

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
g-index

144
all docs

144
docs citations

144
times ranked

31238
citing authors

#	ARTICLE	IF	CITATIONS
1	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	27.8	2,860
2	Taxonomic structure and functional association of foxtail millet root microbiome. <i>GigaScience</i> , 2017, 6, 1-12.	6.4	1,228
3	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
4	The gut microbiome in atherosclerotic cardiovascular disease. <i>Nature Communications</i> , 2017, 8, 845.	12.8	1,029
5	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
6	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
7	The genome sequences of <i>Arachis duranensis</i> and <i>Arachis ipaensis</i> , the diploid ancestors of cultivated peanut. <i>Nature Genetics</i> , 2016, 48, 438-446.	21.4	761
8	The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. <i>Nature Biotechnology</i> , 2011, 29, 735-741.	17.5	699
9	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
10	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	21.4	577
11	An atlas of the protein-coding genes in the human, pig, and mouse brain. <i>Science</i> , 2020, 367, .	12.6	517
12	Single-Cell Exome Sequencing and Monoclonal Evolution of a JAK2-Negative Myeloproliferative Neoplasm. <i>Cell</i> , 2012, 148, 873-885.	28.9	503
13	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra</i>) TJ ETQq1 1 0,784314 r gBT /Ov	17.5	479
14	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
15	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	12.6	436
16	The <i>Symbiodinium kawagutii</i> genome illuminates dinoflagellate gene expression and coral symbiosis. <i>Science</i> , 2015, 350, 691-694.	12.6	430
17	A reference gene catalogue of the pig gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16161.	13.3	416
18	The genome sequence of the orchid <i>Phalaenopsis equestris</i> . <i>Nature Genetics</i> , 2015, 47, 65-72.	21.4	413

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19	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. <i>Nature Biotechnology</i> , 2019, 37, 179-185.	17.5	402
20	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	9.3	391
21	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
22	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
23	Structural genomic changes underlie alternative reproductive strategies in the ruff (<i>Philomachus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	21.4	340
24	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , 2018, 361, .	12.6	339
25	Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing. <i>Nature Communications</i> , 2014, 5, 4340.	12.8	332
26	Genomes of Subaerial Zygnematophyceae Provide Insights into Land Plant Evolution. <i>Cell</i> , 2019, 179, 1057-1067.e14.	28.9	320
27	The structure and function of the global citrus rhizosphere microbiome. <i>Nature Communications</i> , 2018, 9, 4894.	12.8	304
28	Redefining the structural motifs that determine <scp>RNA</scp> binding and <scp>RNA</scp> editing by pentatricopeptide repeat proteins in land plants. <i>Plant Journal</i> , 2016, 85, 532-547.	5.7	267
29	Draft genome of the living fossil <i>Ginkgo biloba</i> . <i>GigaScience</i> , 2016, 5, 49.	6.4	232
30	A reference human genome dataset of the BGISEQ-500 sequencer. <i>GigaScience</i> , 2017, 6, 1-9.	6.4	219
31	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
32	Allelic diversity in an NLR gene <i>BPH9</i> enables rice to combat planthopper variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12850-12855.	7.1	196
33	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
34	10KP: A phylodiverse genome sequencing plan. <i>GigaScience</i> , 2018, 7, 1-9.	6.4	169
35	The pearl oyster <i>Pinctada fucata martensii</i> genome and multi-omic analyses provide insights into biomineralization. <i>GigaScience</i> , 2017, 6, 1-12.	6.4	160
36	Bph6 encodes an exocyst-localized protein and confers broad resistance to planthoppers in rice. <i>Nature Genetics</i> , 2018, 50, 297-306.	21.4	158

