

Wen Wang

List of Publications by Year in descending order

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Version: 2024-02-01

120
papers

12,547
citations

71004

43
h-index

30277

107
g-index

129
all docs

129
docs citations

129
times ranked

17666
citing authors

#	ARTICLE	IF	CITATIONS
1	Ruminant-specific genes identified using high-quality genome data and their roles in rumen evolution. <i>Science Bulletin</i> , 2022, 67, 825-835.	4.3	3
2	High-quality reference genomes of swallowtail butterflies provide insights into their coloration evolution. <i>Zoological Research</i> , 2022, 43, 367-379.	0.9	6
3	Modes of genetic adaptations underlying functional innovations in the rumen. <i>Science China Life Sciences</i> , 2021, 64, 1-21.	2.3	19
4	Chromosome-level genome assembly of <i>Paralithodes platypus</i> provides insights into evolution and adaptation of king crabs. <i>Molecular Ecology Resources</i> , 2021, 21, 511-525.	2.2	14
5	Chromatin accessibility profiling provides insights into larval cuticle color and adult longevity in butterflies. <i>Zoological Research</i> , 2021, 42, 614-619.	0.9	5
6	The Genomes of Two Billfishes Provide Insights into the Evolution of Endothermy in Teleosts. <i>Molecular Biology and Evolution</i> , 2021, 38, 2413-2427.	3.5	15
7	The mitochondrial genome of one twisted-wing parasite <i>Xenos cf. moutoni</i> (Insecta, Strepsiptera). <i>Trends in Microbiology</i> , 2021, 29, 512-514.	0.2	2
8	Genome-wide identification and gene-editing of pigment transporter genes in the swallowtail butterfly <i>Papilio xuthus</i> . <i>BMC Genomics</i> , 2021, 22, 120.	1.2	7
9	A towering genome: Experimentally validated adaptations to high blood pressure and extreme stature in the giraffe. <i>Science Advances</i> , 2021, 7, .	4.7	31
10	Tracing the genetic footprints of vertebrate landing in non-teleost ray-finned fishes. <i>Cell</i> , 2021, 184, 1377-1391.e14.	13.5	66
11	African lungfish genome sheds light on the vertebrate water-to-land transition. <i>Cell</i> , 2021, 184, 1362-1376.e18.	13.5	99
12	Large-scale sequencing of flatfish genomes provides insights into the polyphyletic origin of their specialized body plan. <i>Nature Genetics</i> , 2021, 53, 742-751.	9.4	30
13	The genome of a new anemone species (Actiniaria: Hormathiidae) provides insights into deep-sea adaptation. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2021, 170, 103492.	0.6	11
14	Chromosome-level genome of Himalayan yew provides insights into the origin and evolution of the paclitaxel biosynthetic pathway. <i>Molecular Plant</i> , 2021, 14, 1199-1209.	3.9	46
15	Molecular cloning, characterization, and evolution analysis of the luciferase genes from three sympatric sibling fireflies (Lampyridae: Lampyrinae, Diaphanes). <i>Photochemical and Photobiological Sciences</i> , 2021, 20, 1053-1067.	1.6	3
16	<i>Giraffa camelopardalis</i> . <i>Trends in Genetics</i> , 2021, 37, 860-861.	2.9	0
17	The Elite Alleles of OsSPL4 Regulate Grain Size and Increase Grain Yield in Rice. <i>Rice</i> , 2021, 14, 90.	1.7	23
18	Molecular mechanisms and topological consequences of drastic chromosomal rearrangements of muntjac deer. <i>Nature Communications</i> , 2021, 12, 6858.	5.8	23

