

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Gene expression responses in zebrafish to short-term high-hydrostatic pressure. Zoological Research, 2022, 43, 188-191.	2.1	3
2	Ruminant-specific genes identified using high-quality genome data and their roles in rumen evolution. Science Bulletin, 2022, 67, 825-835.	9.0	3
3	Modes of genetic adaptations underlying functional innovations in the rumen. Science China Life Sciences, 2021, 64, 1-21.	4.9	19
4	Chromosomeâ€level genome assembly of <i>Paralithodes platypus</i> provides insights into evolution and adaptation of king crabs. Molecular Ecology Resources, 2021, 21, 511-525.	4.8	14
5	Chromosomeâ€level genome assembly of <i>Lethenteron reissneri</i> provides insights into lamprey evolution. Molecular Ecology Resources, 2021, 21, 448-463.	4.8	25
6	The Genomes of Two Billfishes Provide Insights into the Evolution of Endothermy in Teleosts. Molecular Biology and Evolution, 2021, 38, 2413-2427.	8.9	15
7	A towering genome: Experimentally validated adaptations to high blood pressure and extreme stature in the giraffe. Science Advances, 2021, 7, .	10.3	31
8	Tracing the genetic footprints of vertebrate landing in non-teleost ray-finned fishes. Cell, 2021, 184, 1377-1391.e14.	28.9	66
9	African lungfish genome sheds light on the vertebrate water-to-land transition. Cell, 2021, 184, 1362-1376.e18.	28.9	99
10	The genome of a new anemone species (Actiniaria: Hormathiidae) provides insights into deep-sea adaptation. Deep-Sea Research Part I: Oceanographic Research Papers, 2021, 170, 103492.	1.4	11
11	Structural Variants Selected during Yak Domestication Inferred from Long-Read Whole-Genome Sequencing. Molecular Biology and Evolution, 2021, 38, 3676-3680.	8.9	21
12	An integrated gene catalog and over 10,000 metagenome-assembled genomes from the gastrointestinal microbiome of ruminants. Microbiome, 2021, 9, 137.	11.1	110
13	Giraffa camelopardalis. Trends in Genetics, 2021, 37, 860-861.	6.7	0
14	Bacterial communities in the solid, liquid, dorsal, and ventral epithelium fractions of yak (<i>Bos) Tj ETQq0 0 0 rg</i>	BT /Overlo	pck_{43}^{10} Tf 50
15	Chromosome-level genome assembly reveals the unique genome evolution of the swimming crab (Portunus trituberculatus). GigaScience, 2020, 9,	6.4	44
16	Allele-aware chromosome-level genome assembly and efficient transgene-free genome editing for the autotetraploid cultivated alfalfa. Nature Communications, 2020, 11, 2494.	12.8	224

QIANG QIU

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19	The sequence and de novo assembly of the wild yak genome. Scientific Data, 2020, 7, 66.	5.3	16
20	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. Science, 2019, 364, .	12.6	266
21	Biological adaptations in the Arctic cervid, the reindeer (<i>Rangifer tarandus</i>). Science, 2019, 364,	12.6	58
22	Genetic basis of ruminant headgear and rapid antler regeneration. Science, 2019, 364, .	12.6	121
23	Identification of a molecular subtyping system associated with the prognosis of Asian hepatocellular carcinoma patients receiving liver resection. Scientific Reports, 2019, 9, 7073.	3.3	7
24	Effect of dietary energy on digestibilities, rumen fermentation, urinary purine derivatives and serum metabolites in Tibetan and smallâ€ŧailed Han sheep. Journal of Animal Physiology and Animal Nutrition, 2019, 103, 977-987.	2.2	6
25	Morphology and genome of a snailfish from the Mariana Trench provide insights into deep-sea adaptation. Nature Ecology and Evolution, 2019, 3, 823-833.	7.8	99
26	Chromosomal level reference genome of <i>Tachypleus tridentatus</i> provides insights into evolution and adaptation of horseshoe crabs. Molecular Ecology Resources, 2019, 19, 744-756.	4.8	25
27	Draft genome of the milu (Elaphurus davidianus). GigaScience, 2018, 7, .	6.4	22
28	Effect of supplemental dietary slowâ€release urea on growth performance and physiological status of dairy heifers. Animal Science Journal, 2018, 89, 966-971.	1.4	1
29	The completed chloroplast genome of Ostrya trichocarpa. Conservation Genetics Resources, 2018, 10, 579-581.	0.8	8
30	Complete mitochondrial genome of bovine species Gayal (Bos frontalis). Conservation Genetics Resources, 2018, 10, 889-891.	0.8	9
31	Incomplete lineage sorting rather than hybridization explains the inconsistent phylogeny of the wisent. Communications Biology, 2018, 1, 169.	4.4	84
32	Genome Sequence of the Freshwater Yangtze Finless Porpoise. Genes, 2018, 9, 213.	2.4	16
33	Postpartum oestrous cycling resumption of yak cows following different calf weaning strategies under range conditions. Animal Science Journal, 2018, 89, 1492-1503.	1.4	8
34	The genome sequence of the wisent (Bison bonasus). GigaScience, 2017, 6, 1-5.	6.4	22
35	Draft genome of the reindeer (Rangifer tarandus). GigaScience, 2017, 6, 1-5.	6.4	41
36	Draft genome of the Marco Polo Sheep (Ovis ammon polii). GigaScience, 2017, 6, 1-7.	6.4	25

QIANG QIU

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37	Genome-wide patterns of copy number variation in the Chinese yak genome. BMC Genomics, 2016, 17, 379.	2.8	66
38	Convergent Evolution of Rumen Microbiomes in High-Altitude Mammals. Current Biology, 2016, 26, 1873-1879.	3.9	281
39	Yak whole-genome resequencing reveals domestication signatures and prehistoric population expansions. Nature Communications, 2015, 6, 10283.	12.8	214
40	Comparative transcriptomic analysis revealed adaptation mechanism of Phrynocephalus erythrurus, the highest altitude Lizard living in the Qinghai-Tibet Plateau. BMC Evolutionary Biology, 2015, 15, 101.	3.2	50
41	Convergent evolution of SOCS4 between yak and Tibetan antelope in response to high-altitude stress. Gene, 2015, 572, 298-302.	2.2	15
42	Genomeâ€wide variation within and between wild and domestic yak. Molecular Ecology Resources, 2014, 14, 794-801.	4.8	40
43	Development and Characterization of EST-SSR Markers in Ostryopsis (Betulaceae). Applications in Plant Sciences, 2014, 2, 1300062.	2.1	4
44	The Yak genome database: an integrative database for studying yak biology and high-altitude adaption. BMC Genomics, 2012, 13, 600.	2.8	33
45	The yak genome and adaptation to life at high altitude. Nature Genetics, 2012, 44, 946-949.	21.4	708
46	Genome-scale transcriptome analysis of the desert poplar, Populus euphratica. Tree Physiology, 2011, 31, 452-461.	3.1	179
47	Isolation and characterization of microsatellite loci in Ostryopsis davidiana (Betulaceae). Conservation Genetics, 2009, 10, 751-753.	1.5	1

Phylogeographic analyses suggest that a deciduous species (<i>Ostryopsis davidiana</i> Decne.,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3.0 108 2009, 36, 2148-2155.