

Guo-Jie Zhang

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/890101/guo-jie-zhang-publications-by-year.pdf>

Version: 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

210
papers

23,089
citations

69
h-index

151
g-index

247
ext. papers

29,592
ext. citations

15.5
avg, IF

6.01
L-index

#	Paper	IF	Citations
210	The mutationathon highlights the importance of reaching standardization in estimates of pedigree-based germline mutation rates.. <i>ELife</i> , 2022 , 11,	8.9	2
209	The Earth BioGenome Project 2020: Starting the clock.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	15
208	The era of reference genomes in conservation genomics.. <i>Trends in Ecology and Evolution</i> , 2022 ,	10.9	8
207	Standards recommendations for the Earth BioGenome Project.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	4
206	Why sequence all eukaryotes?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	6
205	Validation of Potential Reference Genes for Real-Time qPCR Analysis in Pharaoh Ant, (Hymenoptera: Formicidae).. <i>Frontiers in Physiology</i> , 2022 , 13, 852357	4.6	0
204	Probing the genomic limits of de-extinction in the Christmas Island rat.. <i>Current Biology</i> , 2022 ,	6.3	1
203	Incomplete lineage sorting and phenotypic evolution in marsupials.. <i>Cell</i> , 2022 ,	56.2	5
202	Response of an Afro-Palaearctic bird migrant to glaciation cycles.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	6
201	Phylogenomic analyses of the genus <i>Drosophila</i> reveals genomic signals of climate adaptation. <i>Molecular Ecology Resources</i> , 2021 ,	8.4	3
200	Labour classified by cervical dilatation & fetal membrane rupture demonstrates differential impact on RNA-seq data for human myometrium tissues. <i>PLoS ONE</i> , 2021 , 16, e0260119	3.7	0
199	Evolutionary history of the extinct Sardinian dhole. <i>Current Biology</i> , 2021 ,	6.3	2
198	Studying mutation rate evolution in primates-a need for systematic comparison of computational pipelines. <i>GigaScience</i> , 2021 , 10,	7.6	1
197	Tracing the genetic footprints of vertebrate landing in non-teleost ray-finned fishes. <i>Cell</i> , 2021 , 184, 1377-1391.e14	56.2	15
196	African lungfish genome sheds light on the vertebrate water-to-land transition. <i>Cell</i> , 2021 , 184, 1362-1376.e1827	56.2	15
195	The evolution of ancestral and species-specific adaptations in snowfinches at the Qinghai-Tibet Plateau. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	2
194	Evolutionary and biomedical insights from a marmoset diploid genome assembly. <i>Nature</i> , 2021 , 594, 227-233	50.4	10

193	Variation in predicted COVID-19 risk among lemurs and lorises. <i>American Journal of Primatology</i> , 2021 , 83, e23255	2.5	3
192	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737-746	46.4	161
191	The germline mutational process in rhesus macaque and its implications for phylogenetic dating. <i>GigaScience</i> , 2021 , 10,	7.6	6
190	Relaxed selection underlies genome erosion in socially parasitic ant species. <i>Nature Communications</i> , 2021 , 12, 2918	17.4	3
189	Large-scale genomic analysis reveals the genetic cost of chicken domestication. <i>BMC Biology</i> , 2021 , 19, 118	7.3	6
188	Testing cophylogeny between coral reef invertebrates and their bacterial and archaeal symbionts. <i>Molecular Ecology</i> , 2021 , 30, 3768-3782	5.7	1
187	Historical population declines prompted significant genomic erosion in the northern and southern white rhinoceros (<i>Ceratotherium simum</i>). <i>Molecular Ecology</i> , 2021 , 30, 6355-6369	5.7	5
186	Modes of genetic adaptations underlying functional innovations in the rumen. <i>Science China Life Sciences</i> , 2021 , 64, 1-21	8.5	7
185	Multiple origins of a frameshift insertion in a mitochondrial gene in birds and turtles. <i>GigaScience</i> , 2021 , 10,	7.6	2
184	Dynamic evolution of transposable elements, demographic history, and gene content of paleognathous birds. <i>Zoological Research</i> , 2021 , 42, 51-61	3.4	3
183	A new duck genome reveals conserved and convergently evolved chromosome architectures of birds and mammals. <i>GigaScience</i> , 2021 , 10,	7.6	9
182	Phylogeny and sex chromosome evolution of palaeognathae. <i>Journal of Genetics and Genomics</i> , 2021 , 49, 109-109	4	3
181	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. <i>Cell</i> , 2021 , 184, 4874-4885.e16	56.2	6
180	<i>Callithrix jacchus</i> (the common marmoset). <i>Trends in Genetics</i> , 2021 , 37, 948-949	8.5	
179	A new emu genome illuminates the evolution of genome configuration and nuclear architecture of avian chromosomes. <i>Genome Research</i> , 2021 , 31, 497-511	9.7	9
178	Platypus and echidna genomes reveal mammalian biology and evolution. <i>Nature</i> , 2021 , 592, 756-762	50.4	28
177	Gut Microbiota Linked with Reduced Fear of Humans in Red Junglefowl Has Implications for Early Domestication. <i>Genetics & Genomics Next</i> , 2021 , 2, 2100018	1.2	1
176	A novel method for using RNA-seq data to identify imprinted genes in social Hymenoptera with multiply mated queens. <i>Journal of Evolutionary Biology</i> , 2020 , 33, 1770-1782	2.3	1

