

Bisong Yue

List of Publications by Year in descending order

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141
papers

2,009
citations

304743

22
h-index

345221

36
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all docs

142
docs citations

142
times ranked

2434
citing authors

#	ARTICLE	IF	CITATIONS
1	Intraspecific variation in microhabitat selection in reintroduced Chinese giant salamanders. <i>Environmental Epigenetics</i> , 2023, 69, 121-127.	1.8	2
2	Blood transcriptome analysis revealed the immune changes and immunological adaptation of wildness training giant pandas. <i>Molecular Genetics and Genomics</i> , 2022, 297, 227-239.	2.1	4
3	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
4	Comparative transcriptomes of three different skin sites for the Asiatic toad (<i>Bufo</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 Td (gar	2.0	1
5	GCâ€“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
6	Antibacterial and anti-virulence effects of furazolidone on <i>Trueperella pyogenes</i> and <i>Pseudomonas aeruginosa</i> . <i>BMC Veterinary Research</i> , 2022, 18, 114.	1.9	4
7	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
8	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
9	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
10	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
11	Heterologous Prime-Boost Immunization with DNA Vaccine and Modified Recombinant Proteins Enhances Immune Response against <i>Trueperella pyogenes</i> in Mice. <i>Vaccines</i> , 2022, 10, 839.	4.4	4
12	Complete mitochondrial genome of <i>Episymphloce splendens</i> (Blattodea: Ectobiidae): A large intergenic spacer and lacking of two tRNA genes. <i>PLoS ONE</i> , 2022, 17, e0268064.	2.5	4
13	Pyfastx: a robust Python package for fast random access to sequences from plain and gzipped FASTA/Q files. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	10
14	Immune profiles of male giant panda (<i>Ailuropoda melanoleuca</i>) during the breeding season. <i>BMC Genomics</i> , 2021, 22, 143.	2.8	3
15	Characterization of Olfactory Receptor Repertoires in the Endangered Snow Leopard Based on the Chromosome-Level Genome. <i>DNA and Cell Biology</i> , 2021, 40, 293-302.	1.9	3
16	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
17	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
18	Gene Expression Differences Between Developmental Stages of the Fall Armyworm (<i>Spodoptera</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	1.9	2

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19	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
20	Metabolic cold adaptation in the Asiatic toad: intraspecific comparison along an altitudinal gradient. <i>Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology</i> , 2021, 191, 765-776.	1.5	7
21	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
22	Sex-specific gene expression in the blood of four primates. <i>Genomics</i> , 2021, 113, 2605-2613.	2.9	7
23	Unraveling the content of tail displays in an Asian agamid lizard. <i>Behavioral Ecology and Sociobiology</i> , 2021, 75, 1.	1.4	3
24	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
25	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
26	Genome-wide analysis sheds light on the high-altitude adaptation of the buff-throated partridge (<i>Tetraophasis szechenyii</i>). <i>Molecular Genetics and Genomics</i> , 2020, 295, 31-46.	2.1	11
27	First demonstration of giant panda's immune response to canine distemper vaccine. <i>Developmental and Comparative Immunology</i> , 2020, 102, 103489.	2.3	13
28	Genomic evidence sheds light on the genetic mechanisms of musk secretion in muskrats. <i>International Journal of Biological Macromolecules</i> , 2020, 145, 1189-1198.	7.5	3
29	PSMD: An extensive database for pan-species microsatellite investigation and marker development. <i>Molecular Ecology Resources</i> , 2020, 20, 283-291.	4.8	9
30	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
31	Age-related gene expression and DNA methylation changes in rhesus macaque. <i>Genomics</i> , 2020, 112, 5147-5156.	2.9	13
32	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
33	The complete mitochondrial genome of Robin Accentor (<i>Prunella rubeculoides</i>) (Passeriformes:). <i>TJ ETQq1 1 0.784314 rgBT /Ove</i>	0.4	0
34	Comprehensive analysis of lncRNA and mRNA expression changes in Tibetan chicken lung tissue between three developmental stages. <i>Animal Genetics</i> , 2020, 51, 731-740.	1.7	4
35	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
36	Assigning the Sex-Specific Markers via Genotyping-by-Sequencing onto the Y Chromosome for a Torrent Frog <i>Amolops mantzorum</i> . <i>Genes</i> , 2020, 11, 727.	2.4	7

