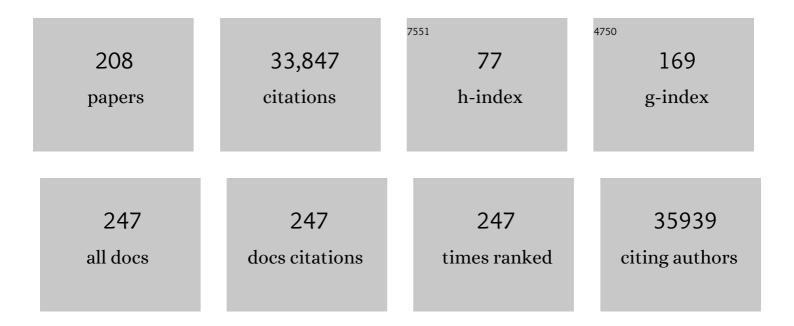
## **Guo-Jie Zhang**

List of Publications by Year in descending order

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CUO-LIE ZHANC

| #  | Article   | IF   | CITATIONS           |
|----|---|------|---------------------|
| 1  | The oyster genome reveals stress adaptation and complexity of shell formation. Nature, 2012, 490, 49-54.  | 13.7 | 1,966               |
| 2  | Whole-genome analyses resolve early branches in the tree of life of modern birds. Science, 2014, 346, 1320-1331.  | 6.0  | 1,583               |
| 3  | The genome of the cucumber, Cucumis sativus L Nature Genetics, 2009, 41, 1275-1281.   | 9.4  | 1,317               |
| 4  | Analyses of pig genomes provide insight into porcine demography and evolution. Nature, 2012, 491, 393-398.  | 13.7 | 1,190               |
| 5  | Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.  | 13.7 | 1,139               |
| 6  | The sequence and de novo assembly of the giant panda genome. Nature, 2010, 463, 311-317.  | 13.7 | 1,058               |
| 7  | Comparative genomics reveals insights into avian genome evolution and adaptation. Science, 2014, 346, 1311-1320.  | 6.0  | 895                 |
| 8  | The diploid genome sequence of an Asian individual. Nature, 2008, 456, 60-65.   | 13.7 | 834                 |
| 9  | Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. Nature Biotechnology, 2012, 30, 105-111.           | 9.4  | 818                 |
| 10 | Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse.<br>Nature, 2013, 499, 74-78.  | 13.7 | 717                 |
| 11 | The yak genome and adaptation to life at high altitude. Nature Genetics, 2012, 44, 946-949.   | 9.4  | 708                 |
| 12 | Whole-genome sequence of a flatfish provides insights into ZW sex chromosome evolution and adaptation to a benthic lifestyle. Nature Genetics, 2014, 46, 253-260.       | 9.4  | 685                 |
| 13 | Earth BioGenome Project: Sequencing life for the future of life. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4325-4333. | 3.3  | 652                 |
| 14 | Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species.<br>GigaScience, 2013, 2, 10.   | 3.3  | 582                 |
| 15 | Comparative Analysis of Bat Genomes Provides Insight into the Evolution of Flight and Immunity.<br>Science, 2013, 339, 456-460.   | 6.0  | 522                 |
| 16 | Genome sequencing reveals insights into physiology and longevity of the naked mole rat. Nature, 2011, 479, 223-227.   | 13.7 | 517                 |
| 17 | Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (Capra) Tj ETQq1   | 1    | 4 rgBT /Ovei<br>479 |
| 18 | The half-life of DNA in bone: measuring decay kinetics in 158 dated fossils. Proceedings of the Royal<br>Society B: Biological Sciences, 2012, 279, 4724-4733.          | 1.2  | 478                 |

