

Ling-Ling Chen

List of Publications by Year in descending order

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87
papers

7,481
citations

145106

33
h-index

68831

81
g-index

98
all docs

98
docs citations

98
times ranked

11764
citing authors

#	ARTICLE	IF	CITATIONS
1	Oil plant genomes: current state of the science. <i>Journal of Experimental Botany</i> , 2022, 73, 2859-2874.	2.4	16
2	BnPIR: <i>Brassica napus</i> pan-genome information resource for 1689 accessions. <i>Plant Biotechnology Journal</i> , 2021, 19, 412-414.	4.1	51
3	Analysis of Rice Transcriptome Reveals the LncRNA/CircRNA Regulation in Tissue Development. <i>Rice</i> , 2021, 14, 14.	1.7	26
4	CharPlant: A De Novo Open Chromatin Region Prediction Tool for Plant Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 860-871.	3.0	4
5	Cotton pan-genome retrieves the lost sequences and genes during domestication and selection. <i>Genome Biology</i> , 2021, 22, 119.	3.8	76
6	Advances in guide RNA design for editing plant genomes using CRISPR-Cas systems. , 2021, , 147-174.		0
7	Designing multi-epitope vaccine against <i>Staphylococcus aureus</i> by employing subtractive proteomics, reverse vaccinology and immuno-informatics approaches. <i>Computers in Biology and Medicine</i> , 2021, 132, 104389.	3.9	73
8	Two gap-free reference genomes and a global view of the centromere architecture in rice. <i>Molecular Plant</i> , 2021, 14, 1757-1767.	3.9	133
9	Development of a Novel Multi-Epitope Vaccine Against Crimean-Congo Hemorrhagic Fever Virus: An Integrated Reverse Vaccinology, Vaccine Informatics and Biophysics Approach. <i>Frontiers in Immunology</i> , 2021, 12, 669812.	2.2	34
10	Phasing analysis of the transcriptome and epigenome in a rice hybrid reveals the inheritance and difference in DNA methylation and allelic transcription regulation. <i>Plant Communications</i> , 2021, 2, 100185.	3.6	10
11	CRISPR-Cereal: a guide RNA design tool integrating regulome and genomic variation for wheat, maize and rice. <i>Plant Biotechnology Journal</i> , 2021, 19, 2141-2143.	4.1	10
12	An inferred functional impact map of genetic variants in rice. <i>Molecular Plant</i> , 2021, 14, 1584-1599.	3.9	48
13	Probing the structural basis of Citrus phytochrome B using computational modelling and molecular dynamics simulation approaches. <i>Journal of Molecular Liquids</i> , 2021, 340, 116895.	2.3	11
14	Structural probing of HapR to identify potent phytochemicals to control <i>Vibrio cholera</i> through integrated computational approaches. <i>Computers in Biology and Medicine</i> , 2021, 138, 104929.	3.9	17
15	High-quality reference genome sequences of two coconut cultivars provide insights into evolution of monocot chromosomes and differentiation of fiber content and plant height. <i>Genome Biology</i> , 2021, 22, 304.	3.8	32
16	Eight high-quality genomes reveal pan-genome architecture and ecotype differentiation of <i>Brassica napus</i> . <i>Nature Plants</i> , 2020, 6, 34-45.	4.7	449
17	Identification and analysis of micro-exons in AP2/ERF and MADS gene families. <i>FEBS Open Bio</i> , 2020, 10, 2564-2577.	1.0	4
18	Discovery of human coronaviruses pan-papain-like protease inhibitors using computational approaches. <i>Journal of Pharmaceutical Analysis</i> , 2020, 10, 546-559.	2.4	67

