Ling-Ling Chen

List of Publications by Year
in descending order

87 papers	7,481 citations	126901 33 h-index	60616 81 g-index
98 all docs	98 docs citations	98 times ranked	10742 citing authors

#	Article	IF	Citations
1	Oil plant genomes: current state of the science. Journal of Experimental Botany, 2022, 73, 2859-2874.	4.8	16
2	BnPIR: <i>Brassica napus</i> panâ€genome information resource for 1689 accessions. Plant Biotechnology Journal, 2021, 19, 412-414.	8.3	51
3	Analysis of Rice Transcriptome Reveals the LncRNA/CircRNA Regulation in Tissue Development. Rice, 2021, 14, 14.	4.0	26
4	CharPlant: A De Novo Open Chromatin Region Prediction Tool for Plant Genomes. Genomics, Proteomics and Bioinformatics, 2021, 19, 860-871.	6.9	4
5	Cotton pan-genome retrieves the lost sequences and genes during domestication and selection. Genome Biology, 2021, 22, 119.	8.8	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 Staphylococcus aureus by employing subtractive proteomics, reverse vaccinology and immuno-informatics approaches. Computers in Biology and Medicine, 2021, 132, 104389.	7.0	73
8	Two gap-free reference genomes and a global view of the centromere architecture in rice. Molecular Plant, 2021, 14, 1757-1767.	8.3	133
9	Development of a Novel Multi-Epitope Vaccine Against Crimean-Congo Hemorrhagic Fever Virus: An Integrated Reverse Vaccinology, Vaccine Informatics and Biophysics Approach. Frontiers in Immunology, 2021, 12, 669812.	4.8	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. Plant Communications, 2021, 2, 100185.	7.7	10
11	CRISPRâ€Cereal: a guide RNA design tool integrating regulome and genomic variation for wheat, maize and rice. Plant Biotechnology Journal, 2021, 19, 2141-2143.	8.3	10
12	An inferred functional impact map of genetic variants in rice. Molecular Plant, 2021, 14, 1584-1599.	8.3	48
13	Probing the structural basis of Citrus phytochrome B using computational modelling and molecular dynamics simulation approaches. Journal of Molecular Liquids, 2021, 340, 116895.	4.9	11
14	Structural probing of HapR to identify potent phytochemicals to control Vibrio cholera through integrated computational approaches. Computers in Biology and Medicine, 2021, 138, 104929.	7.0	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. Genome Biology, 2021, 22, 304.	8.8	32
16	Eight high-quality genomes reveal pan-genome architecture and ecotype differentiation of Brassica napus. Nature Plants, 2020, 6, 34-45.	9.3	449
17	Identification and analysis of microâ€exons in AP2/ERF and MADS gene families. FEBS Open Bio, 2020, 10, 2564-2577.	2.3	4
18	Discovery of human coronaviruses pan-papain-like protease inhibitors using computational approaches. Journal of Pharmaceutical Analysis, 2020, 10, 546-559.	5.3	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. Plant Genome, 2020, 13, e20046.	2.8	15
21	Reverse vaccinology assisted designing of multiepitope-based subunit vaccine against SARS-CoV-2. Infectious Diseases of Poverty, 2020, 9, 132.	3.7	61
22	Conserved Imprinted Genes between Intra-Subspecies and Inter-Subspecies Are Involved in Energy Metabolism and Seed Development in Rice. International Journal of Molecular Sciences, 2020, 21, 9618.	4.1	8
23	Selection of a subspecies-specific diterpene gene cluster implicated in rice disease resistance. Nature Plants, 2020, 6, 1447-1454.	9.3	66
24	Structural basis of SARS-CoV-2 3CLpro and anti-COVID-19 drug discovery from medicinal plants. Journal of Pharmaceutical Analysis, 2020, 10, 313-319.	5.3	721
25	The genome of jojoba (*Simmondsia chinensis*): A taxonomically isolated species that directs wax ester accumulation in its seeds. Science Advances, 2020, 6, eaay3240.	10.3	53
26	Influenza infection elicits an expansion of gut population of endogenous Bifidobacterium animalis which protects mice against infection. Genome Biology, 2020, 21, 99.	8.8	73
27	Designing of a next generation multiepitope based vaccine (MEV) against SARS-COV-2: Immunoinformatics and in silico approaches. PLoS ONE, 2020, 15, e0244176.	2.5	81
28	Identification and Analysis of Micro-Exon Genes in the Rice Genome. International Journal of Molecular Sciences, 2019, 20, 2685.	4.1	6
29	Comparative analysis of miniature inverted€"repeat transposable elements (MITEs) and long terminal repeat (LTR) retrotransposons in six Citrus species. BMC Plant Biology, 2019, 19, 140.	3.6	20
30	Patterns of genome-wide allele-specific expression in hybrid rice and the implications on the genetic basis of heterosis. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5653-5658.	7.1	130
31	ppsPCP: a plant presence/absence variants scanner and pan-genome construction pipeline. Bioinformatics, 2019, 35, 4156-4158.	4.1	24
32	A deep learning model based on sparse auto-encoder for prioritizing cancer-related genes and drug target combinations. Carcinogenesis, 2019, 40, 624-632.	2.8	14
33	Evolutionary dynamics of linc RNA transcription in nine citrus species. Plant Journal, 2019, 98, 912-927.	5.7	43
34	Plant ISOform sequencing database (PISO): a comprehensive repertory of full€length transcripts in plants. Plant Biotechnology Journal, 2019, 17, 1001-1003.	8.3	4
35	Reference genome sequences of two cultivated allotetraploid cottons, Gossypium hirsutum and Gossypium barbadense. Nature Genetics, 2019, 51, 224-229.	21.4	468
36	CRISPR-Local: a local single-guide RNA (sgRNA) design tool for non-reference plant genomes. Bioinformatics, 2019, 35, 2501-2503.	4.1	28

