Huan Liu

List of Publications by Year in descending order

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Version: 2024-02-01

236925 289244 2,074 69 25 40 citations h-index g-index papers 92 92 92 2752 citing authors all docs docs citations times ranked

#	Article	IF	CITATIONS
1	Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. Nature Plants, 2020, 6, 95-106.	9.3	146
2	The sequence and analysis of a Chinese pig genome. GigaScience, 2012, 1, 16.	6.4	125
3	The draft genomes of five agriculturally important African orphan crops. GigaScience, 2019, 8, .	6.4	108
4	Deciphering the Composition and Functional Profile of the Microbial Communities in Chinese Moutai Liquor Starters. Frontiers in Microbiology, 2019, 10, 1540.	3. 5	98
5	The genome of Prasinoderma coloniale unveils the existence of a third phylum within green plants. Nature Ecology and Evolution, 2020, 4, 1220-1231.	7.8	84
6	The Cycas genome and the early evolution of seed plants. Nature Plants, 2022, 8, 389-401.	9.3	80
7	The Distribution of Tryptophan-Dependent Indole-3-Acetic Acid Synthesis Pathways in Bacteria Unraveled by Large-Scale Genomic Analysis. Molecules, 2019, 24, 1411.	3.8	76
8	African Orphan Crops Consortium (AOCC): status of developing genomic resources for African orphan crops. Planta, 2019, 250, 989-1003.	3.2	73
9	Genomic and transcriptomic analysis unveils population evolution and development of pesticide resistance in fall armyworm Spodoptera frugiperda. Protein and Cell, 2022, 13, 513-531.	11.0	72
10	Whole-genome resequencing of 445 Lactuca accessions reveals the domestication history of cultivated lettuce. Nature Genetics, 2021, 53, 752-760.	21.4	64
11	The preceding root system drives the composition and function of the rhizosphere microbiome. Genome Biology, 2020, 21, 89.	8.8	61
12	PIK3R1 negatively regulates the epithelial-mesenchymal transition and stem-like phenotype of renal cancer cells through the AKT/GSK3β/CTNNB1 signaling pathway. Scientific Reports, 2015, 5, 8997.	3.3	56
13	Mycorrhizal symbiosis modulates the rhizosphere microbiota to promote rhizobia–legume symbiosis. Molecular Plant, 2021, 14, 503-516.	8.3	56
14	Establishment of a Macaca fascicularis gut microbiome gene catalog and comparison with the human, pig, and mouse gut microbiomes. GigaScience, 2018, 7, .	6.4	53
15	Plastid phylogenomic insights into the evolution of the Caprifoliaceae s.l. (Dipsacales). Molecular Phylogenetics and Evolution, 2020, 142, 106641.	2.7	52
16	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
17	Chloranthus genome provides insights into the early diversification of angiosperms. Nature Communications, 2021, 12, 6930.	12.8	44
18	Announcing the Genome Atlas of Bamboo and Rattan (GABR) project: promoting research in evolution and in economically and ecologically beneficial plants. GigaScience, 2017, 6, 1-7.	6.4	42