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19	Effectiveness of Conventional Crop Improvement Strategies vs. Omics. , 2020, , 253-284.		5
20	Pan-genome: A promising resource for noncoding RNA discovery in plants. <i>Plant Genome</i> , 2020, 13, e20046.	1.6	15
21	Reverse vaccinology assisted designing of multiepitope-based subunit vaccine against SARS-CoV-2. <i>Infectious Diseases of Poverty</i> , 2020, 9, 132.	1.5	61
22	Conserved Imprinted Genes between Intra-Subspecies and Inter-Subspecies Are Involved in Energy Metabolism and Seed Development in Rice. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9618.	1.8	8
23	Selection of a subspecies-specific diterpene gene cluster implicated in rice disease resistance. <i>Nature Plants</i> , 2020, 6, 1447-1454.	4.7	66
24	Structural basis of SARS-CoV-2 3CLpro and anti-COVID-19 drug discovery from medicinal plants. <i>Journal of Pharmaceutical Analysis</i> , 2020, 10, 313-319.	2.4	721
25	The genome of jojoba (<i>Simmondsia chinensis</i>): A taxonomically isolated species that directs wax ester accumulation in its seeds. <i>Science Advances</i> , 2020, 6, eaay3240.	4.7	53
26	Influenza infection elicits an expansion of gut population of endogenous <i>Bifidobacterium animalis</i> which protects mice against infection. <i>Genome Biology</i> , 2020, 21, 99.	3.8	73
27	Designing of a next generation multiepitope based vaccine (MEV) against SARS-COV-2: Immunoinformatics and in silico approaches. <i>PLoS ONE</i> , 2020, 15, e0244176.	1.1	81
28	Identification and Analysis of Micro-Exon Genes in the Rice Genome. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2685.	1.8	6
29	Comparative analysis of miniature inverted-repeat transposable elements (MITEs) and long terminal repeat (LTR) retrotransposons in six Citrus species. <i>BMC Plant Biology</i> , 2019, 19, 140.	1.6	20
30	Patterns of genome-wide allele-specific expression in hybrid rice and the implications on the genetic basis of heterosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5653-5658.	3.3	130
31	ppsPCP: a plant presence/absence variants scanner and pan-genome construction pipeline. <i>Bioinformatics</i> , 2019, 35, 4156-4158.	1.8	24
32	A deep learning model based on sparse auto-encoder for prioritizing cancer-related genes and drug target combinations. <i>Carcinogenesis</i> , 2019, 40, 624-632.	1.3	14
33	Evolutionary dynamics of linc RNA transcription in nine citrus species. <i>Plant Journal</i> , 2019, 98, 912-927.	2.8	43
34	Plant ISOform sequencing database (PISO): a comprehensive repertory of full-length transcripts in plants. <i>Plant Biotechnology Journal</i> , 2019, 17, 1001-1003.	4.1	4
35	Reference genome sequences of two cultivated allotetraploid cottons, <i>Gossypium hirsutum</i> and <i>Gossypium barbadense</i> . <i>Nature Genetics</i> , 2019, 51, 224-229.	9.4	468
36	CRISPR-Local: a local single-guide RNA (sgRNA) design tool for non-reference plant genomes. <i>Bioinformatics</i> , 2019, 35, 2501-2503.	1.8	28