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37	Rice Information GateWay: A Comprehensive Bioinformatics Platform for Indica Rice Genomes. Molecular Plant, 2018, 11, 505-507.	8.3	33
38	Analyzing AbrB-Knockout Effects through Genome and Transcriptome Sequencing of Bacillus licheniformis DW2. Frontiers in Microbiology, 2018, 9, 307.	3.5	24
39	Inference of Transcriptional Regulation from Expression Data Using Model Integration. Current Bioinformatics, 2018, 13, 426-434.	1.5	1
40	CRISPR-P 2.0: An Improved CRISPR-Cas9 Tool forÂGenome Editing in Plants. Molecular Plant, 2017, 10, 530-532.	8.3	498
41	Genomic analyses of primitive, wild and cultivated citrus provide insights into asexual reproduction. Nature Genetics, 2017, 49, 765-772.	21.4	316
42	Contributions of Zea mays subspecies mexicana haplotypes to modern maize. Nature Communications, 2017, 8, 1874.	12.8	102
43	Identifying prognostic signature in ovarian cancer using DirGenerank. Oncotarget, 2017, 8, 46398-46413.	1.8	27
44	Prediction of Proteinâ€"Protein Interactions by Evidence Combining Methods. International Journal of Molecular Sciences, 2016, 17, 1946.	4.1	28
45	Recent Advances in Genome Editing Using CRISPR/Cas9. Frontiers in Plant Science, 2016, 7, 703.	3.6	94
46	Diverse alternative back-splicing and alternative splicing landscape of circular RNAs. Genome Research, 2016, 26, 1277-1287.	5.5	799
47	Prediction and characterization of protein-protein interaction network in Bacillus licheniformis WX-02. Scientific Reports, 2016, 6, 19486.	3.3	12
48	Extensive sequence divergence between the reference genomes of two elite <i>indica</i> rice varieties Zhenshan 97 and Minghui 63. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5163-71.	7.1	211
49	Comparative genomic and functional analyses: unearthing the diversity and specificity of nematicidal factors in Pseudomonas putida strain 1A00316. Scientific Reports, 2016, 6, 29211.	3.3	15
50	Functional analysis of long intergenic non-coding RNAs in phosphate-starved rice using competing endogenous RNA network. Scientific Reports, 2016, 6, 20715.	3.3	64
51	A novel proposal of a simplified bacterial gene set and the neo-construction of a general minimized metabolic network. Scientific Reports, 2016, 6, 35082.	3.3	8
52	Building two indica rice reference genomes with PacBio long-read and Illumina paired-end sequencing data. Scientific Data, 2016, 3, 160076.	5.3	34
53	Construction and analysis of a genome-scale metabolic network for Bacillus licheniformis WX-02. Research in Microbiology, 2016, 167, 282-289.	2.1	8
54	Identification, characterization and expression analysis of lineage-specific genes within sweet orange (Citrus sinensis). BMC Genomics, 2015, 16, 995.	2.8	24