175	The evolutionary history of extinct and living lions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 10927-10934	11.5	31
174	Genome and single-cell RNA-sequencing of the earthworm <i>Eisenia andrei</i> identifies cellular mechanisms underlying regeneration. <i>Nature Communications</i> , 2020 , 11, 2656	17.4	16
173	The origin of domestication genes in goats. <i>Science Advances</i> , 2020 , 6, eaaz5216	14.3	28
172	Developmental plasticity shapes social traits and selection in a facultatively eusocial bee. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 13615-13625	11.5	16
171	863 genomes reveal the origin and domestication of chicken. <i>Cell Research</i> , 2020 , 30, 693-701	24.7	49
170	Chromatin accessibility and transcriptome landscapes of <i>Monomorium pharaonis</i> brain. <i>Scientific Data</i> , 2020 , 7, 217	8.2	4
169	Genomic regions influencing aggressive behavior in honey bees are defined by colony allele frequencies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 17135-17141	11.5	8
168	A draft genome sequence of the elusive giant squid, <i>Architeuthis dux</i> . <i>GigaScience</i> , 2020 , 9,	7.6	17
167	A draft genome assembly of spotted hyena, <i>Crocuta crocuta</i> . <i>Scientific Data</i> , 2020 , 7, 126	8.2	2
166	Neuroprotectants attenuate hypobaric hypoxia-induced brain injuries in cynomolgus monkeys. <i>Zoological Research</i> , 2020 , 41, 3-19	3.4	5
165	High-quality chromosome-level genome assembly and full-length transcriptome analysis of the pharaoh ant <i>Monomorium pharaonis</i> . <i>GigaScience</i> , 2020 , 9,	7.6	3
164	Diverse coral reef invertebrates exhibit patterns of phyllosymbiosis. <i>ISME Journal</i> , 2020 , 14, 2211-2222	11.9	12
163	Evolutionary History, Genomic Adaptation to Toxic Diet, and Extinction of the Carolina Parakeet. <i>Current Biology</i> , 2020 , 30, 108-114.e5	6.3	16
162	An Indo-Pacific Humpback Dolphin Genome Reveals Insights into Chromosome Evolution and the Demography of a Vulnerable Species. <i>IScience</i> , 2020 , 23, 101640	6.1	8
161	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, <i>Homotherium latidens</i> . <i>Current Biology</i> , 2020 , 30, 5018-5025.e5	6.3	18
160	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. <i>Nature</i> , 2020 , 587, 246-251	50.4	53
159	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020 , 587, 252-257	50.4	89
158	Pre-extinction Demographic Stability and Genomic Signatures of Adaptation in the Woolly Rhinoceros. <i>Current Biology</i> , 2020 , 30, 3871-3879.e7	6.3	16

