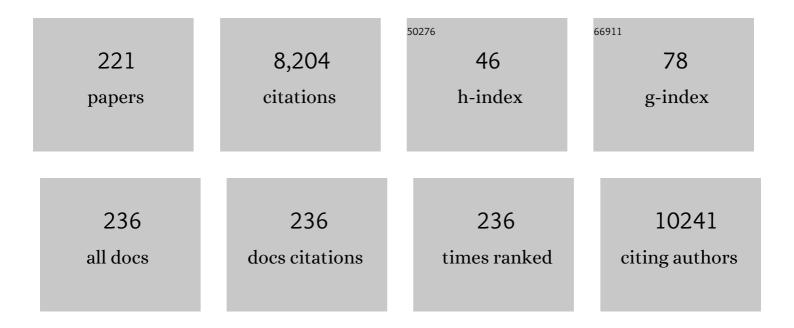
Ya-Ping Zhang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4981623/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Best practices for analyzing imputed genotypes from low-pass sequencing in dogs. Mammalian Genome, 2022, 33, 213-229.	2.2	10
2	Electrochemical sensor for human norovirus based on covalent organic framework/pillararene heterosupramolecular nanocomposites. Talanta, 2022, 237, 122896.	5.5	26
3	Initiation of the Primate Genome Project. Zoological Research, 2022, 43, 147-149.	2.1	7
4	Genomic adaptations for arboreal locomotion in Asian flying treefrogs. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2116342119.	7.1	6
5	Species Persistence with Hybridization in Toad-Headed Lizards Driven by Divergent Selection and Low Recombination. Molecular Biology and Evolution, 2022, 39, .	8.9	3
6	The twin-beginnings of COVID-19 in Asia and Europe—one prevails quickly. National Science Review, 2022, 9, nwab223.	9.5	22
7	Genome-wide investigations reveal the population structure and selection signatures of Nigerian cattle adaptation in the sub-Saharan tropics. BMC Genomics, 2022, 23, 306.	2.8	4
8	Discovery of a wild, genetically pure Chinese giant salamander creates new conservation opportunities. Zoological Research, 2022, 43, 469-480.	2.1	14
9	Comparative genome anatomy reveals evolutionary insights into a unique amphitriploid fish. Nature Ecology and Evolution, 2022, 6, 1354-1366.	7.8	29
10	Herpetological phylogeographic analyses support a Miocene focal point of Himalayan uplift and biological diversification. National Science Review, 2021, 8, nwaa263.	9.5	46
11	Hematologic and spirometric characteristics of Tajik and Kyrgyz highlanders in the Pamir Mountains. American Journal of Human Biology, 2021, 33, e23459.	1.6	2
12	Ultrasensitive supersandwich-type electrochemical sensor for SARS-CoV-2 from the infected COVID-19 patients using a smartphone. Sensors and Actuators B: Chemical, 2021, 327, 128899.	7.8	303
13	Tracing the Genetic Legacy of the Tibetan Empire in the Balti. Molecular Biology and Evolution, 2021, 38, 1529-1536.	8.9	13
14	Genomes reveal selective sweeps in kiang and donkey for high-altitude adaptation. Zoological Research, 2021, 42, 450-460.	2.1	9
15	Behavioral evidence for the origin of Chinese Kunming dog. Environmental Epigenetics, 2021, 67, 469-471.	1.8	2
16	Integrating Genomic and Transcriptomic Data to Reveal Genetic Mechanisms Underlying Piao Chicken Rumpless Trait. Genomics, Proteomics and Bioinformatics, 2021, 19, 787-799.	6.9	7
17	Genetic variation of Nigerian cattle inferred from maternal and paternal genetic markers. PeerJ, 2021, 9, e10607.	2.0	10
18	Genetic Architecture Underlying Nascent Speciation—The Evolution of Eurasian Pigs under Domestication. Molecular Biology and Evolution, 2021, 38, 3556-3566.	8.9	3

#	Article	IF	CITATIONS
19	Dog10K_Boxer_Tasha_1.0: A Long-Read Assembly of the Dog Reference Genome. Genes, 2021, 12, 847.	2.4	19
20	Mitochondrial DNA variation of Nigerian dromedary camel (<i>CamelusÂdromedarius</i>). Animal Genetics, 2021, 52, 570-572.	1.7	1
21	The concordance between the evolutionary trend and the clinical manifestation of the two SARS-CoV-2 variants. National Science Review, 2021, 8, nwab073.	9.5	2
22	Genomic Analyses Unveil Helmeted Guinea Fowl (<i>Numida meleagris</i>) Domestication in West Africa. Genome Biology and Evolution, 2021, 13, .	2.5	6
23	Large-scale genomic analysis reveals the genetic cost of chicken domestication. BMC Biology, 2021, 19, 118.	3.8	22
24	Whole-Genome Sequencing Reveals Lactase Persistence Adaptation in European Dogs. Molecular Biology and Evolution, 2021, 38, 4884-4890.	8.9	7
25	On the origin of SARS-CoV-2—The blind watchmaker argument. Science China Life Sciences, 2021, 64, 1560-1563.	4.9	18
