## Wen Wang

## List of Publications by Year in descending order

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26613 61984 12,547 120 43 107 citations h-index g-index papers 129 129 129 15933 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	The sequence and de novo assembly of the giant panda genome. Nature, 2010, 463, 311-317.	27.8	1,058
2	Resequencing 302 wild and cultivated accessions identifies genes related to domestication and improvement in soybean. Nature Biotechnology, 2015, 33, 408-414.	17.5	1,023
3	A Draft Sequence for the Genome of the Domesticated Silkworm ( <i>Bombyx mori</i> ). Science, 2004, 306, 1937-1940.	12.6	994
4	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. Nature Biotechnology, 2012, 30, 105-111.	17.5	818
5	The Genomes of Oryza sativa: A History of Duplications. PLoS Biology, 2005, 3, e38.	5.6	808
6	COLD1 Confers Chilling Tolerance in Rice. Cell, 2015, 160, 1209-1221.	28.9	724
7	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (Capra) Tj ETQq $1\ 1$	0.784314 17.5	FrgBT /Over
8	The sheep genome illuminates biology of the rumen and lipid metabolism. Science, 2014, 344, 1168-1173.	12.6	436
9	Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm () Tj ETQq $1\ 1\ 0.784$	1314 rgBT 12.6	/Overlock 10
10	Heterotrimeric G proteins regulate nitrogen-use efficiency in rice. Nature Genetics, 2014, 46, 652-656.	21.4	338
11	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. Science, 2019, 364, .	12.6	266
12	The Genome of Dendrobium officinale Illuminates the Biology of the Important Traditional Chinese Orchid Herb. Molecular Plant, 2015, 8, 922-934.	8.3	228
13	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
14	Application of protoplast technology to CRISPR/Cas9 mutagenesis: from singleâ€cell mutation detection to mutant plant regeneration. Plant Biotechnology Journal, 2018, 16, 1295-1310.	8.3	222
15	Design and Characterization of a 52K SNP Chip for Goats. PLoS ONE, 2014, 9, e86227.	2.5	220
16	High Rate of Chimeric Gene Origination by Retroposition in Plant Genomes. Plant Cell, 2006, 18, 1791-1802.	6.6	207
17	Genomic Analyses Reveal Potential Independent Adaptation to High Altitude in Tibetan Chickens. Molecular Biology and Evolution, 2015, 32, 1880-1889.	8.9	193
18	An intercross population study reveals genes associated with body size and plumage color in ducks. Nature Communications, 2018, 9, 2648.	12.8	167

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19	Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies. Nature Communications, 2015, 6, 8212.	12.8	146
20	Engineering yeast for the production of breviscapine by genomic analysis and synthetic biology approaches. Nature Communications, 2018, 9, 448.	12.8	146
21	Constructing a synthetic pathway for acetyl-coenzyme A from one-carbon through enzyme design. Nature Communications, 2019, 10, 1378.	12.8	128
22	Genetic basis of ruminant headgear and rapid antler regeneration. Science, 2019, 364, .	12.6	121
23	The evolutionary road from wild moth to domestic silkworm. Nature Ecology and Evolution, 2018, 2, 1268-1279.	7.8	112
24	Detecting lineage-specific adaptive evolution of brain-expressed genes in human using rhesus macaque as outgroup. Genomics, 2006, 88, 745-751.	2.9	111
25	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.	2.8	103
26	Building a Genetic Manipulation Tool Box for Orchid Biology: Identification of Constitutive Promoters and Application of CRISPR/Cas9 in the Orchid, Dendrobium officinale. Frontiers in Plant Science, 2016, 7, 2036.	3.6	102
27	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
28	African lungfish genome sheds light on the vertebrate water-to-land transition. Cell, 2021, 184, 1362-1376.e18.	28.9	99
29	Rapid and Parallel Chromosomal Number Reductions in Muntjac Deer Inferred from Mitochondrial DNA Phylogeny. Molecular Biology and Evolution, 2000, 17, 1326-1333.	8.9	95
30	Origin and evolution of new exons in rodents. Genome Research, 2005, 15, 1258-1264.	5.5	91
31	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. GigaScience, 2020, 9, .	6.4	90
32	Duplication-degeneration as a mechanism of gene fission and the origin of new genes in Drosophila species. Nature Genetics, 2004, 36, 523-527.	21.4	88
33	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. BMC Genomics, 2015, 16, 538.	2.8	86
34	The origin of domestication genes in goats. Science Advances, 2020, 6, eaaz5216.	10.3	86
35	Origins of New Genes and Evolution of Their Novel Functions. Annual Review of Ecology, Evolution, and Systematics, 2012, 43, 345-363.	8.3	<b>7</b> 5
36	Hybrid de novo genome assembly of the Chinese herbal plant danshen (Salvia miltiorrhiza Bunge). GigaScience, 2015, 4, 62.	6.4	73