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19	Molecular digitization of a botanical garden: high-depth whole-genome sequencing of 689 vascular plant species from the Ruili Botanical Garden. GigaScience, 2019, 8, .	6.4	39
20	Draft genome sequence of Solanum aethiopicum provides insights into disease resistance, drought tolerance, and the evolution of the genome. GigaScience, 2019, 8, .	6.4	38
21	Thioredoxin-interacting protein regulates lipid metabolism via Akt/mTOR pathway in diabetic kidney disease. International Journal of Biochemistry and Cell Biology, 2016, 79, 1-13.	2.8	35
22	Factors Determining the Efficiency of Porcine Somatic Cell Nuclear Transfer: Data Analysis with Over 200,000 Reconstructed Embryos. Cellular Reprogramming, 2015, 17, 463-471.	0.9	32
23	The genome of Magnolia biondii Pamp. provides insights into the evolution of Magnoliales and biosynthesis of terpenoids. Horticulture Research, 2021, 8, 38.	6.3	32
24	Single cell atlas for 11 non-model mammals, reptiles and birds. Nature Communications, 2021, 12, 7083.	12.8	32
25	Comparative Plastome Analysis of Root- and Stem-Feeding Parasites of Santalales Untangle the Footprints of Feeding Mode and Lifestyle Transitions. Genome Biology and Evolution, 2020, 12, 3663-3676.	2.5	30
26	Draft Genomes of Two Artocarpus Plants, Jackfruit (A. heterophyllus) and Breadfruit (A. altilis). Genes, 2020, 11, 27.	2.4	30
27	A chromosome-level genome assembly of rugged rose (Rosa rugosa) provides insights into its evolution, ecology, and floral characteristics. Horticulture Research, 2021, 8, 141.	6.3	29
28	The Amount of RNA Editing Sites in Liverwort Organellar Genes Is Correlated with GC Content and Nuclear PPR Protein Diversity. Genome Biology and Evolution, 2019, 11, 3233-3239.	2.5	27
29	Deciphering the Microbial Taxonomy and Functionality of Two Diverse Mangrove Ecosystems and Their Potential Abilities To Produce Bioactive Compounds. MSystems, 2020, 5, .	3.8	23
30	Genome-wide analyses across Viridiplantae reveal the origin and diversification of small RNA pathway-related genes. Communications Biology, 2021, 4, 412.	4.4	22
31	Mitochondrial genomes of the early land plant lineage liverworts (Marchantiophyta): conserved genome structure, and ongoing low frequency recombination. BMC Genomics, 2019, 20, 953.	2.8	21
32	The chromosomeâ€scale genomes of <i>Dipterocarpus turbinatus</i> and <i>Hopea hainanensis</i> (Dipterocarpaceae) provide insights into fragrant oleoresin biosynthesis and hardwood formation. Plant Biotechnology Journal, 2022, 20, 538-553.	8.3	21
33	Genomes shed light on the evolution of <i>Begonia</i> , a megaâ€diverse genus. New Phytologist, 2022, 234, 295-310.	7.3	18
34	Metagenomic Analysis Reveals Microbial Community Structure and Metabolic Potential for Nitrogen Acquisition in the Oligotrophic Surface Water of the Indian Ocean. Frontiers in Microbiology, 2021, 12, 518865.	3.5	17
35	Dissecting the genome of star fruit (Averrhoa carambola L.). Horticulture Research, 2020, 7, 94.	6.3	16
36	Generation of outbred Ace2 knockout mice by RNA transfection of TALENs displaying colitis reminiscent pathophysiology and inflammation. Transgenic Research, 2015, 24, 433-446.	2.4	14

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37	Molecular evidence for origin, diversification and ancient gene duplication of plant subtilases (SBTs). Scientific Reports, 2019, 9, 12485.	3.3	14
38	An Indo-Pacific Humpback Dolphin Genome Reveals Insights into Chromosome Evolution and the Demography of a Vulnerable Species. IScience, 2020, 23, 101640.	4.1	14
39	Genome of <i>Hippophae rhamnoides</i> provides insights into a conserved molecular mechanism in actinorhizal and rhizobial symbioses. New Phytologist, 2022, 235, 276-291.	7.3	14
40	Chromosome-scale genomes provide new insights into subspecies divergence and evolutionary characteristics of the giant panda. Science Bulletin, 2021, 66, 2002-2013.	9.0	13
41	VThunter: a database for single-cell screening of virus target cells in the animal kingdom. Nucleic Acids Research, 2022, 50, D934-D942.	14.5	13
42	Phylogeographic Analysis and Genetic Structure of an Endemic Sino-Japanese Disjunctive Genus Diabelia (Caprifoliaceae). Frontiers in Plant Science, 2019, 10, 913.	3.6	12
43	Draft genome of the aquatic moss Fontinalis antipyretica (Fontinalaceae, Bryophyta). GigaByte, 0, 2020, 1-9.	0.0	12
44	The Clausena lansium (Wampee) genome reveal new insights into the carbazole alkaloids biosynthesis pathway. Genomics, 2021, 113, 3696-3704.	2.9	11
45	Chromosome-Level Genome Assemblies of Two Hypnales (Mosses) Reveal High Intergeneric Synteny. Genome Biology and Evolution, 2022, 14, .	2.5	11
46	Transgenic Wuzhishan minipigs designed to express a dominant-negative porcine growth hormone receptor display small stature and a perturbed insulin/IGF-1 pathway. Transgenic Research, 2015, 24, 1029-1042.	2.4	10
47	Phylogenomics Provides New Insights into Gains and Losses of Selenoproteins among Archaeplastida. International Journal of Molecular Sciences, 2019, 20, 3020.	4.1	10
48	Development of Transgenic Minipigs with Expression of Antimorphic Human Cryptochrome 1. PLoS ONE, 2013, 8, e76098.	2.5	9
49	Improving Species Identification of Ancient Mammals Based on Next-Generation Sequencing Data. Genes, 2019, 10, 509.	2.4	8
50	Are fungiâ€derived genomic regions related to antagonism towards fungi in mosses?. New Phytologist, 2020, 228, 1169-1175.	7.3	8
51	Comparative transcriptomic analyses of chlorogenic acid and luteolosides biosynthesis pathways at different flowering stages of diploid and tetraploid <i>Lonicera japonica</i> . PeerJ, 2020, 8, e8690.	2.0	8
52	Comparative Analyses of 3,654 Plastid Genomes Unravel Insights Into Evolutionary Dynamics and Phylogenetic Discordance of Green Plants. Frontiers in Plant Science, 2022, 13, 808156.	3.6	8
53	Chromosomeâ€scale assembly and wholeâ€genome sequencing of 266 giant panda roundworms provide insights into their evolution, adaptation and potential drug targets. Molecular Ecology Resources, 2022, 22, 768-785.	4.8	6
54	An efficient pipeline for ancient DNA mapping and recovery of endogenous ancient DNA from wholeâ€genome sequencing data. Ecology and Evolution, 2021, 11, 390-401.	1.9	6

