

Weiwei Zhai

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

8,038
citations

236833

25
h-index

233338

45
g-index

46
all docs

46
docs citations

46
times ranked

14642
citing authors

#	ARTICLE	IF	CITATIONS
1	A Draft Sequence of the Neandertal Genome. <i>Science</i> , 2010, 328, 710-722.	6.0	3,588
2	Bystander CD8+ T cells are abundant and phenotypically distinct in human tumour infiltrates. <i>Nature</i> , 2018, 557, 575-579.	13.7	942
3	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. <i>Science</i> , 2011, 334, 94-98.	6.0	675
4	Genomic landscape of lung adenocarcinoma in East Asians. <i>Nature Genetics</i> , 2020, 52, 177-186.	9.4	281
5	The genomics of selection in dogs and the parallel evolution between dogs and humans. <i>Nature Communications</i> , 2013, 4, 1860.	5.8	275
6	Out of southern East Asia: the natural history of domestic dogs across the world. <i>Cell Research</i> , 2016, 26, 21-33.	5.7	271
7	Two Evolutionary Histories in the Genome of Rice: the Roles of Domestication Genes. <i>PLoS Genetics</i> , 2011, 7, e1002100.	1.5	188
8	Novel therapeutic targets on the horizon for lung cancer. <i>Lancet Oncology</i> , The, 2016, 17, e347-e362.	5.1	156
9	Genetic Convergence in the Adaptation of Dogs and Humans to the High-Altitude Environment of the Tibetan Plateau. <i>Genome Biology and Evolution</i> , 2014, 6, 2122-2128.	1.1	146
10	Elucidating the genomic architecture of Asian EGFR-mutant lung adenocarcinoma through multi-region exome sequencing. <i>Nature Communications</i> , 2018, 9, 216.	5.8	136
11	Development of a new patient-derived xenograft humanised mouse model to study human-specific tumour microenvironment and immunotherapy. <i>Gut</i> , 2018, 67, 1845-1854.	6.1	134
12	Genome sequencing analysis identifies Epstein-Barr virus subtypes associated with high risk of nasopharyngeal carcinoma. <i>Nature Genetics</i> , 2019, 51, 1131-1136.	9.4	133
13	Rapid growth of a hepatocellular carcinoma and the driving mutations revealed by cell-population genetic analysis of whole-genome data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12042-12047.	3.3	117
14	The spatial organization of intra-tumour heterogeneity and evolutionary trajectories of metastases in hepatocellular carcinoma. <i>Nature Communications</i> , 2017, 8, 4565.	5.8	117
15	An Investigation of the Statistical Power of Neutrality Tests Based on Comparative and Population Genetic Data. <i>Molecular Biology and Evolution</i> , 2009, 26, 273-283.	3.5	100
16	Clonal <i>MET</i> Amplification as a Determinant of Tyrosine Kinase Inhibitor Resistance in Epidermal Growth Factor Receptor-Mutant Non-Small-Cell Lung Cancer. <i>Journal of Clinical Oncology</i> , 2019, 37, 876-884.	0.8	91
17	Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. <i>National Science Review</i> , 2019, 6, 810-824.	4.6	65
18	Non-terminally exhausted tumor-resident memory HBV-specific T cell responses correlate with relapse-free survival in hepatocellular carcinoma. <i>Immunity</i> , 2021, 54, 1825-1840.e7.	6.6	64