157	Multi-omic detection of in archaeological human dental calculus. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020 , 375, 20190584	5.8	13
156	The gene expression network regulating queen brain remodeling after insemination and its parallel use in ants with reproductive workers. <i>Science Advances</i> , 2020 , 6,	14.3	5
155	Hi-C chromosome conformation capture sequencing of avian genomes using the BGISEQ-500 platform. <i>GigaScience</i> , 2020 , 9,	7.6	2
154	High-coverage genomes to elucidate the evolution of penguins. <i>GigaScience</i> , 2019 , 8,	7.6	6
153	Mitogenomes Uncover Extinct Penguin Taxa and Reveal Island Formation as a Key Driver of Speciation. <i>Molecular Biology and Evolution</i> , 2019 , 36, 784-797	8.3	23
152	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. <i>Science</i> , 2019 , 364,	33.3	120
151	Genetic basis of ruminant headgear and rapid antler regeneration. <i>Science</i> , 2019 , 364,	33.3	61
150	Comparative study on pattern recognition receptors in non-teleost ray-finned fishes and their evolutionary significance in primitive vertebrates. <i>Science China Life Sciences</i> , 2019 , 62, 566-578	8.5	10
149	Dynamic evolutionary history and gene content of sex chromosomes across diverse songbirds. <i>Nature Ecology and Evolution</i> , 2019 , 3, 834-844	12.3	48
148	Genomic and transcriptomic investigations of the evolutionary transition from oviparity to viviparity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 3646-3655	11.5	21
147	Avian Binocularity and Adaptation to Nocturnal Environments: Genomic Insights from a Highly Derived Visual Phenotype. <i>Genome Biology and Evolution</i> , 2019 , 11, 2244-2255	3.9	6
146	31°South: The physiology of adaptation to arid conditions in a passerine bird. <i>Molecular Ecology</i> , 2019 , 28, 3709-3721	5.7	6
145	Comparative Phylogenomics, a Stepping Stone for Bird Biodiversity Studies. <i>Diversity</i> , 2019 , 11, 115	2.5	16
144	An integrated chromosome-scale genome assembly of the Masai giraffe (<i>Giraffa camelopardalis tippelskirchi</i>). <i>GigaScience</i> , 2019 , 8,	7.6	5
143	The Vertebrate TLR Supergene Family Evolved Dynamically by Gene Gain/Loss and Positive Selection Revealing a Host-Pathogen Arms Race in Birds. <i>Diversity</i> , 2019 , 11, 131	2.5	9
142	Chromosomal level assembly and population sequencing of the Chinese tree shrew genome. <i>Zoological Research</i> , 2019 , 40, 506-521	3.4	31
141	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. <i>Genome Research</i> , 2019 , 29, 576-589	9.7	15
140	Identification and evolution of avian endogenous foamy viruses. <i>Virus Evolution</i> , 2019 , 5, vez049	3.7	6

139	Detoxification Genes Differ Between Cactus-, Fruit-, and Flower-Feeding <i>Drosophila</i> . <i>Journal of Heredity</i> , 2019 , 110, 80-91	2.4	9
138	Draft Genome Assembly and Population Genetics of an Agricultural Pollinator, the Solitary Alkali Bee (Halictidae:). <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 625-634	3.2	6
137	A near-chromosome-scale genome assembly of the gemsbok (<i>Oryx gazella</i>): an iconic antelope of the Kalahari desert. <i>GigaScience</i> , 2019 , 8,	7.6	34
136	The Genomic Footprints of the Fall and Recovery of the Crested Ibis. <i>Current Biology</i> , 2019 , 29, 340-349.e73	6.3	42
135	Draft genome of the milu (<i>Elaphurus davidianus</i>). <i>GigaScience</i> , 2018 , 7,	7.6	17
134	Earth BioGenome Project: Sequencing life for the future of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 4325-4333	11.5	334
133	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018 , 2, 659-668	12.3	64
132	Red fox genome assembly identifies genomic regions associated with tame and aggressive behaviours. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1479-1491	12.3	74
131	The genome of the golden apple snail <i>Pomacea canaliculata</i> provides insight into stress tolerance and invasive adaptation. <i>GigaScience</i> , 2018 , 7,	7.6	32
130	Construction of Red Fox Chromosomal Fragments from the Short-Read Genome Assembly. <i>Genes</i> , 2018 , 9,	4.2	8
129	Genomic Takeover by Transposable Elements in the Strawberry Poison Frog. <i>Molecular Biology and Evolution</i> , 2018 , 35, 2913-2927	8.3	27
128	The bird@-eye view on chromosome evolution. <i>Genome Biology</i> , 2018 , 19, 201	18.3	6
127	Towards reconstructing the ancestral brain gene-network regulating caste differentiation in ants. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1782-1791	12.3	23
126	The first AsiaEvo conference, connecting Asian evolutionary biologists to the world. <i>National Science Review</i> , 2018 , 5, 614-616	10.8	1
125	Functional roles of Aves class-specific cis-regulatory elements on macroevolution of bird-specific features. <i>Nature Communications</i> , 2017 , 8, 14229	17.4	44
124	The genome and transcriptome of Japanese flounder provide insights into flatfish asymmetry. <i>Nature Genetics</i> , 2017 , 49, 119-124	36.3	133
123	Sequencing, de novo assembling, and annotating the genome of the endangered Chinese crocodile lizard <i>Shinisaurus crocodilurus</i> . <i>GigaScience</i> , 2017 , 6, 1-6	7.6	15
122	Constrained vertebrate evolution by pleiotropic genes. <i>Nature Ecology and Evolution</i> , 2017 , 1, 1722-1730	12.3	48

