Qiye Li

List of Publications by Year in Descending Order

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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.

papers	citations	h-index	g-index
43	4,991	28	48

ext. papers	ext. citations	avg, IF	L-index
48	6,540	15.3	4.27

#	Paper	IF	Citations
43	Labour classified by cervical dilatation & fetal membrane rupture demonstrates differential impact on RNA-seq data for human myometrium tissues. *PLoS ONE*, **2021**, 16, e0260119	3.7	0
42	Limits to the cellular control of sequestered cryptophyte prey in the marine ciliate Mesodinium rubrum. *ISME Journal*, **2021**, 15, 1056-1072	11.9	5
41	Platypus and echidna genomes reveal mammalian biology and evolution. *Nature*, **2021**, 592, 756-762	50.4	28
40	A novel method for using RNA-seq data to identify imprinted genes in social Hymenoptera with multiply mated queens. *Journal of Evolutionary Biology*, **2020**, 33, 1770-1782	2.3	1
39	Chromatin accessibility and transcriptome landscapes of Monomorium pharaonis brain. *Scientific Data*, **2020**, 7, 217	8.2	4
38	A draft genome sequence of the elusive giant squid, Architeuthis dux. *GigaScience*, **2020**, 9,	7.6	17
37	A draft genome assembly of spotted hyena, Crocuta crocuta. *Scientific Data*, **2020**, 7, 126	8.2	2
36	Dense sampling of bird diversity increases power of comparative genomics. *Nature*, **2020**, 587, 252-257	50.4	89
35	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. *Science*, **2019**, 364,	33.3	120
34	An integrated chromosome-scale genome assembly of the Masai giraffe (Giraffa camelopardalis tippelskirchi). *GigaScience*, **2019**, 8,	7.6	5
33	A draft genome assembly of the solar-powered sea slug Elysia chlorotica. *Scientific Data*, **2019**, 6, 190022	8.2	30
32	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. *Genome Research*, **2019**, 29, 576-589	9.7	15
31	Transcriptome of Gonads From High Temperature Induced Sex Reversal During Sex Determination and Differentiation in Chinese Tongue Sole,. *Frontiers in Genetics*, **2019**, 10, 1128	4.5	23
30	A near-chromosome-scale genome assembly of the gemsbok (Oryx gazella): an iconic antelope of the Kalahari desert. *GigaScience*, **2019**, 8,	7.6	34
29	Sequencing, de novo assembling, and annotating the genome of the endangered Chinese crocodile lizard Shinisaurus crocodilurus. *GigaScience*, **2017**, 6, 1-6	7.6	15
28	RED-ML: a novel, effective RNA editing detection method based on machine learning. *GigaScience*, **2017**, 6, 1-8	7.6	19
27	RES-Scanner: a software package for genome-wide identification of RNA-editing sites. *GigaScience*, **2016**, 5, 37	7.6	33

26	Draft genome of the leopard gecko, Eublepharis macularius. *GigaScience*, **2016**, 5, 47	7.6	32
25	Anchoring genome sequence to chromosomes of the central bearded dragon (Pogona vitticeps) enables reconstruction of ancestral squamate macrochromosomes and identifies sequence content of the Z chromosome. *BMC Genomics*, **2016**, 17, 447	4.5	24
24	Genetic blueprint of the zoonotic pathogen Toxocara canis. *Nature Communications*, **2015**, 6, 6145	17.4	77
23	The Genome of Dendrobium officinale Illuminates the Biology of the Important Traditional Chinese Orchid Herb. *Molecular Plant*, **2015**, 8, 922-34	14.4	145
22	Genomic Analyses Reveal Potential Independent Adaptation to High Altitude in Tibetan Chickens. *Molecular Biology and Evolution*, **2015**, 32, 1880-9	8.3	114
21	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	4.5	60
20	Stable recombination hotspots in birds. *Science*, **2015**, 350, 928-32	33.3	187
19	High-coverage sequencing and annotated assembly of the genome of the Australian dragon lizard Pogona vitticeps. *GigaScience*, **2015**, 4, 45	7.6	70
18	Epigenetic modification and inheritance in sexual reversal of fish. *Genome Research*, **2014**, 24, 604-15	9.7	244
17	Caste-specific RNA editomes in the leaf-cutting ant Acromyrmex echinatior. *Nature Communications* , **2014**, 5, 4943	17.4	41
16	Whole-genome sequence of a flatfish provides insights into ZW sex chromosome evolution and adaptation to a benthic lifestyle. *Nature Genetics*, **2014**, 46, 253-60	36.3	509
15	The locust genome provides insight into swarm formation and long-distance flight. *Nature Communications*, **2014**, 5, 2957	17.4	294
14	Comparative genomics reveals insights into avian genome evolution and adaptation. *Science*, **2014**, 346, 1311-20	33.3	628
13	Genome-wide and single-base resolution DNA methylomes of the Pacific oyster Crassostrea gigas provide insight into the evolution of invertebrate CpG methylation. *BMC Genomics*, **2014**, 15, 1119	4.5	72
12	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. *GigaScience*, **2014**, 3, 27	7.6	50
11	Advances in genome editing technology and its promising application in evolutionary and ecological studies. *GigaScience*, **2014**, 3, 24	7.6	32
10	Comparative methylomics between domesticated and wild silkworms implies possible epigenetic influences on silkworm domestication. *BMC Genomics*, **2013**, 14, 646	4.5	35
9	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	36.3	299

8	Genome-wide and caste-specific DNA methylomes of the ants Camponotus floridanus and Harpegnathos saltator. *Current Biology*, **2012**, 22, 1755-64	6.3	266
7	Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques. *Nature Biotechnology*, **2011**, 29, 1019-23	44.5	219
6	Computation-assisted SiteFinding- PCR for isolating flanking sequence tags in rice. *BioTechniques*, **2011**, 51, 421-3	2.5	8
5	Genome sequencing reveals insights into physiology and longevity of the naked mole rat. *Nature*, **2011**, 479, 223-7	50.4	410
4	Genomic comparison of the ants Camponotus floridanus and Harpegnathos saltator. *Science*, **2010**, 329, 1068-71	33.3	353
3	Deep RNA sequencing at single base-pair resolution reveals high complexity of the rice transcriptome. *Genome Research*, **2010**, 20, 646-54	9.7	375
2	A draft genome assembly of the eastern banjo frog Limnodynastes dumerilii dumerilii (Anura: Limnodynastidae)		1
1	A draft genome assembly of the eastern banjo frog Limnodynastes dumerilii dumerilii (Anura: Limnodynastidae). *GigaByte*,2020, 1-13		2