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19	Derivedness Index for Estimating Degree of Phenotypic Evolution of Embryos: A Study of Comparative Transcriptomic Analyses of Chordates and Echinoderms. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 749963.	1.8	3
20	Pattern of New Gene Origination in a Special Fish Lineage, the Flatfishes. <i>Genes</i> , 2021, 12, 1819.	1.0	2
21	Integrated Analysis of Transcriptome and Proteome to Reveal Pupal Color Switch in <i>Papilio xuthus</i> Butterflies. <i>Frontiers in Genetics</i> , 2021, 12, 795115.	1.1	1
22	Second Rhagophthalmid Luciferase Cloned from Chinese Glowworm <i>Menghuoius giganteus</i> (Rhagophthalmidae: Elateroidea). <i>Photochemistry and Photobiology</i> , 2020, 96, 46-54.	1.3	6
23	Chromosome-level genome assembly reveals the unique genome evolution of the swimming crab (<i>Portunus trituberculatus</i>). <i>GigaScience</i> , 2020, 9, .	3.3	44
24	Genome size variation in butterflies (Insecta, Lepidoptera, Papilionoidea): a thorough phylogenetic comparison. <i>Systematic Entomology</i> , 2020, 45, 571-582.	1.7	22
25	Convergent genomic signatures of high-altitude adaptation among domestic mammals. <i>National Science Review</i> , 2020, 7, 952-963.	4.6	52
26	Genomic and experimental data provide new insights into luciferin biosynthesis and bioluminescence evolution in fireflies. <i>Scientific Reports</i> , 2020, 10, 15882.	1.6	14
27	Genomic insights of body plan transitions from bilateral to pentameral symmetry in Echinoderms. <i>Communications Biology</i> , 2020, 3, 371.	2.0	34
28	Improved de novo Assembly of the Achlorophyllous Orchid <i>Gastrodia elata</i> . <i>Frontiers in Genetics</i> , 2020, 11, 580568.	1.1	11
29	Identification of Key Genes for the Ultrahigh Yield of Rice Using Dynamic Cross-tissue Network Analysis. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 256-270.	3.0	9
30	Comparison of the two up-to-date sequencing technologies for genome assembly: HiFi reads of Pacific Biosciences Sequel II system and ultralong reads of Oxford Nanopore. <i>GigaScience</i> , 2020, 9, .	3.3	90
31	The Draft Genome of Red Lechwe, <i>Kobus lechwe lechwe</i> . <i>Frontiers in Genetics</i> , 2020, 11, 582638.	1.1	0
32	Allele-aware chromosome-level genome assembly and efficient transgene-free genome editing for the autotetraploid cultivated alfalfa. <i>Nature Communications</i> , 2020, 11, 2494.	5.8	224
33	Chromosome-level reference genome assembly and gene editing of the dead-leaf butterfly <i>Kallima inachus</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 1080-1092.	2.2	22
34	De Novo Genome Assembly of Limpet <i>Bathycypraea lactea</i> (Gastropoda: Pectinodontidae): The First Reference Genome of a Deep-Sea Gastropod Endemic to Cold Seeps. <i>Genome Biology and Evolution</i> , 2020, 12, 905-910.	1.1	15
35	The origin of domestication genes in goats. <i>Science Advances</i> , 2020, 6, eaaz5216.	4.7	86
36	Neo-functionalization of a Teosinte branched 1 homologue mediates adaptations of upland rice. <i>Nature Communications</i> , 2020, 11, 725.	5.8	40

