## Xiangjiang Zhan

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Whole-genome analyses resolve early branches in the tree of life of modern birds. Science, 2014, 346, 1320-1331.	6.0	1,583
2	Comparative genomics reveals insights into avian genome evolution and adaptation. Science, 2014, 346, 1311-1320.	6.0	895
3	Whole-genome sequencing of giant pandas provides insights into demographic history and local adaptation. Nature Genetics, 2013, 45, 67-71.	9.4	303
4	Molecular censusing doubles giant panda population estimate in a key nature reserve. Current Biology, 2006, 16, R451-R452.	1.8	183
5	Peregrine and saker falcon genome sequences provide insights into evolution of a predatory lifestyle. Nature Genetics, 2013, 45, 563-566.	9.4	141
6	The Value of Ecosystem Services from Giant Panda Reserves. Current Biology, 2018, 28, 2174-2180.e7.	1.8	112
7	Spatial genetic structure and dispersal of giant pandas on a mountain-range scale. Conservation Genetics, 2010, 11, 2145-2155.	0.8	72
8	Genetic consequences of historical anthropogenic and ecological events on giant pandas. Ecology, 2013, 94, 2346-2357.	1.5	64
9	Prospects and challenges for the conservation of farm animal genomic resources, 2015-2025. Frontiers in Genetics, 2015, 6, 314.	1.1	64
10	Molecular evidence for Pleistocene refugia at the eastern edge of the Tibetan Plateau. Molecular Ecology, 2011, 20, 3014-3026.	2.0	57
11	Climate-driven flyway changes and memory-based long-distance migration. Nature, 2021, 591, 259-264.	13.7	49
12	Spatial patterns and conservation of genetic and phylogenetic diversity of wildlife in China. Science Advances, 2021, 7, .	4.7	47
13	Genomic analysis of the domestication and post-Spanish conquest evolution of the llama and alpaca. Genome Biology, 2020, 21, 159.	3.8	46
14	Population transcriptomes reveal synergistic responses of <scp>DNA</scp> polymorphism and <scp>RNA</scp> expression to extreme environments on the Qinghai–Tibetan Plateau in a predatory bird. Molecular Ecology, 2017, 26, 2993-3010.	2.0	39
15	The Stem Cell Factor Sox2 Is a Positive Timer of Oligodendrocyte Development in the Postnatal Murine Spinal Cord. Molecular Neurobiology, 2018, 55, 9001-9015.	1.9	34
16	Mitochondrial complex I bridges a connection between regulation of carbon flexibility and gastrointestinal commensalism in the human fungal pathogen Candida albicans. PLoS Pathogens, 2017, 13, e1006414.	2.1	34
17	Wildlife conservation and management in China: achievements, challenges and perspectives. National Science Review, 2021, 8, nwab042.	4.6	26
18	Convergent genomic signatures of flight loss in birds suggest a switch of main fuel. Nature Communications, 2019, 10, 2756.	5.8	24

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19	A new method for quantifying genotyping errors for noninvasive genetic studies. Conservation Genetics, 2010, 11, 1567-1571.	0.8	18
20	Genetics, morphology and ecology reveal a cryptic pika lineage in the Sikkim Himalaya. Molecular Phylogenetics and Evolution, 2017, 106, 55-60.	1.2	17
21	Evidence for deleterious effects of harness-mounted satellite transmitters on Saker Falcons <i>Falco cherrug</i> . Bird Study, 2016, 63, 96-106.	0.4	15
22	Characteristics of home range areas used by Saker Falcons ( <i>Falco cherrug</i> ) wintering on the Qinghai-Tibetan Plateau. Bird Conservation International, 2017, 27, 525-536.	0.7	12
23	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. Integrative Zoology, 2018, 13, 553-568.	1.3	11
24	A single mutation underlying phenotypic convergence for hypoxia adaptation on the Qinghai-Tibetan Plateau. Cell Research, 2021, 31, 1032-1035.	5.7	11
25	Evolutionary Conservation Genomics Reveals Recent Speciation and Local Adaptation in Threatened Takins. Molecular Biology and Evolution, 2022, 39, .	3.5	7
26	Genotyping faeces of red pandas (Ailurus fulgens): implications for population estimation. European Journal of Wildlife Research, 2011, 57, 1231-1235.	0.7	5
27	Transcription-Associated Mutation Promotes RNA Complexity in Highly Expressed Genes—A Major New Source of Selectable Variation. Molecular Biology and Evolution, 2018, 35, 1104-1119.	3.5	5
28	Deeply digging the interaction effect in multiple linear regressions using a fractional-power interaction term. MethodsX, 2020, 7, 101067.	0.7	3
29	Status of the saker falcon in China. Science China Life Sciences, 2021, 64, 828-831.	2.3	0
30	Enhanced Transcriptomic Resilience following Increased Alternative Splicing and Differential Isoform Production between Air Pollution Conurbations. Atmosphere, 2021, 12, 959.	1.0	0
31	RNA-combine: a toolkit for comprehensive analyses on transcriptome data from different sequencing platforms. BMC Bioinformatics, 2022, 23, 26.	1.2	0