

Weiwei Zhai

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

8,038
citations

236925

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docs citations

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times ranked

14642
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic promoter alterations in GI tumour immune-editing and resistance to immune checkpoint inhibition. <i>Gut</i> , 2022, 71, 1277-1288.	12.1	23
2	Dynamic phenotypic heterogeneity and the evolution of multiple RNA subtypes in hepatocellular carcinoma: the PLANET study. <i>National Science Review</i> , 2022, 9, nwab192.	9.5	15
3	Obtaining spatially resolved tumor purity maps using deep multiple instance learning in a pan-cancer study. <i>Patterns</i> , 2022, 3, 100399.	5.9	6
4	Ancient DNA reveals the maternal genetic history of East Asian domestic pigs. <i>Journal of Genetics and Genomics</i> , 2022, 49, 537-546.	3.9	4
5	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.	3.7	45
6	MADE: A Computational Tool for Predicting Vaccine Effectiveness for the Influenza A(H3N2) Virus Adapted to Embryonated Eggs. <i>Vaccines</i> , 2022, 10, 907.	4.4	1
7	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, .	7.1	22
8	On the origin of SARS-CoV-2: The blind watchmaker argument. <i>Science China Life Sciences</i> , 2021, 64, 1560-1563.	4.9	18
9	Delineating the longitudinal tumor evolution using organoid models. <i>Journal of Genetics and Genomics</i> , 2021, 48, 560-570.	3.9	7
10	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.	14.3	64
11	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.	8.1	56
12	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.	9.5	36
13	Structures of Echovirus 30 in complex with its receptors inform a rational prediction for enterovirus receptor usage. <i>Nature Communications</i> , 2020, 11, 4421.	12.8	18
14	Genomic landscape of lung adenocarcinoma in East Asians. <i>Nature Genetics</i> , 2020, 52, 177-186.	21.4	281
15	Genome sequencing analysis identifies Epstein-Barr virus subtypes associated with high risk of nasopharyngeal carcinoma. <i>Nature Genetics</i> , 2019, 51, 1131-1136.	21.4	133
16	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.	13.3	48
17	Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. <i>National Science Review</i> , 2019, 6, 810-824.	9.5	65
18	Clonal MET 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.	1.6	91

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19	Passage Adaptation Correlates With the Reduced Efficacy of the Influenza Vaccine. <i>Clinical Infectious Diseases</i> , 2019, 69, 1198-1204.	5.8	18
20	PSiTE: a Phylogeny guided Simulator for Tumor Evolution. <i>Bioinformatics</i> , 2019, 35, 3148-3150.	4.1	4
21	Elucidating the genomic architecture of Asian EGFR-mutant lung adenocarcinoma through multi-region exome sequencing. <i>Nature Communications</i> , 2018, 9, 216.	12.8	136
22	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.	12.1	134
23	Whole-Genome Sequencing of African Dogs Provides Insights into Adaptations against Tropical Parasites. <i>Molecular Biology and Evolution</i> , 2018, 35, 287-298.	8.9	41
24	Bystander CD8+ T cells are abundant and phenotypically distinct in human tumour infiltrates. <i>Nature</i> , 2018, 557, 575-579.	27.8	942
25	The origin of chow chows in the light of the East Asian breeds. <i>BMC Genomics</i> , 2017, 18, 174.	2.8	8
26	The spatial organization of intra-tumour heterogeneity and evolutionary trajectories of metastases in hepatocellular carcinoma. <i>Nature Communications</i> , 2017, 8, 4565.	12.8	117
27	Novel Computational Approaches and Applications in Cancer Research. <i>BioMed Research International</i> , 2017, 2017, 1-2.	1.9	1
28	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.	7.1	56
29	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.	8.9	16
30	Novel therapeutic targets on the horizon for lung cancer. <i>Lancet Oncology</i> , The, 2016, 17, e347-e362.	10.7	156
31	Out of southern East Asia: the natural history of domestic dogs across the world. <i>Cell Research</i> , 2016, 26, 21-33.	12.0	271
32	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.	2.5	146
33	The Evolution of Small Insertions and Deletions in the Coding Genes of <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2013, 30, 2699-2708.	8.9	6
34	Pseudo-Sanger sequencing: massively parallel production of long and near error-free reads using NGS technology. <i>BMC Genomics</i> , 2013, 14, 711.	2.8	12
35	The genomics of selection in dogs and the parallel evolution between dogs and humans. <i>Nature Communications</i> , 2013, 4, 1860.	12.8	275
36	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.	3.5	16

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37	Looking for Darwin in Genomic Sequences—Validity and Success of Statistical Methods. <i>Molecular Biology and Evolution</i> , 2012, 29, 2889-2893.	8.9	28
38	Whole Genome Sequencing and Evolutionary Analysis of Human Papillomavirus Type 16 in Central China. <i>PLoS ONE</i> , 2012, 7, e36577.	2.5	27
39	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. <i>Science</i> , 2011, 334, 94-98.	12.6	675
40	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.	7.1	117
41	Two Evolutionary Histories in the Genome of Rice: the Roles of Domestication Genes. <i>PLoS Genetics</i> , 2011, 7, e1002100.	3.5	188
42	A Draft Sequence of the Neandertal Genome. <i>Science</i> , 2010, 328, 710-722.	12.6	3,588
43	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.	8.9	100
44	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.	1.8	15
45	Is haplotype block identification useful for association mapping studies?. <i>Genetic Epidemiology</i> , 2004, 27, 80-83.	1.3	12