121	A soft selective sweep during rapid evolution of gentle behaviour in an Africanized honeybee. <i>Nature Communications</i> , 2017 , 8, 1550	17.4	16
120	Genome sequence of a diabetes-prone rodent reveals a mutation hotspot around the ParaHox gene cluster. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 7677-7682	11.5	20
119	Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. <i>GigaScience</i> , 2017 , 6, 1-13	7.6	88
118	Draft genome of the Marco Polo Sheep (<i>Ovis ammon polii</i>). <i>GigaScience</i> , 2017 , 6, 1-7	7.6	15
117	Reciprocal genomic evolution in the ant-fungus agricultural symbiosis. <i>Nature Communications</i> , 2016 , 7, 12233	17.4	74
116	Evolutionary trajectories of snake genes and genomes revealed by comparative analyses of five-pacer viper. <i>Nature Communications</i> , 2016 , 7, 13107	17.4	50
115	RES-Scanner: a software package for genome-wide identification of RNA-editing sites. <i>GigaScience</i> , 2016 , 5, 37	7.6	33
114	Draft genome of the leopard gecko, <i>Eublepharis macularius</i> . <i>GigaScience</i> , 2016 , 5, 47	7.6	32
113	Whole-Genome Identification, Phylogeny, and Evolution of the Cytochrome P450 Family 2 (CYP2) Subfamilies in Birds. <i>Genome Biology and Evolution</i> , 2016 , 8, 1115-31	3.9	15
112	Bone-associated gene evolution and the origin of flight in birds. <i>BMC Genomics</i> , 2016 , 17, 371	4.5	5
111	The genome of the largest bony fish, ocean sunfish (<i>Mola mola</i>), provides insights into its fast growth rate. <i>GigaScience</i> , 2016 , 5, 36	7.6	23
110	Avianbase: a community resource for bird genomics. <i>Genome Biology</i> , 2015 , 16, 21	18.3	22
109	Whole-genome sequence of the Tibetan frog <i>Nanorana parkeri</i> and the comparative evolution of tetrapod genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E1257-62	11.5	122
108	Olfactory Receptor Subgenomes Linked with Broad Ecological Adaptations in Sauropsida. <i>Molecular Biology and Evolution</i> , 2015 , 32, 2832-43	8.3	47
107	A genomic comparison of two termites with different social complexity. <i>Frontiers in Genetics</i> , 2015 , 6, 9	4.5	36
106	Temporal Dynamics of Avian Populations during Pleistocene Revealed by Whole-Genome Sequences. <i>Current Biology</i> , 2015 , 25, 1375-80	6.3	135
105	Phylogenomic analyses data of the avian phylogenomics project. <i>GigaScience</i> , 2015 , 4, 4	7.6	54
104	The Genome of <i>Dendrobium officinale</i> Illuminates the Biology of the Important Traditional Chinese Orchid Herb. <i>Molecular Plant</i> , 2015 , 8, 922-34	14.4	145

