

Qiye Li

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

7,339
citations

172457

29
h-index

265206

42
g-index

48
all docs

48
docs citations

48
times ranked

11438
citing authors

#	ARTICLE	IF	CITATIONS
1	A single-cell transcriptomic atlas tracking the neural basis of division of labour in an ant superorganism. <i>Nature Ecology and Evolution</i> , 2022, 6, 1191-1204.	7.8	15
2	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.	9.8	15
3	Platypus and echidna genomes reveal mammalian biology and evolution. <i>Nature</i> , 2021, 592, 756-762.	27.8	85
4	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.	2.5	1
5	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	27.8	251
6	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.	1.7	3
7	Chromatin accessibility and transcriptome landscapes of <i>Monomorium pharaonis</i> brain. <i>Scientific Data</i> , 2020, 7, 217.	5.3	10
8	A draft genome sequence of the elusive giant squid, <i>Architeuthis dux</i> . <i>GigaScience</i> , 2020, 9, .	6.4	37
9	A draft genome assembly of spotted hyena, <i>Crocuta crocuta</i> . <i>Scientific Data</i> , 2020, 7, 126.	5.3	6
10	An integrated chromosome-scale genome assembly of the Masai giraffe (<i>Giraffa camelopardalis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	6.4	13
11	A draft genome assembly of the solar-powered sea slug <i>Elysia chlorotica</i> . <i>Scientific Data</i> , 2019, 6, 190022.	5.3	48
12	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. <i>Science</i> , 2019, 364, .	12.6	266
13	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. <i>Genome Research</i> , 2019, 29, 576-589.	5.5	39
14	Transcriptome of Gonads From High Temperature Induced Sex Reversal During Sex Determination and Differentiation in Chinese Tongue Sole, <i>Cynoglossus semilaevis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 1128.	2.3	38
15	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, .	6.4	138
16	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.	6.4	23
17	RED-ML: a novel, effective RNA editing detection method based on machine learning. <i>GigaScience</i> , 2017, 6, 1-8.	6.4	29
18	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.	2.8	47

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19	RES-Scanner: a software package for genome-wide identification of RNA-editing sites. <i>GigaScience</i> , 2016, 5, 37.	6.4	55
20	Draft genome of the leopard gecko, <i>Eublepharis macularius</i> . <i>GigaScience</i> , 2016, 5, 47.	6.4	55
21	High-coverage sequencing and annotated assembly of the genome of the Australian dragon lizard <i>Pogona vitticeps</i> . <i>GigaScience</i> , 2015, 4, 45.	6.4	97
22	Genetic blueprint of the zoonotic pathogen <i>Toxocara canis</i> . <i>Nature Communications</i> , 2015, 6, 6145.	12.8	103
23	The Genome of <i>Dendrobium officinale</i> Illuminates the Biology of the Important Traditional Chinese Orchid Herb. <i>Molecular Plant</i> , 2015, 8, 922-934.	8.3	228
24	Genomic Analyses Reveal Potential Independent Adaptation to High Altitude in Tibetan Chickens. <i>Molecular Biology and Evolution</i> , 2015, 32, 1880-1889.	8.9	193
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.	2.8	103
26	Stable recombination hotspots in birds. <i>Science</i> , 2015, 350, 928-932.	12.6	280
27	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, 253-260.	21.4	685
28	The locust genome provides insight into swarm formation and long-distance flight. <i>Nature Communications</i> , 2014, 5, 2957.	12.8	437
29	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	12.6	895
30	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.	2.8	110
31	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. <i>GigaScience</i> , 2014, 3, 27.	6.4	72
32	Advances in genome editing technology and its promising application in evolutionary and ecological studies. <i>GigaScience</i> , 2014, 3, 24.	6.4	47
33	Epigenetic modification and inheritance in sexual reversal of fish. <i>Genome Research</i> , 2014, 24, 604-615.	5.5	356
34	Caste-specific RNA editomes in the leaf-cutting ant <i>Acromyrmex echinatior</i> . <i>Nature Communications</i> , 2014, 5, 4943.	12.8	60
35	Comparative methylomics between domesticated and wild silkworms implies possible epigenetic influences on silkworm domestication. <i>BMC Genomics</i> , 2013, 14, 646.	2.8	47
36	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.	21.4	409

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37	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, 1755-1764.	3.9	361
38	Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques. <i>Nature Biotechnology</i> , 2011, 29, 1019-1023.	17.5	284
39	Computation-assisted SiteFinding- PCR for isolating flanking sequence tags in rice. <i>BioTechniques</i> , 2011, 51, 421-423.	1.8	9
40	Genome sequencing reveals insights into physiology and longevity of the naked mole rat. <i>Nature</i> , 2011, 479, 223-227.	27.8	517
41	Genomic Comparison of the Ants <i>Camponotus floridanus</i> and <i>Harpegnathos saltator</i> . <i>Science</i> , 2010, 329, 1068-1071.	12.6	420
42	Deep RNA sequencing at single base-pair resolution reveals high complexity of the rice transcriptome. <i>Genome Research</i> , 2010, 20, 646-654.	5.5	435
43	A draft genome assembly of the eastern banjo frog <i>Limnodynastes dumerilii dumerilii</i> (Anura:Limnodynastidae). <i>GigaByte</i> , 0, 2020, 1-13.	0.0	8