

Xin Liu

List of Publications by Year in descending order

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Version: 2024-02-01

137
papers

23,598
citations

23567

58
h-index

10445

139
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144
docs citations

144
times ranked

31238
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic and transcriptomic analysis unveils population evolution and development of pesticide resistance in fall armyworm <i>Spodoptera frugiperda</i> . <i>Protein and Cell</i> , 2022, 13, 513-531.	11.0	72
2	Two divergent haplotypes from a highly heterozygous lychee genome suggest independent domestication events for early and late-maturing cultivars. <i>Nature Genetics</i> , 2022, 54, 73-83.	21.4	88
3	Long- read sequencing and de novo assembly of the cynomolgus macaque genome. <i>Journal of Genetics and Genomics</i> , 2022, , .	3.9	1
4	The <i>Cycas</i> genome and the early evolution of seed plants. <i>Nature Plants</i> , 2022, 8, 389-401.	9.3	80
5	The microbial diversity in industrial effluents makes high-throughput sequencing-based source tracking of the effluents possible. <i>Environmental Research</i> , 2022, 212, 113640.	7.5	5
6	Chromosome-level genome assembly of <i>Lethenteron reissneri</i> provides insights into lamprey evolution. <i>Molecular Ecology Resources</i> , 2021, 21, 448-463.	4.8	25
7	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. <i>Scientific Data</i> , 2021, 8, 50.	5.3	38
8	Whole-genome resequencing of 445 <i>Lactuca</i> accessions reveals the domestication history of cultivated lettuce. <i>Nature Genetics</i> , 2021, 53, 752-760.	21.4	64
9	Enhancing CRISPR-Cas9 gRNA efficiency prediction by data integration and deep learning. <i>Nature Communications</i> , 2021, 12, 3238.	12.8	81
10	The complete chloroplast genome of a shrub species, <i>Smilax glabra</i> (Smilacaceae) from Guangdong, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3064-3066.	0.4	1
11	Analysis of 427 genomes reveals moso bamboo population structure and genetic basis of property traits. <i>Nature Communications</i> , 2021, 12, 5466.	12.8	24
12	The genome of the naturally evolved obesity-prone Ossabaw miniature pig. <i>IScience</i> , 2021, 24, 103081.	4.1	9
13	<i>Chloranthus</i> genome provides insights into the early diversification of angiosperms. <i>Nature Communications</i> , 2021, 12, 6930.	12.8	44
14	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	27.8	106
15	Genome-wide analysis of epigenetic and transcriptional changes associated with heterosis in pigeonpea. <i>Plant Biotechnology Journal</i> , 2020, 18, 1697-1710.	8.3	38
16	Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. <i>Nature Plants</i> , 2020, 6, 95-106.	9.3	146
17	Comparative Plastome Analysis of Root- and Stem-Feeding Parasites of Santalales Untangle the Footprints of Feeding Mode and Lifestyle Transitions. <i>Genome Biology and Evolution</i> , 2020, 12, 3663-3676.	2.5	30
18	The Chromosome-Based Rubber Tree Genome Provides New Insights into Spurge Genome Evolution and Rubber Biosynthesis. <i>Molecular Plant</i> , 2020, 13, 336-350.	8.3	73