| #  | Article   | IF        | CITATIONS      |
|----|---|-----------|----------------|
| 19 | The locust genome provides insight into swarm formation and long-distance flight. Nature Communications, 2014, 5, 2957.   | 5.8       | 437            |
| 20 | Deep RNA sequencing at single base-pair resolution reveals high complexity of the rice transcriptome.<br>Genome Research, 2010, 20, 646-654.  | 2.4       | 435            |
| 21 | Genomic Comparison of the Ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> .<br>Science, 2010, 329, 1068-1071.  | 6.0       | 420            |
| 22 | The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. Nature Genetics, 2013, 45, 701-706. | 9.4       | 409            |
| 23 | Whole-genome sequence of Schistosoma haematobium. Nature Genetics, 2012, 44, 221-225.   | 9.4       | 383            |
| 24 | Convergent transcriptional specializations in the brains of humans and song-learning birds. Science, 2014, 346, 1256846.  | 6.0       | 379            |
| 25 | Molecular traces of alternative social organization in a termite genome. Nature Communications, 2014, 5, 3636.  | 5.8       | 371            |
| 26 | Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. Cell, 2014, 157, 785-794.  | 13.5      | 363            |
| 27 | Genome-wide and Caste-Specific DNA Methylomes of the Ants Camponotus floridanus and<br>Harpegnathos saltator. Current Biology, 2012, 22, 1755-1764.                                 | 1.8       | 361            |
| 28 | The i5K Initiative: Advancing Arthropod Genomics for Knowledge, Human Health, Agriculture, and the<br>Environment. Journal of Heredity, 2013, 104, 595-600.                         | 1.0       | 358            |
| 29 | Genomic signatures of evolutionary transitions from solitary to group living. Science, 2015, 348, 1139-1143.  | 6.0       | 357            |
| 30 | Epigenetic modification and inheritance in sexual reversal of fish. Genome Research, 2014, 24, 604-615.   | 2.4       | 356            |
| 31 | Single base–resolution methylome of the silkworm reveals a sparse epigenomic map. Nature<br>Biotechnology, 2010, 28, 516-520.   | 9.4       | 349            |
| 32 | Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm () Tj ETQq0 0 0 r  | gBT/Overl | ock 10 Tf 50 2 |
| 33 | Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. Science, 2014, 346, 1254449.   | 6.0       | 300            |
| 34 | Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques. Nature Biotechnology, 2011, 29, 1019-1023.                      | 9.4       | 284            |
| 35 | Genome of the Chinese tree shrew. Nature Communications, 2013, 4, 1426.   | 5.8       | 284            |
| 36 | Single-base resolution maps of cultivated and wild rice methylomes and regulatory roles of DNA methylation in plant gene expression. BMC Genomics, 2012, 13, 300.                   | 1.2       | 266            |

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|----|--|------|-----------|
| 37 | Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits.<br>Science, 2019, 364, .  | 6.0  | 266       |
| 38 | Complex evolutionary trajectories of sex chromosomes across bird taxa. Science, 2014, 346, 1246338.  | 6.0  | 258       |
| 39 | Progressive Cactus is a multiple-genome aligner for the thousand-genome era. Nature, 2020, 587, 246-251.   | 13.7 | 256       |
| 40 | Dense sampling of bird diversity increases power of comparative genomics. Nature, 2020, 587, 252-257.  | 13.7 | 251       |
| 41 | Ascaris suum draft genome. Nature, 2011, 479, 529-533.   | 13.7 | 246       |
| 42 | Complementary symbiont contributions to plant decomposition in a fungus-farming termite.<br>Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14500-14505.                       | 3.3  | 243       |
| 43 | Temporal Dynamics of Avian Populations during Pleistocene Revealed by Whole-Genome Sequences.<br>Current Biology, 2015, 25, 1375-1380.   | 1.8  | 243       |
| 44 | On the origin of new genes in <i>Drosophila</i> . Genome Research, 2008, 18, 1446-1455.  | 2.4  | 240       |
| 45 | Genomic Diversity and Evolution of the Head Crest in the Rock Pigeon. Science, 2013, 339, 1063-1067.   | 6.0  | 230       |
| 46 | Draft genome sequence of the Tibetan antelope. Nature Communications, 2013, 4, 1858.   | 5.8  | 229       |
| 47 | The Genome of Dendrobium officinale Illuminates the Biology of the Important Traditional Chinese<br>Orchid Herb. Molecular Plant, 2015, 8, 922-934.  | 3.9  | 228       |
| 48 | Genome analysis reveals insights into physiology and longevity of the Brandt's bat Myotis brandtii.<br>Nature Communications, 2013, 4, 2212.   | 5.8  | 213       |
| 49 | The genome of the leaf-cutting ant <i>Acromyrmex echinatior</i> suggests key adaptations to advanced social life and fungus farming. Genome Research, 2011, 21, 1339-1348.   | 2.4  | 210       |
| 50 | High Rate of Chimeric Gene Origination by Retroposition in Plant Genomes. Plant Cell, 2006, 18,<br>1791-1802.  | 3.1  | 207       |
| 51 | The genome and transcriptome of Japanese flounder provide insights into flatfish asymmetry. Nature<br>Genetics, 2017, 49, 119-124.   | 9.4  | 178       |
| 52 | Genomic legacy of the African cheetah, Acinonyx jubatus. Genome Biology, 2015, 16, 277.  | 3.8  | 167       |
| 53 | Adaptations to a Subterranean Environment and Longevity Revealed by the Analysis of Mole Rat<br>Genomes. Cell Reports, 2014, 8, 1354-1364.   | 2.9  | 162       |
| 54 | 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. | 3.3  | 159       |