26	Evolutionary analysis and lineage designation of SARS-CoV-2 genomes. Science Bulletin, 2021, 66, 2297-2311.	9.0	26
27	Single-cell RNA Sequencing Reveals Thoracolumbar Vertebra Heterogeneity and Rib-genesis in Pigs. Genomics, Proteomics and Bioinformatics, 2021, 19, 423-436.	6.9	6
28	The high diversity of SARS-CoV-2-related coronaviruses in pangolins alters potential ecological risks. Zoological Research, 2021, 42, 833-843.	2.1	20
29	Convergent genomic signatures of high-altitude adaptation among domestic mammals. National Science Review, 2020, 7, 952-963.	9.5	52
30	Ambient Temperature is A Strong Selective Factor Influencing Human Development and Immunity. Genomics, Proteomics and Bioinformatics, 2020, 18, 489-500.	6.9	5
31	Comparative population genomic analysis uncovers novel genomic footprints and genes associated with small body size in Chinese pony. BMC Genomics, 2020, 21, 496.	2.8	14
32	Ancient Hybridization with an Unknown Population Facilitated High-Altitude Adaptation of Canids. Molecular Biology and Evolution, 2020, 37, 2616-2629.	8.9	46
33	From asymmetrical to balanced genomic diversification during rediploidization: Subgenomic evolution in allotetraploid fish. Science Advances, 2020, 6, eaaz7677.	10.3	59
34	Whole genome resequencing of the Iranian native dogs and wolves to unravel variome during dog domestication. BMC Genomics, 2020, 21, 207.	2.8	6
35	863 genomes reveal the origin and domestication of chicken. Cell Research, 2020, 30, 693-701.	12.0	144
36	Genomic consequences of population decline in critically endangered pangolins and their demographic histories. National Science Review, 2020, 7, 798-814.	9.5	45

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37	Mitochondrial DNA variation of Nigerian Muscovy duck (<i>Cairina moschata</i>). Animal Genetics, 2020, 51, 485-486.	1.7	4
38	The wild species genome ancestry of domestic chickens. BMC Biology, 2020, 18, 13.	3.8	61
39	Genomic regions under selection in the feralization of the dingoes. Nature Communications, 2020, 11, 671.	12.8	49
40	Defining Individual-Level Genetic Diversity and Similarity Profiles. Scientific Reports, 2020, 10, 5805.	3.3	12
41	Genome-wide genetic structure and selection signatures for color in 10 traditional Chinese yellow-feathered chicken breeds. BMC Genomics, 2020, 21, 316.	2.8	27
42	Whole genome resequencing reveals an association of ABCC4 variants with preaxial polydactyly in pigs. BMC Genomics, 2020, 21, 268.	2.8	3
43	Potential dual expansion of domesticated donkeys revealed by worldwide analysis on mitochondrial sequences. Zoological Research, 2020, 41, 51-60.	2.1	9
44	OrthReg: a tool to predict <i>cis</i> -regulatory elements based on cross-species orthologous sequence conservation. Zoological Research, 2020, 41, 471-475.	2.1	3
45	Genome-wide identification of imprinted genes in pigs and their different imprinting status compared with other mammals. Zoological Research, 2020, 41, 721-725.	2.1	9
46	CaptureProbe: a java tool for designing probes for capture Hi-C applications. Zoological Research, 2020, 41, 94-96.	2.1	1
47	Structural variation during dog domestication: insights from gray wolf and dhole genomes. National Science Review, 2019, 6, 110-122.	9.5	30
48	Population Genomics Analysis Revealed Origin and High-altitude Adaptation of Tibetan Pigs. Scientific Reports, 2019, 9, 11463.	3.3	44
49	Identity-by-Descent Analysis Reveals Susceptibility Loci for Severe Acne in Chinese Han Cohort. Journal of Investigative Dermatology, 2019, 139, 2049-2051.e20.	0.7	5
50	Maternal genomic variability of the wild boar (<i>Sus scrofa</i>) reveals the uniqueness of East aucasian and Central Italian populations. Ecology and Evolution, 2019, 9, 9467-9478.	1.9	15