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19	Draft Genomes of Two Artocarpus Plants, Jackfruit (<i>A. heterophyllus</i>) and Breadfruit (<i>A. altilis</i>). <i>Genes</i> , 2020, 11, 27.	2.4	30
20	Chromosome-Level Comprehensive Genome of Mangrove Sediment-Derived Fungus <i>Penicillium variable</i> HXQ-H-1. <i>Journal of Fungi</i> (Basel, Switzerland), 2020, 6, 7.	3.5	6
21	The Chromosome Level Genome and Genome-wide Association Study for the Agronomic Traits of <i>Panax Notoginseng</i> . <i>IScience</i> , 2020, 23, 101538.	4.1	34
22	An Indo-Pacific Humpback Dolphin Genome Reveals Insights into Chromosome Evolution and the Demography of a Vulnerable Species. <i>IScience</i> , 2020, 23, 101640.	4.1	14
23	Performance of copy number variants detection based on whole-genome sequencing by DNBSEQ platforms. <i>BMC Bioinformatics</i> , 2020, 21, 518.	2.6	10
24	Beaver and Naked Mole Rat Genomes Reveal Common Paths to Longevity. <i>Cell Reports</i> , 2020, 32, 107949.	6.4	26
25	Deciphering the Microbial Taxonomy and Functionality of Two Diverse Mangrove Ecosystems and Their Potential Abilities To Produce Bioactive Compounds. <i>MSystems</i> , 2020, 5, .	3.8	23
26	African Arowana Genome Provides Insights on Ancient Teleost Evolution. <i>IScience</i> , 2020, 23, 101662.	4.1	3
27	Family-Based Whole Genome Sequencing Identified Novel Variants in <i>ABCA5</i> Gene in a Patient with Idiopathic Ventricular Tachycardia. <i>Pediatric Cardiology</i> , 2020, 41, 1783-1794.	1.3	1
28	TGS-GapCloser: A fast and accurate gap closer for large genomes with low coverage of error-prone long reads. <i>GigaScience</i> , 2020, 9, .	6.4	156
29	Initial data release and announcement of the 10,000 Fish Genomes Project (Fish10K). <i>GigaScience</i> , 2020, 9, .	6.4	47
30	Genome sequencing of deep-sea hydrothermal vent snails reveals adaptations to extreme environments. <i>GigaScience</i> , 2020, 9, .	6.4	5
31	The White-Spotted Bamboo Shark Genome Reveals Chromosome Rearrangements and Fast-Evolving Immune Genes of Cartilaginous Fish. <i>IScience</i> , 2020, 23, 101754.	4.1	36
32	The genome of Mekong tiger perch (<i>Datnioides undecimradiatus</i>) provides insights into the phylogenetic position of Lobotiformes and biological conservation. <i>Scientific Reports</i> , 2020, 10, 8164.	3.3	3
33	Complete Chloroplast Genomes of 14 Mangroves: Phylogenetic and Comparative Genomic Analyses. <i>BioMed Research International</i> , 2020, 2020, 1-13.	1.9	14
34	Dissecting the genome of star fruit (<i>Averrhoa carambola</i> L.). <i>Horticulture Research</i> , 2020, 7, 94.	6.3	16
35	The genome of <i>Prasinoderma coloniale</i> unveils the existence of a third phylum within green plants. <i>Nature Ecology and Evolution</i> , 2020, 4, 1220-1231.	7.8	84
36	An atlas of the protein-coding genes in the human, pig, and mouse brain. <i>Science</i> , 2020, 367, .	12.6	517

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37	Haplotyping by CRISPR-mediated DNA circularization (CRISPR-hapC) broadens allele-specific gene editing. <i>Nucleic Acids Research</i> , 2020, 48, e25-e25.	14.5	8
38	Lineage-specific evolution of mangrove plastid genomes. <i>Plant Genome</i> , 2020, 13, e20019.	2.8	4
39	Deciphering the Composition and Functional Profile of the Microbial Communities in Chinese Moutai Liquor Starters. <i>Frontiers in Microbiology</i> , 2019, 10, 1540.	3.5	98
40	African Orphan Crops Consortium (AOCC): status of developing genomic resources for African orphan crops. <i>Planta</i> , 2019, 250, 989-1003.	3.2	73
41	A chromosome-level assembly of the Atlantic herring genome—detection of a supergene and other signals of selection. <i>Genome Research</i> , 2019, 29, 1919-1928.	5.5	84
42	Genomes of Subaerial Zygnematophyceae Provide Insights into Land Plant Evolution. <i>Cell</i> , 2019, 179, 1057-1067.e14.	28.9	320
43	Molecular evidence for origin, diversification and ancient gene duplication of plant subtilases (SBTs). <i>Scientific Reports</i> , 2019, 9, 12485.	3.3	14
44	Transcriptomic analyses reveal new genes and networks response to H5N1 influenza viruses in duck (<i>Anas platyrhynchos</i>). <i>Journal of Integrative Agriculture</i> , 2019, 18, 1460-1472.	3.5	7
45	Resequencing 545 ginkgo genomes across the world reveals the evolutionary history of the living fossil. <i>Nature Communications</i> , 2019, 10, 4201.	12.8	99
46	Draft genome sequence of <i>Solanum aethiopicum</i> provides insights into disease resistance, drought tolerance, and the evolution of the genome. <i>GigaScience</i> , 2019, 8, .	6.4	38
47	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. <i>Nature Communications</i> , 2019, 10, 470.	12.8	156
48	Molecular digitization of a botanical garden: high-depth whole-genome sequencing of 689 vascular plant species from the Ruili Botanical Garden. <i>GigaScience</i> , 2019, 8, .	6.4	39
49	New insights from <i>Opisthorchis felineus</i> genome: update on genomics of the epidemiologically important liver flukes. <i>BMC Genomics</i> , 2019, 20, 399.	2.8	29
50	Phylogenomics Provides New Insights into Gains and Losses of Selenoproteins among Archaeplastida. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3020.	4.1	10
51	A chromosome-level genome of black rockfish, <i>Sebastes schlegelii</i> , provides insights into the evolution of live birth. <i>Molecular Ecology Resources</i> , 2019, 19, 1309-1321.	4.8	44
52	Resequencing of 429 chickpea accessions from 45 countries provides insights into genome diversity, domestication and agronomic traits. <i>Nature Genetics</i> , 2019, 51, 857-864.	21.4	219
53	The complete plastid genomes of four species from Brassicales. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 124-125.	0.4	1
54	LION: a simple and rapid method to achieve CRISPR gene editing. <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 2633-2645.	5.4	3

