

Wen Wang

List of Publications by Year in descending order

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Version: 2024-02-01

120
papers

12,547
citations

61984

43
h-index

26613

107
g-index

129
all docs

129
docs citations

129
times ranked

15933
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.	9.0	3
2	High-quality reference genomes of swallowtail butterflies provide insights into their coloration evolution. <i>Zoological Research</i> , 2022, 43, 367-379.	2.1	6
3	Modes of genetic adaptations underlying functional innovations in the rumen. <i>Science China Life Sciences</i> , 2021, 64, 1-21.	4.9	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.	4.8	14
5	Chromatin accessibility profiling provides insights into larval cuticle color and adult longevity in butterflies. <i>Zoological Research</i> , 2021, 42, 614-619.	2.1	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.	8.9	15
7	The mitochondrial genome of one twisted-wing parasite <i>Xenos cf. moutoni</i> (Insecta, Strepsiptera.) <i>Tj ETQq1 1 0.784314 rgBT</i> 0.4 2 6, 512-514.	0.4	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.	2.8	7
9	A towering genome: Experimentally validated adaptations to high blood pressure and extreme stature in the giraffe. <i>Science Advances</i> , 2021, 7, .	10.3	31
10	Tracing the genetic footprints of vertebrate landing in non-teleost ray-finned fishes. <i>Cell</i> , 2021, 184, 1377-1391.e14.	28.9	66
11	African lungfish genome sheds light on the vertebrate water-to-land transition. <i>Cell</i> , 2021, 184, 1362-1376.e18.	28.9	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.	21.4	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.	1.4	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.	8.3	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.	2.9	3
16	<i>Giraffa camelopardalis</i> . <i>Trends in Genetics</i> , 2021, 37, 860-861.	6.7	0
17	The Elite Alleles of OsSPL4 Regulate Grain Size and Increase Grain Yield in Rice. <i>Rice</i> , 2021, 14, 90.	4.0	23
18	Molecular mechanisms and topological consequences of drastic chromosomal rearrangements of muntjac deer. <i>Nature Communications</i> , 2021, 12, 6858.	12.8	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.	3.7	3
20	Pattern of New Gene Origination in a Special Fish Lineage, the Flatfishes. <i>Genes</i> , 2021, 12, 1819.	2.4	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.	2.3	1
22	Second Rhagophthalmid Luciferase Cloned from Chinese Glowworm <i>Menghuoius giganteus</i> (Rhagophthalmidae: Elateroidea). <i>Photochemistry and Photobiology</i> , 2020, 96, 46-54.	2.5	6
23	Chromosome-level genome assembly reveals the unique genome evolution of the swimming crab (<i>Portunus trituberculatus</i>). <i>GigaScience</i> , 2020, 9, .	6.4	44
24	Genome size variation in butterflies (Insecta, Lepidoptera, Papilionoidea): a thorough phylogenetic comparison. <i>Systematic Entomology</i> , 2020, 45, 571-582.	3.9	22
25	Convergent genomic signatures of high-altitude adaptation among domestic mammals. <i>National Science Review</i> , 2020, 7, 952-963.	9.5	52
26	Genomic and experimental data provide new insights into luciferin biosynthesis and bioluminescence evolution in fireflies. <i>Scientific Reports</i> , 2020, 10, 15882.	3.3	14
27	Genomic insights of body plan transitions from bilateral to pentameral symmetry in Echinoderms. <i>Communications Biology</i> , 2020, 3, 371.	4.4	34
28	Improved de novo Assembly of the Achlorophyllous Orchid <i>Gastrodia elata</i> . <i>Frontiers in Genetics</i> , 2020, 11, 580568.	2.3	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.	6.9	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, .	6.4	90
31	The Draft Genome of Red Lechwe, <i>Kobus lechwe lechwe</i> . <i>Frontiers in Genetics</i> , 2020, 11, 582638.	2.3	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.	12.8	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.	4.8	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.	2.5	15
35	The origin of domestication genes in goats. <i>Science Advances</i> , 2020, 6, eaaz5216.	10.3	86
36	Neo-functionalization of a Teosinte branched 1 homologue mediates adaptations of upland rice. <i>Nature Communications</i> , 2020, 11, 725.	12.8	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.	4.9	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.	3.9	13
39	The genome assembly of asparagus bean, <i>Vigna unguiculata</i> ssp. <i>sesquipedialis</i> . <i>Scientific Data</i> , 2019, 6, 124.	5.3	18
40	Elimination of a Retrotransposon for Quenching Genome Instability in Modern Rice. <i>Molecular Plant</i> , 2019, 12, 1395-1407.	8.3	12
41	Phylogenetic analysis provides insights into the evolution of Asian fireflies and adult bioluminescence. <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106600.	2.7	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, .	6.4	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.	0.4	5
44	Artificial selection on storage protein 1 possibly contributes to increase of hatchability during silkworm domestication. <i>PLoS Genetics</i> , 2019, 15, e1007616.	3.5	21
45	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. <i>Science</i> , 2019, 364, .	12.6	266
46	Biological adaptations in the Arctic cervid, the reindeer (<i>Rangifer tarandus</i>). <i>Science</i> , 2019, 364, .	12.6	58
47	Genetic basis of ruminant headgear and rapid antler regeneration. <i>Science</i> , 2019, 364, .	12.6	121
48	Constructing a synthetic pathway for acetyl-coenzyme A from one-carbon through enzyme design. <i>Nature Communications</i> , 2019, 10, 1378.	12.8	128
49	Cloning and Characterization of Luciferase from the Chinese Firefly <i>Lamprigera yunnana</i> . <i>Photochemistry and Photobiology</i> , 2019, 95, 1186-1194.	2.5	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.	7.8	99
51	The genomic basis for colonizing the freezing Southern Ocean revealed by Antarctic toothfish and Patagonian robalo genomes. <i>GigaScience</i> , 2019, 8, .	6.4	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.	4.8	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.	0.8	2

