

List of Publications by Citations

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

43
papers

4,991
citations

28
h-index

48
g-index

48
ext. papers

6,540
ext. citations

15.3
avg, IF

4.27
L-index

#	Paper	IF	Citations
43	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014 , 346, 1311-20	33.3	628
42	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
41	Genome sequencing reveals insights into physiology and longevity of the naked mole rat. <i>Nature</i> , 2011 , 479, 223-7	50.4	410
40	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
39	Genomic comparison of the ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Science</i> , 2010 , 329, 1068-71	33.3	353
38	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
37	The locust genome provides insight into swarm formation and long-distance flight. <i>Nature Communications</i> , 2014 , 5, 2957	17.4	294
36	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
35	Epigenetic modification and inheritance in sexual reversal of fish. <i>Genome Research</i> , 2014 , 24, 604-15	9.7	244
34	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
33	Stable recombination hotspots in birds. <i>Science</i> , 2015 , 350, 928-32	33.3	187
32	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
31	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. <i>Science</i> , 2019 , 364,	33.3	120
30	Genomic Analyses Reveal Potential Independent Adaptation to High Altitude in Tibetan Chickens. <i>Molecular Biology and Evolution</i> , 2015 , 32, 1880-9	8.3	114
29	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020 , 587, 252-257	50.4	89
28	Genetic blueprint of the zoonotic pathogen <i>Toxocara canis</i> . <i>Nature Communications</i> , 2015 , 6, 6145	17.4	77
27	Genome-wide and single-base resolution DNA methylomes of the Pacific oyster <i>Crassostrea gigas</i> provide insight into the evolution of invertebrate CpG methylation. <i>BMC Genomics</i> , 2014 , 15, 1119	4.5	72

26	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
25	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
24	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
23	Caste-specific RNA editomes in the leaf-cutting ant <i>Acromyrmex echinatior</i> . <i>Nature Communications</i> , 2014 , 5, 4943	17.4	41
22	Comparative methylomics between domesticated and wild silkworms implies possible epigenetic influences on silkworm domestication. <i>BMC Genomics</i> , 2013 , 14, 646	4.5	35
21	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
20	RES-Scanner: a software package for genome-wide identification of RNA-editing sites. <i>GigaScience</i> , 2016 , 5, 37	7.6	33
19	Draft genome of the leopard gecko, <i>Eublepharis macularius</i> . <i>GigaScience</i> , 2016 , 5, 47	7.6	32
18	Advances in genome editing technology and its promising application in evolutionary and ecological studies. <i>GigaScience</i> , 2014 , 3, 24	7.6	32
17	A draft genome assembly of the solar-powered sea slug <i>Elysia chlorotica</i> . <i>Scientific Data</i> , 2019 , 6, 190023.2	8.2	30
16	Platypus and echidna genomes reveal mammalian biology and evolution. <i>Nature</i> , 2021 , 592, 756-762	50.4	28
15	Anchoring genome sequence to chromosomes of the central bearded dragon (<i>Pogona vitticeps</i>) enables reconstruction of ancestral squamate macrochromosomes and identifies sequence content of the Z chromosome. <i>BMC Genomics</i> , 2016 , 17, 447	4.5	24
14	Transcriptome of Gonads From High Temperature Induced Sex Reversal During Sex Determination and Differentiation in Chinese Tongue Sole,. <i>Frontiers in Genetics</i> , 2019 , 10, 1128	4.5	23
13	RED-ML: a novel, effective RNA editing detection method based on machine learning. <i>GigaScience</i> , 2017 , 6, 1-8	7.6	19
12	A draft genome sequence of the elusive giant squid, <i>Architeuthis dux</i> . <i>GigaScience</i> , 2020 , 9,	7.6	17
11	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
10	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
9	Computation-assisted SiteFinding- PCR for isolating flanking sequence tags in rice. <i>BioTechniques</i> , 2011 , 51, 421-3	2.5	8

8	An integrated chromosome-scale genome assembly of the Masai giraffe (<i>Giraffa camelopardalis tippelskirchi</i>). <i>GigaScience</i> , 2019 , 8,	7.6	5
7	Limits to the cellular control of sequestered cryptophyte prey in the marine ciliate <i>Mesodinium rubrum</i> . <i>ISME Journal</i> , 2021 , 15, 1056-1072	11.9	5
6	Chromatin accessibility and transcriptome landscapes of <i>Monomorium pharaonis</i> brain. <i>Scientific Data</i> , 2020 , 7, 217	8.2	4
5	A draft genome assembly of spotted hyena, <i>Crocuta crocuta</i> . <i>Scientific Data</i> , 2020 , 7, 126	8.2	2
4	A draft genome assembly of the eastern banjo frog <i>Limnodynastes dumerilii dumerilii</i> (Anura: Limnodynastidae). <i>GigaByte</i> , 2020, 1-13		2
3	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
2	A draft genome assembly of the eastern banjo frog <i>Limnodynastes dumerilii dumerilii</i> (Anura: Limnodynastidae)		
1	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