| #  | Article   | IF   | CITATIONS |
|----|---|------|-----------|
| 55 | Preparation of Pd–Au/C catalysts with different alloying degree and their electrocatalytic performance for formic acid oxidation. Applied Catalysis B: Environmental, 2011, 102, 614-619. | 10.8 | 155       |
| 56 | Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies. Nature Communications, 2015, 6, 8212.  | 5.8  | 146       |
| 57 | 863 genomes reveal the origin and domestication of chicken. Cell Research, 2020, 30, 693-701.   | 5.7  | 144       |
| 58 | The Genome of the Clonal Raider Ant Cerapachys biroi. Current Biology, 2014, 24, 451-458.   | 1.8  | 143       |
| 59 | A near-chromosome-scale genome assembly of the gemsbok ( <i>Oryx gazella</i> ): an iconic antelope of the Kalahari desert. GigaScience, 2019, 8, .  | 3.3  | 138       |
| 60 | The era of reference genomes in conservation genomics. Trends in Ecology and Evolution, 2022, 37, 197-202.  | 4.2  | 138       |
| 61 | Comparative performance of the BCISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. GigaScience, 2017, 6, 1-13.  | 3.3  | 137       |
| 62 | Bird sequencing project takes off. Nature, 2015, 522, 34-34.  | 13.7 | 136       |
| 63 | Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. Nature Communications, 2014, 5, 5594.   | 5.8  | 135       |
| 64 | Comparative genomics of parasitic silkworm microsporidia reveal an association between genome expansion and host adaptation. BMC Genomics, 2013, 14, 186.                                 | 1.2  | 127       |
| 65 | Genome of <i>Drosophila suzukii</i> , the Spotted Wing <i>Drosophila</i> . G3: Genes, Genomes,<br>Genetics, 2013, 3, 2257-2271.   | 0.8  | 126       |
| 66 | The sequence and analysis of a Chinese pig genome. GigaScience, 2012, 1, 16.  | 3.3  | 125       |
| 67 | Reference-assisted chromosome assembly. Proceedings of the National Academy of Sciences of the<br>United States of America, 2013, 110, 1785-1790.   | 3.3  | 124       |
| 68 | Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. Nature Ecology and Evolution, 2018, 2, 659-668.   | 3.4  | 124       |
| 69 | The Earth BioGenome Project 2020: Starting the clock. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .                                       | 3.3  | 124       |
| 70 | Genetic basis of ruminant headgear and rapid antler regeneration. Science, 2019, 364, .   | 6.0  | 121       |
| 71 | Comparative genomic data of the Avian Phylogenomics Project. GigaScience, 2014, 3, 26.  | 3.3  | 117       |
| 72 | Red fox genome assembly identifies genomic regions associated with tame and aggressive behaviours.<br>Nature Ecology and Evolution, 2018, 2, 1479-1491.                                   | 3.4  | 113       |

| #  | Article   | IF   | CITATIONS |
|----|---|------|-----------|
| 73 | The genomic consequences of adaptive divergence and reproductive isolation between species of manakins. Molecular Ecology, 2013, 22, 3304-3317.   | 2.0  | 108       |
| 74 | Reciprocal genomic evolution in the ant–fungus agricultural symbiosis. Nature Communications, 2016, 7, 12233.   | 5.8  | 106       |
| 75 | Reference genome of wild goat (capra aegagrus) and sequencing of goat breeds provide insight into genic basis of goat domestication. BMC Genomics, 2015, 16, 431.                               | 1.2  | 103       |
| 76 | Evidence for a single loss of mineralized teeth in the common avian ancestor. Science, 2014, 346, 1254390.  | 6.0  | 99        |
| 77 | African lungfish genome sheds light on the vertebrate water-to-land transition. Cell, 2021, 184, 1362-1376.e18.   | 13.5 | 99        |
| 78 | High-coverage sequencing and annotated assembly of the genome of the Australian dragon lizard<br>Pogona vitticeps. GigaScience, 2015, 4, 45.  | 3.3  | 97        |
| 79 | The Genomic Footprints of the Fall and Recovery of the Crested Ibis. Current Biology, 2019, 29, 340-349.e7.   | 1.8  | 94        |
| 80 | Evolutionary trajectories of snake genes and genomes revealed by comparative analyses of five-pacer viper. Nature Communications, 2016, 7, 13107.   | 5.8  | 88        |
| 81 | The origin of domestication genes in goats. Science Advances, 2020, 6, eaaz5216.  | 4.7  | 86        |
| 82 | Platypus and echidna genomes reveal mammalian biology and evolution. Nature, 2021, 592, 756-762.  | 13.7 | 85        |
| 83 | Dynamic evolution of the alpha (α) and beta (β) keratins has accompanied integument diversification and the adaptation of birds into novel lifestyles. BMC Evolutionary Biology, 2014, 14, 249. | 3.2  | 84        |
| 84 | Genomic signatures of near-extinction and rebirth of the crested ibis and other endangered bird species. Genome Biology, 2014, 15, 557.   | 3.8  | 83        |
| 85 | High-coverage sequencing and annotated assemblies of the budgerigar genome. GigaScience, 2014, 3, 11.   | 3.3  | 75        |
| 86 | Olfactory Receptor Subgenomes Linked with Broad Ecological Adaptations in Sauropsida. Molecular<br>Biology and Evolution, 2015, 32, 2832-2843.  | 3.5  | 73        |
| 87 | The draft genome of a socially polymorphic halictid bee, Lasioglossum albipes. Genome Biology, 2013,<br>14, R142.   | 13.9 | 72        |
| 88 | Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. GigaScience, 2014, 3, 27.                             | 3.3  | 72        |
| 89 | Phylogenomic analyses data of the avian phylogenomics project. GigaScience, 2015, 4, 4.   | 3.3  | 72        |
| 90 | Constrained vertebrate evolution by pleiotropic genes. Nature Ecology and Evolution, 2017, 1, 1722-1730.  | 3.4  | 72        |