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37	Whole-Genome Sequencing and Analysis of the Chinese Herbal Plant Panax notoginseng. Molecular Plant, 2017, 10, 899-902.	8.3	71
38	Genome of Plant Maca (Lepidium meyenii) Illuminates Genomic Basis for High-Altitude Adaptation in the Central Andes. Molecular Plant, 2016, 9, 1066-1077.	8.3	69
39	Tracing the genetic footprints of vertebrate landing in non-teleost ray-finned fishes. Cell, 2021, 184, 1377-1391.e14.	28.9	66
40	Biological adaptations in the Arctic cervid, the reindeer ( <i>Rangifer tarandus</i> ). Science, 2019, 364,	12.6	58
41	Improved hybrid de novo genome assembly of domesticated apple (Malus x domestica). GigaScience, 2016, 5, 35.	6.4	56
42	Hagfish and lamprey Hox genes reveal conservation of temporal colinearity in vertebrates. Nature Ecology and Evolution, 2018, 2, 859-866.	7.8	55
43	Convergent genomic signatures of high-altitude adaptation among domestic mammals. National Science Review, 2020, 7, 952-963.	9.5	52
44	Genome and Comparative Transcriptomics of African Wild Rice Oryza longistaminata Provide Insights into Molecular Mechanism of Rhizomatousness and Self-Incompatibility. Molecular Plant, 2015, 8, 1683-1686.	8.3	49
45	Genomes and virulence difference between two physiological races of Phytophthora nicotianae. GigaScience, 2016, 5, 3.	6.4	49
46	Advances in genome editing technology and its promising application in evolutionary and ecological studies. GigaScience, 2014, 3, 24.	6.4	47
47	The genomic basis for colonizing the freezing Southern Ocean revealed by Antarctic toothfish and Patagonian robalo genomes. GigaScience, 2019, 8, .	6.4	47
48	Identification of selection signals by large-scale whole-genome resequencing of cashmere goats. Scientific Reports, 2017, 7, 15142.	3.3	46
49	Chromosome-level genome of Himalayan yew provides insights into the origin and evolution of the paclitaxel biosynthetic pathway. Molecular Plant, 2021, 14, 1199-1209.	8.3	46
50	Chromosome-level genome assembly reveals the unique genome evolution of the swimming crab (Portunus trituberculatus). GigaScience, 2020, 9, .	6.4	44
51	Decrease of gene expression diversity during domestication of animals and plants. BMC Evolutionary Biology, 2019, 19, 19.	3.2	42
52	Protein polymorphism and genetic divergence in slow loris (genusNycticebus). Primates, 1998, 39, 79-84.	1.1	41
53	Draft genome of the reindeer (Rangifer tarandus). GigaScience, 2017, 6, 1-5.	6.4	41
54	Neo-functionalization of a Teosinte branched $1$ homologue mediates adaptations of upland rice. Nature Communications, 2020, $11$ , $725$ .	12.8	40

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55	A genomic perspective on the important genetic mechanisms of upland adaptation of rice. BMC Plant Biology, 2014, 14, 160.	3.6	39
56	Generation of biallelic knock-out sheep via gene-editing and somatic cell nuclear transfer. Scientific Reports, 2016, 6, 33675.	3.3	39
57	Population genomic data reveal genes related to important traits of quail. GigaScience, 2018, 7, .	6.4	38
58	Neo-sex chromosomes in the black muntjac recapitulate incipient evolution of mammalian sex chromosomes. Genome Biology, 2008, 9, R98.	9.6	36
59	Genomic insights of body plan transitions from bilateral to pentameral symmetry in Echinoderms. Communications Biology, 2020, 3, 371.	4.4	34
60	A towering genome: Experimentally validated adaptations to high blood pressure and extreme stature in the giraffe. Science Advances, 2021, 7, .	10.3	31
61	A Phylogeny of Chinese Leaf Monkeys Using Mitochondrial ND3-ND4 Gene Sequences. International Journal of Primatology, 1997, 18, 305-320.	1.9	30
62	Large-scale sequencing of flatfish genomes provides insights into the polyphyletic origin of their specialized body plan. Nature Genetics, 2021, 53, 742-751.	21.4	30
63	Pleiotropy of the de novo-originated gene MDF1. Scientific Reports, 2014, 4, 7280.	3.3	28
64	Unravelling miRNA regulation in yield of rice (Oryza sativa) based on differential network model. Scientific Reports, 2018, 8, 8498.	3.3	28
65	Chromosomal-level reference genome of Chinese peacock butterfly (Papilio bianor) based on third-generation DNA sequencing and Hi-C analysis. GigaScience, 2019, 8, .	6.4	26
66	Systematic evaluation of sericin protein as a substitute for fetal bovine serum in cell culture. Scientific Reports, 2016, 6, 31516.	3.3	25
67	Draft genome of the Marco Polo Sheep (Ovis ammon polii). GigaScience, 2017, 6, 1-7.	6.4	25
68	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
69	Comparative transcriptome analyses on silk glands of six silkmoths imply the genetic basis of silk structure and coloration. BMC Genomics, 2015, 16, 203.	2.8	24
70	Phylogenetic analysis provides insights into the evolution of Asian fireflies and adult bioluminescence. Molecular Phylogenetics and Evolution, 2019, 140, 106600.	2.7	24
71	Draft genome of the gayal, Bos frontalis. GigaScience, 2017, 6, 1-7.	6.4	23
72	The Elite Alleles of OsSPL4 Regulate Grain Size and Increase Grain Yield in Rice. Rice, 2021, 14, 90.	4.0	23

