Jiang Libo

List of Publications by Year
in descending order

69 papers	951 citations	516710 16 h-index	552781 26 g-index
74 all docs	74 docs citations	74 times ranked	973 citing authors

#	Article	IF	Citations
1	Plant grafting: how genetic exchange promotes vascular reconnection. New Phytologist, 2017, 214, 56-65.	7.3	130
2	The genetic architecture of floral traits in the woody plant Prunus mume. Nature Communications, 2018, 9, 1702.	12.8	73
3	Deep-sequencing transcriptome analysis of low temperature perception in a desert tree, Populus euphratica. BMC Genomics, 2014, 15, 326.	2.8	54
4	Integrating Evolutionary Game Theory into Mechanistic Genotype–Phenotype Mapping. Trends in Genetics, 2016, 32, 256-268.	6.7	44
5	Genome-Wide Analysis of the NAC Domain Transcription Factor Gene Family in Theobroma cacao. Genes, 2020, 11, 35.	2.4	37
6	Novel Mutation Sites in the Development of Vancomycin- Intermediate Resistance in Staphylococcus aureus. Frontiers in Microbiology, 2016, 7, 2163.	3.5	34
7	Recovering dynamic networks in big static datasets. Physics Reports, 2021, 912, 1-57.	25.6	29
8	Epigenetic game theory: How to compute the epigenetic control of maternal-to-zygotic transition. Physics of Life Reviews, 2017, 20, 126-137.	2.8	23
9	A mapping framework of competition–cooperation QTLs that drive community dynamics. Nature Communications, 2018, 9, 3010.	12.8	23
10	Long–read genome assembly and genetic architecture of fruit shape in the bottle gourd. Plant Journal, 2021, 107, 956-968.	5.7	23
11	Plastic expression of heterochrony quantitative trait loci (hQTLs) for leaf growth in the common bean (*P*haseolus vulgaris). New Phytologist, 2015, 207, 872-882.	7.3	20
12	2HiGWAS: a unifying high-dimensional platform to infer the global genetic architecture of trait development. Briefings in Bioinformatics, 2015, 16, 905-911.	6.5	20
13	The genetic architecture of shoot–root covariation during seedling emergence of a desert tree, *Populus euphratica*. Plant Journal, 2017, 90, 918-928.	5.7	20
14	An omnidirectional visualization model of personalized gene regulatory networks. Npj Systems Biology and Applications, 2019, 5, 38.	3.0	20
15	Modeling genome-wide by environment interactions through omnigenic interactome networks. Cell Reports, 2021, 35, 109114.	6.4	20
16	Network mapping of root–microbe interactions in Arabidopsis thaliana. Npj Biofilms and Microbiomes, 2021, 7, 72.	6.4	19
17	Functional mapping of N deficiency–induced response in wheat yield–component traits by implementing high–throughput phenotyping. Plant Journal, 2019, 97, 1105-1119.	5.7	18
18	Genome-wide association studies of callus differentiation for the desert tree, *Populus euphratica*. Tree Physiology, 2020, 40, 1762-1777.	3.1	18

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19	Constructing a linkage–linkage disequilibrium map using dominant-segregating markers. DNA Research, 2016, 23, dsv031.	3.4	16
20	A computational framework for mapping the timing of vegetative phase change. New Phytologist, 2016, 211, 750-760.	7.3	16
21	Computational identification of genes modulating stem height–diameter allometry. Plant Biotechnology Journal, 2016, 14, 2254-2264.	8.3	15
22	HpQTL: a geometric morphometric platform to compute the genetic architecture of heterophylly. Briefings in Bioinformatics, 2018, 19, 603-612.	6.5	15
23	How trees allocate carbon for optimal growth: insight from a game-theoretic model. Briefings in Bioinformatics, 2018, 19, 593-602.	6.5	14
24	Two-stage identification of SNP effects on dynamic poplar growth. Plant Journal, 2018, 93, 286-296.	5.7	14
25	Recursive Test of Hardy-Weinberg Equilibrium in Tetraploids. Trends in Genetics, 2021, 37, 504-513.	6.7	14
26	A skellam model to identify differential patterns of gene expression induced by environmental signals. BMC Genomics, 2014, 15, 772.	2.8	11
27	A Drive to Driven Model of Mapping Intraspecific Interaction Networks. IScience, 2019, 22, 109-122.	4.1	11
28	A behavioral model for mapping the genetic architecture of gut-microbiota networks. Gut Microbes, 2021, 13, 1820847.	9.8	11
29	Identification of Quantitative Trait Loci for Altitude Adaptation of Tree Leaf Shape With Populus szechuanica in the Qinghai-Tibetan Plateau. Frontiers in Plant Science, 2020, 11, 632.	3.6	11
30	Analysis of quasi-dynamic ordinary differential equations and the quasi-dynamic replicator. Physica A: Statistical Mechanics and Its Applications, 2020, 555, 124422.	2.6	11
31	Cloning of the Cryptochrome-Encoding PeCRY1 Gene from Populus euphratica and Functional Analysis in Arabidopsis. PLoS ONE, 2014, 9, e115201.	2.5	10
32	Inferring the evolutionary history of outcrossing populations through computing a multiallelic linkage–linkage disequilibrium map. Methods in Ecology and Evolution, 2015, 6, 1259-1269.	5.2	10
33	Landscaping Crossover Interference Across a Genome. Trends in Plant Science, 2017, 22, 894-907.	8.8	9
34	Computational Identification of Gene Networks as a Biomarker of Neuroblastoma Risk. Cancers, 2020, 12, 2086.	3.7	8
35	The genetic control of leaf allometry in the common bean, Phaseolus vulgaris. BMC Genetics, 2020, 21, 29.	2.7	8
36	Functional physiological phenotyping with functional mapping: A general framework to bridge the phenotype-genotype gap in plant physiology. IScience, 2021, 24, 102846.	4.1	8