51	Dog10K: the International Consortium of Canine Genome Sequencing. National Science Review, 2019, 6, 611-613.	9.5	9
52	Genomic Approaches Reveal an Endemic Subpopulation of Gray Wolves in Southern China. IScience, 2019, 20, 110-118.	4.1	6
53	Higherâ€level phylogenetic affinities of the Neotropical genus <i>Mastigodryas</i> Amaral, 1934 (Serpentes: Colubridae), speciesâ€group definition and description of a new genus for <i>Mastigodryas bifossatus</i> . Journal of Zoological Systematics and Evolutionary Research, 2019, 57, 205-239.	1.4	8
54	Canine transmissible venereal tumor genome reveals ancient introgression from coyotes to pre-contact dogs in North America. Cell Research, 2019, 29, 592-595.	12.0	7

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55	Large-scale molecular phylogeny, morphology, divergence-time estimation, and the fossil record of advanced caenophidian snakes (Squamata: Serpentes). PLoS ONE, 2019, 14, e0216148.	2.5	116
56	A Global Deal For Nature: Guiding principles, milestones, and targets. Science Advances, 2019, 5, eaaw2869.	10.3	477
57	The evolutionary genetics of lactase persistence in seven ethnic groups across the Iranian plateau. Human Genomics, 2019, 13, 7.	2.9	11
58	Phenotypic and morphometric differentiation of indigenous chickens from Kenya and other tropical countries augments perspectives for genetic resource improvement and conservation. Poultry Science, 2019, 98, 2747-2755.	3.4	12
59	Asymmetric biotic interchange across the Bering land bridge between Eurasia and North America. National Science Review, 2019, 6, 739-745.	9.5	43
60	Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. National Science Review, 2019, 6, 810-824.	9.5	65
61	Artificial selection drives differential gene expression during pig domestication. Journal of Genetics and Genomics, 2019, 46, 97-100.	3.9	6
62	Genomic and transcriptomic investigations of the evolutionary transition from oviparity to viviparity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3646-3655.	7.1	43
63	Hybrid assembly of ultra-long Nanopore reads augmented with 10x-Genomics contigs: Demonstrated with a human genome. Genomics, 2019, 111, 1896-1901.	2.9	26
64	Local origin or external input: modern horse origin in East Asia. BMC Evolutionary Biology, 2019, 19, 217.	3.2	1
65	The Origin and Population History of the Endangered Golden Snub-Nosed Monkey (<i>Rhinopithecus) Tj ETQq1</i>	1 0,78431 8.9	4 rgBT /Overl
66	iDog: an integrated resource for domestic dogs and wild canids. Nucleic Acids Research, 2019, 47, D793-D800.	14.5	33
67	Complete mitochondrial genome of Sri Lankan Junglefowl (Gallus lafayetti) and phylogenetic study. Mitochondrial DNA Part B: Resources, 2018, 3, 83-84.	0.4	0
68	Altered hemoglobin co-factor sensitivity does not underlie the evolution of derived fossorial specializations in the family Talpidae. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2018, 224, 150-155.	1.6	2
69	Origin of new genes after zygotic genome activation in vertebrate. Journal of Molecular Cell Biology, 2018, 10, 139-146.	3.3	1
70	Mitochondrial DNA sequence variation in Iranian native dogs. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 394-402.	0.7	1
71	Whole-Genome Sequencing of African Dogs Provides Insights into Adaptations against Tropical Parasites. Molecular Biology and Evolution, 2018, 35, 287-298.	8.9	41
72	Out of Southern East Asia of the Brown Rat Revealed by Large-Scale Genome Sequencing. Molecular Biology and Evolution, 2018, 35, 149-158.	8.9	36

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73	Mitochondrial genomes uncover the maternal history of the Pamir populations. European Journal of Human Genetics, 2018, 26, 124-136.	2.8	21
74	Was chicken domesticated in northern China? New evidence from mitochondrial genomes. Science Bulletin, 2018, 63, 743-746.	9.0	17
