

Xiangjiang Zhan

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

30
papers

2,777
citations

15
h-index

32
g-index

32
ext. papers

3,479
ext. citations

11.6
avg, IF

3.55
L-index

#	Paper	IF	Citations
30	RNA-combine: a toolkit for comprehensive analyses on transcriptome data from different sequencing platforms.. <i>BMC Bioinformatics</i> , 2022 , 23, 26	3.6	
29	Wildlife conservation and management in China: achievements, challenges and perspectives. <i>National Science Review</i> , 2021 , 8, nwab042	10.8	5
28	Climate-driven flyway changes and memory-based long-distance migration. <i>Nature</i> , 2021 , 591, 259-264	50.4	9
27	A single mutation underlying phenotypic convergence for hypoxia adaptation on the Qinghai-Tibetan Plateau. <i>Cell Research</i> , 2021 , 31, 1032-1035	24.7	3
26	Enhanced Transcriptomic Resilience following Increased Alternative Splicing and Differential Isoform Production between Air Pollution Conurbations. <i>Atmosphere</i> , 2021 , 12, 959	2.7	
25	Status of the saker falcon in China. <i>Science China Life Sciences</i> , 2021 , 64, 828-831	8.5	
24	Spatial patterns and conservation of genetic and phylogenetic diversity of wildlife in China. <i>Science Advances</i> , 2021 , 7,	14.3	10
23	Deeply digging the interaction effect in multiple linear regressions using a fractional-power interaction term. <i>MethodsX</i> , 2020 , 7, 101067	1.9	1
22	Genomic analysis of the domestication and post-Spanish conquest evolution of the llama and alpaca. <i>Genome Biology</i> , 2020 , 21, 159	18.3	22
21	Convergent genomic signatures of flight loss in birds suggest a switch of main fuel. <i>Nature Communications</i> , 2019 , 10, 2756	17.4	15
20	The Stem Cell Factor Sox2 Is a Positive Timer of Oligodendrocyte Development in the Postnatal Murine Spinal Cord. <i>Molecular Neurobiology</i> , 2018 , 55, 9001-9015	6.2	17
19	Transcription-Associated Mutation Promotes RNA Complexity in Highly Expressed Genes-A Major New Source of Selectable Variation. <i>Molecular Biology and Evolution</i> , 2018 , 35, 1104-1119	8.3	2
18	Integrated tool for microsatellite isolation and validation from the reference genome and their application in the study of breeding turnover in an endangered avian population. <i>Integrative Zoology</i> , 2018 , 13, 553-568	1.9	6
17	The Value of Ecosystem Services from Giant Panda Reserves. <i>Current Biology</i> , 2018 , 28, 2174-2180.e7	6.3	75
16	Characteristics of home range areas used by Saker Falcons (<i>Falco cherrug</i>) wintering on the Qinghai-Tibetan Plateau. <i>Bird Conservation International</i> , 2017 , 27, 525-536	1.7	8
15	Population transcriptomes reveal synergistic responses of DNA polymorphism and RNA expression to extreme environments on the Qinghai-Tibetan Plateau in a predatory bird. <i>Molecular Ecology</i> , 2017 , 26, 2993-3010	5.7	24
14	Genetics, morphology and ecology reveal a cryptic pika lineage in the Sikkim Himalaya. <i>Molecular Phylogenetics and Evolution</i> , 2017 , 106, 55-60	4.1	10

13	Mitochondrial complex I bridges a connection between regulation of carbon flexibility and gastrointestinal commensalism in the human fungal pathogen <i>Candida albicans</i> . <i>PLoS Pathogens</i> , 2017 , 13, e1006414	7.6	19
12	Evidence for deleterious effects of harness-mounted satellite transmitters on Saker Falcons <i>Falco cherrug</i> . <i>Bird Study</i> , 2016 , 63, 96-106	0.7	10
11	Prospects and challenges for the conservation of farm animal genomic resources, 2015-2025. <i>Frontiers in Genetics</i> , 2015 , 6, 314	4.5	50
10	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014 , 346, 1320-31	33.3	1182
9	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014 , 346, 1311-20	33.3	628
8	Peregrine and saker falcon genome sequences provide insights into evolution of a predatory lifestyle. <i>Nature Genetics</i> , 2013 , 45, 563-6	36.3	119
7	Whole-genome sequencing of giant pandas provides insights into demographic history and local adaptation. <i>Nature Genetics</i> , 2013 , 45, 67-71	36.3	219
6	Genetic consequences of historical anthropogenic and ecological events on giant pandas. <i>Ecology</i> , 2013 , 94, 2346-57	4.6	54
5	Molecular evidence for Pleistocene refugia at the eastern edge of the Tibetan Plateau. <i>Molecular Ecology</i> , 2011 , 20, 3014-26	5.7	53
4	Genotyping faeces of red pandas (<i>Ailurus fulgens</i>): implications for population estimation. <i>European Journal of Wildlife Research</i> , 2011 , 57, 1231-1235	2	3
3	A new method for quantifying genotyping errors for noninvasive genetic studies. <i>Conservation Genetics</i> , 2010 , 11, 1567-1571	2.6	16
2	Spatial genetic structure and dispersal of giant pandas on a mountain-range scale. <i>Conservation Genetics</i> , 2010 , 11, 2145-2155	2.6	59
1	Molecular censusing doubles giant panda population estimate in a key nature reserve. <i>Current Biology</i> , 2006 , 16, R451-2	6.3	158