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55	The complete plastid genomes of two Fabaceae orphan crops from Africa. Mitochondrial DNA Part B: Resources, 2019, 4, 93-94.	0.4	5
56	The Draft Genome of the Small, Spineless Green Alga Desmodesmus costato-granulatus (Sphaeropleales, Chlorophyta). Protist, 2019, 170, 125697.	1.5	4
57	The Draft Genome of the Centric Diatom Conticribra weissflogii (Coscinodiscophyceae, Ochrophyta). Protist, 2021, 172, 125845.	1.5	4
58	Fugacium Spliced Leader Genes Identified from Stranded RNA-Seq Datasets. Microorganisms, 2019, 7, 171.	3.6	3
59	The draft genome of mandrill (Mandrillus sphinx): An Old World monkey. Scientific Reports, 2020, 10, 2431.	3.3	3
60	The draft genome assembly of the critically endangered Nyssa yunnanensis, a plant species with extremely small populations endemic to Yunnan Province, China. GigaByte, 0, 2020, 1-12.	0.0	3
61	Chromosome-Scale Genome of Masked Palm Civet (Paguma larvata) Shows Genomic Signatures of Its Biological Characteristics and Evolution. Frontiers in Genetics, 2021, 12, 819493.	2.3	3
62	The Draft Genome of Coelastrum proboscideum (Sphaeropleales, Chlorophyta). Protist, 2020, 171, 125758.	1.5	2
63	Targeted enrichment of novel chloroplast-based probes reveals a large-scale phylogeny of 412 bamboos. BMC Plant Biology, 2021, 21, 76.	3.6	2
64	Chromosomeâ€evel genome of <i>Pedinomonas minor</i> (Chlorophyta) unveils adaptations to abiotic stress in a rapidly fluctuating environment. New Phytologist, 2022, , .	7.3	2
65	Genome-Wide Analysis of the MADS-Box Gene Family in Holoparasitic Plants (Balanophora) Tj ETQq $1\ 1\ 0.7843$	14 rgBT /Ov	verl <u>o</u> ck 10 TF
66	The Draft Genome of Hariotina reticulata (Sphaeropleales, Chlorophyta) Provides Insight into the Evolution of Scenedesmaceae. Protist, 2019, 170, 125684.	1.5	1
67	Viral receptor profiles of masked palm civet revealed by single-cell transcriptomics. Journal of Genetics and Genomics, 2022, , .	3.9	1
68	Establishment of regeneration system of callus pathway for Iris sanguinea Donn ex Horn. In Vitro Cellular and Developmental Biology - Plant, 2020, 56, 694-702.	2.1	0
69	Large Differentiation of Extremely Threatened Chinese Pangolins Provide New Genomic Cues for Their Conservation. SSRN Electronic Journal, 0, , .	0.4	0