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19	Point mutations in the major outer membrane protein drive hypervirulence of a rapidly expanding clone of <i>Campylobacter jejuni</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10690-10695.	3.3	56
20	Radioembolisation with Y90-resin microspheres followed by nivolumab for advanced hepatocellular carcinoma (CA 209-678): a single arm, single centre, phase 2 trial. <i>The Lancet Gastroenterology and Hepatology</i> , 2021, 6, 1025-1035.	3.7	56
21	Proteomic profiling of HIV-1 infection of human CD4+ T cells identifies PSGL-1 as an HIV restriction factor. <i>Nature Microbiology</i> , 2019, 4, 813-825.	5.9	48
22	Uncoupling immune trajectories of response and adverse events from anti-PD-1 immunotherapy in hepatocellular carcinoma. <i>Journal of Hepatology</i> , 2022, 77, 683-694.	1.8	45
23	Whole-Genome Sequencing of African Dogs Provides Insights into Adaptations against Tropical Parasites. <i>Molecular Biology and Evolution</i> , 2018, 35, 287-298.	3.5	41
24	Rapid phenotypic evolution with shallow genomic differentiation during early stages of high elevation adaptation in Eurasian Tree Sparrows. <i>National Science Review</i> , 2020, 7, 113-127.	4.6	36
25	Looking for Darwin in Genomic Sequences—Validity and Success of Statistical Methods. <i>Molecular Biology and Evolution</i> , 2012, 29, 2889-2893.	3.5	28
26	Whole Genome Sequencing and Evolutionary Analysis of Human Papillomavirus Type 16 in Central China. <i>PLoS ONE</i> , 2012, 7, e36577.	1.1	27
27	Epigenetic promoter alterations in GI tumour immune-editing and resistance to immune checkpoint inhibition. <i>Gut</i> , 2022, 71, 1277-1288.	6.1	23
28	The evolution of ancestral and species-specific adaptations in snowfinches at the Qinghai-Tibet Plateau. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	22
29	Passage Adaptation Correlates With the Reduced Efficacy of the Influenza Vaccine. <i>Clinical Infectious Diseases</i> , 2019, 69, 1198-1204.	2.9	18
30	Structures of Echovirus 30 in complex with its receptors inform a rational prediction for enterovirus receptor usage. <i>Nature Communications</i> , 2020, 11, 4421.	5.8	18
31	On the origin of SARS-CoV-2—The blind watchmaker argument. <i>Science China Life Sciences</i> , 2021, 64, 1560-1563.	2.3	18
32	Age-Dependent Transition from Cell-Level to Population-Level Control in Murine Intestinal Homeostasis Revealed by Coalescence Analysis. <i>PLoS Genetics</i> , 2013, 9, e1003326.	1.5	16
33	Dynamic Convergent Evolution Drives the Passage Adaptation across 48 Years—History of H3N2 Influenza Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 3133-3143.	3.5	16
34	Exploring Variation in the d N /d S Ratio Among Sites and Lineages Using Mutational Mappings: Applications to the Influenza Virus. <i>Journal of Molecular Evolution</i> , 2007, 65, 340-348.	0.8	15
35	Dynamic phenotypic heterogeneity and the evolution of multiple RNA subtypes in hepatocellular carcinoma: the PLANET study. <i>National Science Review</i> , 2022, 9, nwab192.	4.6	15
36	Is haplotype block identification useful for association mapping studies?. <i>Genetic Epidemiology</i> , 2004, 27, 80-83.	0.6	12

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37	Pseudo-Sanger sequencing: massively parallel production of long and near error-free reads using NGS technology. BMC Genomics, 2013, 14, 711.	1.2	12
38	The origin of chow chows in the light of the East Asian breeds. BMC Genomics, 2017, 18, 174.	1.2	8
39	Delineating the longitudinal tumor evolution using organoid models. Journal of Genetics and Genomics, 2021, 48, 560-570.	1.7	7
40	The Evolution of Small Insertions and Deletions in the Coding Genes of Drosophila melanogaster. Molecular Biology and Evolution, 2013, 30, 2699-2708.	3.5	6
41	Obtaining spatially resolved tumor purity maps using deep multiple instance learning in a pan-cancer study. Patterns, 2022, 3, 100399.	3.1	6
42	PSiTE: a Phylogeny guided Simulator for Tumor Evolution. Bioinformatics, 2019, 35, 3148-3150.	1.8	4
43	Ancient DNA reveals the maternal genetic history of East Asian domestic pigs. Journal of Genetics and Genomics, 2022, 49, 537-546.	1.7	4
44	Novel Computational Approaches and Applications in Cancer Research. BioMed Research International, 2017, 2017, 1-2.	0.9	1
45	MADE: A Computational Tool for Predicting Vaccine Effectiveness for the Influenza A(H3N2) Virus Adapted to Embryonated Eggs. Vaccines, 2022, 10, 907.	2.1	1