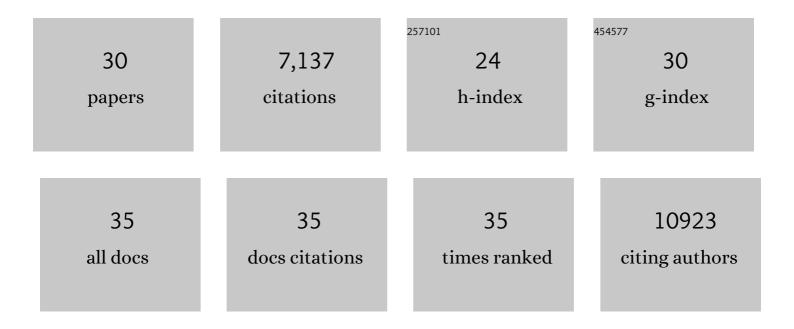
## Shi-Ping Liu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7190484/publications.pdf Version: 2024-02-01



SHI-DING LIU

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

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#	Article	IF	CITATIONS
19	Genomic legacy of the African cheetah, Acinonyx jubatus. Genome Biology, 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. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1257-62.	3.3	159
21	Genomic signatures of near-extinction and rebirth of the crested ibis and other endangered bird species. Genome Biology, 2014, 15, 557.	3.8	83
22	Whole-genome analyses resolve early branches in the tree of life of modern birds. Science, 2014, 346, 1320-1331.	6.0	1,583
23	Comparative genomics reveals insights into avian genome evolution and adaptation. Science, 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. GigaScience, 2014, 3, 27.	3.3	72
25	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. Cell, 2014, 157, 785-794.	13.5	363
26	Decoding the Ascaris suum 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 Schistosoma haematobium. Nature Genetics, 2012, 44, 221-225.	9.4	383
28	Ascaris suum draft genome. Nature, 2011, 479, 529-533.	13.7	246
29	The sequence and de novo assembly of the giant panda genome. Nature, 2010, 463, 311-317.	13.7	1,058

30 Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm () Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 3