| #   | Article  | IF   | CITATIONS |
|-----|--|------|-----------|
| 91  | The evolutionary history of extinct and living lions. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10927-10934.       | 3.3  | 70        |
| 92  | A Young Drosophila Duplicate Gene Plays Essential Roles in Spermatogenesis by Regulating Several<br>Y-Linked Male Fertility Genes. PLoS Genetics, 2010, 6, e1001255. | 1.5  | 68        |
| 93  | The genome of the golden apple snail Pomacea canaliculata provides insight into stress tolerance and invasive adaptation. GigaScience, 2018, 7, .                    | 3.3  | 68        |
| 94  | Dynamic evolutionary history and gene content of sex chromosomes across diverse songbirds.<br>Nature Ecology and Evolution, 2019, 3, 834-844.                        | 3.4  | 68        |
| 95  | Tracing the genetic footprints of vertebrate landing in non-teleost ray-finned fishes. Cell, 2021, 184, 1377-1391.e14.   | 13.5 | 66        |
| 96  | Deciphering neo-sex and B chromosome evolution by the draft genome of Drosophila albomicans. BMC Genomics, 2012, 13, 109.  | 1.2  | 64        |
| 97  | Functional roles of Aves class-specific cis-regulatory elements on macroevolution of bird-specific features. Nature Communications, 2017, 8, 14229.                  | 5.8  | 61        |
| 98  | Low frequency of paleoviral infiltration across the avian phylogeny. Genome Biology, 2014, 15, 539.  | 3.8  | 60        |
| 99  | Caste-specific RNA editomes in the leaf-cutting ant Acromyrmex echinatior. Nature Communications, 2014, 5, 4943.   | 5.8  | 60        |
| 100 | A genomic comparison of two termites with different social complexity. Frontiers in Genetics, 2015, 6,<br>9.   | 1.1  | 60        |
| 101 | Gene loss, adaptive evolution and the co-evolution of plumage coloration genes with opsins in birds.<br>BMC Genomics, 2015, 16, 751.                                 | 1.2  | 58        |
| 102 | RES-Scanner: a software package for genome-wide identification of RNA-editing sites. GigaScience, 2016, 5, 37.   | 3.3  | 55        |
| 103 | Draft genome of the leopard gecko, Eublepharis macularius. GigaScience, 2016, 5, 47.   | 3.3  | 55        |
| 104 | Cephalopod genomics: A plan of strategies and organization. Standards in Genomic Sciences, 2012, 7, 175-188.   | 1.5  | 53        |
| 105 | Response to Comment on "Whole-genome analyses resolve early branches in the tree of life of modern<br>birds― Science, 2015, 349, 1460-1460.                          | 6.0  | 53        |
| 106 | Why sequence all eukaryotes?. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .  | 3.3  | 51        |
| 107 | Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. Cell, 2021, 184, 4874-4885.e16.  | 13.5 | 49        |
| 108 | Comparative methylomics between domesticated and wild silkworms implies possible epigenetic influences on silkworm domestication. BMC Genomics, 2013, 14, 646.       | 1.2  | 47        |