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55	Allele-specific expression and alternative splicing in horse \times monkey and cattle \times yak hybrids. Zoological Research, 2019, 40, 293-304.	2.1	18
56	Genomic insights into ruminant evolution: from past to future prospects. Zoological Research, 2019, 40, 476-487.	2.1	11
57	HMOD: An Omics Database for Herbal Medicine Plants. Molecular Plant, 2018, 11, 757-759.	8.3	22
58	Draft genome of the milu (<i>Elaphurus davidianus</i>). GigaScience, 2018, 7, .	6.4	22
59	Engineering yeast for the production of breviscapine by genomic analysis and synthetic biology approaches. Nature Communications, 2018, 9, 448.	12.8	146
60	Hagfish and lamprey Hox genes reveal conservation of temporal colinearity in vertebrates. Nature Ecology and Evolution, 2018, 2, 859-866.	7.8	55
61	Weighted gene co-expression network analysis reveals potential genes involved in early metamorphosis process in sea cucumber <i>Apostichopus japonicus</i> . Biochemical and Biophysical Research Communications, 2018, 495, 1395-1402.	2.1	15
62	Application of protoplast technology to CRISPR/Cas9 mutagenesis: from single \times cell mutation detection to mutant plant regeneration. Plant Biotechnology Journal, 2018, 16, 1295-1310.	8.3	222
63	Population genomic data reveal genes related to important traits of quail. GigaScience, 2018, 7, .	6.4	38
64	The evolutionary road from wild moth to domestic silkworm. Nature Ecology and Evolution, 2018, 2, 1268-1279.	7.8	112
65	An intercross population study reveals genes associated with body size and plumage color in ducks. Nature Communications, 2018, 9, 2648.	12.8	167
66	Complete mitochondrial genome sequence of the mountain nyala (<i>Tragelaphus buxtoni</i>). Conservation Genetics Resources, 2018, 10, 547-550.	0.8	0
67	Unravelling miRNA regulation in yield of rice (<i>Oryza sativa</i>) based on differential network model. Scientific Reports, 2018, 8, 8498.	3.3	28
68	Whole-Genome Sequencing and Analysis of the Chinese Herbal Plant <i>Panax notoginseng</i> . Molecular Plant, 2017, 10, 899-902.	8.3	71
69	Draft genome of the gayal, <i>Bos frontalis</i> . GigaScience, 2017, 6, 1-7.	6.4	23
70	Genome-wide Target Enrichment-aided Chip Design: a 66 \times 10 ⁶ SNP Chip for Cashmere Goat. Scientific Reports, 2017, 7, 8621.	3.3	11
71	Identification of selection signals by large-scale whole-genome resequencing of cashmere goats. Scientific Reports, 2017, 7, 15142.	3.3	46
72	Genome editing in the butterfly type \times species <i>Papilio machaon</i> . Insect Science, 2017, 24, 708-711.	3.0	10