75	Understanding the cryptic introgression and mixed ancestry of Red Junglefowl in India. PLoS ONE, 2018, 13, e0204351.	2.5	6
76	Species groups distributed across elevational gradients reveal convergent and continuous genetic adaptation to high elevations. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10634-E10641.	7.1	57
77	Space for nature. Science, 2018, 361, 1051-1051.	12.6	72
78	Pervasive introgression facilitated domestication and adaptation in the Bos species complex. Nature Ecology and Evolution, 2018, 2, 1139-1145.	7.8	157
79	The Chinese giant salamander exemplifies the hidden extinction of cryptic species. Current Biology, 2018, 28, R590-R592.	3.9	71
80	Selection and environmental adaptation along a path to speciation in the Tibetan frog <i>Nanorana parkeri</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5056-E5065.	7.1	49
81	Comparative genomic investigation of high-elevation adaptation in ectothermic snakes. Proceedings of the United States of America, 2018, 115, 8406-8411.	7.1	119
82	Genome wide analyses uncover allele-specific RNA editing in human and mouse. Nucleic Acids Research, 2018, 46, 8888-8897.	14.5	47
83	A parallel mechanism underlying frizzle in domestic chickens. Journal of Molecular Cell Biology, 2018, 10, 589-591.	3.3	19
84	Genetic Diversity and Population Structure of East Asian Raccoon Dog (<i>Nyctereutes) Tj ETQq0 0 0 rgBT /Over 249-259.</i>	lock 10 Tf 0.7	50 307 Td (p 13
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86	The origin of chow chows in the light of the East Asian breeds. BMC Genomics, 2017, 18, 174.	2.8	8
87	Ultrasensitive electrochemical detection of Dicer1 3′UTR for the fast analysis of alternative cleavage and polyadenylation. Nanoscale, 2017, 9, 4272-4282.	5.6	13
88	Draft genome of the gayal, Bos frontalis. GigaScience, 2017, 6, 1-7.	6.4	23
89	An Evolutionary Genomic Perspective on the Breeding of Dwarf Chickens. Molecular Biology and Evolution, 2017, 34, 3081-3088.	8.9	42
90	Rapid Evolution of Genes Involved in Learning and Energy Metabolism for Domestication of the Laboratory Rat. Molecular Biology and Evolution, 2017, 34, 3148-3153.	8.9	14

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91	Barcoding utility in a mega-diverse, cross-continental genus: keeping pace with Cyrtodactylus geckos. Scientific Reports, 2017, 7, 5592.	3.3	24
92	Sri Lankan pig ancestry revealed by mitochondrial <scp>DNA</scp> , Yâ€chromosome, and <i><scp>MC</scp>1R</i> . Animal Genetics, 2017, 48, 622-623.	1.7	0
93	PigVar: a database of pig variations and positive selection signatures. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	11
94	Analysis of the genetic variation in mitochondrial DNA, Y-chromosome sequences, and MC1R sheds light on the ancestry of Nigerian indigenous pigs. Genetics Selection Evolution, 2017, 49, 52.	3.0	8
95	A novel multilocus phylogenetic estimation reveals unrecognized diversity in Asian horned toads, genus Megophrys sensu lato (Anura: Megophryidae). Molecular Phylogenetics and Evolution, 2017, 106, 28-43.	2.7	78
96	A cryptic mitochondrial DNA link between North European and West African dogs. Journal of Genetics and Genomics, 2017, 44, 163-170.	3.9	11
97	The first mangrove genomes sequenced as the sea level rises. National Science Review, 2017, 4, 735-735.	9.5	0
98	Annotating long intergenic non-coding RNAs under artificial selection during chicken domestication. BMC Evolutionary Biology, 2017, 17, 192.	3.2	12
99	Identification of HNF4A Mutation p.T130I and HNF1A Mutations p.I27L and p.S487N in a Han Chinese Family with Early-Onset Maternally Inherited Type 2 Diabetes. Journal of Diabetes Research, 2016, 2016, 1-8.	2.3	12