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55	Genomic variants identified from whole-genome resequencing of indicine cattle breeds from Pakistan. PLoS ONE, 2019, 14, e0215065.	2.5	28
56	Sequencing of the MHC region defines <i>HLA-DQA1</i> as the major genetic risk for seropositive rheumatoid arthritis in Han Chinese population. Annals of the Rheumatic Diseases, 2019, 78, 773-780.	0.9	27
57	The first chromosome-level genome for a marine mammal as a resource to study ecology and evolution. Molecular Ecology Resources, 2019, 19, 944-956.	4.8	27
58	Enhancement of de novo sequencing, assembly and annotation of the Mongolian gerbil genome with transcriptome sequencing and assembly from several different tissues. BMC Genomics, 2019, 20, 903.	2.8	5
59	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
60	Chromosome level comparative analysis of Brassica genomes. Plant Molecular Biology, 2019, 99, 237-249.	3.9	14
61	Integrated transcriptome, small RNA and degradome sequencing approaches provide insights into Ascochyta blight resistance in chickpea. Plant Biotechnology Journal, 2019, 17, 914-931.	8.3	66
62	The draft genomes of five agriculturally important African orphan crops. GigaScience, 2019, 8, .	6.4	108
63	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. Nature Biotechnology, 2019, 37, 179-185.	17.5	402
64	Natural selection and repeated patterns of molecular evolution following allopatric divergence. ELife, 2019, 8, .	6.0	18
65	A survey of the sperm whale (<i>Physeter catodon</i>) commensal microbiome. PeerJ, 2019, 7, e7257.	2.0	15
66	10KP: A phylodiverse genome sequencing plan. GigaScience, 2018, 7, 1-9.	6.4	169
67	Genome-wide determination of on-target and off-target characteristics for RNA-guided DNA methylation by dCas9 methyltransferases. GigaScience, 2018, 7, 1-19.	6.4	64
68	Bph6 encodes an exocyst-localized protein and confers broad resistance to planthoppers in rice. Nature Genetics, 2018, 50, 297-306.	21.4	158
69	The genetic architecture of floral traits in the woody plant <i>Prunus mume</i> . Nature Communications, 2018, 9, 1702.	12.8	73
70	Is there foul play in the leaf pocket? The metagenome of floating fern <i>Azolla</i> reveals endophytes that do not fix N ₂ but may denitrify. New Phytologist, 2018, 217, 453-466.	7.3	42
71	The structure and function of the global citrus rhizosphere microbiome. Nature Communications, 2018, 9, 4894.	12.8	304
72	Whole-genome sequencing of 175 Mongolians uncovers population-specific genetic architecture and gene flow throughout North and East Asia. Nature Genetics, 2018, 50, 1696-1704.	21.4	38

