

# Bisong Yue

## List of Publications by Year in descending order

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141  
papers

2,009  
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304743

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345221

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142  
docs citations

142  
times ranked

2434  
citing authors

#	ARTICLE	IF	CITATIONS
1	Hypoxia Adaptations in the Grey Wolf ( <i>Canis lupus chanco</i> ) from Qinghai-Tibet Plateau. <i>PLoS Genetics</i> , 2014, 10, e1004466.	3.5	169
2	Worldwide patterns of genomic variation and admixture in gray wolves. <i>Genome Research</i> , 2016, 26, 163-173.	5.5	160
3	Krait: an ultrafast tool for genome-wide survey of microsatellites and primer design. <i>Bioinformatics</i> , 2018, 34, 681-683.	4.1	120
4	Age-associated microbiome shows the giant panda lives on hemicelluloses, not on cellulose. <i>ISME Journal</i> , 2018, 12, 1319-1328.	9.8	89
5	Whole-Genome Sequencing of Tibetan Macaque ( <i>Macaca thibetana</i> ) Provides New Insight into the Macaque Evolutionary History. <i>Molecular Biology and Evolution</i> , 2014, 31, 1475-1489.	8.9	49
6	Chitosan-DNA nanoparticles enhanced the immunogenicity of multivalent DNA vaccination on mice against <i>Trueperella pyogenes</i> infection. <i>Journal of Nanobiotechnology</i> , 2018, 16, 8.	9.1	44
7	TesG is a type I secretion effector of <i>Pseudomonas aeruginosa</i> that suppresses the host immune response during chronic infection. <i>Nature Microbiology</i> , 2019, 4, 459-469.	13.3	44
8	Assessing genetic diversity of wild populations of Prenant's schizothoracin, <i>Schizothorax prenanti</i> , using AFLP markers. <i>Environmental Biology of Fishes</i> , 2006, 77, 79-86.	1.0	41
9	Ancient hybridization and admixture in macaques (genus <i>Macaca</i> ) inferred from whole genome sequences. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 376-386.	2.7	38
10	Behavioral heterogeneity in quorum sensing can stabilize social cooperation in microbial populations. <i>BMC Biology</i> , 2019, 17, 20.	3.8	37
11	The complete mitochondrial genome of <i>Epicauta chinensis</i> (Coleoptera: Meloidae) and phylogenetic analysis among Coleopteran insects. <i>Gene</i> , 2016, 578, 274-280.	2.2	35
12	Mitochondrial genomes of blister beetles (Coleoptera, Meloidae) and two large intergenic spacers in <i>Hycleus</i> genera. <i>BMC Genomics</i> , 2017, 18, 698.	2.8	34
13	Verifying an F <sub>1</sub> screen for identification and quantification of rare <i>Bacillus thuringiensis</i> resistance alleles in field populations of the sugarcane borer, <i>Diatraea saccharalis</i> . <i>Entomologia Experimentalis Et Applicata</i> , 2008, 129, 172-180.	1.4	33
14	Population genetic diversity of Prenant's schizothoracin, <i>Schizothorax prenanti</i> , inferred from the mitochondrial DNA control region. <i>Environmental Biology of Fishes</i> , 2008, 81, 247-252.	1.0	31
15	Nutrient reduction induced stringent responses promote bacterial quorum-sensing divergence for population fitness. <i>Scientific Reports</i> , 2016, 6, 34925.	3.3	29
16	Relationship between human disturbance and Endangered giant panda <i>Ailuropoda melanoleuca</i> habitat use in the Daxiangling Mountains. <i>Oryx</i> , 2017, 51, 146-152.	1.0	27
17	The draft genome sequence of forest musk deer ( <i>Moschus berezovskii</i> ). <i>GigaScience</i> , 2018, 7, .	6.4	26
18	DNA barcoding of 18 species of Bovidae. <i>Science Bulletin</i> , 2011, 56, 164-168.	1.7	25