100	Genomic analysis of snub-nosed monkeys (Rhinopithecus) identifies genes and processes related to high-altitude adaptation. Nature Genetics, 2016, 48, 947-952.	21.4	109
101	Positive selection rather than relaxation of functional constraint drives the evolution of vision during chicken domestication. Cell Research, 2016, 26, 556-573.	12.0	69
102	Questioning the evidence for a Central Asian domestication origin of dogs. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2554-5.	7.1	6
103	An ancient record of an avian hybrid and the potential uses of art in ecology and conservation. Ibis, 2016, 158, 444-445.	1.9	5
104	Olfactory genes in Tibetan wild boar. Nature Genetics, 2016, 48, 972-973.	21.4	6
105	A new genus of anthophilous drosophilids, Impatiophila (Diptera, Drosophilidae): morphology, DNA barcoding and molecular phylogeny, with descriptions of thirty-nine new species . Zootaxa, 2016, 4120, 1.	0.5	10
106	Genetic variations associated with six-white-point coat pigmentation in Diannan small-ear pigs. Scientific Reports, 2016, 6, 27534.	3.3	22
107	Large numbers of vertebrates began rapid population decline in the late 19th century. Proceedings of the United States of America, 2016, 113, 14079-14084.	7.1	50
108	Comparative population genomics reveals genetic basis underlying body size of domestic chickens. Journal of Molecular Cell Biology, 2016, 8, 542-552.	3.3	41

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109	A sodium channel inhibitor ISTX-I with a novel structure provides a new hint at the evolutionary link between two toxin folds. Scientific Reports, 2016, 6, 29691.	3.3	6
110	Cellular responses to HSV-1 infection are linked to specific types of alterations in the host transcriptome. Scientific Reports, 2016, 6, 28075.	3.3	61
111	Biotic interchange between the Indian subcontinent and mainland Asia through time. Nature Communications, 2016, 7, 12132.	12.8	110
112	Was ADH1B under Selection in European Populations?. American Journal of Human Genetics, 2016, 99, 1217-1219.	6.2	3
113	Spatiotemporal Diversification of the True Frogs (Genus <i>Rana</i>): A Historical Framework for a Widely Studied Group of Model Organisms. Systematic Biology, 2016, 65, 824-842.	5.6	125
114	Genomic incompatibilities in the diploid and tetraploid offspring of the goldfish × common carp cross. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1327-1332.	7.1	119
115	Out of southern East Asia: the natural history of domestic dogs across the world. Cell Research, 2016, 26, 21-33.	12.0	271
116	Population Variation Reveals Independent Selection toward Small Body Size in Chinese Debao Pony. Genome Biology and Evolution, 2016, 8, 42-50.	2.5	57
117	Reconciling the conflicts between mitochondrial DNA haplogroup trees of Canis lupus. Forensic Science International: Genetics, 2016, 23, 83-85.	3.1	8
118	DNA barcoding reveals commercial fraud related to yak jerky sold in China. Science China Life Sciences, 2016, 59, 106-108.	4.9	8
119	The geographical distribution of grey wolves () in China: a systematic review. Zoological Research, 2016, 37, 315-326.	2.1	9
120	Re-evaluating data quality of dog mitochondrial, Y chromosomal, and autosomal SNPs genotyped by SNP array. Zoological Research, 2016, 37, 356-360.	2.1	0
121	DNA methylation signatures of long intergenic noncoding RNAs in porcine adipose and muscle tissues. Scientific Reports, 2015, 5, 15435.	3.3	29
122	Transcriptomes reveal the genetic mechanisms underlying ionic regulatory adaptations to salt in the crab-eating frog. Scientific Reports, 2015, 5, 17551.	3.3	14
123	Genetic adaptations of the plateau zokor in high-elevation burrows. Scientific Reports, 2015, 5, 17262.	3.3	48
124	Evaluating the association between <i>CACNA1C</i> rs1006737 and schizophrenia risk: A meta-analysis. Asia-Pacific Psychiatry, 2015, 7, 260-267.	2.2	18
