

Xin Liu

List of Publications by Year in Descending Order

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Version: 2024-04-20

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

134
papers

15,382
citations

49
h-index

123
g-index

144
ext. papers

20,537
ext. citations

14.8
avg, IF

6.69
L-index

#	Paper	IF	Citations
134	Long- read sequencing and de novo assembly of the cynomolgus macaque genome.. <i>Journal of Genetics and Genomics</i> , 2022 ,	4	0
133	Two divergent haplotypes from a highly heterozygous lychee genome suggest independent domestication events for early and late-maturing cultivars.. <i>Nature Genetics</i> , 2022 ,	36.3	5
132	The Cycas genome and the early evolution of seed plants.. <i>Nature Plants</i> , 2022 ,	11.5	5
131	Chloranthus genome provides insights into the early diversification of angiosperms. <i>Nature Communications</i> , 2021 , 12, 6930	17.4	5
130	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021 , 599, 622-627	30.4	15
129	Whole-genome resequencing of 445 Lactuca accessions reveals the domestication history of cultivated lettuce. <i>Nature Genetics</i> , 2021 , 53, 752-760	36.3	9
128	Enhancing CRISPR-Cas9 gRNA efficiency prediction by data integration and deep learning. <i>Nature Communications</i> , 2021 , 12, 3238	17.4	13
127	Chromosome-level genome assembly of Lethenteron reissneri provides insights into lamprey evolution. <i>Molecular Ecology Resources</i> , 2021 , 21, 448-463	8.4	10
126	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. <i>Scientific Data</i> , 2021 , 8, 50	8.2	13
125	The complete chloroplast genome of a shrub species, (Smilacaceae) from Guangdong, China. <i>Mitochondrial DNA Part B: Resources</i> , 2021 , 6, 3064-3066	0.5	1
124	Analysis of 427 genomes reveals moso bamboo population structure and genetic basis of property traits. <i>Nature Communications</i> , 2021 , 12, 5466	17.4	3
123	The genome of the naturally evolved obesity-prone Ossabaw miniature pig. <i>iScience</i> , 2021 , 24, 103081	6.1	2
122	The White-Spotted Bamboo Shark Genome Reveals Chromosome Rearrangements and Fast-Evolving Immune Genes of Cartilaginous Fish. <i>iScience</i> , 2020 , 23, 101754	6.1	8
121	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	4.9	0
120	Complete Chloroplast Genomes of 14 Mangroves: Phylogenetic and Comparative Genomic Analyses. <i>BioMed Research International</i> , 2020 , 2020, 8731857	3	7
119	Dissecting the genome of star fruit (L.). <i>Horticulture Research</i> , 2020 , 7, 94	7.7	8
118	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	12.3	31

117	An atlas of the protein-coding genes in the human, pig, and mouse brain. <i>Science</i> , 2020 , 367,	33.3	130
116	Haplotyping by CRISPR-mediated DNA circularization (CRISPR-hapC) broadens allele-specific gene editing. <i>Nucleic Acids Research</i> , 2020 , 48, e25	20.1	3
115	Lineage-specific evolution of mangrove plastid genomes. <i>Plant Genome</i> , 2020 , 13, e20019	4.4	2
114	Genome-wide analysis of epigenetic and transcriptional changes associated with heterosis in pigeonpea. <i>Plant Biotechnology Journal</i> , 2020 , 18, 1697-1710	11.6	17
113	Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. <i>Nature Plants</i> , 2020 , 6, 95-106	11.5	73
112	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	2.9	16
111	The Chromosome-Based Rubber Tree Genome Provides New Insights into Spurge Genome Evolution and Rubber Biosynthesis. <i>Molecular Plant</i> , 2020 , 13, 336-350	14.4	29
110	The Chromosome Level Genome and Genome-wide Association Study for the Agronomic Traits of. <i>IScience</i> , 2020 , 23, 101538	6.1	12
109	An Indo-Pacific Humpback Dolphin Genome Reveals Insights into Chromosome Evolution and the Demography of a Vulnerable Species. <i>IScience</i> , 2020 , 23, 101640	6.1	8
108	Performance of copy number variants detection based on whole-genome sequencing by DNBSEQ platforms. <i>BMC Bioinformatics</i> , 2020 , 21, 518	3.6	3
107	Beaver and Naked Mole Rat Genomes Reveal Common Paths to Longevity. <i>Cell Reports</i> , 2020 , 32, 107949	10.6	10
106	Genomic and transcriptomic analysis unveils population evolution and development of pesticide resistance in fall armyworm <i>Spodoptera frugiperda</i> . <i>Protein and Cell</i> , 2020 , 1	7.2	20
105	Deciphering the Microbial Taxonomy and Functionality of Two Diverse Mangrove Ecosystems and Their Potential Abilities To Produce Bioactive Compounds. <i>MSystems</i> , 2020 , 5,	7.6	5
104	African Arowana Genome Provides Insights on Ancient Teleost Evolution. <i>IScience</i> , 2020 , 23, 101662	6.1	1
103	Family-Based Whole Genome Sequencing Identified Novel Variants in ABCA5 Gene in a Patient with Idiopathic Ventricular Tachycardia. <i>Pediatric Cardiology</i> , 2020 , 41, 1783-1794	2.1	0
102	TGS-GapCloser: A fast and accurate gap closer for large genomes with low coverage of error-prone long reads. <i>GigaScience</i> , 2020 , 9,	7.6	30
101	Initial data release and announcement of the 10,000 Fish Genomes Project (Fish10K). <i>GigaScience</i> , 2020 , 9,	7.6	12
100	Genome sequencing of deep-sea hydrothermal vent snails reveals adaptations to extreme environments. <i>GigaScience</i> , 2020 , 9,	7.6	2