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19	First insights into the giant panda ( <i>Ailuropoda melanoleuca</i> ) blood transcriptome: a resource for novel gene loci and immunogenetics. <i>Molecular Ecology Resources</i> , 2015, 15, 1001-1013.	4.8	25
20	Mitochondrial Genome and Nuclear Markers Provide New Insight into the Evolutionary History of Macaques. <i>PLoS ONE</i> , 2016, 11, e0154665.	2.5	25
21	Genome-wide mining and comparative analysis of microsatellites in three macaque species. <i>Molecular Genetics and Genomics</i> , 2017, 292, 537-550.	2.1	25
22	Genes as Early Responders Regulate Quorum-Sensing and Control Bacterial Cooperation in <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2014, 9, e101887.	2.5	24
23	Phylogenomics and Evolutionary Dynamics of the Family Actinomycetaceae. <i>Genome Biology and Evolution</i> , 2014, 6, 2625-2633.	2.5	24
24	The gut microbiome and antibiotic resistome of chronic diarrhea rhesus macaques ( <i>Macaca mulatta</i> ) and its similarity to the human gut microbiome. <i>Microbiome</i> , 2022, 10, 29.	11.1	24
25	Characterization of perfect microsatellite based on genome-wide and chromosome level in Rhesus monkey ( <i>Macaca mulatta</i> ). <i>Gene</i> , 2016, 592, 269-275.	2.2	23
26	<i>Pseudomonas aeruginosa</i> Quorum-Sensing and Type VI Secretion System Can Direct Interspecific Coexistence During Evolution. <i>Frontiers in Microbiology</i> , 2018, 9, 2287.	3.5	22
27	Molecular phylogenetics and phylogeographic structure of <i>Sorex bedfordiae</i> based on mitochondrial and nuclear DNA sequences. <i>Molecular Phylogenetics and Evolution</i> , 2015, 84, 245-253.	2.7	21
28	DNA vaccination based on pyolysin co-immunized with IL-1 $\beta$ enhances host antibacterial immunity against <i>Trueperella pyogenes</i> infection. <i>Vaccine</i> , 2016, 34, 3469-3477.	3.8	21
29	Analysis of the phenolic compounds in root exudates produced by a subalpine coniferous species as responses to experimental warming and nitrogen fertilisation. <i>Chemistry and Ecology</i> , 2014, 30, 555-565.	1.6	19
30	Conservation of the Endangered giant panda <i>Ailuropoda melanoleuca</i> in China: successes and challenges. <i>Oryx</i> , 2009, 43, 176.	1.0	18
31	Quorum-sensing molecules N-acyl homoserine lactones inhibit <i>Trueperella pyogenes</i> infection in mouse model. <i>Veterinary Microbiology</i> , 2018, 213, 89-94.	1.9	18
32	Diversification and historical demography of the rapid racerunner ( <i>Eremias velox</i> ) in relation to geological history and Pleistocene climatic oscillations in arid Central Asia. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 244-258.	2.7	18
33	MicroRNA-302/367 Cluster Impacts Host Antimicrobial Defense via Regulation of Mitophagic Response Against <i>Pseudomonas aeruginosa</i> Infection. <i>Frontiers in Immunology</i> , 2020, 11, 569173.	4.8	18
34	Transcriptome analysis reveals immune-related gene expression changes with age in giant panda ( <i>Ailuropoda melanoleuca</i> ) blood. <i>Aging</i> , 2019, 11, 249-262.	3.1	17
35	Comparative Genomics Reveals the Genetic Mechanisms of Musk Secretion and Adaptive Immunity in Chinese Forest Musk Deer. <i>Genome Biology and Evolution</i> , 2019, 11, 1019-1032.	2.5	17
36	PCR-CTPP: a rapid and reliable genotyping technique based on ZFX/ZFY alleles for sex identification of tiger ( <i>Panthera tigris</i> ) and four other endangered felids. <i>Conservation Genetics</i> , 2008, 9, 225-228.	1.5	16