| #   | Article   | IF   | CITATIONS |
|-----|---|------|-----------|
| 109 | Advances in genome editing technology and its promising application in evolutionary and ecological studies. GigaScience, 2014, 3, 24.   | 3.3  | 47        |
| 110 | A flock of genomes. Science, 2014, 346, 1308-1309.  | 6.0  | 46        |
| 111 | Genomic takeover by transposable elements in the Strawberry poison frog. Molecular Biology and Evolution, 2014, 35, 2913-2927.  | 3.5  | 45        |
| 112 | Genomic and transcriptomic investigations of the evolutionary transition from oviparity to<br>viviparity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116,<br>3646-3655. | 3.3  | 43        |
| 113 | Genome and single-cell RNA-sequencing of the earthworm Eisenia andrei identifies cellular mechanisms underlying regeneration. Nature Communications, 2020, 11, 2656.  | 5.8  | 43        |
| 114 | Diverse coral reef invertebrates exhibit patterns of phylosymbiosis. ISME Journal, 2020, 14, 2211-2222.   | 4.4  | 43        |
| 115 | Chromosomal level assembly and population sequencing of the Chinese tree shrew genome.<br>Zoological Research, 2019, 40, 506-521.   | 0.9  | 43        |
| 116 | Incomplete lineage sorting and phenotypic evolution in marsupials. Cell, 2022, 185, 1646-1660.e18.  | 13.5 | 43        |
| 117 | Evolutionary and biomedical insights from a marmoset diploid genome assembly. Nature, 2021, 594, 227-233.   | 13.7 | 42        |
| 118 | Temporal genomic evolution of bird sex chromosomes. BMC Evolutionary Biology, 2014, 14, 250.  | 3.2  | 41        |
| 119 | Pre-extinction Demographic Stability and Genomic Signatures of Adaptation in the Woolly<br>Rhinoceros. Current Biology, 2020, 30, 3871-3879.e7.   | 1.8  | 41        |
| 120 | Towards reconstructing the ancestral brain gene-network regulating caste differentiation in ants.<br>Nature Ecology and Evolution, 2018, 2, 1782-1791.  | 3.4  | 40        |
| 121 | Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. Genome Research, 2019, 29, 576-589.  | 2.4  | 39        |
| 122 | Historical population declines prompted significant genomic erosion in the northern and southern white rhinoceros ( <i>Ceratotherium simum</i> ). Molecular Ecology, 2021, 30, 6355-6369.                           | 2.0  | 39        |
| 123 | Identification and characterization of insect-specific proteins by genome data analysis. BMC Genomics, 2007, 8, 93.   | 1.2  | 38        |
| 124 | The Mutationathon highlights the importance of reaching standardization in estimates of pedigree-based germline mutation rates. ELife, 2022, 11, .  | 2.8  | 38        |
| 125 | Developmental plasticity shapes social traits and selection in a facultatively eusocial bee. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13615-13625.               | 3.3  | 37        |
| 126 | A draft genome sequence of the elusive giant squid, Architeuthis dux. GigaScience, 2020, 9, .   | 3.3  | 37        |