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37	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. <i>Nature Communications</i> , 2019, 10, 470.	12.8	156
38	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
39	Landscape of genomic diversity and trait discovery in soybean. <i>Scientific Reports</i> , 2016, 6, 23598.	3.3	151
40	Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. <i>Nature Plants</i> , 2020, 6, 95-106.	9.3	146
41	The genetic basis for ecological adaptation of the Atlantic herring revealed by genome sequencing. <i>ELife</i> , 2016, 5, .	6.0	143
42	Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. <i>Nature Communications</i> , 2014, 5, 5594.	12.8	135
43	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
44	The draft genomes of five agriculturally important African orphan crops. <i>GigaScience</i> , 2019, 8, .	6.4	108
45	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	27.8	106
46	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
47	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
48	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
49	Baiji genomes reveal low genetic variability and new insights into secondary aquatic adaptations. <i>Nature Communications</i> , 2013, 4, 2708.	12.8	93
50	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
51	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
52	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
53	Enhancing CRISPR-Cas9 gRNA efficiency prediction by data integration and deep learning. <i>Nature Communications</i> , 2021, 12, 3238.	12.8	81
54	The <i>Cycas</i> genome and the early evolution of seed plants. <i>Nature Plants</i> , 2022, 8, 389-401.	9.3	80

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55	A western Sahara centre of domestication inferred from pearl millet genomes. <i>Nature Ecology and Evolution</i> , 2018, 2, 1377-1380.	7.8	78
56	Recent breeding programs enhanced genetic diversity in both desi and kabuli varieties of chickpea (<i>Cicer arietinum</i> L.). <i>Scientific Reports</i> , 2016, 6, 38636.	3.3	77
57	The sacred lotus genome provides insights into the evolution of flowering plants. <i>Plant Journal</i> , 2013, 76, 557-567.	5.7	75
58	The genetic architecture of floral traits in the woody plant <i>Prunus mume</i> . <i>Nature Communications</i> , 2018, 9, 1702.	12.8	73
59	African Orphan Crops Consortium (AOCC): status of developing genomic resources for African orphan crops. <i>Planta</i> , 2019, 250, 989-1003.	3.2	73
60	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
61	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
62	Integrated transcriptome, small RNA and degradome sequencing approaches provide insights into <i>Ascochyta</i> blight resistance in chickpea. <i>Plant Biotechnology Journal</i> , 2019, 17, 914-931.	8.3	66
63	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
64	Genome-wide determination of on-target and off-target characteristics for RNA-guided DNA methylation by dCas9 methyltransferases. <i>GigaScience</i> , 2018, 7, 1-19.	6.4	64
65	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
66	Genome-Wide Characterization of Nonreference Transposons Reveals Evolutionary Propensities of Transposons in Soybean. <i>Plant Cell</i> , 2012, 24, 4422-4436.	6.6	51
67	PGA: an R/Bioconductor package for identification of novel peptides using a customized database derived from RNA-Seq. <i>BMC Bioinformatics</i> , 2016, 17, 244.	2.6	48
68	Initial data release and announcement of the 10,000 Fish Genomes Project (Fish10K). <i>GigaScience</i> , 2020, 9, .	6.4	47
69	Genome Annotation of a Model Diatom <i>Phaeodactylum tricorutum</i> Using an Integrated Proteogenomic Pipeline. <i>Molecular Plant</i> , 2018, 11, 1292-1307.	8.3	44
70	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
71	Chloranthus genome provides insights into the early diversification of angiosperms. <i>Nature Communications</i> , 2021, 12, 6930.	12.8	44
72	Analysis of elite variety tag SNPs reveals an important allele in upland rice. <i>Nature Communications</i> , 2013, 4, 2138.	12.8	43