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55	Construction of a genome‐scale metabolic network of the plant pathogen *Pectobacterium carotovorum* provides new strategies for bactericide discovery. FEBS Letters, 2015, 589, 285-294.	2.8	18
56	Comprehensive transcriptome and improved genome annotation of *Bacillus licheniformis* WX‐02. FEBS Letters, 2015, 589, 2372-2381.	2.8	19
57	Citrus sinensis Annotation Project (CAP): A Comprehensive Database for Sweet Orange Genome. PLoS ONE, 2014, 9, e87723.	2.5	47
58	Dissecting the chromatin interactome of microRNA genes. Nucleic Acids Research, 2014, 42, 3028-3043.	14.5	27
59	RiceWiki: a wiki-based database for community curation of rice genes. Nucleic Acids Research, 2014, 42, D1222-D1228.	14.5	19
60	CRISPR-P: A Web Tool for Synthetic Single-Guide RNA Design of CRISPR-System in Plants. Molecular Plant, 2014, 7, 1494-1496.	8.3	591
61	Prediction and functional analysis of the sweet orange protein-protein interaction network. BMC Plant Biology, 2014, 14, 213.	3.6	30
62	Recognition of Protein-coding Genes Based on Z-curve Algorithms. Current Genomics, 2014, 15, 95-103.	1.6	3
63	Prediction and characterization of protein‐protein interaction network in Xanthomonas oryzae pv. oryzae PXO99A. Research in Microbiology, 2013, 164, 1035-1044.	2.1	12
64	The draft genome of sweet orange (Citrus sinensis). Nature Genetics, 2013, 45, 59-66.	21.4	837
65	Genome‐wide characterization and expression analysis of genetic variants in sweet orange. Plant Journal, 2013, 75, 954-964.	5.7	22
66	The Differential Transcription Network between Embryo and Endosperm in the Early Developing Maize Seed Â Â Â. Plant Physiology, 2013, 162, 440-455.	4.8	76
67	Improved annotation of a plant pathogen genome *Xanthomonas oryzae* pv. *oryzae* PXO99A. Journal of Biomolecular Structure and Dynamics, 2013, 31, 342-350.	3.5	6
68	PlantNATsDB: a comprehensive database of plant natural antisense transcripts. Nucleic Acids Research, 2012, 40, D1187-D1193.	14.5	76
69	Pseudorabies Virus Infected Porcine Epithelial Cell Line Generates a Diverse Set of Host MicroRNAs and a Special Cluster of Viral MicroRNAs. PLoS ONE, 2012, 7, e30988.	2.5	46
70	Protein Domain Structure Uncovers the Origin of Aerobic Metabolism and the Rise of Planetary Oxygen. Structure, 2012, 20, 67-76.	3.3	53
71	Theoretical Prediction and Experimental Verification of Protein-Coding Genes in Plant Pathogen Genome Agrobacterium tumefaciens Strain C58. PLoS ONE, 2012, 7, e43176.	2.5	18
72	Plant siRNAs from introns mediate DNA methylation of host genes. Rna, 2011, 17, 1012-1024.	3.5	35

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73	Historical Variation of Structural Novelty in a Natural Product Library. Chemistry and Biodiversity, 2011, 8, 1968-1977.	2.1	24
74	DIGAP - a Database of Improved Gene Annotation for Phytopathogens. BMC Genomics, 2010, 11, 54.	2.8	4
75	Evolutionary inspirations for drug discovery. Trends in Pharmacological Sciences, 2010, 31, 443-448.	8.7	31
76	Theoretical methods for identifying important functional genes in bacterial genomes. Research in Microbiology, 2010, 161, 1-8.	2.1	6
77	Gene Expression Analysis of Four Radiation-resistant Bacteria. Genomics Insights, 2009, 2, GEI.S2380.	3.0	10
78	Analyzing S-Adenosylhomocysteine Hydrolase Gene Sequences in Deuterostome Genomes. Journal of Biomolecular Structure and Dynamics, 2009, 27, 371-380.	3.5	12
79	Reannotation of hypothetical ORFs in plant pathogen <i>Erwiniaâ€ƒcarotovora</i> subsp. <i>atroseptica</i> SCRI1043. FEBS Journal, 2008, 275, 198-206.	4.7	16
80	Sterol biosynthesis and prokaryotes-to-eukaryotes evolution. Biochemical and Biophysical Research Communications, 2007, 363, 885-888.	2.1	44
81	Identification of genomic islands in six plant pathogens. Gene, 2006, 374, 134-141.	2.2	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. Nucleic Acids Research, 2006, 34, e3-e3.	14.5	67
83	Detection of nucleolar organizer and mitochondrial DNA insertion regions based on the isochore map of Arabidopsis thaliana. FEBS Journal, 2005, 272, 3328-3336.	4.7	4
84	Gene expression analysis of six GC-rich Gram-negative phytopathogens. Biochemical and Biophysical Research Communications, 2005, 332, 380-387.	2.1	8
85	Seven GC-rich microbial genomes adopt similar codon usage patterns regardless of their phylogenetic lineages. Biochemical and Biophysical Research Communications, 2003, 306, 310-317.	2.1	27
86	ZCURVE_CoV: a new system to recognize protein coding genes in coronavirus genomes, and its applications in analyzing SARS-CoV genomes. Biochemical and Biophysical Research Communications, 2003, 307, 382-388.	2.1	34
87	Gene Recognition from Questionable ORFs in Bacterial and Archaeal Genomes. Journal of Biomolecular Structure and Dynamics, 2003, 21, 99-109.	3.5	9