

Yao-Cheng Lin

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

10,812
citations

186265

28
h-index

254184

43
g-index

47
all docs

47
docs citations

47
times ranked

15001
citing authors

#	ARTICLE	IF	CITATIONS
1	The map-based sequence of the rice genome. <i>Nature</i> , 2005, 436, 793-800.	27.8	3,365
2	The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013, 497, 579-584.	27.8	1,303
3	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008, 452, 88-92.	27.8	1,003
4	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9166-9171.	7.1	640
5	The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. <i>Nature</i> , 2016, 530, 331-335.	27.8	460
6	Pan genome of the phytoplankton <i>Emiliania hirsutum</i> underpins its global distribution. <i>Nature</i> , 2013, 499, 209-213.	27.8	448
7	Genome sequence of the recombinant protein production host <i>Pichia pastoris</i> . <i>Nature Biotechnology</i> , 2009, 27, 561-566.	17.5	422
8	Genome dynamics of the human embryonic kidney 293 lineage in response to cell biology manipulations. <i>Nature Communications</i> , 2014, 5, 4767.	12.8	421
9	The <i>Apostasia</i> genome and the evolution of orchids. <i>Nature</i> , 2017, 549, 379-383.	27.8	305
10	The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D1028-D1033.	14.5	295
11	The Plant Genome Integrative Explorer Resource: PlantGen<sc>IE</sc>.org. <i>New Phytologist</i> , 2015, 208, 1149-1156.	7.3	282
12	Curated genome annotation of <i>Oryza sativa</i> ssp. <i>japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	5.5	218
13	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. <i>New Phytologist</i> , 2012, 194, 1001-1013.	7.3	210
14	A rice gene activation/knockout mutant resource for high throughput functional genomics. <i>Plant Molecular Biology</i> , 2007, 63, 351-364.	3.9	197
15	GOLVEN Secretory Peptides Regulate Auxin Carrier Turnover during Plant Gravitropic Responses. <i>Developmental Cell</i> , 2012, 22, 678-685.	7.0	182
16	A Comprehensive Analysis of Genes Encoding Small Secreted Proteins Identifies Candidate Effectors in <i>Melampsora larici-populina</i> (Poplar Leaf Rust). <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 279-293.	2.6	150
17	The biosynthetic gene cluster for sophorolipids: a biotechnological interesting biosurfactant produced by <i>Sarcoma bombicicola</i> . <i>Molecular Microbiology</i> , 2013, 88, 501-509.	2.5	94
18	Functional and evolutionary genomic inferences in <i>Populus</i> through genome and population sequencing of American and European aspen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10970-E10978.	7.1	84

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19	Oil Bodies and Oleosins in <i>Physcomitrella</i> Possess Characteristics Representative of Early Trends in Evolution. <i>Plant Physiology</i> , 2009, 150, 1192-1203.	4.8	73
20	Expanding the repertoire of secretory peptides controlling root development with comparative genome analysis and functional assays. <i>Journal of Experimental Botany</i> , 2015, 66, 5257-5269.	4.8	71
21	Development and implementation of a highly-multiplexed SNP array for genetic mapping in maritime pine and comparative mapping with loblolly pine. <i>BMC Genomics</i> , 2011, 12, 368.	2.8	66
22	Genome-Wide Analysis Reveals Diverged Patterns of Codon Bias, Gene Expression, and Rates of Sequence Evolution in <i>Picea</i> Gene Families. <i>Genome Biology and Evolution</i> , 2015, 7, 1002-1015.	2.5	63
23	Open access to sequence: Browsing the <i>Pichia pastoris</i> genome. <i>Microbial Cell Factories</i> , 2009, 8, 53.	4.0	55
24	A rice phenomics study—phenotype scoring and seed propagation of a T-DNA insertion-induced rice mutant population. <i>Plant Molecular Biology</i> , 2007, 65, 427-438.	3.9	52
25	Systems genetics reveals a transcriptional network associated with susceptibility in the maize “grey leaf spot” pathosystem. <i>Plant Journal</i> , 2017, 89, 746-763.	5.7	49
26	<i>Candida bombicola</i> as a platform organism for the production of tailor-made biomolecules. <i>Biotechnology and Bioengineering</i> , 2013, 110, 2494-2503.	3.3	42
27	DNA-free CRISPR-Cas9 gene editing of wild tetraploid tomato <i>Solanum peruvianum</i> using protoplast regeneration. <i>Plant Physiology</i> , 2022, 188, 1917-1930.	4.8	39
28	Draft genome of <i>Cercospora zeina</i> , <i>Fusarium pininemorale</i> , <i>Hawksworthiomyces lignivorus</i> , <i>Huntia decipiens</i> and <i>Ophiostoma ips</i> . <i>IMA Fungus</i> , 2017, 8, 385-396.	3.8	37
29	Comparative in silico analysis of EST-SSRs in angiosperm and gymnosperm tree genera. <i>BMC Plant Biology</i> , 2014, 14, 220.	3.6	29
30	Small RNA profiling in <i>Pinus pinaster</i> reveals the transcriptome of developing seeds and highlights differences between zygotic and somatic embryos. <i>Scientific Reports</i> , 2019, 9, 11327.	3.3	28
31	Serendipitous Meta-Transcriptomics: The Fungal Community of Norway Spruce (<i>Picea abies</i>). <i>PLoS ONE</i> , 2015, 10, e0139080.	2.5	27
32	SILAC-Based Proteome Analysis of <i>Starmerella bombicola</i> Sophorolipid Production. <i>Journal of Proteome Research</i> , 2013, 12, 4376-4392.	3.7	22
33	miRNA profiling in leaf and cork tissues of <i>Quercus suber</i> reveals novel miRNAs and tissue-specific expression patterns. <i>Tree Genetics and Genomes</i> , 2014, 10, 721-737.	1.6	20
34	Reference genome and comparative genome analysis for the WHO reference strain for <i>Mycobacterium bovis</i> BCG Danish, the present tuberculosis vaccine. <i>BMC Genomics</i> , 2019, 20, 561.	2.8	16
35	Efficient and Economical Targeted Insertion in Plant Genomes via Protoplast Regeneration. <i>CRISPR Journal</i> , 2021, 4, 752-760.	2.9	9
36	Draft Genome Assembly of the False Spider Mite <i>Brevipalpus yothersi</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	6

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37	Comparative Genomic Analysis Uncovered Evolution of Pathogenicity Factors, Horizontal Gene Transfer Events, and Heavy Metal Resistance Traits in Citrus Canker Bacterium <i>Xanthomonas citri</i> subsp. <i>citri</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 731711.	3.5	5
38	Whole genome resequencing and complementation tests reveal candidate loci contributing to bacterial wilt (<i>Ralstonia</i> sp.) resistance in tomato. <i>Scientific Reports</i> , 2022, 12, 8374.	3.3	5
39	Comparative in silico analysis of SSRs in coding regions of high confidence predicted genes in Norway spruce (<i>Picea abies</i>) and Loblolly pine (<i>Pinus taeda</i>). <i>BMC Genetics</i> , 2015, 16, 149.	2.7	3
40	Automatic Leaf Counting Using Improved YOLOv3. , 2020, , .		3
41	Toward automatic plant phenotyping: starting from leaf counting. <i>Multimedia Tools and Applications</i> , 2022, 81, 11865-11879.	3.9	3
42	Complete Genome Sequence of <i>Bacillus cereus</i> C1L, a Plant Growth-Promoting Rhizobacterium from the Rhizosphere of Formosa Lily in Taiwan. <i>Genome Announcements</i> , 2017, 5, .	0.8	2