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37	Bacterial Genetic Architecture of Ecological Interactions in Co-culture by GWAS-Taking Escherichia coli and Staphylococcus aureus as an Example. Frontiers in Microbiology, 2017, 8, 2332.	3.5	7
38	A computational–experimental framework for mapping plant coexistence. Methods in Ecology and Evolution, 2018, 9, 1335-1352.	5.2	7
39	An ecophysiologically based mapping model identifies a major pleiotropic QTL for leaf growth trajectories of Phaseolus vulgaris. Plant Journal, 2018, 95, 775-784.	5.7	7
40	np^2QTL: networking phenotypic plasticity quantitative trait loci across heterogeneous environments. Plant Journal, 2019, 99, 796-806.	5.7	7
41	Interrogation of Internal Workings in Microbial Community Assembly: Play a Game through a Behavioral Network?. MSystems, 2019, 4, .	3.8	7
42	A dissection model for mapping complex traits. Plant Journal, 2019, 97, 1168-1182.	5.7	7
43	Functional mapping of seasonal transition in perennial plants. Briefings in Bioinformatics, 2015, 16, 526-535.	6.5	6
44	A reciprocal cross design to map the genetic architecture of complex traits in apomictic plants. New Phytologist, 2015, 205, 1360-1367.	7.3	6
45	A Computational Model for Inferring QTL Control Networks Underlying Developmental Covariation. Frontiers in Plant Science, 2019, 10, 1557.	3.6	6
46	Computational characterization of double reduction in autotetraploid natural populations. Plant Journal, 2021, 105, 1703-1709.	5.7	5
47	A Single-Cell Omics Network Model of Cell Crosstalk during the Formation of Primordial Follicles. Cells, 2022, 11, 332.	4.1	5
48	A high-dimensional linkage analysis model for characterizing crossover interference. Briefings in Bioinformatics, 2017, 18, 382-393.	6.5	4
49	SEGN: Inferring real-time gene networks mediating phenotypic plasticity. Computational and Structural Biotechnology Journal, 2020, 18, 2510-2521.	4.1	4
50	Mapping Covariation Quantitative Trait Loci That Control Organ Growth and Whole-Plant Biomass. Frontiers in Plant Science, 2019, 10, 719.	3.6	3
51	A rewiring model of intratumoral interaction networks. Computational and Structural Biotechnology Journal, 2020, 18, 45-51.	4.1	3
52	Interaction analyses based on growth parameters of GWAS between Escherichia coli and Staphylococcus aureus. AMB Express, 2021, 11, 34.	3.0	3
53	Heterophylly Quantitative Trait Loci Respond to Salt Stress in the Desert Tree Populus euphratica. Frontiers in Plant Science, 2021, 12, 692494.	3.6	3
54	A quantitative decision theory of animal conflict. Heliyon, 2021, 7, e07621.	3.2	3

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55	Genetic Architecture of Multiphasic Growth Covariation as Revealed by a Nonlinear Mixed Mapping Framework. Frontiers in Plant Science, 2021, 12, 711219.	3.6	3
56	A Computational Atlas of Tissue-specific Regulatory Networks. Frontiers in Systems Biology, 2021, 1, .	0.7	3
57	AlloMap6: an R package for genetic linkage analysis in allohexaploids. Briefings in Bioinformatics, 2016, 18, bbw085.	6.5	2
58	Evo-Devo-EpiR: a genome-wide search platform for epistatic control on the evolution of development. Briefings in Bioinformatics, 2016, 18, bbw062.	6.5	2
59	A computing platform to map ecological metabolism by integrating functional mapping and the metabolic theory of ecology. Briefings in Bioinformatics, 2017, 18, 137-144.	6.5	2
60	Integration of epigenetic game theory and developmental principles. Physics of Life Reviews, 2017, 20, 166-169.	2.8	2
61	The Genomic Landscape of Crossover Interference in the Desert Tree Populus euphratica. Frontiers in Genetics, 2019, 10, 440.	2.3	2
62	Functional Mapping: How to Map Genes for Phenotypic Plasticity of Development. , 2015, , 3-17.		1
63	<i>HiG</i>was: how to compute longitudinal GWAS data in population designs. Bioinformatics, 2020, 36, 4222-4224.	4.1	1
64	Modeling Genome-Wide by Environment Interactions Through Omnigenic Interactome Networks. SSRN Electronic Journal, 0, , .	0.4	1
65	Functional Mapping of Phenotypic Plasticity of Staphylococcus aureus Under Vancomycin Pressure. Frontiers in Microbiology, 2021, 12, 696730.	3.5	1
66	Systems Mapping for Hematopoietic Progenitor Cell Heterogeneity. PLoS ONE, 2015, 10, e0126937.	2.5	1
67	A Holling Functional Response Model for Mapping QTLs Governing Interspecific Interactions. Frontiers in Genetics, 2021, 12, 766372.	2.3	0
68	Transcriptional differentiation driving Cucumis sativusâ€"Botrytis cinerea interactions based on the Skellam model and Bayesian networks. AMB Express, 2021, 11, 138.	3.0	0
69	A Quantitative Theory of War and Peace in the Gut Microbiota. SSRN Electronic Journal, 0, , .	0.4	0