99	Molecular evidence for origin, diversification and ancient gene duplication of plant subtilases (SBTs). <i>Scientific Reports</i> , 2019 , 9, 12485	4.9	5
98	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	3.2	2
97	Resequencing 545 ginkgo genomes across the world reveals the evolutionary history of the living fossil. <i>Nature Communications</i> , 2019 , 10, 4201	17.4	41
96	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,	7.6	24
95	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. <i>Nature Communications</i> , 2019 , 10, 470	17.4	84
94	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,	7.6	24
93	New insights from <i>Opisthorchis felinus</i> genome: update on genomics of the epidemiologically important liver flukes. <i>BMC Genomics</i> , 2019 , 20, 399	4.5	17
92	Phylogenomics Provides New Insights into Gains and Losses of Selenoproteins among Archaeplastida. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	8
91	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	8.4	25
90	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	36.3	116
89	LION: a simple and rapid method to achieve CRISPR gene editing. <i>Cellular and Molecular Life Sciences</i> , 2019 , 76, 2633-2645	10.3	3
88	Genomic variants identified from whole-genome resequencing of indicine cattle breeds from Pakistan. <i>PLoS ONE</i> , 2019 , 14, e0215065	3.7	9
87	Sequencing of the MHC region defines as the major genetic risk for seropositive rheumatoid arthritis in Han Chinese population. <i>Annals of the Rheumatic Diseases</i> , 2019 , 78, 773-780	2.4	16
86	The first chromosome-level genome for a marine mammal as a resource to study ecology and evolution. <i>Molecular Ecology Resources</i> , 2019 , 19, 944-956	8.4	15
85	Deciphering the Composition and Functional Profile of the Microbial Communities in Chinese Moutai Liquor Starters. <i>Frontiers in Microbiology</i> , 2019 , 10, 1540	5.7	29
84	African Orphan Crops Consortium (AOCC): status of developing genomic resources for African orphan crops. <i>Planta</i> , 2019 , 250, 989-1003	4.7	42
83	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	9.7	49
82	Genomes of Subaerial Zygnematophyceae Provide Insights into Land Plant Evolution. <i>Cell</i> , 2019 , 179, 1057-1067.e14	56.2	151

81	Natural selection and repeated patterns of molecular evolution following allopatric divergence. <i>ELife</i> , 2019 , 8,	8.9	7
80	A survey of the sperm whale () commensal microbiome. <i>PeerJ</i> , 2019 , 7, e7257	3.1	6
79	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. <i>Nature Biotechnology</i> , 2019 , 37, 179-185	44.5	213
78	Draft Genomes of Two Artocarpus Plants, Jackfruit (<i>A. heterophyllus</i>) and Breadfruit (<i>A. altilis</i>). <i>Genes</i> , 2019 , 11,	4.2	12
77	Chromosome-Level Comprehensive Genome of Mangrove Sediment-Derived Fungus HXQ-H-1. <i>Journal of Fungi (Basel, Switzerland)</i> , 2019 , 6,	5.6	1
76	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	4.5	2
75	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	8.4	19
74	Chromosome level comparative analysis of Brassica genomes. <i>Plant Molecular Biology</i> , 2019 , 99, 237-249	4.6	7
73	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	11.6	35
72	The draft genomes of five agriculturally important African orphan crops. <i>GigaScience</i> , 2019 , 8,	7.6	68
71	10KP: A phylo diverse genome sequencing plan. <i>GigaScience</i> , 2018 , 7, 1-9	7.6	108
70	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	7.6	43
69	Bph6 encodes an exocyst-localized protein and confers broad resistance to planthoppers in rice. <i>Nature Genetics</i> , 2018 , 50, 297-306	36.3	88
68	The genetic architecture of floral traits in the woody plant <i>Prunus mume</i> . <i>Nature Communications</i> , 2018 , 9, 1702	17.4	46
67	Is there foul play in the leaf pocket? The metagenome of floating fern <i>Azolla</i> reveals endophytes that do not fix N but may denitrify. <i>New Phytologist</i> , 2018 , 217, 453-466	9.8	17
66	A western Sahara centre of domestication inferred from pearl millet genomes. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1377-1380	12.3	48
65	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,	7.6	14
64	Central and Peripheral Nervous System Progenitors Derived from Human Pluripotent Stem Cells Reveal a Unique Temporal and Cell-Type Specific Expression of PMCAs. <i>Frontiers in Cell and Developmental Biology</i> , 2018 , 6, 5	5.7	1