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37	Major histocompatibility complex Class II<i>DRB</i> exonâ€² diversity of the Eurasian lynx (<i>Lynx</i> Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 62	0.5	16
38	A reliable, non-invasive PCR method for giant panda ( <i>Ailuropoda melanoleuca</i> ) sex identification. Conservation Genetics, 2008, 9, 739-741.	1.5	15
39	Genetic diversities of the giant panda ( <i>Ailuropoda melanoleuca</i> ) in Wanglang and Baoxing Nature Reserves. Conservation Genetics, 2008, 9, 1541-1546.	1.5	14
40	High intra-population genetic variability and inter-population differentiation in a plateau specialized fish, <i>Triplophysa orientalis</i> . Environmental Biology of Fishes, 2012, 93, 519-530.	1.0	14
41	A novel mitochondrial genome of <i>Arborophila</i> and new insight into <i>Arborophila</i> evolutionary history. PLoS ONE, 2017, 12, e0181649.	2.5	14
42	Comparative genomics sheds light on the predatory lifestyle of accipitrids and owls. Scientific Reports, 2019, 9, 2249.	3.3	14
43	Validation of daily otolith increments in larval and juvenile Chinese sucker, <i>Myxocyprinus asiaticus</i> . Environmental Biology of Fishes, 2008, 82, 165-171.	1.0	13
44	Cloning, Expression and Effects of <i>P. americana</i> Thymosin on Wound Healing. International Journal of Molecular Sciences, 2019, 20, 4932.	4.1	13
45	First demonstration of giant panda's immune response to canine distemper vaccine. Developmental and Comparative Immunology, 2020, 102, 103489.	2.3	13
46	Age-related gene expression and DNA methylation changes in rhesus macaque. Genomics, 2020, 112, 5147-5156.	2.9	13
47	Taxonomic implications from phylogenetic relationships of subspecies of <i>Schizopygopsis malacanthus</i> (Pisces: Cyprinidae) based on sequence analysis of cytochrome b mitochondrial DNA control region. Journal of Natural History, 2006, 40, 2569-2576.	0.5	12
48	Six microsatellite loci in forest musk deer, <i>Moschus berezovskii</i> . Molecular Ecology Notes, 2006, 6, 113-115.	1.7	12
49	Applying DNA barcoding to conservation practice: a case study of endangered birds and large mammals in China. Biodiversity and Conservation, 2017, 26, 653-668.	2.6	12
50	Genome-wide mining of perfect microsatellites and tetranucleotide orthologous microsatellites estimates in six primate species. Gene, 2018, 643, 124-132.	2.2	12
51	The complete mitochondrial genome of the Chinese Sika deer ( <i>Cervus nippon</i> Temminck, 1838), and phylogenetic analysis among Cervidae, Moschidae and Bovidae. Journal of Natural History, 2012, 46, 1747-1759.	0.5	11
52	Genome-wide analysis sheds light on the high-altitude adaptation of the buff-throated partridge ( <i>Tetraophasis szechenyii</i> ). Molecular Genetics and Genomics, 2020, 295, 31-46.	2.1	11
53	Limited genetic diversity of an endemic subspecies <i>Schizopygopsis chengi baoxingensis</i> as inferred from the mitochondrial DNA control region. Hydrobiologia, 2009, 632, 371-376.	2.0	10
54	The complete mitochondrial genome and phylogenetic analysis of forest musk deer ( <i>Moschus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62	0.5	10