103	Social evolution. Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 2015 , 348, 1139-43	33.3	256
102	Response to Comment on "Whole-genome analyses resolve early branches in the tree of life of modern birds". <i>Science</i> , 2015 , 349, 1460	33.3	37
101	Reference genome of wild goat (<i>capra aegagrus</i>) and sequencing of goat breeds provide insight into genic basis of goat domestication. <i>BMC Genomics</i> , 2015 , 16, 431	4.5	60
100	Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies. <i>Nature Communications</i> , 2015 , 6, 8212	17.4	111
99	Ancient population genomics and the study of evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015 , 370, 20130381	5.8	14
98	High-coverage sequencing and annotated assembly of the genome of the Australian dragon lizard <i>Pogona vitticeps</i> . <i>GigaScience</i> , 2015 , 4, 45	7.6	70
97	Gene loss, adaptive evolution and the co-evolution of plumage coloration genes with opsins in birds. <i>BMC Genomics</i> , 2015 , 16, 751	4.5	37
96	Genomics: Bird sequencing project takes off. <i>Nature</i> , 2015 , 522, 34	50.4	97
95	Improving the ostrich genome assembly using optical mapping data. <i>GigaScience</i> , 2015 , 4, 24	7.6	22
94	Genomic legacy of the African cheetah, <i>Acinonyx jubatus</i> . <i>Genome Biology</i> , 2015 , 16, 277	18.3	99
93	The genome of the clonal raider ant <i>Cerapachys biroi</i> . <i>Current Biology</i> , 2014 , 24, 451-8	6.3	110
92	Population genomics reveal recent speciation and rapid evolutionary adaptation in polar bears. <i>Cell</i> , 2014 , 157, 785-94	56.2	242
91	Epigenetic modification and inheritance in sexual reversal of fish. <i>Genome Research</i> , 2014 , 24, 604-15	9.7	244
90	Caste-specific RNA editomes in the leaf-cutting ant <i>Acromyrmex echinatior</i> . <i>Nature Communications</i> , 2014 , 5, 4943	17.4	41
89	High-coverage sequencing and annotated assemblies of the budgerigar genome. <i>GigaScience</i> , 2014 , 3, 11	7.6	67
88	Complementary symbiont contributions to plant decomposition in a fungus-farming termite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 14500-5	11.5	163
87	Turtle ghrelin. <i>Nature Genetics</i> , 2014 , 46, 526	36.3	
86	Molecular traces of alternative social organization in a termite genome. <i>Nature Communications</i> , 2014 , 5, 3636	17.4	250

85	Evolutionary genomics and adaptive evolution of the Hedgehog gene family (Shh, Ihh and Dhh) in vertebrates. <i>PLoS ONE</i> , 2014 , 9, e74132	3.7	18
84	Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. <i>Nature Communications</i> , 2014 , 5, 5594	17.4	89
83	Dynamic evolution of the alpha (α) and beta (β) keratins has accompanied integument diversification and the adaptation of birds into novel lifestyles. <i>BMC Evolutionary Biology</i> , 2014 , 14, 249	3	66
82	Genomic signatures of near-extinction and rebirth of the crested ibis and other endangered bird species. <i>Genome Biology</i> , 2014 , 15, 557	18.3	56
81	Temporal genomic evolution of bird sex chromosomes. <i>BMC Evolutionary Biology</i> , 2014 , 14, 250	3	31
80	Low frequency of paleoviral infiltration across the avian phylogeny. <i>Genome Biology</i> , 2014 , 15, 539	18.3	43
79	Whole-genome sequence of a flatfish provides insights into ZW sex chromosome evolution and adaptation to a benthic lifestyle. <i>Nature Genetics</i> , 2014 , 46, 253-60	36.3	509
78	The locust genome provides insight into swarm formation and long-distance flight. <i>Nature Communications</i> , 2014 , 5, 2957	17.4	294
77	Convergent transcriptional specializations in the brains of humans and song-learning birds. <i>Science</i> , 2014 , 346, 1256846	33.3	283
76	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014 , 346, 1254449	33.3	231
75	Evidence for a single loss of mineralized teeth in the common avian ancestor. <i>Science</i> , 2014 , 346, 1254390	33.3	74
74	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014 , 346, 1320-31	33.3	1182
73	Avian genomes. A flock of genomes. Introduction. <i>Science</i> , 2014 , 346, 1308-9	33.3	39
72	Complex evolutionary trajectories of sex chromosomes across bird taxa. <i>Science</i> , 2014 , 346, 1246338	33.3	184
71	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014 , 346, 1311-20	33.3	628
70	Adaptations to a subterranean environment and longevity revealed by the analysis of mole rat genomes. <i>Cell Reports</i> , 2014 , 8, 1354-64	10.6	124
69	Comparative genomic data of the Avian Phylogenomics Project. <i>GigaScience</i> , 2014 , 3, 26	7.6	91
68	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. <i>GigaScience</i> , 2014 , 3, 27	7.6	50