63	The chromosome-level genome assemblies of two rattans (<i>Calamus simplicifolius</i> and <i>Daemonorops jenkinsiana</i>). <i>GigaScience</i> , 2018 , 7,	7.6	11
62	The structure and function of the global citrus rhizosphere microbiome. <i>Nature Communications</i> , 2018 , 9, 4894	17.4	157
61	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	36.3	27
60	Chromosome-level genome assembly of the spotted sea bass, <i>Lateolabrax maculatus</i> . <i>GigaScience</i> , 2018 , 7,	7.6	16
59	Genome Annotation of a Model Diatom <i>Phaeodactylum tricornutum</i> Using an Integrated Proteogenomic Pipeline. <i>Molecular Plant</i> , 2018 , 11, 1292-1307	14.4	24
58	CRISPR-C: circularization of genes and chromosome by CRISPR in human cells. <i>Nucleic Acids Research</i> , 2018 , 46, e131	20.1	23
57	Phylogenomics reveals multiple losses of nitrogen-fixing root nodule symbiosis. <i>Science</i> , 2018 , 361,	33.3	167
56	Population genomic data reveal genes related to important traits of quail. <i>GigaScience</i> , 2018 , 7,	7.6	16
55	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018 , 4, 460-475	47.5	176
54	Patient iPSC-Derived Neurons for Disease Modeling of Frontotemporal Dementia with Mutation in CHMP2B. <i>Stem Cell Reports</i> , 2017 , 8, 648-658	8	52
53	A novel Enterovirus 96 circulating in China causes hand, foot, and mouth disease. <i>Virus Genes</i> , 2017 , 53, 352-356	2.3	1
52	Draft genome sequence of the Tibetan medicinal herb <i>Rhodiola crenulata</i> . <i>GigaScience</i> , 2017 , 6, 1-5	7.6	20
51	A reference human genome dataset of the BGISEQ-500 sequencer. <i>GigaScience</i> , 2017 , 6, 1-9	7.6	141
50	Retinoic acid combined with spermatogonial stem cell conditions facilitate the generation of mouse germ-like cells. <i>Bioscience Reports</i> , 2017 , 37,	4.1	6
49	The gut microbiome in atherosclerotic cardiovascular disease. <i>Nature Communications</i> , 2017 , 8, 845	17.4	575
48	Taxonomic structure and functional association of foxtail millet root microbiome. <i>GigaScience</i> , 2017 , 6, 1-12	7.6	1155
47	Whole-genome duplication and molecular evolution in <i>Cornus</i> L. (Cornaceae) - Insights from transcriptome sequences. <i>PLoS ONE</i> , 2017 , 12, e0171361	3.7	10
46	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017 , 35, 969-976	44.5	197