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55	Identification of deer species (Cervidae, Cetartiodactyla) in China using mitochondrial cytochrome c oxidase subunit I (mtDNA COI). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4240-4243.	0.7	10
56	Comparative transcriptome analysis of <i>Trueperella pyogenes</i> reveals a novel antimicrobial strategy. Archives of Microbiology, 2017, 199, 649-655.	2.2	10
57	Genome-wide analysis reveals the genomic features of the turkey vulture ( <i>Cathartes aura</i> ) as a scavenger. Molecular Genetics and Genomics, 2019, 294, 679-692.	2.1	10
58	Pyfastx: a robust Python package for fast random access to sequences from plain and gzipped FASTA/Q files. Briefings in Bioinformatics, 2021, 22, .	6.5	10
59	Cooperative breeding by Buff-throated Partridge <i>Tetraophasis szechenyii</i> : a case in the Galliformes. Journal of Ornithology, 2011, 152, 695-700.	1.1	9
60	A triple-primer PCR approach for the sex identification of endangered Phasianidae birds. European Journal of Wildlife Research, 2012, 58, 289-294.	1.4	9
61	Transcriptome-Derived Tetranucleotide Microsatellites and Their Associated Genes from the Giant Panda ( <i>Ailuropoda melanoleuca</i> ). Journal of Heredity, 2016, 107, 423-430.	2.4	9
62	The first draft genome of <i>Lophophorus</i> : A step forward for Phasianidae genomic diversity and conservation. Genomics, 2019, 111, 1209-1215.	2.9	9
63	MTOR involved in bacterial elimination against <i>Trueperella pyogenes</i> infection based on mice model by transcriptome and biochemical analysis. Veterinary Microbiology, 2019, 235, 199-208.	1.9	9
64	PSMD: An extensive database for pan-species microsatellite investigation and marker development. Molecular Ecology Resources, 2020, 20, 283-291.	4.8	9
65	Otolith Microstructure of Larval <i>Gymnocypris potanini</i> Herzenstein from the Minjiang River in China. Environmental Biology of Fishes, 2006, 75, 431-438.	1.0	8
66	Complete mitogenome of Chinese shrew mole <i>Uropsilus soricipes</i> (Milne-Edwards, 1871) (Mammalia: Tj ETQq0 0 0 rgBT /Overlock 10 Tf History, 2014, 48, 1467-1483.	0.5	8
67	Molecular phylogenetic relationships among Asiatic shrewlike moles inferred from the complete mitogenomes. Journal of Zoological Systematics and Evolutionary Research, 2015, 53, 155-160.	1.4	8
68	The Draft Genome of the Endangered Sichuan Partridge ( <i>Arborophila rufipectus</i> ) with Evolutionary Implications. Genes, 2019, 10, 677.	2.4	8
69	Genetic diversity analysis of <i>Macaca thibetana</i> based on mitochondrial DNA control region sequences. DNA Sequence, 2008, 19, 446-452.	0.7	7
70	Phylogenetic lineages of <i>Monopterus albus</i> (Synbranchiformes: Synbranchidae) in China inferred from mitochondrial control region. Journal of Zoological Systematics and Evolutionary Research, 2013, 51, 38-44.	1.4	7
71	Assigning the Sex-Specific Markers via Genotyping-by-Sequencing onto the Y Chromosome for a Torrent Frog <i>Amolops mantzorum</i> . Genes, 2020, 11, 727.	2.4	7
72	Metabolic cold adaptation in the Asiatic toad: intraspecific comparison along an altitudinal gradient. Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology, 2021, 191, 765-776.	1.5	7