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73	Chromosome-level genome assembly of the spotted sea bass, <i>Lateolabrax maculatus</i> . <i>GigaScience</i> , 2018, 7, .	6.4	39
74	Genome Annotation of a Model Diatom <i>Phaeodactylum tricornutum</i> Using an Integrated Proteogenomic Pipeline. <i>Molecular Plant</i> , 2018, 11, 1292-1307.	8.3	44
75	CRISPR-C: circularization of genes and chromosome by CRISPR in human cells. <i>Nucleic Acids Research</i> , 2018, 46, e131.	14.5	39
76	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , 2018, 361, .	12.6	339
77	Population genomic data reveal genes related to important traits of quail. <i>GigaScience</i> , 2018, 7, .	6.4	38
78	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	9.3	391
79	A western Sahara centre of domestication inferred from pearl millet genomes. <i>Nature Ecology and Evolution</i> , 2018, 2, 1377-1380.	7.8	78
80	Chromosome-level reference genome of the Siamese fighting fish <i>Betta splendens</i> , a model species for the study of aggression. <i>GigaScience</i> , 2018, 7, .	6.4	25
81	Central and Peripheral Nervous System Progenitors Derived from Human Pluripotent Stem Cells Reveal a Unique Temporal and Cell-Type Specific Expression of PMCs. <i>Frontiers in Cell and Developmental Biology</i> , 2018, 6, 5.	3.7	3
82	The chromosome-level genome assemblies of two rattans (<i>Calamus simplicifolius</i> and <i>Daemonorops</i>) Tj ETQq0 0 0 ggBT /Overlock 10 Tf 6.4 28	6.4	28
83	Patient iPSC-Derived Neurons for Disease Modeling of Frontotemporal Dementia with Mutation in CHMP2B. <i>Stem Cell Reports</i> , 2017, 8, 648-658.	4.8	65
84	A novel Enterovirus 96 circulating in China causes hand, foot, and mouth disease. <i>Virus Genes</i> , 2017, 53, 352-356.	1.6	3
85	Draft genome sequence of the Tibetan medicinal herb <i>Rhodiola crenulata</i> . <i>GigaScience</i> , 2017, 6, 1-5.	6.4	33
86	A reference human genome dataset of the BGISEQ-500 sequencer. <i>GigaScience</i> , 2017, 6, 1-9.	6.4	219
87	Retinoic acid combined with spermatogonial stem cell conditions facilitate the generation of mouse germ-like cells. <i>Bioscience Reports</i> , 2017, 37, .	2.4	8
88	The gut microbiome in atherosclerotic cardiovascular disease. <i>Nature Communications</i> , 2017, 8, 845.	12.8	1,029
89	Taxonomic structure and functional association of foxtail millet root microbiome. <i>GigaScience</i> , 2017, 6, 1-12.	6.4	1,228
90	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	17.5	356

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91	Genome-wide Target Enrichment-aided Chip Design: a 66â€‰%K SNP Chip for Cashmere Goat. Scientific Reports, 2017, 7, 8621.	3.3	11
92	RED-ML: a novel, effective RNA editing detection method based on machine learning. GigaScience, 2017, 6, 1-8.	6.4	29
93	Deep whole-genome sequencing of 90 Han Chinese genomes. GigaScience, 2017, 6, 1-7.	6.4	36
94	The pearl oyster <i>Pinctada fucata martensii</i> genome and multi-omic analyses provide insights into biomineralization. GigaScience, 2017, 6, 1-12.	6.4	160
95	Improvement of peptide identification with considering the abundance of mRNA and peptide. BMC Bioinformatics, 2017, 18, 109.	2.6	7
96	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
97	Whole-genome duplication and molecular evolution in <i>Cornus L.</i> (Cornaceae) â€“ Insights from transcriptome sequences. PLoS ONE, 2017, 12, e0171361.	2.5	17
98	The genetic basis for ecological adaptation of the Atlantic herring revealed by genome sequencing. ELife, 2016, 5, .	6.0	143
99	Redefining the structural motifs that determine <sc>RNA</sc> binding and <sc>RNA</sc> editing by pentatricopeptide repeat proteins in land plants. Plant Journal, 2016, 85, 532-547.	5.7	267
100	Recent breeding programs enhanced genetic diversity in both desi and kabuli varieties of chickpea (<i>Cicer arietinum L.</i>). Scientific Reports, 2016, 6, 38636.	3.3	77
101	Landscape of genomic diversity and trait discovery in soybean. Scientific Reports, 2016, 6, 23598.	3.3	151
102	First documented case of avian influenza (H5N1) virus infection in a lion. Emerging Microbes and Infections, 2016, 5, 1-3.	6.5	15
103	Draft genome of the living fossil <i>Ginkgo biloba</i> . GigaScience, 2016, 5, 49.	6.4	232
104	A reference gene catalogue of the pig gut microbiome. Nature Microbiology, 2016, 1, 16161.	13.3	416
105	Allelic diversity in an NLR gene <i>BPH9</i> enables rice to combat planthopper variation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12850-12855.	7.1	196
106	PGA: an R/Bioconductor package for identification of novel peptides using a customized database derived from RNA-Seq. BMC Bioinformatics, 2016, 17, 244.	2.6	48
107	Complete Genome Sequence of a <i>Salivirus</i> in Respiratory Specimens from a Child with Adenovirus Infection. Genome Announcements, 2016, 4, .	0.8	2
108	The genome sequences of <i>Arachis duranensis</i> and <i>Arachis ipaensis</i> , the diploid ancestors of cultivated peanut. Nature Genetics, 2016, 48, 438-446.	21.4	761