45	Genome-wide Target Enrichment-aided Chip Design: a 66 K SNP Chip for Cashmere Goat. <i>Scientific Reports</i> , 2017 , 7, 8621	4.9	5
44	RED-ML: a novel, effective RNA editing detection method based on machine learning. <i>GigaScience</i> , 2017 , 6, 1-8	7.6	19
43	Deep whole-genome sequencing of 90 Han Chinese genomes. <i>GigaScience</i> , 2017 , 6, 1-7	7.6	22
42	The pearl oyster <i>Pinctada fucata martensii</i> genome and multi-omic analyses provide insights into biomineralization. <i>GigaScience</i> , 2017 , 6, 1-12	7.6	116
41	Improvement of peptide identification with considering the abundance of mRNA and peptide. <i>BMC Bioinformatics</i> , 2017 , 18, 109	3.6	6
40	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	7.6	22
39	Draft genome of the living fossil <i>Ginkgo biloba</i> . <i>GigaScience</i> , 2016 , 5, 49	7.6	161
38	A reference gene catalogue of the pig gut microbiome. <i>Nature Microbiology</i> , 2016 , 1, 16161	26.6	233
37	Allelic diversity in an NLR gene 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	11.5	120
36	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	3.6	39
35	Complete Genome Sequence of a Salivirus in Respiratory Specimens from a Child with Adenovirus Infection. <i>Genome Announcements</i> , 2016 , 4,		1
34	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, 438-46	36.3	498
33	Structural genomic changes underlie alternative reproductive strategies in the ruff (<i>Philomachus pugnax</i>). <i>Nature Genetics</i> , 2016 , 48, 84-8	36.3	214
32	The genetic basis for ecological adaptation of the Atlantic herring revealed by genome sequencing. <i>ELife</i> , 2016 , 5,	8.9	103
31	Redefining the structural motifs that determine RNA binding and RNA editing by pentatricopeptide repeat proteins in land plants. <i>Plant Journal</i> , 2016 , 85, 532-47	6.9	176
30	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	4.9	53
29	Landscape of genomic diversity and trait discovery in soybean. <i>Scientific Reports</i> , 2016 , 6, 23598	4.9	112
28	First documented case of avian influenza (H5N1) virus infection in a lion. <i>Emerging Microbes and Infections</i> , 2016 , 5, e125	18.9	11

27	Genome sequence of cultivated Upland cotton (<i>Gossypium hirsutum</i> TM-1) provides insights into genome evolution. <i>Nature Biotechnology</i> , 2015 , 33, 524-30	44.5	683
26	A genome draft of the legless anguid lizard, <i>Ophisaurus gracilis</i> . <i>GigaScience</i> , 2015 , 4, 17	7.6	19
25	The Symbiodinium <i>kawagutii</i> genome illuminates dinoflagellate gene expression and coral symbiosis. <i>Science</i> , 2015 , 350, 691-4	33.3	283
24	Appraisal of the Missing Proteins Based on the mRNAs Bound to Ribosomes. <i>Journal of Proteome Research</i> , 2015 , 14, 4976-84	5.6	1
23	The genome sequence of the orchid <i>Phalaenopsis equestris</i> . <i>Nature Genetics</i> , 2015 , 47, 65-72	36.3	265
22	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, 319-30	4	16
21	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	18.3	131
20	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	18.3	97
19	Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing. <i>Nature Communications</i> , 2014 , 5, 4340	17.4	230
18	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014 , 344, 1168-1173	33.3	294
17	Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. <i>Nature Communications</i> , 2014 , 5, 5594	17.4	89
16	Genomic landscapes of Chinese hamster ovary cell lines as revealed by the <i>Cricetulus griseus</i> draft genome. <i>Nature Biotechnology</i> , 2013 , 31, 759-65	44.5	289
15	The sacred lotus genome provides insights into the evolution of flowering plants. <i>Plant Journal</i> , 2013 , 76, 557-67	6.9	55
14	A genomic variation map provides insights into the genetic basis of cucumber domestication and diversity. <i>Nature Genetics</i> , 2013 , 45, 1510-5	36.3	307
13	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra hircus</i>). <i>Nature Biotechnology</i> , 2013 , 31, 135-41	44.5	355
12	The <i>Tarenaya hassleriana</i> genome provides insight into reproductive trait and genome evolution of crucifers. <i>Plant Cell</i> , 2013 , 25, 2813-30	11.6	67
11	Baiji genomes reveal low genetic variability and new insights into secondary aquatic adaptations. <i>Nature Communications</i> , 2013 , 4, 2708	17.4	76
10	Analysis of elite variety tag SNPs reveals an important allele in upland rice. <i>Nature Communications</i> , 2013 , 4, 2138	17.4	27

9	Single-cell exome sequencing and monoclonal evolution of a JAK2-negative myeloproliferative neoplasm. <i>Cell</i> , 2012 , 148, 873-85	56.2	431
8	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012 , 44, 803-7	36.3	470
7	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012 , 485, 635-41	50.4	2138
6	Genome sequence of foxtail millet (<i>Setaria italica</i>) provides insights into grass evolution and biofuel potential. <i>Nature Biotechnology</i> , 2012 , 30, 549-54	44.5	447
5	Genome-wide characterization of nonreference transposons reveals evolutionary propensities of transposons in soybean. <i>Plant Cell</i> , 2012 , 24, 4422-36	11.6	42
4	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2011 , 30, 105-11	44.5	635
3	The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. <i>Nature Biotechnology</i> , 2011 , 29, 735-41	44.5	584
2	Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection. <i>Nature Genetics</i> , 2010 , 42, 1053-9	36.3	754
1	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> , 2020, 1-12		1