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73	Announcing the Genome Atlas of Bamboo and Rattan (GABR) project: promoting research in evolution and in economically and ecologically beneficial plants. <i>GigaScience</i> , 2017, 6, 1-7.	6.4	42
74	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. <i>New Phytologist</i> , 2018, 217, 453-466.	7.3	42
75	Chromosome-level genome assembly of the spotted sea bass, <i>Lateolabrax maculatus</i> . <i>GigaScience</i> , 2018, 7, .	6.4	39
76	CRISPR-C: circularization of genes and chromosome by CRISPR in human cells. <i>Nucleic Acids Research</i> , 2018, 46, e131.	14.5	39
77	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
78	Whole-genome sequencing of 175 Mongolians uncovers population-specific genetic architecture and gene flow throughout North and East Asia. <i>Nature Genetics</i> , 2018, 50, 1696-1704.	21.4	38
79	Population genomic data reveal genes related to important traits of quail. <i>GigaScience</i> , 2018, 7, .	6.4	38
80	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
81	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
82	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. <i>Scientific Data</i> , 2021, 8, 50.	5.3	38
83	Deep whole-genome sequencing of 90 Han Chinese genomes. <i>GigaScience</i> , 2017, 6, 1-7.	6.4	36
84	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
85	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
86	Draft genome sequence of the Tibetan medicinal herb <i>Rhodiola crenulata</i> . <i>GigaScience</i> , 2017, 6, 1-5.	6.4	33
87	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
88	Draft Genomes of Two <i>Artocarpus</i> Plants, Jackfruit (<i>A. heterophyllus</i>) and Breadfruit (<i>A. altilis</i>). <i>Genes</i> , 2020, 11, 27.	2.4	30
89	RED-ML: a novel, effective RNA editing detection method based on machine learning. <i>GigaScience</i> , 2017, 6, 1-8.	6.4	29
90	New insights from <i>Opisthorchis felinus</i> genome: update on genomics of the epidemiologically important liver flukes. <i>BMC Genomics</i> , 2019, 20, 399.	2.8	29

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91	The chromosome-level genome assemblies of two rattans (<i>Calamus simplicifolius</i> and <i>Daemonorops</i>) Tj ETQq1 1 0.784314 rgBT /Ove	6.4	28
92	Genomic variants identified from whole-genome resequencing of indicine cattle breeds from Pakistan. PLoS ONE, 2019, 14, e0215065.	2.5	28
93	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
94	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
95	Beaver and Naked Mole Rat Genomes Reveal Common Paths to Longevity. Cell Reports, 2020, 32, 107949.	6.4	26
96	Chromosome-level reference genome of the Siamese fighting fish <i>Betta splendens</i> , a model species for the study of aggression. GigaScience, 2018, 7, .	6.4	25
97	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
98	Chromosome-level genome assembly of <i>Lethenteron reissneri</i> provides insights into lamprey evolution. Molecular Ecology Resources, 2021, 21, 448-463.	4.8	25
99	Analysis of 427 genomes reveals moso bamboo population structure and genetic basis of property traits. Nature Communications, 2021, 12, 5466.	12.8	24
100	A genome draft of the legless anguid lizard, <i>Ophisaurus gracilis</i> . GigaScience, 2015, 4, 17.	6.4	23
101	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
102	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. Journal of Genetics and Genomics, 2015, 42, 319-330.	3.9	18
103	Natural selection and repeated patterns of molecular evolution following allopatric divergence. ELife, 2019, 8, .	6.0	18
104	Whole-genome duplication and molecular evolution in <i>Cornus</i> L. (Cornaceae) – Insights from transcriptome sequences. PLoS ONE, 2017, 12, e0171361.	2.5	17
105	Dissecting the genome of star fruit (<i>Averrhoa carambola</i> L.). Horticulture Research, 2020, 7, 94.	6.3	16
106	First documented case of avian influenza (H5N1) virus infection in a lion. Emerging Microbes and Infections, 2016, 5, 1-3.	6.5	15
107	A survey of the sperm whale (<i>Physeter catodon</i>) commensal microbiome. PeerJ, 2019, 7, e7257.	2.0	15
108	Molecular evidence for origin, diversification and ancient gene duplication of plant subtilases (SBTs). Scientific Reports, 2019, 9, 12485.	3.3	14

