

Ling-Ling Chen

List of Publications by Year in Descending Order

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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.

89
papers

4,514
citations

28
h-index

66
g-index

98
ext. papers

6,284
ext. citations

8.9
avg, IF

5.94
L-index

#	Paper	IF	Citations
89	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	18.3	3
88	Oil plant genomes: current state of the science. <i>Journal of Experimental Botany</i> , 2021 ,	7	3
87	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	7	8
86	Cotton pan-genome retrieves the lost sequences and genes during domestication and selection. <i>Genome Biology</i> , 2021 , 22, 119	18.3	10
85	Advances in guide RNA design for editing plant genomes using CRISPR-Cas systems 2021 , 147-174		
84	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	7	33
83	Two gap-free reference genomes and a global view of the centromere architecture in rice. <i>Molecular Plant</i> , 2021 , 14, 1757-1767	14.4	15
82	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	8.4	15
81	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, 100183	9	2
80	BnPIR: Brassica napus pan-genome information resource for 1689 accessions. <i>Plant Biotechnology Journal</i> , 2021 , 19, 412-414	11.6	19
79	Analysis of Rice Transcriptome Reveals the LncRNA/CircRNA Regulation in Tissue Development. <i>Rice</i> , 2021 , 14, 14	5.8	4
78	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	11.6	2
77	An inferred functional impact map of genetic variants in rice. <i>Molecular Plant</i> , 2021 , 14, 1584-1599	14.4	3
76	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	6	5
75	Selection of a subspecies-specific diterpene gene cluster implicated in rice disease resistance. <i>Nature Plants</i> , 2020 , 6, 1447-1454	11.5	25
74	Structural basis of SARS-CoV-2 3CL and anti-COVID-19 drug discovery from medicinal plants. <i>Journal of Pharmaceutical Analysis</i> , 2020 , 10, 313-319	14	477
73	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	14.3	28

72	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	18.3	31
71	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	3.7	43
70	Eight high-quality genomes reveal pan-genome architecture and ecotype differentiation of <i>Brassica napus</i> . <i>Nature Plants</i> , 2020 , 6, 34-45	11.5	204
69	Identification and analysis of micro-exons in AP2/ERF and MADS gene families. <i>FEBS Open Bio</i> , 2020 , 10, 2564-2577	2.7	0
68	Discovery of human coronaviruses pan-papain-like protease inhibitors using computational approaches. <i>Journal of Pharmaceutical Analysis</i> , 2020 , 10, 546-559	14	35
67	Effectiveness of Conventional Crop Improvement Strategies vs. Omics 2020 , 253-284		4
66	Pan-genome: A promising resource for noncoding RNA discovery in plants. <i>Plant Genome</i> , 2020 , 13, e20044	4.4	7
65	Reverse vaccinology assisted designing of multiepitope-based subunit vaccine against SARS-CoV-2. <i>Infectious Diseases of Poverty</i> , 2020 , 9, 132	10.4	38
64	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,	6.3	3
63	Identification and Analysis of Micro-Exon Genes in the Rice Genome. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	4
62	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	5.3	9
61	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	11.5	45
60	ppsPCP: a plant presence/absence variants scanner and pan-genome construction pipeline. <i>Bioinformatics</i> , 2019 , 35, 4156-4158	7.2	12
59	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	4.6	8
58	Evolutionary dynamics of lincRNA transcription in nine citrus species. <i>Plant Journal</i> , 2019 , 98, 912-927	6.9	10
57	Plant ISOform sequencing database (PISO): a comprehensive repertory of full-length transcripts in plants. <i>Plant Biotechnology Journal</i> , 2019 , 17, 1001-1003	11.6	1
56	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	36.3	266
55	CRISPR-Local: a local single-guide RNA (sgRNA) design tool for non-reference plant genomes. <i>Bioinformatics</i> , 2019 , 35, 2501-2503	7.2	20

54	Rice Information GateWay: A Comprehensive Bioinformatics Platform for Indica Rice Genomes. <i>Molecular Plant</i> , 2018 , 11, 505-507	14.4	22
53	Analyzing AbrB-Knockout Effects through Genome and Transcriptome Sequencing of DW2. <i>Frontiers in Microbiology</i> , 2018 , 9, 307	5.7	11
52	Inference of Transcriptional Regulation from Expression Data Using Model Integration. <i>Current Bioinformatics</i> , 2018 , 13, 426-434	4.7	1
51	CRISPR-P 2.0: An Improved CRISPR-Cas9 Tool for Genome Editing in Plants. <i>Molecular Plant</i> , 2017 , 10, 530-532	14.4	253
50	Genomic analyses of primitive, wild and cultivated citrus provide insights into asexual reproduction. <i>Nature Genetics</i> , 2017 , 49, 765-772	36.3	194
49	Contributions of <i>Zea mays</i> subspecies <i>mexicana</i> haplotypes to modern maize. <i>Nature Communications</i> , 2017 , 8, 1874	17.4	62
48	Identifying prognostic signature in ovarian cancer using DirGenerank. <i>Oncotarget</i> , 2017 , 8, 46398-46413	3.3	9
47	Extensive sequence divergence between the reference genomes of two elite indica 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	11.5	141
46	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	4.9	10
45	Functional analysis of long intergenic non-coding RNAs in phosphate-starved rice using competing endogenous RNA network. <i>Scientific Reports</i> , 2016 , 6, 20715	4.9	44
44	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	4.9	7
43	Building two indica rice reference genomes with PacBio long-read and Illumina paired-end sequencing data. <i>Scientific Data</i> , 2016 , 3, 160076	8.2	19
42	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	4	6
41	Prediction of Protein-Protein Interactions by Evidence Combining Methods. <i>International Journal of Molecular Sciences</i> , 2016 , 17,	6.3	22
40	Recent Advances in Genome Editing Using CRISPR/Cas9. <i>Frontiers in Plant Science</i> , 2016 , 7, 703	6.2	75
39	Diverse alternative back-splicing and alternative splicing landscape of circular RNAs. <i>Genome Research</i> , 2016 , 26, 1277-87	9.7	482
38	Prediction and characterization of protein-protein interaction network in <i>Bacillus licheniformis</i> WX-02. <i>Scientific Reports</i> , 2016 , 6, 19486	4.9	10
37	Comprehensive transcriptome and improved genome annotation of <i>Bacillus licheniformis</i> WX-02. <i>FEBS Letters</i> , 2015 , 589, 2372-81	3.8	11