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73	Sex-specific gene expression in the blood of four primates. <i>Genomics</i> , 2021, 113, 2605-2613.	2.9	7
74	Characterization of olfactory receptor repertoires provides insights into the high-altitude adaptation of the yak based on the chromosome-level genome. <i>International Journal of Biological Macromolecules</i> , 2022, 209, 220-230.	7.5	7
75	Identification and characterization of ten polymorphic microsatellite loci in the red panda <i>Ailurus fulgens</i> . <i>Conservation Genetics</i> , 2008, 9, 787-790.	1.5	6
76	Effects of temperature, starvation and photoperiod on otolith increments in larval Chinese sucker, <i>Myxocyprinus asiaticus</i> . <i>Environmental Biology of Fishes</i> , 2009, 84, 159-171.	1.0	6
77	The complete mitochondrial genome of <i>Cricetulus kamensis</i> (Rodentia: Cricetidae). <i>Mitochondrial DNA</i> , 2016, 27, 976-977.	0.6	6
78	The complete mitochondrial genome of the <i>Vibrissaphora boringii</i> (Anura: Megophryidae). <i>Mitochondrial DNA</i> , 2016, 27, 758-759.	0.6	6
79	Effects of Supplementary Feeding on the Breeding Ecology of the Buff-Throated Partridge in a Tibetan Sacred Site, China. <i>PLoS ONE</i> , 2016, 11, e0146568.	2.5	6
80	Genomic Copy Number Variation Study of Nine <i>Macaca</i> Species Provides New Insights into Their Genetic Divergence, Adaptation, and Biomedical Application. <i>Genome Biology and Evolution</i> , 2020, 12, 2211-2230.	2.5	6
81	Molecular cloning and sequence analysis of the gene encoding interleukin-6 of the giant panda ( <i>Ailuropoda melanoleuca</i> ). <i>Journal of Natural History</i> , 2008, 42, 2585-2591.	0.5	5
82	Complete mitochondrial genome of <i>Tetraophasis szechenyii</i> (Madarász, 1885 (Aves: Galliformes)). <i>Journal of Natural History</i> , 2010, 44, 2955-2964.	0.5	5
83	Molecular phylogeny of major lineages of the avian family Phasianidae inferred from complete mitochondrial genome sequences. <i>Journal of Natural History</i> , 2012, 46, 757-767.	0.5	5
84	Complete mitochondrial genomes of two blattid cockroaches, <i>Periplaneta australasiae</i> and <i>Neostylopyga rhombifolia</i> , and phylogenetic relationships within the Blattaria. <i>PLoS ONE</i> , 2017, 12, e0177162.	2.5	5
85	Phenotypic and genetic characterization of <i>Pseudomonas aeruginosa</i> isolate COP2 from the lungs of COPD patients in China. <i>Pathogens and Disease</i> , 2019, 77, .	2.0	5
86	Coexistence of Microbial Species in Structured Communities by Forming a Hawk-Dove Game Like Interactive Relationship. <i>Frontiers in Microbiology</i> , 2019, 10, 807.	3.5	5
87	A High-quality Draft Genome Assembly of the Black-necked Crane ( <i>Grus nigricollis</i> ) Based on Nanopore Sequencing. <i>Genome Biology and Evolution</i> , 2019, 11, 3332-3340.	2.5	5
88	Transcriptome analyses provide insights into maternal immune changes at several critical phases of giant panda reproduction. <i>Developmental and Comparative Immunology</i> , 2020, 110, 103699.	2.3	5
89	Identification and characterization of microRNAs in American cockroach ( <i>Periplaneta americana</i> ). <i>Gene</i> , 2020, 743, 144610.	2.2	5
90	Characterization of microsatellites in the endangered snow leopard based on the chromosome-level genome. <i>Mammal Research</i> , 2021, 66, 385-398.	1.3	5