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109	Structural genomic changes underlie alternative reproductive strategies in the ruff (<i>Philomachus</i>) Tj ETQq1 1 0.784314 rgBT /Overloc	21.4	340
110	Fast-Suppressor Screening for New Components in Protein Trafficking, Organelle Biogenesis and Silencing Pathway in <i>Arabidopsis thaliana</i> Using DEX-Inducible FREE1-RNAi Plants. <i>Journal of Genetics and Genomics</i> , 2015, 42, 319-330.	3.9	18
111	Genome sequence of cultivated Upland cotton (<i>Gossypium hirsutum</i> TM-1) provides insights into genome evolution. <i>Nature Biotechnology</i> , 2015, 33, 524-530.	17.5	1,064
112	A genome draft of the legless anguid lizard, <i>Ophisaurus gracilis</i> . <i>GigaScience</i> , 2015, 4, 17.	6.4	23
113	The <i>Symbiodinium kawagutii</i> genome illuminates dinoflagellate gene expression and coral symbiosis. <i>Science</i> , 2015, 350, 691-694.	12.6	430
114	Appraisal of the Missing Proteins Based on the mRNAs Bound to Ribosomes. <i>Journal of Proteome Research</i> , 2015, 14, 4976-4984.	3.7	1
115	The genome sequence of the orchid <i>Phalaenopsis equestris</i> . <i>Nature Genetics</i> , 2015, 47, 65-72.	21.4	413
116	Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. <i>Nature Communications</i> , 2014, 5, 5594.	12.8	135
117	Whole-genome bisulfite sequencing of multiple individuals reveals complementary roles of promoter and gene body methylation in transcriptional regulation. <i>Genome Biology</i> , 2014, 15, 408.	8.8	173
118	Comparative population genomics reveals the domestication history of the peach, <i>Prunus persica</i> , and human influences on perennial fruit crops. <i>Genome Biology</i> , 2014, 15, 415.	8.8	134
119	Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing. <i>Nature Communications</i> , 2014, 5, 4340.	12.8	332
120	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	12.6	436
121	Comparative population genomics reveals the domestication history of the peach., <i>Genome Biology</i> , 2014, 15, 415.	9.6	3
122	Genomic landscapes of Chinese hamster ovary cell lines as revealed by the <i>Cricetulus griseus</i> draft genome. <i>Nature Biotechnology</i> , 2013, 31, 759-765.	17.5	340
123	The sacred lotus genome provides insights into the evolution of flowering plants. <i>Plant Journal</i> , 2013, 76, 557-567.	5.7	75
124	A genomic variation map provides insights into the genetic basis of cucumber domestication and diversity. <i>Nature Genetics</i> , 2013, 45, 1510-1515.	21.4	472
125	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra</i>) Tj ETQq1 1 0.784314 rgBT /Over	17.5	479
126	The <i>Tarenaya hassleriana</i> Genome Provides Insight into Reproductive Trait and Genome Evolution of Crucifers. <i>Plant Cell</i> , 2013, 25, 2813-2830.	6.6	95

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127	Baiji genomes reveal low genetic variability and new insights into secondary aquatic adaptations. <i>Nature Communications</i> , 2013, 4, 2708.	12.8	93
128	Analysis of elite variety tag SNPs reveals an important allele in upland rice. <i>Nature Communications</i> , 2013, 4, 2138.	12.8	43
129	Genome-Wide Characterization of Nonreference Transposons Reveals Evolutionary Propensities of Transposons in Soybean. <i>Plant Cell</i> , 2012, 24, 4422-4436.	6.6	51
130	Single-Cell Exome Sequencing and Monoclonal Evolution of a JAK2-Negative Myeloproliferative Neoplasm. <i>Cell</i> , 2012, 148, 873-885.	28.9	503
131	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	21.4	577
132	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
133	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	27.8	2,860
134	Genome sequence of foxtail millet (<i>Setaria italica</i>) provides insights into grass evolution and biofuel potential. <i>Nature Biotechnology</i> , 2012, 30, 549-554.	17.5	636
135	The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. <i>Nature Biotechnology</i> , 2011, 29, 735-741.	17.5	699
136	Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection. <i>Nature Genetics</i> , 2010, 42, 1053-1059.	21.4	987
137	The draft genome assembly of the critically endangered <i>Nyssa yunnanensis</i> , a plant species with extremely small populations endemic to Yunnan Province, China. <i>GigaByte</i> , 0, 2020, 1-12.	0.0	3