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73	Molecular mechanisms and topological consequences of drastic chromosomal rearrangements of muntjac deer. Nature Communications, 2021, 12, 6858.	12.8	23
74	HMOD: An Omics Database for Herbal Medicine Plants. Molecular Plant, 2018, 11, 757-759.	8.3	22
75	Draft genome of the milu (Elaphurus davidianus). GigaScience, 2018, 7, .	6.4	22
76	Genome size variation in butterflies (Insecta, Lepidotera, Papilionoidea): a thorough phylogenetic comparison. Systematic Entomology, 2020, 45, 571-582.	3.9	22
77	Chromosomeâ€level reference genome assembly and gene editing of the deadâ€leaf butterfly <i>Kallima inachus</i> . Molecular Ecology Resources, 2020, 20, 1080-1092.	4.8	22
78	Artificial selection on storage protein 1 possibly contributes to increase of hatchability during silkworm domestication. PLoS Genetics, 2019, 15, e1007616.	3.5	21
79	Modes of genetic adaptations underlying functional innovations in the rumen. Science China Life Sciences, 2021, 64, 1-21.	4.9	19
80	The genome assembly of asparagus bean, Vigna unguiculata ssp. sesquipedialis. Scientific Data, 2019, 6, 124.	5.3	18
81	Allele-specific expression and alternative splicing in horseè«onkey and cattleè®ak hybrids. Zoological Research, 2019, 40, 293-304.	2.1	18
82	14ç§èç«è™«(éž~ç¿ç>®:èçç°)基å>组å§å°çš"测定. Zoological Research, 2017, 38, 449-458.	2.1	15
83	Weighted gene co-expression network analysis reveals potential genes involved in early metamorphosis process in sea cucumber Apostichopus japonicus. Biochemical and Biophysical Research Communications, 2018, 495, 1395-1402.	2.1	15
84	De Novo Genome Assembly of Limpet Bathyacmaea lactea (Gastropoda: Pectinodontidae): The First Reference Genome of a Deep-Sea Gastropod Endemic to Cold Seeps. Genome Biology and Evolution, 2020, 12, 905-910.	2.5	15
85	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
86	Genomic and experimental data provide new insights into luciferin biosynthesis and bioluminescence evolution in fireflies. Scientific Reports, 2020, 10, 15882.	3.3	14
87	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
88	Advances and perspectives in the application of CRISPR/Cas9 in insects. Zoological Research, 2016, 37, 220-8.	0.6	14
89	Molecular microevolution and epigenetic patterns of the long non-coding gene H19 show its potential function in pig domestication and breed divergence. BMC Evolutionary Biology, 2016, 16, 87.	3.2	13
90	Demography and adaptation promoting evolutionary transitions in a mammalian genus that diversified during the Pleistocene. Molecular Ecology, 2020, 29, 2777-2792.	3.9	13