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37	Raising the production of phloretin by alleviation of by-product of chalcone synthase in the engineered yeast. <i>Science China Life Sciences</i> , 2020, 63, 1734-1743.	2.3	11
38	Demography and adaptation promoting evolutionary transitions in a mammalian genus that diversified during the Pleistocene. <i>Molecular Ecology</i> , 2020, 29, 2777-2792.	2.0	13
39	The genome assembly of asparagus bean, <i>Vigna unguiculata</i> ssp. <i>sesquipedialis</i> . <i>Scientific Data</i> , 2019, 6, 124.	2.4	18
40	Elimination of a Retrotransposon for Quenching Genome Instability in Modern Rice. <i>Molecular Plant</i> , 2019, 12, 1395-1407.	3.9	12
41	Phylogenetic analysis provides insights into the evolution of Asian fireflies and adult bioluminescence. <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106600.	1.2	24
42	Chromosomal-level reference genome of Chinese peacock butterfly (<i>Papilio bianor</i>) based on third-generation DNA sequencing and Hi-C analysis. <i>GigaScience</i> , 2019, 8, .	3.3	26
43	The mitochondrial genome of the first luminous click-beetle (<i>Coleoptera</i> : Elateridae) recorded in Asia. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 565-567.	0.2	5
44	Artificial selection on storage protein 1 possibly contributes to increase of hatchability during silkworm domestication. <i>PLoS Genetics</i> , 2019, 15, e1007616.	1.5	21
45	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. <i>Science</i> , 2019, 364, .	6.0	266
46	Biological adaptations in the Arctic cervid, the reindeer (<i>Rangifer tarandus</i>). <i>Science</i> , 2019, 364, .	6.0	58
47	Genetic basis of ruminant headgear and rapid antler regeneration. <i>Science</i> , 2019, 364, .	6.0	121
48	Constructing a synthetic pathway for acetyl-coenzyme A from one-carbon through enzyme design. <i>Nature Communications</i> , 2019, 10, 1378.	5.8	128
49	Cloning and Characterization of Luciferase from the Chinese Firefly <i>Lamprigera yunnana</i> . <i>Photochemistry and Photobiology</i> , 2019, 95, 1186-1194.	1.3	7
50	Morphology and genome of a snailfish from the Mariana Trench provide insights into deep-sea adaptation. <i>Nature Ecology and Evolution</i> , 2019, 3, 823-833.	3.4	99
51	The genomic basis for colonizing the freezing Southern Ocean revealed by Antarctic toothfish and Patagonian robalo genomes. <i>GigaScience</i> , 2019, 8, .	3.3	47
52	Chromosomal level reference genome of <i>Tachypleus tridentatus</i> provides insights into evolution and adaptation of horseshoe crabs. <i>Molecular Ecology Resources</i> , 2019, 19, 744-756.	2.2	25
53	Decrease of gene expression diversity during domestication of animals and plants. <i>BMC Evolutionary Biology</i> , 2019, 19, 19.	3.2	42
54	Complete mitochondrial genome sequence of the Przewalski's gazelle (<i>Procapra przewalskii</i>). <i>Conservation Genetics Resources</i> , 2019, 11, 369-371.	0.4	2

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55	Allele-specific expression and alternative splicing in horse \times monkey and cattle \times yak hybrids. <i>Zoological Research</i> , 2019, 40, 293-304.	0.9	18
56	Genomic insights into ruminant evolution: from past to future prospects. <i>Zoological Research</i> , 2019, 40, 476-487.	0.9	11
57	HMOD: An Omics Database for Herbal Medicine Plants. <i>Molecular Plant</i> , 2018, 11, 757-759.	3.9	22
58	Draft genome of the milu (<i>Elaphurus davidianus</i>). <i>GigaScience</i> , 2018, 7, .	3.3	22
59	Engineering yeast for the production of breviscapine by genomic analysis and synthetic biology approaches. <i>Nature Communications</i> , 2018, 9, 448.	5.8	146
60	Hagfish and lamprey Hox genes reveal conservation of temporal colinearity in vertebrates. <i>Nature Ecology and Evolution</i> , 2018, 2, 859-866.	3.4	55
61	Weighted gene co-expression network analysis reveals potential genes involved in early metamorphosis process in sea cucumber <i>Apostichopus japonicus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 1395-1402.	1.0	15
62	Application of protoplast technology to CRISPR/Cas9 mutagenesis: from single \times cell mutation detection to mutant plant regeneration. <i>Plant Biotechnology Journal</i> , 2018, 16, 1295-1310.	4.1	222
63	Population genomic data reveal genes related to important traits of quail. <i>GigaScience</i> , 2018, 7, .	3.3	38
64	The evolutionary road from wild moth to domestic silkworm. <i>Nature Ecology and Evolution</i> , 2018, 2, 1268-1279.	3.4	112
65	An intercross population study reveals genes associated with body size and plumage color in ducks. <i>Nature Communications</i> , 2018, 9, 2648.	5.8	167
66	Complete mitochondrial genome sequence of the mountain nyala (<i>Tragelaphus buxtoni</i>). <i>Conservation Genetics Resources</i> , 2018, 10, 547-550.	0.4	0
67	Unravelling miRNA regulation in yield of rice (<i>Oryza sativa</i>) based on differential network model. <i>Scientific Reports</i> , 2018, 8, 8498.	1.6	28
68	Whole-Genome Sequencing and Analysis of the Chinese Herbal Plant <i>Panax notoginseng</i> . <i>Molecular Plant</i> , 2017, 10, 899-902.	3.9	71
69	Draft genome of the gayal, <i>Bos frontalis</i> . <i>GigaScience</i> , 2017, 6, 1-7.	3.3	23
70	Genome-wide Target Enrichment-aided Chip Design: a 66 \times 10 ⁶ SNP Chip for Cashmere Goat. <i>Scientific Reports</i> , 2017, 7, 8621.	1.6	11
71	Identification of selection signals by large-scale whole-genome resequencing of cashmere goats. <i>Scientific Reports</i> , 2017, 7, 15142.	1.6	46
72	Genome editing in the butterfly type \times species <i>Papilio machaon</i> . <i>Insect Science</i> , 2017, 24, 708-711.	1.5	10