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109	Chromosome level comparative analysis of Brassica genomes. <i>Plant Molecular Biology</i> , 2019, 99, 237-249.	3.9	14
110	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
111	Complete Chloroplast Genomes of 14 Mangroves: Phylogenetic and Comparative Genomic Analyses. <i>BioMed Research International</i> , 2020, 2020, 1-13.	1.9	14
112	Genome-wide Target Enrichment-aided Chip Design: a 66â€‰K SNP Chip for Cashmere Goat. <i>Scientific Reports</i> , 2017, 7, 8621.	3.3	11
113	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
114	Performance of copy number variants detection based on whole-genome sequencing by DNBSEQ platforms. <i>BMC Bioinformatics</i> , 2020, 21, 518.	2.6	10
115	The genome of the naturally evolved obesity-prone Ossabaw miniature pig. <i>IScience</i> , 2021, 24, 103081.	4.1	9
116	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
117	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
118	Improvement of peptide identification with considering the abundance of mRNA and peptide. <i>BMC Bioinformatics</i> , 2017, 18, 109.	2.6	7
119	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
120	Chromosome-Level Comprehensive Genome of Mangrove Sediment-Derived Fungus <i>Penicillium variable</i> HXQ-H-1. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 7.	3.5	6
121	Enhancement of de novo sequencing, assembly and annotation of the Mongolian gerbil genome with transcriptome sequencing and assembly from several different tissues. <i>BMC Genomics</i> , 2019, 20, 903.	2.8	5
122	Genome sequencing of deep-sea hydrothermal vent snails reveals adaptations to extreme environments. <i>GigaScience</i> , 2020, 9, .	6.4	5
123	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
124	Lineage-specific evolution of mangrove plastid genomes. <i>Plant Genome</i> , 2020, 13, e20019.	2.8	4
125	A novel Enterovirus 96 circulating in China causes hand, foot, and mouth disease. <i>Virus Genes</i> , 2017, 53, 352-356.	1.6	3
126	Central and Peripheral Nervous System Progenitors Derived from Human Pluripotent Stem Cells Reveal a Unique Temporal and Cell-Type Specific Expression of PMCA. <i>Frontiers in Cell and Developmental Biology</i> , 2018, 6, 5.	3.7	3

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127	LION: a simple and rapid method to achieve CRISPR gene editing. Cellular and Molecular Life Sciences, 2019, 76, 2633-2645.	5.4	3
128	African Arowana Genome Provides Insights on Ancient Teleost Evolution. IScience, 2020, 23, 101662.	4.1	3
129	The genome of Mekong tiger perch (<i>Datnioides undecimradiatus</i>) provides insights into the phylogenetic position of Lobotiformes and biological conservation. Scientific Reports, 2020, 10, 8164.	3.3	3
130	Comparative population genomics reveals the domestication history of the peach,. Genome Biology, 2014, 15, 415.	9.6	3
131	The draft genome assembly of the critically endangered <i>Nyssa yunnanensis</i> , a plant species with extremely small populations endemic to Yunnan Province, China. GigaByte, 0, 2020, 1-12.	0.0	3
132	Complete Genome Sequence of a <i>Salivirus</i> in Respiratory Specimens from a Child with Adenovirus Infection. Genome Announcements, 2016, 4, .	0.8	2
133	Appraisal of the Missing Proteins Based on the mRNAs Bound to Ribosomes. Journal of Proteome Research, 2015, 14, 4976-4984.	3.7	1
134	The complete plastid genomes of four species from Brassicales. Mitochondrial DNA Part B: Resources, 2019, 4, 124-125.	0.4	1
135	Family-Based Whole Genome Sequencing Identified Novel Variants in ABCA5 Gene in a Patient with Idiopathic Ventricular Tachycardia. Pediatric Cardiology, 2020, 41, 1783-1794.	1.3	1
136	The complete chloroplast genome of a shrub species, <i>Smilax glabra</i> (Smilacaceae) from Guangdong, China. Mitochondrial DNA Part B: Resources, 2021, 6, 3064-3066.	0.4	1
137	Long- read sequencing and de novo assembly of the cynomolgus macaque genome. Journal of Genetics and Genomics, 2022, , .	3.9	1