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|-----|---|-----|-----------|
| 127 | Mitogenomes Uncover Extinct Penguin Taxa and Reveal Island Formation as a Key Driver of Speciation.<br>Molecular Biology and Evolution, 2019, 36, 784-797.  | 3.5 | 36        |
| 128 | A new duck genome reveals conserved and convergently evolved chromosome architectures of birds and mammals. GigaScience, 2021, 10, .  | 3.3 | 36        |
| 129 | Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, Homotherium<br>latidens. Current Biology, 2020, 30, 5018-5025.e5.   | 1.8 | 34        |
| 130 | A soft selective sweep during rapid evolution of gentle behaviour in an Africanized honeybee. Nature<br>Communications, 2017, 8, 1550.  | 5.8 | 33        |
| 131 | Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .  | 3.3 | 33        |
| 132 | The genome of the largest bony fish, ocean sunfish (Mola mola), provides insights into its fast<br>growth rate. GigaScience, 2016, 5, 36.   | 3.3 | 32        |
| 133 | In-Depth Tanscriptomic Analysis on Giant Freshwater Prawns. PLoS ONE, 2013, 8, e60839.  | 1.1 | 32        |
| 134 | Multi-omic detection of <i>Mycobacterium leprae</i> in archaeological human dental calculus.<br>Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190584.                        | 1.8 | 31        |
| 135 | A flock of genomes. Science, 2014, 346, 1308-1309.  | 6.0 | 31        |
| 136 | Genome sequence of a diabetes-prone rodent reveals a mutation hotspot around the ParaHox gene<br>cluster. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114,<br>7677-7682. | 3.3 | 30        |
| 137 | A new emu genome illuminates the evolution of genome configuration and nuclear architecture of avian chromosomes. Genome Research, 2021, 31, 497-511.   | 2.4 | 30        |
| 138 | Improving the ostrich genome assembly using optical mapping data. GigaScience, 2015, 4, 24.   | 3.3 | 28        |
| 139 | Avianbase: a community resource for bird genomics. Genome Biology, 2015, 16, 21.  | 3.8 | 28        |
| 140 | An Effort to Use Human-Based Exome Capture Methods to Analyze Chimpanzee and Macaque Exomes.<br>PLoS ONE, 2012, 7, e40637.  | 1.1 | 28        |
| 141 | Synthesis and Electrocatalytic Properties of Palladium Network Nanostructures. ChemPlusChem, 2012, 77, 936-940.   | 1.3 | 27        |
| 142 | Evolutionary Genomics and Adaptive Evolution of the Hedgehog Gene Family (Shh, Ihh and Dhh) in Vertebrates. PLoS ONE, 2014, 9, e74132.  | 1.1 | 27        |
| 143 | Comparative Phylogenomics, a Stepping Stone for Bird Biodiversity Studies. Diversity, 2019, 11, 115.  | 0.7 | 26        |
| 144 | The germline mutational process in rhesus macaque and its implications for phylogenetic dating.<br>GigaScience, 2021, 10, .   | 3.3 | 26        |

| #   | Article  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 145 | Draft genome of the Marco Polo Sheep (Ovis ammon polii). GigaScience, 2017, 6, 1-7.  | 3.3 | 25        |
| 146 | The Vertebrate TLR Supergene Family Evolved Dynamically by Gene Gain/Loss and Positive Selection<br>Revealing a Host–Pathogen Arms Race in Birds. Diversity, 2019, 11, 131.  | 0.7 | 25        |
| 147 | Response of an Afro-Palearctic bird migrant to glaciation cycles. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .  | 3.3 | 25        |
| 148 | Evolutionary History, Genomic Adaptation to Toxic Diet, and Extinction of the Carolina Parakeet.<br>Current Biology, 2020, 30, 108-114.e5.   | 1.8 | 24        |
| 149 | Genomic regions influencing aggressive behavior in honey bees are defined by colony allele<br>frequencies. Proceedings of the National Academy of Sciences of the United States of America, 2020,<br>117, 17135-17141. | 3.3 | 24        |
| 150 | Sequencing, de novo assembling, and annotating the genome of the endangered Chinese crocodile<br>lizard Shinisaurus crocodilurus. GigaScience, 2017, 6, 1-6.   | 3.3 | 23        |
| 151 | Deep parallel sequencing reveals conserved and novel miRNAs in gill and hepatopancreas of giant freshwater prawn. Fish and Shellfish Immunology, 2013, 35, 1061-1069.  | 1.6 | 22        |
| 152 | Draft genome of the milu (Elaphurus davidianus). GigaScience, 2018, 7, .   | 3.3 | 22        |
| 153 | The evolution of ancestral and species-specific adaptations in snowfinches at the Qinghai–Tibet<br>Plateau. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .              | 3.3 | 22        |
| 154 | Large-scale genomic analysis reveals the genetic cost of chicken domestication. BMC Biology, 2021, 19, 118.  | 1.7 | 22        |
| 155 | Transcriptome and Network Changes in Climbers at Extreme Altitudes. PLoS ONE, 2012, 7, e31645.   | 1.1 | 21        |
| 156 | Whole-Genome Identification, Phylogeny, and Evolution of the Cytochrome P450 Family 2 (CYP2) Subfamilies in Birds. Genome Biology and Evolution, 2016, 8, 1115-1131.   | 1.1 | 20        |
| 157 | Relaxed selection underlies genome erosion in socially parasitic ant species. Nature Communications, 2021, 12, 2918.   | 5.8 | 20        |
| 158 | Draft Genome Assembly and Population Genetics of an Agricultural Pollinator, the Solitary Alkali Bee<br>(Halictidae: <i>Nomia melanderi</i> ). G3: Genes, Genomes, Genetics, 2019, 9, 625-634.                         | 0.8 | 19        |
| 159 | Modes of genetic adaptations underlying functional innovations in the rumen. Science China Life Sciences, 2021, 64, 1-21.  | 2.3 | 19        |
| 160 | Neuroprotectants attenuate hypobaric hypoxia-induced brain injuries in cynomolgus monkeys.<br>Zoological Research, 2020, 41, 3-19.   | 0.9 | 19        |
| 161 | A complete, telomere-to-telomere human genome sequence presents new opportunities for evolutionary genomics. Nature Methods, 2022, 19, 635-638.  | 9.0 | 19        |
| 162 | Ancient population genomics and the study of evolution. Philosophical Transactions of the Royal<br>Society B: Biological Sciences, 2015, 370, 20130381.  | 1.8 | 18        |