125	Mitochondrial <scp>DNA</scp> variation of <scp>N</scp> igerian domestic helmeted guinea fowl. Animal Genetics, 2015, 46, 576-579.	1.7	9
126	Identification of Valid Reference Genes for the Normalization of RT-qPCR Expression Studies in Human Breast Cancer Cell Lines Treated with and without Transient Transfection. PLoS ONE, 2015, 10, e0117058.	2.5	58

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127	Nocturnal to Diurnal Transition in the Common Ancestor of Haplorrhines: Evidence from Genomic-Scan for Positively Selected Genes. Journal of Genetics and Genomics, 2015, 42, 33-37.	3.9	4
128	DomeTree: a canonical toolkit for mitochondrial <scp>DNA</scp> analyses in domesticated animals. Molecular Ecology Resources, 2015, 15, 1238-1242.	4.8	45
129	DoGSD: the dog and wolf genome SNP database. Nucleic Acids Research, 2015, 43, D777-D783.	14.5	76
130	Evolutionary and Functional Novelty of Pancreatic Ribonuclease: a Study of Musteloidea (order) Tj ETQq0 0 0 rgBT	/Overlock 3.3	10 Tf 50 62 28
131	Whole-genome sequence of the Tibetan frog <i>Nanorana parkeri</i> and the comparative evolution of tetrapod genomes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1257-62.	7.1	159
132	Integrative analyses of RNA editing, alternative splicing, and expression of young genes in human brain transcriptome by deep RNA sequencing. Journal of Molecular Cell Biology, 2015, 7, 314-325.	3.3	12
133	Divergence of dim-light vision among bats (order: Chiroptera) as estimated by molecular and electrophysiological methods. Scientific Reports, 2015, 5, 11531.	3.3	12
134	Caveats about interpretation of ancient chicken mtDNAs from northern China. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1970-1.	7.1	15
135	A genome draft of the legless anguid lizard, Ophisaurus gracilis. GigaScience, 2015, 4, 17.	6.4	23
136	A Positive Correlation between Elevated Altitude and Frequency of Mutant Alleles at the EPAS1 and HBB Loci in Chinese Indigenous Dogs. Journal of Genetics and Genomics, 2015, 42, 173-177.	3.9	9
137	Genomic Analyses Reveal Potential Independent Adaptation to High Altitude in Tibetan Chickens. Molecular Biology and Evolution, 2015, 32, 1880-1889.	8.9	193
138	Ancient inland human dispersals from Myanmar into interior East Asia since the Late Pleistocene. Scientific Reports, 2015, 5, 9473.	3.3	26
139	Proteomic analysis of the skin of Chinese giant salamander (Andrias davidianus). Journal of Proteomics, 2015, 119, 196-208.	2.4	35
140	Data from proteomic analysis of the skin of Chinese giant salamander (Andrias davidianus). Data in Brief, 2015, 3, 99-102.	1.0	1
141	The prion protein gene polymorphisms associated with bovine spongiform encephalopathy susceptibility differ significantly between cattle and buffalo. Infection, Genetics and Evolution, 2015, 36, 531-538.	2.3	15
142	Accelerated evolution of constraint elements for hematophagic adaptation in mosquitoes. Zoological Research, 2015, 36, 320-7.	0.6	0
143	Domestication of the Dog from the Wolf Was Promoted by Enhanced Excitatory Synaptic Plasticity: A Hypothesis. Genome Biology and Evolution, 2014, 6, 3115-3121.	2.5	38
144	Integrative analysis of young genes, positively selected genes and lncRNAs in the development of Drosophila melanogaster. BMC Evolutionary Biology, 2014, 14, 241.	3.2	11

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145	Identification and Characterization of MicroRNAs in Ovary and Testis of Nile Tilapia (Oreochromis) Tj ETQq1 1 0.7	784314 rg 2.5	BT/Overloci
146	Pattern of Mutation Rates in the Germline of Drosophila melanogaster Males from a Large-Scale Mutation Screening Experiment. G3: Genes, Genomes, Genetics, 2014, 4, 1503-1514.	1.8	15
