018, 9, 308.	1.0	14
17	Population-wide sampling of retrotransposon insertion polymorphisms using deep sequencing and efficient detection. <i>GigaScience</i> , 2017, 6, 1-11.	3.3	11
18	Evolution of multiple cell clones over a 29-year period of a CLL patient. <i>Nature Communications</i> , 2016, 7, 13765.	5.8	29

#	ARTICLE	IF	CITATIONS
19	Genomic legacy of the African cheetah, <i>Acinonyx jubatus</i> . <i>Genome Biology</i> , 2015, 16, 277.	3.8	167
20	Whole-genome sequence of the Tibetan frog <i>Nanorana parkeri</i> and the comparative evolution of tetrapod genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1257-62.	3.3	159
21	Genomic signatures of near-extinction and rebirth of the crested ibis and other endangered bird species. <i>Genome Biology</i> , 2014, 15, 557.	3.8	83
22	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	6.0	1,583
23	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	6.0	895
24	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. <i>GigaScience</i> , 2014, 3, 27.	3.3	72
25	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. <i>Cell</i> , 2014, 157, 785-794.	13.5	363
26	Decoding the <i>Ascaris suum</i> Genome using Massively Parallel Sequencing and Advanced Bioinformatic Methods – Unprecedented Prospects for Fundamental and Applied Research. , 2013, , 287-314.		1
27	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012, 44, 221-225.	9.4	383
28	<i>Ascaris suum</i> draft genome. <i>Nature</i> , 2011, 479, 529-533.	13.7	246
29	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	13.7	1,058
30	Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm (<i>Bombyx mori</i>)	6.0	342