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91	Profile of microRNA in Giant Panda Blood: A Resource for Immune-Related and Novel microRNAs. PLoS ONE, 2015, 10, e0143242.	2.5	4
92	The complete mitochondrial genome of lesser long-tailed Hamster <i>Cricetulus longicaudatus</i> (Milne-Edwards, 1867) and phylogenetic implications. Mitochondrial DNA, 2016, 27, 1303-1304.	0.6	4
93	Comparative Transcriptomics Reveals the Expression Differences Between Four Developmental Stages of American Cockroach ( <i>Periplaneta americana</i> ). DNA and Cell Biology, 2019, 38, 1078-1087.	1.9	4
94	Population divergence of <i>Pseudomonas aeruginosa</i> can lead to the coexistence with <i>Escherichia coli</i> in animal suppurative lesions. Veterinary Microbiology, 2019, 231, 169-176.	1.9	4
95	Genome-wide investigation of microsatellite polymorphism in coding region of the giant panda ( <i>Ailuropoda melanoleuca</i> ) genome: a resource for study of phenotype diversity and abnormal traits. Mammal Research, 2019, 64, 353-363.	1.3	4
96	Comprehensive analysis of lncRNA and mRNA expression changes in Tibetan chicken lung tissue between three developmental stages. Animal Genetics, 2020, 51, 731-740.	1.7	4
97	Blood transcriptome analysis revealed the immune changes and immunological adaptation of wildness training giant pandas. Molecular Genetics and Genomics, 2022, 297, 227-239.	2.1	4
98	Antibacterial and anti-virulence effects of furazolidone on <i>Trueperella pyogenes</i> and <i>Pseudomonas aeruginosa</i> . BMC Veterinary Research, 2022, 18, 114.	1.9	4
99	Heterologous Prime-Boost Immunization with DNA Vaccine and Modified Recombinant Proteins Enhances Immune Response against <i>Trueperella pyogenes</i> in Mice. Vaccines, 2022, 10, 839.	4.4	4
100	Complete mitochondrial genome of <i>Episymphloce splendens</i> (Blattodea: Ectobiidae): A large intergenic spacer and lacking of two tRNA genes. PLoS ONE, 2022, 17, e0268064.	2.5	4
101	Isolation and characterization of polymorphic tri- and tetra-nucleotide microsatellite loci for the south China tiger <i>Panthera tigris amoyensis</i> . Journal of Natural History, 2006, 40, 2259-2263.	0.5	3
102	The complete mitochondrial genome of Assamese Macaques ( <i>Macaca assamensis</i> ). Mitochondrial DNA, 2016, 27, 226-227.	0.6	3
103	The complete mitochondrial genome of the <i>Elaphe perlacea</i> (Squamata: Colubridae). Mitochondrial DNA, 2016, 27, 12-13.	0.6	3
104	Experimental warming effects on root nitrogen absorption and mycorrhizal infection in a subalpine coniferous forest. Scandinavian Journal of Forest Research, 2016, 31, 347-354.	1.4	3
105	Comparative Genome-Wide Survey of Single Nucleotide Variation Uncovers the Genetic Diversity and Potential Biomedical Applications among Six <i>Macaca</i> Species. International Journal of Molecular Sciences, 2018, 19, 3123.	4.1	3
106	Genomic evidence sheds light on the genetic mechanisms of musk secretion in muskrats. International Journal of Biological Macromolecules, 2020, 145, 1189-1198.	7.5	3
107	Immune profiles of male giant panda ( <i>Ailuropoda melanoleuca</i> ) during the breeding season. BMC Genomics, 2021, 22, 143.	2.8	3
108	Characterization of Olfactory Receptor Repertoires in the Endangered Snow Leopard Based on the Chromosome-Level Genome. DNA and Cell Biology, 2021, 40, 293-302.	1.9	3

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109	De novo transcriptome assemblies of <i>Epicauta tibialis</i> provide insights into the sexual dimorphism in the production of cantharidin. <i>Archives of Insect Biochemistry and Physiology</i> , 2021, 106, e21784.	1.5	3
110	De Novo Sequencing and High-Contiguity Genome Assembly of <i>Moniezia expansa</i> Reveals Its Specific Fatty Acid Metabolism and Reproductive Stem Cell Regulatory Network. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 693914.	3.9	3
111	Unraveling the content of tail displays in an Asian agamid lizard. <i>Behavioral Ecology and Sociobiology</i> , 2021, 75, 1.	1.4	3
112	Gene expression profiles during postnatal development of the liver and pancreas in giant pandas. <i>Aging</i> , 2020, 12, 15705-15729.	3.1	3
113	Genome-Wide Analyses Provide Insights into the Scavenging Lifestyle of the Striped Hyena ( <i>Hyaena</i> )	1.9	3
114	GC-MS analysis of chemical constituents and determination of the total antioxidant capacity of adult powder of <i>Periplaneta americana</i> . <i>Entomological Research</i> , 2022, 52, 68-76.	1.1	3
115	Transcriptome Analysis Reveals the Alternative Splicing Changes in the Immune-Related Genes of the Giant Panda ( <i>Ailuropoda melanoleuca</i> ), in Response to the Canine Distemper Vaccine. <i>Zoological Science</i> , 2022, 39, .	0.7	3
116	A triple-primer PCR method for sexing endangered caprine species. <i>Conservation Genetics</i> , 2009, 10, 1609-1612.	1.5	2
117	Mitochondrial DNA genetic variation and phylogeography of the recently described vole species <i>Proedromys liangshanensis</i> Liu, Sun, Zeng and Zhao, 2007 (Rodentia: Arvicolinae). <i>Journal of Natural History</i> , 2010, 44, 2693-2703.	0.5	2
118	The complete mitochondrial genome of the <i>Leopoldamys edwardsi</i> (Rodentia: Muridae). <i>Mitochondrial DNA</i> , 2016, 27, 1-3.	0.6	2
119	Identification and characterization of polymorphic Alu insertions in the Tibetan macaque ( <i>Macaca</i> )	1.4	2
120	Phylogenetic analysis of the Black Stork <i>Ciconia nigra</i> (Ciconiiformes: Ciconiidae) based on complete mitochondrial genome. <i>Mitochondrial DNA</i> , 2016, 27, 261-262.	0.6	2
121	Isolation and strategies of novel tetranucleotide microsatellites with polymorphisms from different chromosomes of the rhesus monkey ( <i>Macaca mulatta</i> ). <i>Molecular Biology Reports</i> , 2019, 46, 3955-3966.	2.3	2
122	Characterization of the complete mitochondrial genome and phylogenetic analysis of <i>Otus sunia</i> (Strigiformes: Strigidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 804-805.	0.4	2
123	Two new complete mitochondrial genomes ( <i>Paradoxornis gularis</i> and <i>Niltava davidi</i> ) and their phylogenetic and taxonomic implications. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 820-821.	0.4	2
124	The complete mitochondrial genome of grey-headed canary-flycatcher ( <i>Culicicapa ceylonensis</i> )	0.4	2
125	Gene Expression Differences Between Developmental Stages of the Fall Armyworm (Spodoptera)	1.9	2
126	Single-base-resolution methylome of giant panda's brain, liver and pancreatic tissue. <i>PeerJ</i> , 2019, 7, e7847.	2.0	2