36	Identification, characterization and expression analysis of lineage-specific genes within sweet orange (<i>Citrus sinensis</i>). <i>BMC Genomics</i> , 2015 , 16, 995	4.5	15
35	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, 285-94	3.8	15
34	CRISPR-P: a web tool for synthetic single-guide RNA design of CRISPR-system in plants. <i>Molecular Plant</i> , 2014 , 7, 1494-1496	14.4	389
33	Prediction and functional analysis of the sweet orange protein-protein interaction network. <i>BMC Plant Biology</i> , 2014 , 14, 213	5.3	20
32	Citrus sinensis annotation project (CAP): a comprehensive database for sweet orange genome. <i>PLoS ONE</i> , 2014 , 9, e87723	3.7	30
31	Dissecting the chromatin interactome of microRNA genes. <i>Nucleic Acids Research</i> , 2014 , 42, 3028-43	20.1	22
30	RiceWiki: a wiki-based database for community curation of rice genes. <i>Nucleic Acids Research</i> , 2014 , 42, D1222-8	20.1	18
29	Recognition of Protein-coding Genes Based on Z-curve Algorithms. <i>Current Genomics</i> , 2014 , 15, 95-103	2.6	3
28	Prediction and characterization of protein-protein interaction network in <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99 A. <i>Research in Microbiology</i> , 2013 , 164, 1035-44	4	11
27	The draft genome of sweet orange (<i>Citrus sinensis</i>). <i>Nature Genetics</i> , 2013 , 45, 59-66	36.3	630
26	Genome-wide characterization and expression analysis of genetic variants in sweet orange. <i>Plant Journal</i> , 2013 , 75, 954-64	6.9	20
25	The differential transcription network between embryo and endosperm in the early developing maize seed. <i>Plant Physiology</i> , 2013 , 162, 440-55	6.6	66
24	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, 342-50	3.6	4
23	Protein domain structure uncovers the origin of aerobic metabolism and the rise of planetary oxygen. <i>Structure</i> , 2012 , 20, 67-76	5.2	45
22	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	3.7	41
21	PlantNATsDB: a comprehensive database of plant natural antisense transcripts. <i>Nucleic Acids Research</i> , 2012 , 40, D1187-93	20.1	66
20	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	3.7	16
19	Historical variation of structural novelty in a natural product library. <i>Chemistry and Biodiversity</i> , 2011 , 8, 1968-77	2.5	19

18	Plant siRNAs from introns mediate DNA methylation of host genes. <i>Rna</i> , 2011 , 17, 1012-24	5.8	34
17	Evolutionary inspirations for drug discovery. <i>Trends in Pharmacological Sciences</i> , 2010 , 31, 443-8	13.2	23
16	Theoretical methods for identifying important functional genes in bacterial genomes. <i>Research in Microbiology</i> , 2010 , 161, 1-8	4	5
15	DIGA--a database of improved gene annotation for phytopathogens. <i>BMC Genomics</i> , 2010 , 11, 54	4.5	3
14	Gene Expression Analysis of Four Radiation-resistant Bacteria. <i>Genomics Insights</i> , 2009 , 2, 11-22	0	7
13	Analyzing S-adenosylhomocysteine hydrolase gene sequences in deuterostome genomes. <i>Journal of Biomolecular Structure and Dynamics</i> , 2009 , 27, 371-80	3.6	12
12	Reannotation of hypothetical ORFs in plant pathogen <i>Erwinia carotovora</i> subsp. <i>atroseptica</i> SCRI1043. <i>FEBS Journal</i> , 2008 , 275, 198-206	5.7	16
11	Sterol biosynthesis and prokaryotes-to-eukaryotes evolution. <i>Biochemical and Biophysical Research Communications</i> , 2007 , 363, 885-8	3.4	37
10	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	20.1	62
9	Identification of genomic islands in six plant pathogens. <i>Gene</i> , 2006 , 374, 134-41	3.8	13
8	Gene expression analysis of six GC-rich Gram-negative phytopathogens. <i>Biochemical and Biophysical Research Communications</i> , 2005 , 332, 380-7	3.4	6
7	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, 3328-36	5.7	3
6	Gene recognition from questionable ORFs in bacterial and archaeal genomes. <i>Journal of Biomolecular Structure and Dynamics</i> , 2003 , 21, 99-109	3.6	9
5	Seven GC-rich microbial genomes adopt similar codon usage patterns regardless of their phylogenetic lineages. <i>Biochemical and Biophysical Research Communications</i> , 2003 , 306, 310-7	3.4	25
4	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, 382-8	3.4	28
3	Structural Basis of SARS-CoV-2 3CLpro and Anti-COVID-19 Drug Discovery from Medicinal Plants		8
2	Structural modeling and conserved epitopes prediction against SARS-COV-2 structural proteins for vaccine development		6
1	Designing of a next generation multiepitope based vaccine (MEV) against SARS-COV-2: Immunoinformatics and in silico approaches		14