| #   | Article   | IF         | CITATIONS     |
|-----|---|------------|---------------|
| 163 | High-coverage genomes to elucidate the evolution of penguins. GigaScience, 2019, 8, .   | 3.3        | 18            |
| 164 | Detoxification Genes Differ Between Cactus-, Fruit-, and Flower-Feeding <i>Drosophila</i> . Journal of Heredity, 2019, 110, 80-91.  | 1.0        | 17            |
| 165 | Phylogenomic analyses of the genus <i>Drosophila</i> reveals genomic signals of climate adaptation.<br>Molecular Ecology Resources, 2022, 22, 1559-1581.  | 2.2        | 15            |
| 166 | A single-cell transcriptomic atlas tracking the neural basis of division of labour in an ant superorganism. Nature Ecology and Evolution, 2022, 6, 1191-1204.                                     | 3.4        | 15            |
| 167 | Construction of Red Fox Chromosomal Fragments from the Short-Read Genome Assembly. Genes, 2018, 9, 308.   | 1.0        | 14            |
| 168 | An Indo-Pacific Humpback Dolphin Genome Reveals Insights into Chromosome Evolution and the Demography of a Vulnerable Species. IScience, 2020, 23, 101640.  | 1.9        | 14            |
| 169 | Ancient proteins resolve controversy over the identity of <i>Genyornis</i> eggshell. Proceedings of the United States of America, 2022, 119, .  | 3.3        | 14            |
| 170 | An integrated chromosome-scale genome assembly of the Masai giraffe (Giraffa camelopardalis) Tj ETQq0 0 0 rg  | 3T /Qverlo | ck 10 Tf 50 4 |
| 171 | Triangulation of the human, chimpanzee, and Neanderthal genome sequences identifies potentially compensated mutations. Human Mutation, 2010, 31, 1286-1293.                                       | 1.1        | 12            |
| 172 | Bone-associated gene evolution and the origin of flight in birds. BMC Genomics, 2016, 17, 371.  | 1.2        | 12            |
| 173 | Avian Binocularity and Adaptation to Nocturnal Environments: Genomic Insights from a Highly Derived Visual Phenotype. Genome Biology and Evolution, 2019, 11, 2244-2255.                          | 1.1        | 12            |
| 174 | Comparative study on pattern recognition receptors in non-teleost ray-finned fishes and their evolutionary significance in primitive vertebrates. Science China Life Sciences, 2019, 62, 566-578. | 2.3        | 12            |
| 175 | The gene expression network regulating queen brain remodeling after insemination and its parallel use in ants with reproductive workers. Science Advances, 2020, 6, .                             | 4.7        | 12            |
| 176 | 31° South: The physiology of adaptation to arid conditions in a passerine bird. Molecular Ecology, 2019, 28, 3709-3721.   | 2.0        | 11            |
| 177 | Testing cophylogeny between coral reef invertebrates and their bacterial and archaeal symbionts.<br>Molecular Ecology, 2021, 30, 3768-3782.   | 2.0        | 11            |
| 178 | The bird's-eye view on chromosome evolution. Genome Biology, 2018, 19, 201.   | 3.8        | 10            |
| 179 | Identification and evolution of avian endogenous foamy viruses. Virus Evolution, 2019, 5, vez049.   | 2.2        | 10            |
|     |   |            |               |

<sup>180</sup>Chromatin accessibility and transcriptome landscapes of Monomorium pharaonis brain. Scientific<br/>Data, 2020, 7, 217.2.410

