

Jiang Libo

List of Publications by Year in descending order

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Version: 2024-02-01

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	A Single-Cell Omics Network Model of Cell Crosstalk during the Formation of Primordial Follicles. <i>Cells</i> , 2022, 11, 332.	4.1	5
2	A behavioral model for mapping the genetic architecture of gut-microbiota networks. <i>Gut Microbes</i> , 2021, 13, 1820847.	9.8	11
3	Computational characterization of double reduction in autotetraploid natural populations. <i>Plant Journal</i> , 2021, 105, 1703-1709.	5.7	5
4	Recursive Test of Hardy-Weinberg Equilibrium in Tetraploids. <i>Trends in Genetics</i> , 2021, 37, 504-513.	6.7	14
5	Interaction analyses based on growth parameters of GWAS between <i>Escherichia coli</i> and <i>Staphylococcus aureus</i> . <i>AMB Express</i> , 2021, 11, 34.	3.0	3
6	Recovering dynamic networks in big static datasets. <i>Physics Reports</i> , 2021, 912, 1-57.	25.6	29
7	Modeling genome-wide by environment interactions through omnigenic interactome networks. <i>Cell Reports</i> , 2021, 35, 109114.	6.4	20
8	Heterophylly Quantitative Trait Loci Respond to Salt Stress in the Desert Tree <i>Populus euphratica</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 692494.	3.6	3
9	Long-read genome assembly and genetic architecture of fruit shape in the bottle gourd. <i>Plant Journal</i> , 2021, 107, 956-968.	5.7	23
10	A quantitative decision theory of animal conflict. <i>Heliyon</i> , 2021, 7, e07621.	3.2	3
11	Functional physiological phenotyping with functional mapping: A general framework to bridge the phenotype-genotype gap in plant physiology. <i>IScience</i> , 2021, 24, 102846.	4.1	8
12	Functional Mapping of Phenotypic Plasticity of <i>Staphylococcus aureus</i> Under Vancomycin Pressure. <i>Frontiers in Microbiology</i> , 2021, 12, 696730.	3.5	1
13	Network mapping of root-microbe interactions in <i>Arabidopsis thaliana</i> . <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 72.	6.4	19
14	Genetic Architecture of Multiphasic Growth Covariation as Revealed by a Nonlinear Mixed Mapping Framework. <i>Frontiers in Plant Science</i> , 2021, 12, 711219.	3.6	3
15	A Holling Functional Response Model for Mapping QTLs Governing Interspecific Interactions. <i>Frontiers in Genetics</i> , 2021, 12, 766372.	2.3	0
16	A Computational Atlas of Tissue-specific Regulatory Networks. <i>Frontiers in Systems Biology</i> , 2021, 1, .	0.7	3
17	Transcriptional differentiation driving <i>Cucumis sativus</i> - <i>Botrytis cinerea</i> interactions based on the Skellam model and Bayesian networks. <i>AMB Express</i> , 2021, 11, 138.	3.0	0
18	Genome-Wide Analysis of the NAC Domain Transcription Factor Gene Family in <i>Theobroma cacao</i> . <i>Genes</i> , 2020, 11, 35.	2.4	37

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19	A rewiring model of intratumoral interaction networks. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 45-51.	4.1	3
20	Computational Identification of Gene Networks as a Biomarker of Neuroblastoma Risk. <i>Cancers</i> , 2020, 12, 2086.	3.7	8
21	Genome-wide association studies of callus differentiation for the desert tree, <i>Populus euphratica</i> . <i>Tree Physiology</i> , 2020, 40, 1762-1777.	3.1	18
22	SEGN: Inferring real-time gene networks mediating phenotypic plasticity. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2510-2521.	4.1	4
23	Identification of Quantitative Trait Loci for Altitude Adaptation of Tree Leaf Shape With <i>Populus szechuanica</i> in the Qinghai-Tibetan Plateau. <i>Frontiers in Plant Science</i> , 2020, 11, 632.	3.6	11
24	HiGwas: how to compute longitudinal GWAS data in population designs. <i>Bioinformatics</i> , 2020, 36, 4222-4224.	4.1	1
25	The genetic control of leaf allometry in the common bean, <i>Phaseolus vulgaris</i> . <i>BMC Genetics</i> , 2020, 21, 29.	2.7	8
26	Analysis of quasi-dynamic ordinary differential equations and the quasi-dynamic replicator. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2020, 555, 124422.	2.6	11
27	Mapping Covariation Quantitative Trait Loci That Control Organ Growth and Whole-Plant Biomass. <i>Frontiers in Plant Science</i> , 2019, 10, 719.	3.6	3
28	An omnidirectional visualization model of personalized gene regulatory networks. <i>Npj Systems Biology and Applications</i> , 2019, 5, 38.	3.0	20
29	A Computational Model for Inferring QTL Control Networks Underlying Developmental Covariation. <i>Frontiers in Plant Science</i> , 2019, 10, 1557.	3.6	6
30	The Genomic Landscape of Crossover Interference in the Desert Tree <i>Populus euphratica</i> . <i>Frontiers in Genetics</i> , 2019, 10, 440.	2.3	2
31	np ² QTL: networking phenotypic plasticity quantitative trait loci across heterogeneous environments. <i>Plant Journal</i> , 2019, 99, 796-806.	5.7	7
32	Interrogation of Internal Workings in Microbial Community Assembly: Play a Game through a Behavioral Network?. <i>MSystems</i> , 2019, 4, .	3.8	7
33	A Drive to Driven Model of Mapping Intraspecific Interaction Networks. <i>IScience</i> , 2019, 22, 109-122.	4.1	11
34	Functional mapping of N deficiency-induced response in wheat yield component traits by implementing high-throughput phenotyping. <i>Plant Journal</i> , 2019, 97, 1105-1119.	5.7	18
35	A dissection model for mapping complex traits. <i>Plant Journal</i> , 2019, 97, 1168-1182.	5.7	7
36	A computational-experimental framework for mapping plant coexistence. <i>Methods in Ecology and Evolution</i> , 2018, 9, 1335-1352.	5.2	7