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73	Draft genome of the reindeer (<i>Rangifer tarandus</i>). <i>GigaScience</i> , 2017, 6, 1-5.	3.3	41
74	Draft genome of the Marco Polo Sheep (<i>Ovis ammon polii</i>). <i>GigaScience</i> , 2017, 6, 1-7.	3.3	25
75	14çŞèç«è™«(éž~ç;...ç»:èç\$)ăÿ°ă»„ăŞâ°çş„æµ«ă®š. <i>Zoological Research</i> , 2017, 38, 449-458.	0.9	15
76	Genome of Plant Maca (<i>Lepidium meyenii</i>) Illuminates Genomic Basis for High-Altitude Adaptation in the Central Andes. <i>Molecular Plant</i> , 2016, 9, 1066-1077.	3.9	69
77	Genomes and virulence difference between two physiological races of <i>Phytophthora nicotianae</i> . <i>GigaScience</i> , 2016, 5, 3.	3.3	49
78	Improved hybrid de novo genome assembly of domesticated apple (<i>Malus x domestica</i>). <i>GigaScience</i> , 2016, 5, 35.	3.3	56
79	Generation of biallelic knock-out sheep via gene-editing and somatic cell nuclear transfer. <i>Scientific Reports</i> , 2016, 6, 33675.	1.6	39
80	Systematic evaluation of sericin protein as a substitute for fetal bovine serum in cell culture. <i>Scientific Reports</i> , 2016, 6, 31516.	1.6	25
81	Molecular microevolution and epigenetic patterns of the long non-coding gene H19 show its potential function in pig domestication and breed divergence. <i>BMC Evolutionary Biology</i> , 2016, 16, 87.	3.2	13
82	Building a Genetic Manipulation Tool Box for Orchid Biology: Identification of Constitutive Promoters and Application of CRISPR/Cas9 in the Orchid, <i>Dendrobium officinale</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 2036.	1.7	102
83	Genetic Variation of Goat Interferon Regulatory Factor 3 Gene and Its Implication in Goat Evolution. <i>PLoS ONE</i> , 2016, 11, e0161962.	1.1	2
84	Advances and perspectives in the application of CRISPR/Cas9 in insects. <i>Zoological Research</i> , 2016, 37, 220-8.	0.6	14
85	Genome and Comparative Transcriptomics of African Wild Rice <i>Oryza longistaminata</i> Provide Insights into Molecular Mechanism of Rhizomatousness and Self-Incompatibility. <i>Molecular Plant</i> , 2015, 8, 1683-1686.	3.9	49
86	Single Base-Resolution Methylome of the Dizygotic Sheep. <i>PLoS ONE</i> , 2015, 10, e0142034.	1.1	5
87	Hybrid de novo genome assembly of the Chinese herbal plant danshen (<i>Salvia miltiorrhiza</i> Bunge). <i>GigaScience</i> , 2015, 4, 62.	3.3	73
88	Resequencing 302 wild and cultivated accessions identifies genes related to domestication and improvement in soybean. <i>Nature Biotechnology</i> , 2015, 33, 408-414.	9.4	1,023
89	COLD1 Confers Chilling Tolerance in Rice. <i>Cell</i> , 2015, 160, 1209-1221.	13.5	724
90	Comparative transcriptome analyses on silk glands of six silkmths imply the genetic basis of silk structure and coloration. <i>BMC Genomics</i> , 2015, 16, 203.	1.2	24