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73	Draft genome of the reindeer (<i>Rangifer tarandus</i>). <i>GigaScience</i> , 2017, 6, 1-5.	6.4	41
74	Draft genome of the Marco Polo Sheep (<i>Ovis ammon polii</i>). <i>GigaScience</i> , 2017, 6, 1-7.	6.4	25
75	14çŞèç«è™«(éž~ç;...ç»:èç\$)ăÿâ»ç»„âšâ°çš„æµ«â®š. <i>Zoological Research</i> , 2017, 38, 449-458.	2.1	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.	8.3	69
77	Genomes and virulence difference between two physiological races of <i>Phytophthora nicotianae</i> . <i>GigaScience</i> , 2016, 5, 3.	6.4	49
78	Improved hybrid de novo genome assembly of domesticated apple (<i>Malus x domestica</i>). <i>GigaScience</i> , 2016, 5, 35.	6.4	56
79	Generation of biallelic knock-out sheep via gene-editing and somatic cell nuclear transfer. <i>Scientific Reports</i> , 2016, 6, 33675.	3.3	39
80	Systematic evaluation of sericin protein as a substitute for fetal bovine serum in cell culture. <i>Scientific Reports</i> , 2016, 6, 31516.	3.3	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.	3.6	102
83	Genetic Variation of Goat Interferon Regulatory Factor 3 Gene and Its Implication in Goat Evolution. <i>PLoS ONE</i> , 2016, 11, e0161962.	2.5	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.	8.3	49
86	Single Base-Resolution Methylome of the Dizygotic Sheep. <i>PLoS ONE</i> , 2015, 10, e0142034.	2.5	5
87	Hybrid de novo genome assembly of the Chinese herbal plant danshen (<i>Salvia miltiorrhiza</i> Bunge). <i>GigaScience</i> , 2015, 4, 62.	6.4	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.	17.5	1,023
89	COLD1 Confers Chilling Tolerance in Rice. <i>Cell</i> , 2015, 160, 1209-1221.	28.9	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.	2.8	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.	8.3	228
92	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
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.	2.8	103
94	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015, 16, 538.	2.8	86
95	Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies. <i>Nature Communications</i> , 2015, 6, 8212.	12.8	146
96	Design and Characterization of a 52K SNP Chip for Goats. <i>PLoS ONE</i> , 2014, 9, e86227.	2.5	220
97	Advances in genome editing technology and its promising application in evolutionary and ecological studies. <i>GigaScience</i> , 2014, 3, 24.	6.4	47
98	Heterotrimeric G proteins regulate nitrogen-use efficiency in rice. <i>Nature Genetics</i> , 2014, 46, 652-656.	21.4	338
99	A genomic perspective on the important genetic mechanisms of upland adaptation of rice. <i>BMC Plant Biology</i> , 2014, 14, 160.	3.6	39
100	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	12.6	436
101	Pleiotropy of the de novo-originated gene MDF1. <i>Scientific Reports</i> , 2014, 4, 7280.	3.3	28
102	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	17.5	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.	8.3	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.	17.5	818
105	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	27.8	1,058
106	Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1	12.6	342
107	Neo-sex chromosomes in the black muntjac recapitulate incipient evolution of mammalian sex chromosomes. <i>Genome Biology</i> , 2008, 9, R98.	9.6	36
108	High Rate of Chimeric Gene Origination by Retroposition in Plant Genomes. <i>Plant Cell</i> , 2006, 18, 1791-1802.	6.6	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.	2.9	111
110	The Genomes of <i>Oryza sativa</i> : A History of Duplications. <i>PLoS Biology</i> , 2005, 3, e38.	5.6	808
111	Origin and evolution of new exons in rodents. <i>Genome Research</i> , 2005, 15, 1258-1264.	5.5	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.	21.4	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.	12.6	994
115	Nucleotide Variation and Recombination Along the Fourth Chromosome in <i>Drosophila simulans</i> . <i>Genetics</i> , 2004, 166, 1783-1794.	2.9	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.	8.9	95
117	Protein polymorphism and genetic divergence in slow loris (genus <i>Nycticebus</i>). <i>Primates</i> , 1998, 39, 79-84.	1.1	41
118	A Phylogeny of Chinese Leaf Monkeys Using Mitochondrial ND3-ND4 Gene Sequences. <i>International Journal of Primatology</i> , 1997, 18, 305-320.	1.9	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.	1.7	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.	1.7	0