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37	The genetic architecture of floral traits in the woody plant <i>Prunus mume</i> . <i>Nature Communications</i> , 2018, 9, 1702.	12.8	73
38	HpQTL: a geometric morphometric platform to compute the genetic architecture of heterophylly. <i>Briefings in Bioinformatics</i> , 2018, 19, 603-612.	6.5	15
39	How trees allocate carbon for optimal growth: insight from a game-theoretic model. <i>Briefings in Bioinformatics</i> , 2018, 19, 593-602.	6.5	14
40	Two-stage identification of SNP effects on dynamic poplar growth. <i>Plant Journal</i> , 2018, 93, 286-296.	5.7	14
41	A mapping framework of competition-cooperation QTLs that drive community dynamics. <i>Nature Communications</i> , 2018, 9, 3010.	12.8	23
42	An ecophysiological based mapping model identifies a major pleiotropic QTL for leaf growth trajectories of <i>Phaseolus vulgaris</i> . <i>Plant Journal</i> , 2018, 95, 775-784.	5.7	7
43	A computing platform to map ecological metabolism by integrating functional mapping and the metabolic theory of ecology. <i>Briefings in Bioinformatics</i> , 2017, 18, 137-144.	6.5	2
44	A high-dimensional linkage analysis model for characterizing crossover interference. <i>Briefings in Bioinformatics</i> , 2017, 18, 382-393.	6.5	4
45	The genetic architecture of shoot-root covariation during seedling emergence of a desert tree, <i>Populus euphratica</i> . <i>Plant Journal</i> , 2017, 90, 918-928.	5.7	20
46	Integration of epigenetic game theory and developmental principles. <i>Physics of Life Reviews</i> , 2017, 20, 166-169.	2.8	2
47	Plant grafting: how genetic exchange promotes vascular reconnection. <i>New Phytologist</i> , 2017, 214, 56-65.	7.3	130
48	Landscaping Crossover Interference Across a Genome. <i>Trends in Plant Science</i> , 2017, 22, 894-907.	8.8	9
49	Epigenetic game theory: How to compute the epigenetic control of maternal-to-zygotic transition. <i>Physics of Life Reviews</i> , 2017, 20, 126-137.	2.8	23
50	Bacterial Genetic Architecture of Ecological Interactions in Co-culture by GWAS-Taking <i>Escherichia coli</i> and <i>Staphylococcus aureus</i> as an Example. <i>Frontiers in Microbiology</i> , 2017, 8, 2332.	3.5	7
51	Constructing a linkage-linkage disequilibrium map using dominant-segregating markers. <i>DNA Research</i> , 2016, 23, dsv031.	3.4	16
52	Computational identification of genes modulating stem height-diameter allometry. <i>Plant Biotechnology Journal</i> , 2016, 14, 2254-2264.	8.3	15
53	A computational framework for mapping the timing of vegetative phase change. <i>New Phytologist</i> , 2016, 211, 750-760.	7.3	16
54	AlloMap6: an R package for genetic linkage analysis in allohexaploids. <i>Briefings in Bioinformatics</i> , 2016, 18, bbw085.	6.5	2

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55	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
56	Integrating Evolutionary Game Theory into Mechanistic Genotype-Phenotype Mapping. Trends in Genetics, 2016, 32, 256-268.	6.7	44
57	Novel Mutation Sites in the Development of Vancomycin- Intermediate Resistance in Staphylococcus aureus. Frontiers in Microbiology, 2016, 7, 2163.	3.5	34
58	Plastic expression of heterochrony quantitative trait loci (QTLs) for leaf growth in the common bean (<i>Phaseolus vulgaris</i>). New Phytologist, 2015, 207, 872-882.	7.3	20
59	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
60	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
61	Functional mapping of seasonal transition in perennial plants. Briefings in Bioinformatics, 2015, 16, 526-535.	6.5	6
62	Functional Mapping: How to Map Genes for Phenotypic Plasticity of Development. , 2015, , 3-17.		1
63	A reciprocal cross design to map the genetic architecture of complex traits in apomictic plants. New Phytologist, 2015, 205, 1360-1367.	7.3	6
64	Systems Mapping for Hematopoietic Progenitor Cell Heterogeneity. PLoS ONE, 2015, 10, e0126937.	2.5	1
65	Cloning of the Cryptochrome-Encoding PeCRY1 Gene from Populus euphratica and Functional Analysis in Arabidopsis. PLoS ONE, 2014, 9, e115201.	2.5	10
66	A skellam model to identify differential patterns of gene expression induced by environmental signals. BMC Genomics, 2014, 15, 772.	2.8	11
67	Deep-sequencing transcriptome analysis of low temperature perception in a desert tree, Populus euphratica. BMC Genomics, 2014, 15, 326.	2.8	54
68	Modeling Genome-Wide by Environment Interactions Through Omnigenic Interactome Networks. SSRN Electronic Journal, 0, , .	0.4	1
69	A Quantitative Theory of War and Peace in the Gut Microbiota. SSRN Electronic Journal, 0, , .	0.4	0