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91	Nucleotide Variation and Recombination Along the Fourth Chromosome in <i>Drosophila simulans</i> . Genetics, 2004, 166, 1783-1794.	2.9	13
92	Elimination of a Retrotransposon for Quenching Genome Instability in Modern Rice. Molecular Plant, 2019, 12, 1395-1407.	8.3	12
93	Genome-wide Target Enrichment-aided Chip Design: a 66 K SNP Chip for Cashmere Goat. Scientific Reports, 2017, 7, 8621.	3.3	11
94	Improved de novo Assembly of the Achlorophyllous Orchid Gastrodia elata. Frontiers in Genetics, 2020, 11, 580568.	2.3	11
95	Raising the production of phloretin by alleviation of by-product of chalcone synthase in the engineered yeast. Science China Life Sciences, 2020, 63, 1734-1743.	4.9	11
96	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
97	Genomic insights into ruminant evolution: from past to future prospects. Zoological Research, 2019, 40, 476-487.	2.1	11
98	Genome editing in the butterfly typeâ€species <i>Papilio machaon</i> . Insect Science, 2017, 24, 708-711.	3.0	10
99	Multiple genotypes of mitochondrial DNA within a horse population from a small region in Yunnan province of China. Biochemical Genetics, 1994, 32, 371-378.	1.7	9
100	Identification of Key Genes for the Ultrahigh Yield of Rice Using Dynamic Cross-tissue Network Analysis. Genomics, Proteomics and Bioinformatics, 2020, 18, 256-270.	6.9	9
101	Cloning and Characterization of Luciferase from the Chinese Firefly <i>Lamprigera yunnana</i> Photochemistry and Photobiology, 2019, 95, 1186-1194.	2.5	7
102	Genome-wide identification and gene-editing of pigment transporter genes in the swallowtail butterfly Papilio xuthus. BMC Genomics, 2021, 22, 120.	2.8	7
103	Second Rhagophthalmid Luciferase Cloned from Chinese Glowâ€worm <i>Menghuoius giganteus</i> (Rhagophthalmidae: Elateroidea). Photochemistry and Photobiology, 2020, 96, 46-54.	2.5	6
104	High-quality reference genomes of swallowtail butterflies provide insights into their coloration evolution. Zoological Research, 2022, 43, 367-379.	2.1	6
105	Single Base-Resolution Methylome of the Dizygotic Sheep. PLoS ONE, 2015, 10, e0142034.	2.5	5
106	The mitochondrial genome of the first luminous click-beetle ( <i>Coleoptera</i> : Elateridae) recorded in Asia. Mitochondrial DNA Part B: Resources, 2019, 4, 565-567.	0.4	5
107	Chromatin accessibility profiling provides insights into larval cuticle color and adult longevity in butterflies. Zoological Research, 2021, 42, 614-619.	2.1	5
108	Molecular cloning, characterization, and evolution analysis of the luciferase genes from three sympatric sibling fireflies (Lampyridae: Lampyrinae, Diaphanes). Photochemical and Photobiological Sciences, 2021, 20, 1053-1067.	2.9	3

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109	Derivedness Index for Estimating Degree of Phenotypic Evolution of Embryos: A Study of Comparative Transcriptomic Analyses of Chordates and Echinoderms. Frontiers in Cell and Developmental Biology, 2021, 9, 749963.	3.7	3
110	Ruminant-specific genes identified using high-quality genome data and their roles in rumen evolution. Science Bulletin, 2022, 67, 825-835.	9.0	3
111	Complete mitochondrial genome sequence of the Przewalski's gazelle (Procapra przewalskii). Conservation Genetics Resources, 2019, 11, 369-371.	0.8	2
112	The mitochondrial genome of one â€~twisted-wing parasite' Xenos cf. moutoni (Insecta, Strepsiptera,) Tj ETC 6, 512-514.	)q0 0 0 rgl 0.4	BT /Overlock 2
113	Genetic Variation of Goat Interferon Regulatory Factor 3 Gene and Its Implication in Goat Evolution. PLoS ONE, 2016, 11, e0161962.	2.5	2
114	Pattern of New Gene Origination in a Special Fish Lineage, the Flatfishes. Genes, 2021, 12, 1819.	2.4	2
115	Origin and evolution of new genes. Science Bulletin, 2004, 49, 1681-1686.	1.7	1
116	Integrated Analysis of Transcriptome and Proteome to Reveal Pupal Color Switch in Papilio xuthus Butterflies. Frontiers in Genetics, 2021, 12, 795115.	2.3	1
117	Complete mitochondrial genome sequence of the mountain nyala (Tragelaphus buxtoni). Conservation Genetics Resources, 2018, 10, 547-550.	0.8	O
118	The Draft Genome of Red Lechwe, Kobus leche leche. Frontiers in Genetics, 2020, 11, 582638.	2.3	0
119	Giraffa camelopardalis. Trends in Genetics, 2021, 37, 860-861.	6.7	O
120	Multiple genotypes of mitochondrial DNA within a horse population from a small region in Yunnan province of China. Biochemical Genetics, 1994, 32-32, 371-378.	1.7	0