| #   | Article  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 181 | Phylogeny and sex chromosome evolution of Palaeognathae. Journal of Genetics and Genomics, 2022, 49, 109-119.  | 1.7 | 10        |
| 182 | Adaptation and Cryptic Pseudogenization in Penguin Toll-Like Receptors. Molecular Biology and Evolution, 2022, 39, .   | 3.5 | 10        |
| 183 | High-quality chromosome-level genome assembly and full-length transcriptome analysis of the pharaoh ant <i>Monomorium pharaonis</i> . GigaScience, 2020, 9, .                          | 3.3 | 9         |
| 184 | Room-temperature synthesis and electrocatalysis of carbon nanotubes supported palladium–iron<br>alloy nanoparticles. Electrochimica Acta, 2013, 111, 898-902.                          | 2.6 | 8         |
| 185 | The naked mole rat genome: understanding aging through genome analysis. Aging, 2011, 3, 1124-1124.   | 1.4 | 8         |
| 186 | A draft genome assembly of the eastern banjo frog Limnodynastes dumerilii dumerilii<br>(Anura:ALimnodynastidae). GigaByte, 0, 2020, 1-13.  | 0.0 | 8         |
| 187 | Probing the genomic limits of de-extinction in the Christmas Island rat. Current Biology, 2022, , .  | 1.8 | 8         |
| 188 | Variation in predicted COVIDâ€19 risk among lemurs and lorises. American Journal of Primatology, 2021,<br>83, e23255.  | 0.8 | 7         |
| 189 | Evolutionary history of the extinct Sardinian dhole. Current Biology, 2021, 31, 5571-5579.e6.  | 1.8 | 7         |
| 190 | Initiation of the Primate Genome Project. Zoological Research, 2022, 43, 147-149.  | 0.9 | 7         |
| 191 | Gut Microbiota Linked with Reduced Fear of Humans in Red Junglefowl Has Implications for Early<br>Domestication. Genetics & Genomics Next, 2021, 2, .                                  | 0.8 | 7         |
| 192 | Hi-C chromosome conformation capture sequencing of avian genomes using the BGISEQ-500 platform.<br>GigaScience, 2020, 9, .   | 3.3 | 6         |
| 193 | A draft genome assembly of spotted hyena, Crocuta crocuta. Scientific Data, 2020, 7, 126.  | 2.4 | 6         |
| 194 | Sensory Rewiring in an Echolocator: Genome-Wide Modification of Retinogenic and Auditory Genes in the Bat <i>Myotis davidii</i> . G3: Genes, Genomes, Genetics, 2014, 4, 1825-1835.    | 0.8 | 5         |
| 195 | Ancestral developmental potentials in early bony fish contributed to vertebrate water-to-land transition. Zoological Research, 2021, 42, 135-137.                                      | 0.9 | 5         |
| 196 | Conservation genomics of the endangered Seychelles Magpieâ€Robin ( Copsychus sechellarum ): A<br>unique insight into the history of a precious endemic bird. Ibis, 0, , .              | 1.0 | 4         |
| 197 | Cross-comparison of the genome sequences from human, chimpanzee, Neanderthal and a Denisovan hominin identifies novel potentially compensated mutations. Human Genomics, 2011, 5, 453. | 1.4 | 3         |
| 198 | Adaptive diversity of innate immune receptor family short pentraxins in Murinae. FEBS Letters, 2012, 586, 798-803.   | 1.3 | 3         |

| #   | Article   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 199 | A novel method for using RNAâ€seq data to identify imprinted genes in social Hymenoptera with multiply<br>mated queens. Journal of Evolutionary Biology, 2020, 33, 1770-1782.     | 0.8 | 3         |
| 200 | Multiple origins of a frameshift insertion in a mitochondrial gene in birds and turtles. GigaScience, 2021, 10, .   | 3.3 | 3         |
| 201 | Dynamic evolution of transposable elements, demographic history, and gene content of paleognathous birds. Zoological Research, 2021, 42, 51-61.                                   | 0.9 | 3         |
| 202 | Validation of Potential Reference Genes for Real-Time qPCR Analysis in Pharaoh Ant, Monomorium<br>pharaonis (Hymenoptera: Formicidae). Frontiers in Physiology, 2022, 13, 852357. | 1.3 | 3         |
| 203 | Functional Diversity and Evolution of Bitter Taste Receptors in Egg-Laying Mammals. Molecular<br>Biology and Evolution, 2022, 39, .   | 3.5 | 2         |
| 204 | The first AsiaEvo conference, connecting Asian evolutionary biologists to the world. National Science Review, 2018, 5, 614-616.   | 4.6 | 1         |
| 205 | Studying mutation rate evolution in primates—a need for systematic comparison of computational pipelines. GigaScience, 2021, 10, .  | 3.3 | 1         |
| 206 | Labour classified by cervical dilatation & fetal membrane rupture demonstrates differential impact on RNA-seq data for human myometrium tissues. PLoS ONE, 2021, 16, e0260119.    | 1.1 | 1         |
| 207 | Turtle ghrelin. Nature Genetics, 2014, 46, 526-526.   | 9.4 | 0         |
| 208 | Callithrix jacchus (the common marmoset). Trends in Genetics, 2021, 37, 948-949.  | 2.9 | 0         |