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91	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.	3.9	228
92	Genomic Analyses Reveal Potential Independent Adaptation to High Altitude in Tibetan Chickens. <i>Molecular Biology and Evolution</i> , 2015, 32, 1880-1889.	3.5	193
93	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.	1.2	103
94	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015, 16, 538.	1.2	86
95	Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies. <i>Nature Communications</i> , 2015, 6, 8212.	5.8	146
96	Design and Characterization of a 52K SNP Chip for Goats. <i>PLoS ONE</i> , 2014, 9, e86227.	1.1	220
97	Advances in genome editing technology and its promising application in evolutionary and ecological studies. <i>GigaScience</i> , 2014, 3, 24.	3.3	47
98	Heterotrimeric G proteins regulate nitrogen-use efficiency in rice. <i>Nature Genetics</i> , 2014, 46, 652-656.	9.4	338
99	A genomic perspective on the important genetic mechanisms of upland adaptation of rice. <i>BMC Plant Biology</i> , 2014, 14, 160.	1.6	39
100	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	6.0	436
101	Pleiotropy of the de novo-originated gene MDF1. <i>Scientific Reports</i> , 2014, 4, 7280.	1.6	28
102	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra</i>)	9.4	479
103	Origins of New Genes and Evolution of Their Novel Functions. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2012, 43, 345-363.	3.8	75
104	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2012, 30, 105-111.	9.4	818
105	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	13.7	1,058
106	Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm (<i>Bombyx mori</i>)	6.0	342
107	Neo-sex chromosomes in the black muntjac recapitulate incipient evolution of mammalian sex chromosomes. <i>Genome Biology</i> , 2008, 9, R98.	13.9	36
108	High Rate of Chimeric Gene Origination by Retroposition in Plant Genomes. <i>Plant Cell</i> , 2006, 18, 1791-1802.	3.1	207

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109	Detecting lineage-specific adaptive evolution of brain-expressed genes in human using rhesus macaque as outgroup. <i>Genomics</i> , 2006, 88, 745-751.	1.3	111
110	The Genomes of <i>Oryza sativa</i> : A History of Duplications. <i>PLoS Biology</i> , 2005, 3, e38.	2.6	808
111	Origin and evolution of new exons in rodents. <i>Genome Research</i> , 2005, 15, 1258-1264.	2.4	91
112	Duplication-degeneration as a mechanism of gene fission and the origin of new genes in <i>Drosophila</i> species. <i>Nature Genetics</i> , 2004, 36, 523-527.	9.4	88
113	Origin and evolution of new genes. <i>Science Bulletin</i> , 2004, 49, 1681-1686.	1.7	1
114	A Draft Sequence for the Genome of the Domesticated Silkworm (<i>Bombyx mori</i>). <i>Science</i> , 2004, 306, 1937-1940.	6.0	994
115	Nucleotide Variation and Recombination Along the Fourth Chromosome in <i>Drosophila simulans</i> . <i>Genetics</i> , 2004, 166, 1783-1794.	1.2	13
116	Rapid and Parallel Chromosomal Number Reductions in Muntjac Deer Inferred from Mitochondrial DNA Phylogeny. <i>Molecular Biology and Evolution</i> , 2000, 17, 1326-1333.	3.5	95
117	Protein polymorphism and genetic divergence in slow loris (genus <i>Nycticebus</i>). <i>Primates</i> , 1998, 39, 79-84.	0.7	41
118	A Phylogeny of Chinese Leaf Monkeys Using Mitochondrial ND3-ND4 Gene Sequences. <i>International Journal of Primatology</i> , 1997, 18, 305-320.	0.9	30
119	Multiple genotypes of mitochondrial DNA within a horse population from a small region in Yunnan province of China. <i>Biochemical Genetics</i> , 1994, 32, 371-378.	0.8	9
120	Multiple genotypes of mitochondrial DNA within a horse population from a small region in Yunnan province of China. <i>Biochemical Genetics</i> , 1994, 32-32, 371-378.	0.8	0