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37	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
38	Identification and characterization of microRNAs in American cockroach (<i>Periplaneta americana</i>). <i>Gene</i> , 2020, 743, 144610.	2.2	5
39	Gene expression profiles during postnatal development of the liver and pancreas in giant pandas. <i>Aging</i> , 2020, 12, 15705-15729.	3.1	3
40	Genome-Wide Analyses Provide Insights into the Scavenging Lifestyle of the Striped Hyena (<i>Hyaena</i>)	1.9	3
41	The first draft genome of <i>Lophophorus</i> : A step forward for Phasianidae genomic diversity and conservation. <i>Genomics</i> , 2019, 111, 1209-1215.	2.9	9
42	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
43	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
44	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
45	MTOR involved in bacterial elimination against <i>Trueperella pyogenes</i> infection based on mice model by transcriptome and biochemical analysis. <i>Veterinary Microbiology</i> , 2019, 235, 199-208.	1.9	9
46	Cloning, Expression and Effects of <i>P. americana</i> Thymosin on Wound Healing. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4932.	4.1	13
47	Comparative Transcriptomics Reveals the Expression Differences Between Four Developmental Stages of American Cockroach (<i>Periplaneta americana</i>). <i>DNA and Cell Biology</i> , 2019, 38, 1078-1087.	1.9	4
48	The Draft Genome of the Endangered Sichuan Partridge (<i>Arborophila rufipectus</i>) with Evolutionary Implications. <i>Genes</i> , 2019, 10, 677.	2.4	8
49	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
50	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
51	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
52	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
53	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
54	The complete mitochondrial genome of grey-headed canary-flycatcher (<i>Culicicapa ceylonensis</i>)	0.4	2

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55	Genome-wide analysis reveals the genomic features of the turkey vulture (<i>Cathartes aura</i>) as a scavenger. <i>Molecular Genetics and Genomics</i> , 2019, 294, 679-692.	2.1	10
56	Behavioral heterogeneity in quorum sensing can stabilize social cooperation in microbial populations. <i>BMC Biology</i> , 2019, 17, 20.	3.8	37
57	Comparative genomics sheds light on the predatory lifestyle of accipitrids and owls. <i>Scientific Reports</i> , 2019, 9, 2249.	3.3	14
58	Population divergence of <i>Pseudomonas aeruginosa</i> can lead to the coexistence with <i>Escherichia coli</i> in animal suppurative lesions. <i>Veterinary Microbiology</i> , 2019, 231, 169-176.	1.9	4
59	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
60	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
61	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. <i>Mammal Research</i> , 2019, 64, 353-363.	1.3	4
62	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
63	The complete mitochondrial genome of the Minla cyanouroptera (<i>Passeriformes: Timaliidae</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3610-3611.	0.4	1
64	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
65	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
66	Single-base-resolution methylome of giant panda's brain, liver and pancreatic tissue. <i>PeerJ</i> , 2019, 7, e7847.	2.0	2
67	The draft genome sequence of forest musk deer (<i>Moschus berezovskii</i>). <i>GigaScience</i> , 2018, 7, .	6.4	26
68	Age-associated microbiome shows the giant panda lives on hemicelluloses, not on cellulose. <i>ISME Journal</i> , 2018, 12, 1319-1328.	9.8	89
69	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
70	Krait: an ultrafast tool for genome-wide survey of microsatellites and primer design. <i>Bioinformatics</i> , 2018, 34, 681-683.	4.1	120
71	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
72	Genome-wide mining of perfect microsatellites and tetranucleotide orthologous microsatellites estimates in six primate species. <i>Gene</i> , 2018, 643, 124-132.	2.2	12