67	Sensory rewiring in an echolocator: genome-wide modification of retinogenic and auditory genes in the bat <i>Myotis davidii</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 1825-35	3.2	5
66	Advances in genome editing technology and its promising application in evolutionary and ecological studies. <i>GigaScience</i> , 2014 , 3, 24	7.6	32
65	A flock of genomes. <i>Science</i> , 2014 , 346, 1308-1309	33.3	19
64	Comparative genomics of parasitic silkworm microsporidia reveal an association between genome expansion and host adaptation. <i>BMC Genomics</i> , 2013 , 14, 186	4.5	105
63	Genome analysis reveals insights into physiology and longevity of the Brandt's bat <i>Myotis brandtii</i> . <i>Nature Communications</i> , 2013 , 4, 2212	17.4	160
62	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra hircus</i>). <i>Nature Biotechnology</i> , 2013 , 31, 135-41	44.5	355
61	Comparative methylomics between domesticated and wild silkworms implies possible epigenetic influences on silkworm domestication. <i>BMC Genomics</i> , 2013 , 14, 646	4.5	35
60	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013 , 2, 10	7.6	461
59	Genome of the Chinese tree shrew. <i>Nature Communications</i> , 2013 , 4, 1426	17.4	230
58	Comparative analysis of bat genomes provides insight into the evolution of flight and immunity. <i>Science</i> , 2013 , 339, 456-60	33.3	377
57	Room-temperature synthesis and electrocatalysis of carbon nanotubes supported palladium-iron alloy nanoparticles. <i>Electrochimica Acta</i> , 2013 , 111, 898-902	6.7	6
56	Deep parallel sequencing reveals conserved and novel miRNAs in gill and hepatopancreas of giant freshwater prawn. <i>Fish and Shellfish Immunology</i> , 2013 , 35, 1061-9	4.3	20
55	The genomic consequences of adaptive divergence and reproductive isolation between species of manakins. <i>Molecular Ecology</i> , 2013 , 22, 3304-17	5.7	83
54	Genomic diversity and evolution of the head crest in the rock pigeon. <i>Science</i> , 2013 , 339, 1063-7	33.3	169
53	The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. <i>Nature Genetics</i> , 2013 , 45, 701-706	36.3	299
52	Recalibrating <i>Equus</i> evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013 , 499, 74-8	50.4	563
51	Genome of <i>Drosophila suzukii</i> , the spotted wing drosophila. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 2257-71	3.7	83
50	The i5K Initiative: advancing arthropod genomics for knowledge, human health, agriculture, and the environment. <i>Journal of Heredity</i> , 2013 , 104, 595-600	2.4	253

49	Draft genome sequence of the Tibetan antelope. <i>Nature Communications</i> , 2013 , 4, 1858	17.4	162
48	Reference-assisted chromosome assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 1785-90	11.5	96
47	The draft genome of a socially polymorphic halictid bee, <i>Lasioglossum albipes</i> . <i>Genome Biology</i> , 2013 , 14, R142	18.3	58
46	In-depth transcriptomic analysis on giant freshwater prawns. <i>PLoS ONE</i> , 2013 , 8, e60839	3.7	26
45	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012 , 491, 393-8	50.4	928
44	The half-life of DNA in bone: measuring decay kinetics in 158 dated fossils. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012 , 279, 4724-33	4.4	331
43	Synthesis and Electrocatalytic Properties of Palladium Network Nanostructures. <i>ChemPlusChem</i> , 2012 , 77, 936-940	2.8	26
42	Deciphering neo-sex and B chromosome evolution by the draft genome of <i>Drosophila albomicans</i> . <i>BMC Genomics</i> , 2012 , 13, 109	4.5	59
41	Single-base resolution maps of cultivated and wild rice methylomes and regulatory roles of DNA methylation in plant gene expression. <i>BMC Genomics</i> , 2012 , 13, 300	4.5	202
40	The sequence and analysis of a Chinese pig genome. <i>GigaScience</i> , 2012 , 1, 16	7.6	91
39	The oyster genome reveals stress adaptation and complexity of shell formation. <i>Nature</i> , 2012 , 490, 49-54	50.4	1464
38	Genome-wide and caste-specific DNA methylomes of the ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Current Biology</i> , 2012 , 22, 1755-64	6.3	266
37	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012 , 44, 221-5	36.3	325
36	Transcriptome and network changes in climbers at extreme altitudes. <i>PLoS ONE</i> , 2012 , 7, e31645	3.7	16
35	The yak genome and adaptation to life at high altitude. <i>Nature Genetics</i> , 2012 , 44, 946-9	36.3	472
34	Adaptive diversity of innate immune receptor family short pentraxins in Murinae. <i>FEBS Letters</i> , 2012 , 586, 798-803	3.8	3
33	Cephalopod genomics: A plan of strategies and organization. <i>Standards in Genomic Sciences</i> , 2012 , 7, 175-88		40
32	An effort to use human-based exome capture methods to analyze chimpanzee and macaque exomes. <i>PLoS ONE</i> , 2012 , 7, e40637	3.7	24