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37	Rice Information GateWay: A Comprehensive Bioinformatics Platform for Indica Rice Genomes. <i>Molecular Plant</i> , 2018, 11, 505-507.	3.9	33
38	Analyzing AbrB-Knockout Effects through Genome and Transcriptome Sequencing of <i>Bacillus licheniformis</i> DW2. <i>Frontiers in Microbiology</i> , 2018, 9, 307.	1.5	24
39	Inference of Transcriptional Regulation from Expression Data Using Model Integration. <i>Current Bioinformatics</i> , 2018, 13, 426-434.	0.7	1
40	CRISPR-P 2.0: An Improved CRISPR-Cas9 Tool for Genome Editing in Plants. <i>Molecular Plant</i> , 2017, 10, 530-532.	3.9	498
41	Genomic analyses of primitive, wild and cultivated citrus provide insights into asexual reproduction. <i>Nature Genetics</i> , 2017, 49, 765-772.	9.4	316
42	Contributions of <i>Zea mays</i> subspecies <i>mexicana</i> haplotypes to modern maize. <i>Nature Communications</i> , 2017, 8, 1874.	5.8	102
43	Identifying prognostic signature in ovarian cancer using DirGenerank. <i>Oncotarget</i> , 2017, 8, 46398-46413.	0.8	27
44	Prediction of Protein-Protein Interactions by Evidence Combining Methods. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1946.	1.8	28
45	Recent Advances in Genome Editing Using CRISPR/Cas9. <i>Frontiers in Plant Science</i> , 2016, 7, 703.	1.7	94
46	Diverse alternative back-splicing and alternative splicing landscape of circular RNAs. <i>Genome Research</i> , 2016, 26, 1277-1287.	2.4	799
47	Prediction and characterization of protein-protein interaction network in <i>Bacillus licheniformis</i> WX-02. <i>Scientific Reports</i> , 2016, 6, 19486.	1.6	12
48	Extensive sequence divergence between the reference genomes of two elite <i>indica</i> rice varieties Zhenshan 97 and Minghui 63. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5163-71.	3.3	211
49	Comparative genomic and functional analyses: unearthing the diversity and specificity of nematocidal factors in <i>Pseudomonas putida</i> strain 1A00316. <i>Scientific Reports</i> , 2016, 6, 29211.	1.6	15
50	Functional analysis of long intergenic non-coding RNAs in phosphate-starved rice using competing endogenous RNA network. <i>Scientific Reports</i> , 2016, 6, 20715.	1.6	64
51	A novel proposal of a simplified bacterial gene set and the neo-construction of a general minimized metabolic network. <i>Scientific Reports</i> , 2016, 6, 35082.	1.6	8
52	Building two indica rice reference genomes with PacBio long-read and Illumina paired-end sequencing data. <i>Scientific Data</i> , 2016, 3, 160076.	2.4	34
53	Construction and analysis of a genome-scale metabolic network for <i>Bacillus licheniformis</i> WX-02. <i>Research in Microbiology</i> , 2016, 167, 282-289.	1.0	8
54	Identification, characterization and expression analysis of lineage-specific genes within sweet orange (<i>Citrus sinensis</i>). <i>BMC Genomics</i> , 2015, 16, 995.	1.2	24

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55	Construction of a genome-scale metabolic network of the plant pathogen <i>Pectobacterium carotovorum</i> provides new strategies for bactericide discovery. <i>FEBS Letters</i> , 2015, 589, 285-294.	1.3	18
56	Comprehensive transcriptome and improved genome annotation of <i>Bacillus licheniformis</i> . <i>FEBS Letters</i> , 2015, 589, 2372-2381.	1.3	19
57	Citrus sinensis Annotation Project (CAP): A Comprehensive Database for Sweet Orange Genome. <i>PLoS ONE</i> , 2014, 9, e87723.	1.1	47
58	Dissecting the chromatin interactome of microRNA genes. <i>Nucleic Acids Research</i> , 2014, 42, 3028-3043.	6.5	27
59	RiceWiki: a wiki-based database for community curation of rice genes. <i>Nucleic Acids Research</i> , 2014, 42, D1222-D1228.	6.5	19
60	CRISPR-P: A Web Tool for Synthetic Single-Guide RNA Design of CRISPR-System in Plants. <i>Molecular Plant</i> , 2014, 7, 1494-1496.	3.9	591
61	Prediction and functional analysis of the sweet orange protein-protein interaction network. <i>BMC Plant Biology</i> , 2014, 14, 213.	1.6	30
62	Recognition of Protein-coding Genes Based on Z-curve Algorithms. <i>Current Genomics</i> , 2014, 15, 95-103.	0.7	3
63	Prediction and characterization of protein-protein interaction network in <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. <i>Research in Microbiology</i> , 2013, 164, 1035-1044.	1.0	12
64	The draft genome of sweet orange (<i>Citrus sinensis</i>). <i>Nature Genetics</i> , 2013, 45, 59-66.	9.4	837
65	Genome-wide characterization and expression analysis of genetic variants in sweet orange. <i>Plant Journal</i> , 2013, 75, 954-964.	2.8	22
66	The Differential Transcription Network between Embryo and Endosperm in the Early Developing Maize Seed. <i>Plant Physiology</i> , 2013, 162, 440-455.	2.3	76
67	Improved annotation of a plant pathogen genome <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 342-350.	2.0	6
68	PlantNATsDB: a comprehensive database of plant natural antisense transcripts. <i>Nucleic Acids Research</i> , 2012, 40, D1187-D1193.	6.5	76
69	Pseudorabies Virus Infected Porcine Epithelial Cell Line Generates a Diverse Set of Host MicroRNAs and a Special Cluster of Viral MicroRNAs. <i>PLoS ONE</i> , 2012, 7, e30988.	1.1	46
70	Protein Domain Structure Uncovers the Origin of Aerobic Metabolism and the Rise of Planetary Oxygen. <i>Structure</i> , 2012, 20, 67-76.	1.6	53
71	Theoretical Prediction and Experimental Verification of Protein-Coding Genes in Plant Pathogen Genome <i>Agrobacterium tumefaciens</i> Strain C58. <i>PLoS ONE</i> , 2012, 7, e43176.	1.1	18
72	Plant siRNAs from introns mediate DNA methylation of host genes. <i>Rna</i> , 2011, 17, 1012-1024.	1.6	35