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73	Comparative Genome-Wide Survey of Single Nucleotide Variation Uncovers the Genetic Diversity and Potential Biomedical Applications among Six Macaca Species. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3123.	4.1	3
74	<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
75	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
76	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
77	Comparative transcriptome analysis of <i>Trueperella pyogenes</i> reveals a novel antimicrobial strategy. <i>Archives of Microbiology</i> , 2017, 199, 649-655.	2.2	10
78	Applying DNA barcoding to conservation practice: a case study of endangered birds and large mammals in China. <i>Biodiversity and Conservation</i> , 2017, 26, 653-668.	2.6	12
79	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
80	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
81	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
82	A novel mitochondrial genome of <i>Arborophila</i> and new insight into <i>Arborophila</i> evolutionary history. <i>PLoS ONE</i> , 2017, 12, e0181649.	2.5	14
83	The complete mitochondrial genome of the <i>Leopoldamys edwardsi</i> (Rodentia: Muridae). <i>Mitochondrial DNA</i> , 2016, 27, 1-3.	0.6	2
84	The complete mitochondrial genome of lesser long-tailed Hamster <i>Cricetulus longicaudatus</i> (Milne-Edwards, 1867) and phylogenetic implications. <i>Mitochondrial DNA</i> , 2016, 27, 1303-1304.	0.6	4
85	The complete mitochondrial genome of Assamese Macaques (<i>Macaca assamensis</i>). <i>Mitochondrial DNA</i> , 2016, 27, 226-227.	0.6	3
86	The complete mitochondrial genome of <i>Cricetulus kamensis</i> (Rodentia: Cricetidae). <i>Mitochondrial DNA</i> , 2016, 27, 976-977.	0.6	6
87	The complete mitochondrial genome of the <i>Vibrissaphora boringii</i> (Anura: Megophryidae). <i>Mitochondrial DNA</i> , 2016, 27, 758-759.	0.6	6
88	Mitochondrial Genome and Nuclear Markers Provide New Insight into the Evolutionary History of Macaques. <i>PLoS ONE</i> , 2016, 11, e0154665.	2.5	25
89	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
90	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

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91	Identification of <i>CR1</i> retroposons in <i>Arborophila rufipectus</i> and their application to <i>P. hasianidae</i> phylogeny. <i>Molecular Ecology Resources</i> , 2016, 16, 1037-1049.	4.8	1
92	DNA vaccination based on pyolysin co-immunized with IL-1 β enhances host antibacterial immunity against <i>Trueperella pyogenes</i> infection. <i>Vaccine</i> , 2016, 34, 3469-3477.	3.8	21
93	Transcriptome-Derived Tetranucleotide Microsatellites and Their Associated Genes from the Giant Panda (<i>Ailuropoda melanoleuca</i>). <i>Journal of Heredity</i> , 2016, 107, 423-430.	2.4	9
94	Nutrient reduction induced stringent responses promote bacterial quorum-sensing divergence for population fitness. <i>Scientific Reports</i> , 2016, 6, 34925.	3.3	29
95	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
96	The complete mitochondrial genome of the <i>Elaphe perlacea</i> (Squamata: Colubridae). <i>Mitochondrial DNA</i> , 2016, 27, 12-13.	0.6	3
97	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
98	Worldwide patterns of genomic variation and admixture in gray wolves. <i>Genome Research</i> , 2016, 26, 163-173.	5.5	160
99	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
100	Experimental warming effects on root nitrogen absorption and mycorrhizal infection in a subalpine coniferous forest. <i>Scandinavian Journal of Forest Research</i> , 2016, 31, 347-354.	1.4	3
101	Identification of deer species (Cervidae, Cetartiodactyla) in China using mitochondrial cytochrome c oxidase subunit I (mtDNA COI). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4240-4243.	0.7	10
102	Profile of microRNA in Giant Panda Blood: A Resource for Immune-Related and Novel microRNAs. <i>PLoS ONE</i> , 2015, 10, e0143242.	2.5	4
103	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
104	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
105	Identification and characterization of polymorphic Alu insertions in the Tibetan macaque (<i>Macaca Tj ETQq1 1 0.784314 rgBT₂/Overl</i>	1.4	14
106	Molecular phylogenetic relationships among Asiatic shrewlike moles inferred from the complete mitogenomes. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2015, 53, 155-160.	1.4	8
107	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
108	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