31	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2011 , 30, 105-11	44.5	635
30	Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques. <i>Nature Biotechnology</i> , 2011 , 29, 1019-23	44.5	219
29	Cross-comparison of the genome sequences from human, chimpanzee, Neanderthal and a Denisovan hominin identifies novel potentially compensated mutations. <i>Human Genomics</i> , 2011 , 5, 453-84	6.8	3
28	Genome sequencing reveals insights into physiology and longevity of the naked mole rat. <i>Nature</i> , 2011 , 479, 223-7	50.4	410
27	<i>Ascaris suum</i> draft genome. <i>Nature</i> , 2011 , 479, 529-33	50.4	217
26	Preparation of PdAu/C catalysts with different alloying degree and their electrocatalytic performance for formic acid oxidation. <i>Applied Catalysis B: Environmental</i> , 2011 , 102, 614-619	21.8	140
25	The genome of the leaf-cutting ant <i>Acromyrmex echinatior</i> suggests key adaptations to advanced social life and fungus farming. <i>Genome Research</i> , 2011 , 21, 1339-48	9.7	183
24	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010 , 463, 311-7	50.4	864
23	Single base-resolution methylome of the silkworm reveals a sparse epigenomic map. <i>Nature Biotechnology</i> , 2010 , 28, 516-20	44.5	288
22	Genomic comparison of the ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Science</i> , 2010 , 329, 1068-71	33.3	353
21	Deep RNA sequencing at single base-pair resolution reveals high complexity of the rice transcriptome. <i>Genome Research</i> , 2010 , 20, 646-54	9.7	375
20	A young <i>Drosophila</i> duplicate gene plays essential roles in spermatogenesis by regulating several Y-linked male fertility genes. <i>PLoS Genetics</i> , 2010 , 6, e1001255	6	51
19	Triangulation of the human, chimpanzee, and Neanderthal genome sequences identifies potentially compensated mutations. <i>Human Mutation</i> , 2010 , 31, 1286-93	4.7	12
18	Complete resequencing of 40 genomes reveals domestication events and genes in silkworm (<i>Bombyx</i>). <i>Science</i> , 2009 , 326, 433-6	33.3	277
17	The genome of the cucumber, <i>Cucumis sativus</i> L. <i>Nature Genetics</i> , 2009 , 41, 1275-81	36.3	1031
16	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008 , 456, 60-5	50.4	744
15	On the origin of new genes in <i>Drosophila</i> . <i>Genome Research</i> , 2008 , 18, 1446-55	9.7	191
14	Identification and characterization of insect-specific proteins by genome data analysis. <i>BMC Genomics</i> , 2007 , 8, 93	4.5	33

- 13 High rate of chimeric gene origination by retroposition in plant genomes. *Plant Cell*, **2006**, 18, 1791-802 11.6 183
- 12 A draft genome assembly of the eastern banjo frog *Limnodynastes dumerilii dumerilii* (Anura: Limnodynastidae)
- 11 A draft genome assembly of the eastern banjo frog *Limnodynastes dumerilii dumerilii* (Anura: Limnodynastidae). *GigaByte*, 2020, 1-13 2
- 10 Repetitive element annotation for the eastern banjo frog genome assembly v3 2
- 9 Tracing the origin of a new organ by inferring the genetic basis of rumen evolution 1
- 8 Historical population declines prompted significant genomic erosion in the northern and southern white rhinoceros (*Ceratotherium simum*) 1
- 7 Towards complete and error-free genome assemblies of all vertebrate species 38
- 6 From egg to adult: a developmental table of the ant *Monomorium pharaonis* 1
- 5 Identification and evolution of avian endogenous foamy viruses 1
- 4 Progressive alignment with Cactus: a multiple-genome aligner for the thousand-genome era 15
- 3 Phylogeny, transposable element and sex chromosome evolution of the basal lineage of birds 5
- 2 False gene and chromosome losses affected by assembly and sequence errors 3
- 1 Automated assembly of high-quality diploid human reference genomes 3