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73	Historical Variation of Structural Novelty in a Natural Product Library. <i>Chemistry and Biodiversity</i> , 2011, 8, 1968-1977.	1.0	24
74	DIGAP - a Database of Improved Gene Annotation for Phytopathogens. <i>BMC Genomics</i> , 2010, 11, 54.	1.2	4
75	Evolutionary inspirations for drug discovery. <i>Trends in Pharmacological Sciences</i> , 2010, 31, 443-448.	4.0	31
76	Theoretical methods for identifying important functional genes in bacterial genomes. <i>Research in Microbiology</i> , 2010, 161, 1-8.	1.0	6
77	Gene Expression Analysis of Four Radiation-resistant Bacteria. <i>Genomics Insights</i> , 2009, 2, GEI.S2380.	3.0	10
78	Analyzing S-Adenosylhomocysteine Hydrolase Gene Sequences in Deuterostome Genomes. <i>Journal of Biomolecular Structure and Dynamics</i> , 2009, 27, 371-380.	2.0	12
79	Reannotation of hypothetical ORFs in plant pathogen <i>Erwinia carotovora</i> subsp. <i>atroseptica</i> SCRI1043. <i>FEBS Journal</i> , 2008, 275, 198-206.	2.2	16
80	Sterol biosynthesis and prokaryotes-to-eukaryotes evolution. <i>Biochemical and Biophysical Research Communications</i> , 2007, 363, 885-888.	1.0	44
81	Identification of genomic islands in six plant pathogens. <i>Gene</i> , 2006, 374, 134-141.	1.0	14
82	A novel strategy for the identification of genomic islands by comparative analysis of the contents and contexts of tRNA sites in closely related bacteria. <i>Nucleic Acids Research</i> , 2006, 34, e3-e3.	6.5	67
83	Detection of nucleolar organizer and mitochondrial DNA insertion regions based on the isochore map of <i>Arabidopsis thaliana</i> . <i>FEBS Journal</i> , 2005, 272, 3328-3336.	2.2	4
84	Gene expression analysis of six GC-rich Gram-negative phytopathogens. <i>Biochemical and Biophysical Research Communications</i> , 2005, 332, 380-387.	1.0	8
85	Seven GC-rich microbial genomes adopt similar codon usage patterns regardless of their phylogenetic lineages. <i>Biochemical and Biophysical Research Communications</i> , 2003, 306, 310-317.	1.0	27
86	ZCURVE_CoV: a new system to recognize protein coding genes in coronavirus genomes, and its applications in analyzing SARS-CoV genomes. <i>Biochemical and Biophysical Research Communications</i> , 2003, 307, 382-388.	1.0	34
87	Gene Recognition from Questionable ORFs in Bacterial and Archaeal Genomes. <i>Journal of Biomolecular Structure and Dynamics</i> , 2003, 21, 99-109.	2.0	9