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127	Epigenomic profiling indicates a role for DNA methylation in the postnatal liver and pancreas development of giant pandas. <i>Genomics</i> , 2022, 114, 110342.	2.9	2
128	Intraspecific variation in microhabitat selection in reintroduced Chinese giant salamanders. <i>Environmental Epigenetics</i> , 2023, 69, 121-127.	1.8	2
129	Identification of <i>CR1</i> retroposons in <i>Arborophila rufipectus</i> and their application to <i>Pterodroma hasianidae</i> phylogeny. <i>Molecular Ecology Resources</i> , 2016, 16, 1037-1049.	4.8	1
130	The complete mitochondrial genome of brown-flanked bush warbler ( <i>Horornis fortipes</i> ). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1426-1427.	0.4	1
131	The complete mitochondrial genome of <i>Aquila nipalensis</i> and its phylogenetic position. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2152-2153.	0.4	1
132	The complete mitochondrial genome of the Minla cyanouroptera (Passeriformes: Timaliidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3610-3611.	0.4	1
133	Changes in the MicroRNA Profile of the Giant Panda After Canine Distemper Vaccination and the Integrated Analysis of MicroRNA-Messenger RNA. <i>DNA and Cell Biology</i> , 2021, 40, 595-605.	1.9	1
134	Transcriptomic landscape of persistent diarrhoea in rhesus macaques and comparison with humans and mouse models with inflammatory bowel disease. <i>Gene</i> , 2021, 800, 145837.	2.2	1
135	Comparative transcriptomes of three different skin sites for the Asiatic toad ( <i>Bufo</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 4	2.0	1
136	Whole blood transcriptome profiling identifies candidate genes associated with alopecia in male giant pandas ( <i>Ailuropoda melanoleuca</i> ). <i>BMC Genomics</i> , 2022, 23, 297.	2.8	1
137	Complete mitochondrial genome sequence of Arboreal Brown-toothed Shrew, <i>Episorculus macrurus</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 332-333.	0.4	0
138	Shanxi population of musk deer: species re-identification and genetic relationships with its sister species based on mitochondrial genomes. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 943-944.	0.4	0
139	The complete mitochondrial genome of Robin Accentor <i>Prunella rubeculoides</i> (Passeriformes:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 4	0.4	0
140	MACSNVdb: a high-quality SNV database for interspecies genetic divergence investigation among macaques. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	0
141	Spatiotemporal expression patterns of thymosin and its immune regulation after bacterial stimulation in American cockroach ( <i>Periplaneta americana</i> ). <i>Entomological Research</i> , 2021, 51, 587.	1.1	0