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109	Phylogenomics and Evolutionary Dynamics of the Family Actinomycetaceae. <i>Genome Biology and Evolution</i> , 2014, 6, 2625-2633.	2.5	24
110	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
111	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
112	Complete mitogenome of Chinese shrew mole <i>Uropsilus soricipes</i> (Milne-Edwards, 1871) (Mammalia: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 History, 2014, 48, 1467-1483.	0.5	8
113	Phylogenetic lineages of <i>Monopterus albus</i> (Synbranchiformes: Synbranchidae) in China inferred from mitochondrial control region. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2013, 51, 38-44.	1.4	7
114	The complete mitochondrial genome of the Chinese Sika deer (<i>Cervus nippon</i> Temminck, 1838), and phylogenetic analysis among Cervidae, Moschidae and Bovidae. <i>Journal of Natural History</i> , 2012, 46, 1747-1759.	0.5	11
115	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
116	High intra-population genetic variability and inter-population differentiation in a plateau specialized fish, <i>Triplophysa orientalis</i> . <i>Environmental Biology of Fishes</i> , 2012, 93, 519-530.	1.0	14
117	A triple-primer PCR approach for the sex identification of endangered Phasianidae birds. <i>European Journal of Wildlife Research</i> , 2012, 58, 289-294.	1.4	9
118	Cooperative breeding by Buff-throated Partridge <i>Tetraophaps szechenyii</i> : a case in the Galliformes. <i>Journal of Ornithology</i> , 2011, 152, 695-700.	1.1	9
119	DNA barcoding of 18 species of Bovidae. <i>Science Bulletin</i> , 2011, 56, 164-168.	1.7	25
120	Complete mitochondrial genome of <i>Tetraophaps szechenyii</i> (MadarÁisz, 1885 (Aves: Galliformes: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 <i>Journal of Natural History</i> , 2010, 44, 2955-2964.	0.5	5
121	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
122	Conservation of the Endangered giant panda <i>Ailuropoda melanoleuca</i> in China: successes and challenges. <i>Oryx</i> , 2009, 43, 176.	1.0	18
123	Limited genetic diversity of an endemic subspecies <i>Schizopygopsis chengjaoxingensis</i> as inferred from the mitochondrial DNA control region. <i>Hydrobiologia</i> , 2009, 632, 371-376.	2.0	10
124	A triple-primer PCR method for sexing endangered caprine species. <i>Conservation Genetics</i> , 2009, 10, 1609-1612.	1.5	2
125	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
126	Major histocompatibility complex Class II DRB exon 2 diversity of the Eurasian lynx (<i>Lynx</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.5	16

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127	The complete mitochondrial genome and phylogenetic analysis of forest musk deer (<i>Moschus moschiferus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.5	10
128	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
129	A reliable, non-invasive PCR method for giant panda (<i>Ailuropoda melanoleuca</i>) sex identification. <i>Conservation Genetics</i> , 2008, 9, 739-741.	1.5	15
130	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
131	Genetic diversities of the giant panda (<i>Ailuropoda melanoleuca</i>) in Wanglang and Baoxing Nature Reserves. <i>Conservation Genetics</i> , 2008, 9, 1541-1546.	1.5	14
132	Population genetic diversity of <i>Prenantia</i> '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
133	Validation of daily otolith increments in larval and juvenile Chinese sucker, <i>Myxocyprinus asiaticus</i> . <i>Environmental Biology of Fishes</i> , 2008, 82, 165-171.	1.0	13
134	Verifying an F ₁ 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
135	Genetic diversity analysis of <i>Macaca thibetana</i> based on mitochondrial DNA control region sequences. <i>DNA Sequence</i> , 2008, 19, 446-452.	0.7	7
136	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
137	Taxonomic implications from phylogenetic relationships of subspecies of <i>Schizopygopsis malacanthus</i> (Pisces: Cyprinidae) based on sequence analysis of cytochrome b and mitochondrial DNA control region. <i>Journal of Natural History</i> , 2006, 40, 2569-2576.	0.5	12
138	Six microsatellite loci in forest musk deer, <i>Moschus berezovskii</i> . <i>Molecular Ecology Notes</i> , 2006, 6, 113-115.	1.7	12
139	Otolith Microstructure of Larval <i>Gymnocypris potanini</i> Herzenstein from the Minjiang River in China. <i>Environmental Biology of Fishes</i> , 2006, 75, 431-438.	1.0	8
140	Assessing genetic diversity of wild populations of <i>Prenantia</i> 's schizothoracin, <i>Schizothorax prenanti</i> , using AFLP markers. <i>Environmental Biology of Fishes</i> , 2006, 77, 79-86.	1.0	41
141	Isolation and characterization of polymorphic tri- and tetra-nucleotide microsatellite loci for the south China tiger <i>Panthera tigris amoyensis</i> . <i>Journal of Natural History</i> , 2006, 40, 2259-2263.	0.5	3