147	"Out of Pollen―Hypothesis for Origin of New Genes in Flowering Plants: Study from Arabidopsis thaliana. Genome Biology and Evolution, 2014, 6, 2822-2829.	2.5	28
148	Genome-Wide Identification of Long Intergenic Noncoding RNA Genes and Their Potential Association with Domestication in Pigs. Genome Biology and Evolution, 2014, 6, 1387-1392.	2.5	121
149	Domestication Genomics: Evidence from Animals. Annual Review of Animal Biosciences, 2014, 2, 65-84.	7.4	98
150	Retrieving Y chromosomal haplogroup trees using GWAS data. European Journal of Human Genetics, 2014, 22, 1046-1050.	2.8	9
151	Two new susceptibility loci 1q24.2 and 11p11.2 confer risk to severe acne. Nature Communications, 2014, 5, 2870.	12.8	54
152	Genetic Convergence in the Adaptation of Dogs and Humans to the High-Altitude Environment of the Tibetan Plateau. Genome Biology and Evolution, 2014, 6, 2122-2128.	2.5	146
153	Mitogenomic analyses propose positive selection in mitochondrial genes for high-altitude adaptation in galliform birds. Mitochondrion, 2014, 18, 70-75.	3.4	70
154	No association between Y chromosomal haplogroups and severe acne in the Han Chinese population. Journal of Human Genetics, 2014, 59, 475-476.	2.3	0
155	A Matrilineal Genetic Legacy from the Last Glacial Maximum Confers Susceptibility to Schizophrenia in Han Chinese. Journal of Genetics and Genomics, 2014, 41, 397-407.	3.9	28
156	TNF -308 G/A Polymorphism and Risk of Acne Vulgaris: A Meta-Analysis. PLoS ONE, 2014, 9, e87806.	2.5	20
157	The Updated Phylogenies of the Phasianidae Based on Combined Data of Nuclear and Mitochondrial DNA. PLoS ONE, 2014, 9, e95786.	2.5	18
158	Tamil Merchant in Ancient Mesopotamia. PLoS ONE, 2014, 9, e109331.	2.5	3
159	Balancing Selection on CDH2 May Be Related to the Behavioral Features of the Belgian Malinois. PLoS ONE, 2014, 9, e110075.	2.5	13
160	Molecular phylogeny of European and African Barbus and their West Asian relatives in the Cyprininae (Teleostei: Cypriniformes) and orogenesis of the Qinghai-Tibetan Plateau. Science Bulletin, 2013, 58, 3738-3746.	1.7	22
161	Artificial Selection on Brain-Expressed Genes during the Domestication of Dog. Molecular Biology and Evolution, 2013, 30, 1867-1876.	8.9	74
162	QcReads: An Adapter and Quality Trimming Tool for Next-Generation Sequencing Reads. Journal of Genetics and Genomics, 2013, 40, 639-642.	3.9	5

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163	Cold Code: the global initiative to <scp>DNA</scp> barcode amphibians and nonavian reptiles. Molecular Ecology Resources, 2013, 13, 161-167.	4.8	72
164	The genomics of selection in dogs and the parallel evolution between dogs and humans. Nature Communications, 2013, 4, 1860.	12.8	275
165	Origin of Chinese Goldfish and Sequential Loss of Genetic Diversity Accompanies New Breeds. PLoS ONE, 2013, 8, e59571.	2.5	33
166	<p>Phylogeny of the Cyrtodactylus irregularis species complex (Squamata: Gekkonidae) from Vietnam with the description of two new species</p> . Zootaxa, 2013, 3737, 399.	0.5	29
167	Quaternary palaeoenvironmental oscillations drove the evolution of the Eurasian <i>Carassius auratus</i> complex (Cypriniformes, Cyprinidae). Journal of Biogeography, 2012, 39, 2264-2278.	3.0	52
168	Molecular phylogeny of the New World Dipsadidae (Serpentes: Colubroidea): a reappraisal. Cladistics, 2012, 28, 437-459.	3.3	112
169	Polyploidization and epigenetics. Science Bulletin, 2011, 56, 245-252.	1.7	18
170	Genetic consequences of postglacial colonization by the endemic Yarkand hare (Lepus yarkandensis) of the arid Tarim Basin. Science Bulletin, 2011, 56, 1370-1382.	1.7	23
171	Gene duplication plays a major role in gene co-option: Studies into the evolution of the motilin/ghrelin family and their receptors. Science Bulletin, 2011, 56, 2690-2697.	1.7	9
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